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Refined proposal for an EU Pollinator Monitoring Scheme

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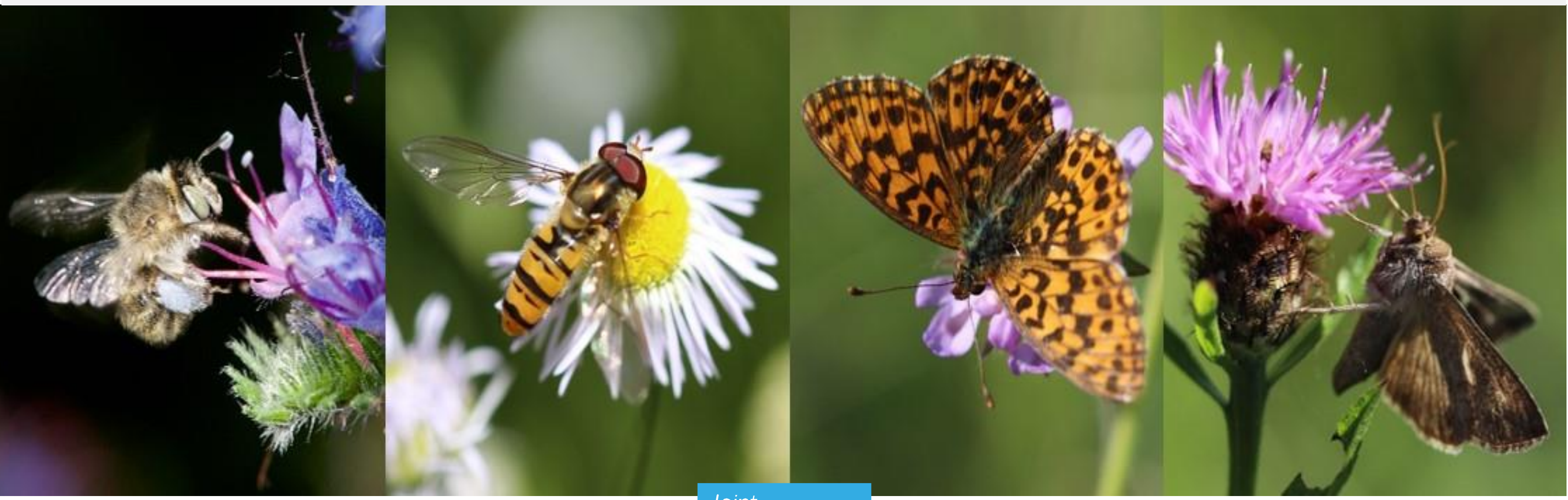

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Contents

Abstract

This report presents refined options for an EU Pollinator Monitoring Scheme (EU PoMS), based on the work of a technical expert group comprising 26 international experts from 12 countries, with members being representatives of universities, research institutes and NGOs. The work presented here was produced during the second part of the STING project (Science and Technology for Pollinating Insects, running from 2022 to 2024). It provides updated methodological options for the standardised monitoring of wild pollinators (bees, hoverflies, butterflies and moths) for the core scheme of the EU PoMS, taking into consideration the data and knowledge generated by the SPRING (Strengthening Pollinator Recovery through Indicators and Monitoring) and other projects. It also provides a refined proposal for a General Pollinator Indicator to support inter alia a legally binding target on reversing pollinators' decline, as well as refined options for a Farmland Pollinator Indicator. The report presents options for data management and models to process and harmonise pollinator data, as well as options for future developments of the scheme (including emerging technologies and genomic monitoring). This work supports Priority I of the revised EU Pollinators Initiative, which aims at improving knowledge of pollinator decline, its causes and consequences, and entails the development of a comprehensive European pollinator monitoring system and indicators.

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Helophilus trivittatus, Adara Pardo

Executive summary

Background and policy context

The revised EU Pollinators Initiative (A New Deal for Pollinators) and more recently the adoption of the Regulation on Nature Restoration provided a new impetus to the setting up of an EU Pollinators Monitoring Scheme (EU PoMS). To meet this renewed ambition, the JRC has been entrusted the task to mobilize high-level experts covering different aspects of the monitoring scheme to be set in place. This scheme will be for its scope and scale the first ever scheme worldwide to help addressing pollinators decline.

European pollinators

Europe supports a rich diversity of wild pollinators, estimated to comprise 2,051 species of bees, 482 species of butterflies, almost 1,000 species of hoverflies plus thousands of species of moths, flies, wasps, beetles and other insects. There is well-established evidence that many European pollinating species are declining. Collectively, pollinators provide a wide range of benefits to society including: more than €15 billion per year contribution to the market value of European crops; important contributions to human diets in terms of fruits, vegetables and nuts with high nutritional value; pollination of around 78% of wild flowering plants, which ensure healthy ecosystem functioning and maintenance of wider biodiversity as well as of culturally important flower-rich landscapes.

There are multiple benefits to an EU monitoring scheme for pollinators, including: societal (e.g. increased food security, agri-food sector employment, protection of pollinator species and habitats), political (e.g. contributing to (inter)-national conservation policy targets, directing policy actions), and scientific (e.g. addressing novel research questions on drivers, biodiversity and ecosystem services).

EU Pollinators Initiative

The revision of the EU Pollinators Initiative (EU PI): a New Deal for Pollinators, under ‘Priority I: Improving knowledge of pollinator decline, its causes and consequences’, called for the establishment of a comprehensive monitoring system. Based on this context, the key points informing the STING2 work were to develop proposals for:

- Options for a standardised approach to collecting annual data on the abundance and diversity of pollinator species across ecosystems in each Member State, with data coming from an adequate number of sites to ensure representativeness across territories.
- The ability to measure changes in pollinator diversity and pollinator populations by 2030, and at least every six years thereafter, in each Member State.
- Identifying options to promote citizen science in the collection of monitoring data.

The STING2 expert group

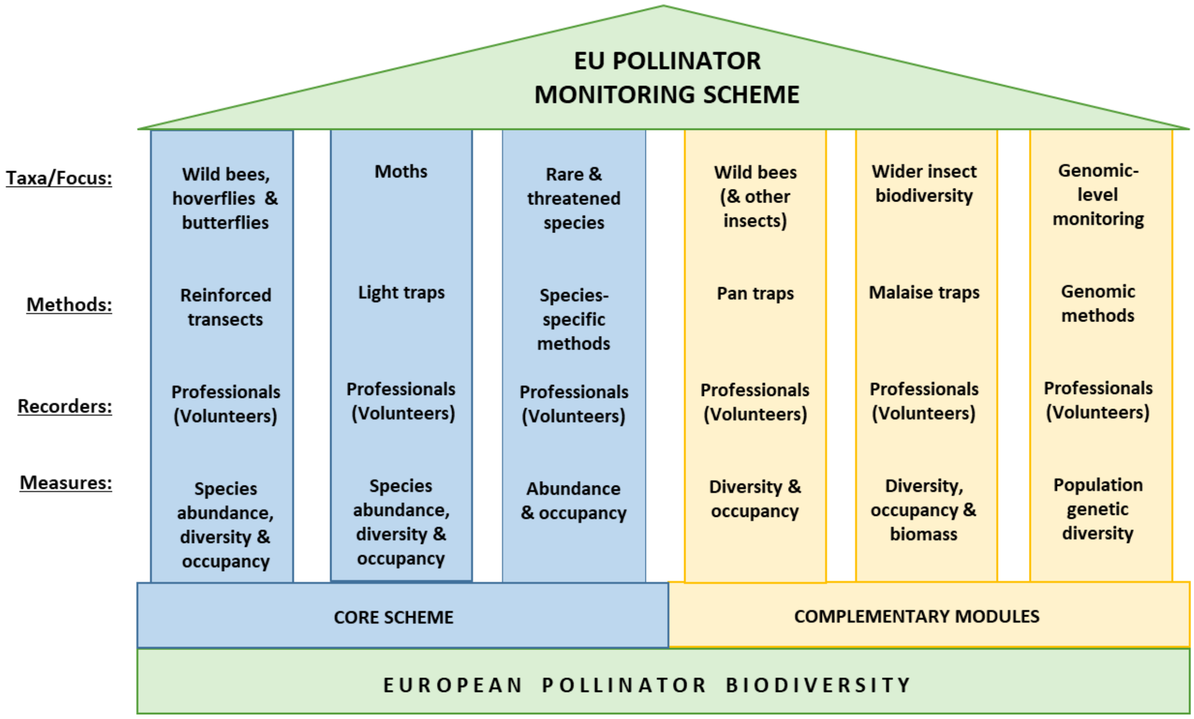
STING2 was tasked with three broad objectives to: (i) provide technical assistance in implementing and fine-tuning the EU pollinator monitoring scheme (EU PoMS); (ii) test, refine and validate the proposals for pollinator indicators; and (3) develop options for data management/storage/access and models to process and harmonise pollinator data.

Options for the EU PoMS design

Overall design

The proposed framework for the EU pollinator monitoring scheme is summarised in Figure i, and comprises two main components: the **core scheme** and **complementary modules**. The core scheme includes those taxa that are essential to monitor as part of EU PoMS (i.e. wild bees, butterflies, hoverflies, moths, as well as rare and threatened species of pollinators).

Figure i. Summary of the EU Pollinator Monitoring Scheme (EU PoMS) proposed design. This consists of the **core scheme**, which includes methods that are ready to be used to monitor: wild bees, hoverflies, and butterflies (using **reinforced transects**); moths (using light traps); and rare and threatened pollinator species (using species-specific methods). In addition, there are three **complementary modules**, which still require further piloting and refinement, and these include pan traps, Malaise traps and genomic methods. For each component of the EU PoMS, the main target taxa, sampling methods, type of recorder, and output measures are given. Recorders are expected to be professionals during the early stages of EU PoMS implementation, with the ambition to move towards an increasingly volunteer-led scheme in the longer-term.



Taxa/Focus:	Wild bees, hoverflies & butterflies	Moths	Rare & threatened species	Wild bees (& other insects)	Wider insect biodiversity	Genomic-level monitoring
Methods:	Reinforced transects	Light traps	Species-specific methods	Pan traps	Malaise traps	Genomic methods
Recorders:	Professionals (Volunteers)	Professionals (Volunteers)	Professionals (Volunteers)	Professionals (Volunteers)	Professionals (Volunteers)	Professionals (Volunteers)
Measures:	Species abundance, diversity & occupancy	Species abundance, diversity & occupancy	Abundance & occupancy	Diversity & occupancy	Diversity, occupancy & biomass	Population genetic diversity

Source: Authors' elaboration.

The first module of the core scheme uses standardised **reinforced transects**[1] (500m timed transect walks) to survey wild bees, hoverflies and butterflies to provide species abundance data. The second module of the core scheme provides species abundance data for moths using standardised **light traps**. The third module of the core scheme uses **species-specific methods** to

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[1] Reinforced transects are standardised transects proposed by STING2 and are sampled with a greater intensity than those transects initially proposed by STING1 (Potts et al., 2021). Full details can be found in section 2.3.

monitor rare and threatened species, which includes all pollinators (e.g. wasps, flies, beetles and other insects), in addition to bees, hoverflies, butterflies and moths.

There are three **complementary modules**, which could provide important measures of: bee diversity using **pan traps**, wider flying insect biodiversity using **Malaise traps**, and genetic diversity of wild pollinator populations using **genomic methods**. These three complementary modules should be prioritised for further piloting and refinement to become part of a core scheme.

For all methods, it is expected that these will be primarily professional led during the early roll out of EU PoMS, though the longer-term ambition is to shift to a hybrid model, with increasing proportions of volunteers trained to be able to implement the various methods in the field. Different Member States will have different starting conditions and capacities to involve volunteers.

Reinforced transects for surveying wild bees, hoverflies and butterflies

Using expert knowledge, SPRING pilot data, data simulations, and state of the art multispecies statistical models we recommend a set of options for EU PoMS that will ensure a high statistical power and that the data collected can directly flow into biodiversity indicators.

Choice of methods

- It was concluded that standardised transect walks, rather than pan traps, are the best method for assessing the species abundance of wild bees, hoverflies and butterflies. While pan traps may detect a wider diversity of wild bees, compared to transects, they have several major limitations: capture rates are strongly affected by the local floral context, making it hard to interpret data for the purposes of pollinator monitoring; they cannot provide abundance data; they are relatively costly; require the large scale storage of material; and citizen scientists are increasingly reluctant to use lethal methods.
- For EU PoMS, based on a power analysis, we recommend the use of reinforced transects of 500 metres in length which are walked first for butterflies and then re-walked for wild bees and hoverflies (though for the final protocol proposed by STING+ these two groups may be walked separately based on further insights from SPRING and the wider expert community). The 500m reinforced transect walks are repeated twice during each site visit to allow characterising species detectability, with 8 rounds per season. The transects are linked to a fixed location in each site, with each 500m walk taking a standardised amount of time (i.e. 30 minutes).
- Reinforced transects will need to be surveyed by professionals to ensure a high proportion of specimens can be identified to species in the field, with the remaining specimens collected in the field and identified in the lab.
- Along the same reinforced transect, flower abundance should also be recorded. While an estimate of flower richness and cover is not needed to estimate trends in pollinators, it is highly informative in understanding the factors driving pollinator trends.

Sampling design

- The proposed sampling design and statistical models have a high power for detecting a statistical trend, but due to the uncertainty introduced by the observation process, the power to precisely identify the strength of the trend, in terms of rates of change, is low.

- We recommend the relevant decline trend to be evaluated to be fixed at 1% per year, in line with studies on overall decline of pollinators and other flying insects. The time interval across which the trend is to be determined (with 80% power) is 6 years. Across all simulations, detecting higher declines is easy with a high power, but realistically declines in aggregated species abundances should be expected on the 1% range.
- Knowledge on the sampling effort required to properly monitor pollinators will increase as more data from the SPRING project is released (at the time of this report some specimens were still being identified), and data becomes available from the first years of the EU PoMS implementation, indicating that revisiting this challenge in the future is important.

Costings

- Information from participants in the SPRING project was used to determine the likely costs of implementing any proposed pollinator monitoring scenario, accounting for variation in wages, pollinator diversity, identification time and expenses between Member States.
- The costs of implementing the monitoring scheme will be heavily influenced by the number of sites, the staff model (balance between professional and volunteer recorders), the number of individual specimens sampled and the complexity of identifying specimens.
- Analysis of general costs indicate that: (i) some costs (e.g. travel) can be reduced through co-location with other monitoring networks; (ii) data management is a significant cost that can be reduced through careful planning (see section 4.2); (iii) the effective, harmonized use of novel technologies and robust metadata standards will reduce the staff effort needed for data entry; (iv) staff retention and training are crucial to long-term cost-effectiveness; and, (v) the initial learning phase of many new recorders will result in higher initial costs, therefore staff retention is key to both capacity building and cost-effectiveness.
- The cost methodology developed can readily be applied to any design variant once finalised for EU PoMS.

Light traps for surveying moths

- There is increasing evidence of the importance of nocturnal pollination, with moths as major contributors.
- An image recognition-based moth monitoring system has been developed and piloted in the SPRING project. The trap consists of a small LED light trap that runs through the night; in the morning, all moths are photographed using an existing app, allowing rapid identification. Moths are released afterwards.
- While in the early stages of EU PoMS, it is likely that professionals will run traps, it is expected that this approach (relative to reinforced transects and rare and threatened species assessments) is particularly amenable to being run by volunteers with comparatively little training required.
- This system has been tested in several European countries and the results are very promising. Based on the analysis of SPRING data, and for the Netherlands in particular, an initial power analysis indicates that around 40 traps run 6 times a year could provide a power of 80% to detect a 1% change in species abundance, in the Netherlands.

- To further develop a monitoring network at the EU scale, we recommend the following options: (i) develop a network of regional moth experts to validate volunteer data and help further develop the image recognition; (ii) support Member State coordinators and an overall EU coordinator; (iii) create and translate user-friendly moth information and identification materials to increase volunteer enthusiasm; (iv) extend the existing app and image recognition systems to prepare for increased usage; and, (v) further develop and test statistical approaches to produce trends and indicators for moths.

Rare and threatened species monitoring

- Many insect species are rare, geographically localised or ecologically highly specialised. A standardised, large-scale monitoring scheme such as the core scheme of EU PoMS is extremely unlikely to sample these species sufficiently to detect changes in their status.
- Therefore, we propose a rare and threatened species module to: (i) provide high quality data for assessing the conservation status of pollinators, reduce the number of Data Deficient and Not Evaluated species on the IUCN Red List, and improve the data for threatened species; and (ii) develop tailored recommendations to inform conservation management.
- A formula for prioritisation is presented to select species with the highest extinction risk (based upon the IUCN Red List) and lowest data availability. Resulting priority lists should be co-developed between the European level and Member States, taking into account both EU and Member State priority species.
- The choice of methods should be based on the most important information needed according to the current status of a species, and the most cost-effective data required to close respective knowledge gaps.
- After an initial survey, recommendations for longer-term monitoring and management could be developed, and follow-on monitoring would provide data to assess the efficacy of conservation actions.
- Two indicators are proposed, based on established methods, to measure the trends of rare and threatened species: (i) the IUCN Red List of Threatened Species, and (ii) the IUCN Green Status of Species. National Red Lists or National Green Status calculations can be considered for national priority species.

Options for monitoring pressures and site co-location

- Five candidate schemes, potentially suitable for co-locating the EU PoMS site network have been identified: Land Use and Cover Area frame Survey (LUCAS); the European Monitoring of Biodiversity in Agricultural Landscapes (EMBAL); the Monitoring of Environmental Pollution using Honey Bees (INSIGNIA); the Integrated European Long-Term Ecosystem, critical zone and socio-ecological Research Infrastructure (eLTER RI); and the EU Farm Sustainability Data Network (FSDN).
- There is no single 'one-size-fits-all' monitoring scheme with which EU PoMS is best aligned with. This is because of limitations due to: (i) limited environmental information (LUCAS, INSIGNIA, eLTER, FSDN); (ii) non-representative coverage of the land cover across the EU (LUCAS Grassland, EMBAL, FSDN); or, (iii) an insufficient number of observation sites (INSIGNIA, eLTER).

- Since EU PoMS should be representative of land cover and habitat types across the EU Member States, there can only be partial alignment with one or multiple other monitoring initiatives, i.e. a subset of EU PoMS sites is aligned to selected monitoring scheme(s), while the other part is (stratified) randomly distributed.
- For the (stratified) random sampling, the LUCAS Master grid is proposed. However, for a subset of EU PoMS sites to be co-located with INSIGNIA, eLTER or FSDN sites, some flexibility to allow for deviations from the gridded approach would be needed. However, aligning with more than one initiative might be challenging in terms of agreements and coordination.
- We recommend the design of EU PoMS is prioritised, and that EMBAL (or maybe LUCAS Grassland) and INSIGNIA co-locate to EU PoMS sites. INSIGNIA could further aim to increase the number of sampling sites considerably and seek options for a more spatially constant sampling design.

Taxonomic and human resource requirements

- Identification of species for monitoring purposes can be done in the field for most butterflies. However, for hoverflies and bees, some work in the lab will need to be undertaken in taxonomic facilities, with access to physical and/or digital collections and expert taxonomists.
- Based on previous studies (such as the Red List of Taxonomists), there is a clear shortage of professional taxonomists to address the anticipated monitoring requirements of EU PoMS. Available taxonomists are not expected to be sufficient to identify all species, across all sites, in all Member States.
- To overcome this shortfall, that varies from negligible to moderate and substantial depending upon Member State, a two-steps plan is proposed, by differentiating a short-term and a long-term approach.
- In the near term, capacity building and training stands as a critical component to allow EU PoMS monitoring to start in timely and efficient manner. This should be based on the “train the trainers” system to enable rapid upscaling over time.
- In addition, a wide variety of training resources will be needed, from basic to intermediate and advanced levels, such as those developed by the Pollinator Academy; resources will include training courses, factsheets, field guides, reference collections, keys and other tools and material that support the experts in their monitoring tasks. These materials will be increasingly important as the workforce evolves from fully professional based to a hybrid format where expert taxonomists combine effort with non-professionals though well-trained volunteers.
- In the longer-term, the sustainability of the model should rely on the consolidation of the monitoring work force to avoid recurrent restarting of the process (with new individuals being recruited continuously). This will benefit continuity and improve cost efficiency.
- To consolidate taxonomic expertise, in addition to training other elements are required including the establishment of academic pathways, widening of professional careers, opening of new positions, and ultimately supporting recognition of taxonomy. Moreover, to attract and secure the commitment of volunteers, will require stronger involvement of local governments, provision of stable structures to taxonomic communities, and supporting their work through a co-participatory model.

- To coordinate and harmonise the building of taxonomic and human capacity initiatives would need to: (i) centralise and provide access to the necessary protocols, best practices, standards, indicators, tools and mechanisms; (ii) facilitate training across borders; (iii) support mobilisation of experts; and, (iv) invest in and foster the use of technologies in support of species identification. This requires appropriate social, technical and, of course, financial structures to be supported over time, leveraging on existing networks and organised communities.

Building Citizen Science capacity for EU PoMS

- Europe has a long and rich tradition of Citizen Science and its innovation. An assessment of the current status of Pollinator Citizen Science shows that most aspects influencing it are at least developing or establishing, indicating that there is already good support and potential for Pollinator Citizen Science.
- Pollinator Citizen Science is more established in northern and western Europe, whereas in southern and eastern Europe, it tends to be at the embryonic or developing stages; embedding Citizen Science as a part of the EU PoMS in these regions will therefore pose the greatest challenge.
- There is considerable scope for further developing Pollinator Citizen Science on farmland by engaging farmers and other members of agricultural communities, though this would require careful reflection on likely motivations to partake and effect support mechanisms.
- Citizen Science has substantial future potential for implementing reinforced transects, with data collection by experienced naturalists for some groups and by specialists for others, and for training and engagement. Transects involving Citizen Science would also benefit greatly from integration with existing schemes, particularly Butterfly Monitoring Schemes, and place-based monitoring (e.g. Nature Reserves).
- Citizen Science also offers important opportunities to support other EU PoMS core scheme methods. Light trapping for moths would be particularly amenable to volunteer involvement and depending upon the priority species selected for the rare and threatened species module, volunteers could also make substantial contributions here.
- For the methods in the complementary modules of the EU PoMS, involvement of citizen scientists would need to be further explored for the use of Malaise traps, pan traps and the collection of specimens for genomic-level monitoring.
- We recommend: (i) supporting co-ordination and development of Citizen Science in all Member States as an integral part of the EU PoMS in the longer-term; (ii) adopting proven Citizen Science approaches, such as Butterfly Monitoring Schemes, in all Member States. The Butterfly Monitoring Scheme could support the monitoring of rare and threatened butterflies and provide a highly cost-effective approach to collect structured data to integrate within EU PoMS pollinator indicators and substantially increase the power to assess trends; (iii) evaluating methods that enable wide participation without requiring high levels of expertise in species identification, and which can be supported by new technologies; (iv) engaging with the farming community at Member State and EU levels to evaluate the potential for their involvement; and, (v) strengthening collaborations between Citizen Science practitioners and social scientists to understand motivation of volunteers and overcoming barriers to participation.

Options for pollinator indicators

General Pollinator Indicator

- Options for a General Pollinator Indicator are described. These indicator options can be used to assess whether there has been a reverse in the decline of pollinators (i.e. a trend should be shifted from a declining to an increasing one), using annually collected data, assessed over a standardised time interval of six years, at the Member State level by a given date. Based on the EU PI and STING expert consensus we recommend species abundance as the core metric for assessing trends.
- A generalised indicator workflow for (pollinator) biodiversity indicators is outlined: pollinator observations > data > species-specific models > species indices > statistical models > indicators. Based on this, options are proposed for converting EU PoMS data into biodiversity indicators, and how these indicators can be used to assess targets, such as those included in the EU PI.
- A set of Essential Biodiversity Variable (EBV) metrics are described that could be derived from EU PoMS data: species abundance, species distribution, taxonomic diversity, and taxon-aggregated abundance. The strengths and limitations of each is highlighted in the context of the EU PI.
- Future work is recommended to: (i) refine and test the statistical models, including their sensitivity to data from rarely observed species, and their ability to detect changes over a six-year window; and (ii) explore options for the assessment of targets within a risk-based framework, including combining indicators from multiple biodiversity metrics.

Farmland Pollinator Indicator

- Agricultural landscapes are significantly shaped by the complex interplay of various drivers, including policy interventions at EU and Member State level and by the individual decisions of farmers. As a result, it is difficult to single out the impact of the CAP on (pollinator) biodiversity. CAP Impact Indicators used so far in the Performance Monitoring and Evaluation Framework (PMEF) are not suitable for this, as they were designed for other purposes.
- A workflow for a two-stage monitoring approach is presented to assess the medium- and long-term status and trends of farmland pollinators in conjunction with the impacts of CAP and other policy interventions: (i) trend monitoring (surveillance monitoring of pollinators), and (ii) monitoring under adaptive management (surveillance monitoring of pollinators together with environmental data).
- Trend monitoring could be based on the sampling methods and sites of the core scheme (though the site allocation approach is to be finalised) and, if necessary, complemented by additional sampling sites within agricultural landscapes to ensure representativeness of farmed landscapes, and for example CAP measures.
- Monitoring under adaptive management could use a citizen science-based approach with farmers conducting the monitoring, as they decide where and when which CAP measures are implemented, and therefore make it possible to evaluate them at the farm level in an efficient way. In monitoring under adaptive management, simplified approaches, compared to the core scheme, could be employed (e.g. monitoring of species groups).

- To ensure that the proposed indicators for farmland pollinators are functional and can be reported in the future, we recommend conducting a pilot study in selected EU agricultural landscapes to test and further develop the two approaches presented here.

Options for EU PoMS data management

Building on existing initiatives (e.g. EuropaBON) and stakeholder requirements, we propose an optimised workflow for data management throughout the entire data life cycle. Specifically, we recommend:

- Establishing a unified central hardware infrastructure fully respecting and compatible with national biodiversity data and information systems;
- Implementing data management solutions based on existing software and tailored to specific EU PoMS requirements;
- Developing both a new EU PoMS app and cooperating with existing Apps, which interface with the central database via an Application Programming Interface (API), to maximise the uptake and impact of EU PoMS;
- Putting in place two levels of validation procedure to guarantee the quality of data;
- Establishing a species referencing table for standardising nomenclature;
- Publishing annual monitoring data with open access and assign citable DOIs, offering flexibility for the download of accumulated multi-year datasets as well as data specific to spatial, temporal, and taxonomic contexts;
- Ensuring data publication policy is openly accessible and clear to volunteers prior to participating in EU PoMS.

Options for future scheme development

Complementary modules

In addition to the core scheme, there are three approaches, which, with further piloting and refinement could be included in a future core scheme.

Pan traps

While the reinforced transects are recommended as the best overall method for monitoring wild bees, hoverflies and butterflies, pan traps also offer the possibility to monitor a wider spectrum of wild bee species richness (but not abundance) and wider flying insect diversity. However, pan trap protocols need further piloting and refinement, and the reluctance of some citizen scientists to use this lethal method would also need considering.

Emerging technologies

Several novel technologies hold considerable promise for enhancing pollinator monitoring efforts; all still require some level of further development and testing before they could be rolled out at scale and integrated into a core scheme:

- DNA barcoding and metabarcoding techniques are well developed and have the potential to reduce costs and expedite specimen identification, and while the availability of reference databases is increasing, they are currently incomplete.

- Image-based methods for identifying (dead) specimens are maturing, though reference databases for pollinators are incomplete.
- Remote sensing approaches to monitor pollinator habitats, including floral resources, are fast emerging.
- Insect camera traps are at an early stage of development, but could provide important phenological and flower visitor data, complementing other methods.
- Acoustic methods are rapidly evolving, but at present, they have limited applicability across insect taxa.

Genomic-level monitoring

Systematically assessing monitoring the genetic diversity of wild pollinator populations is important for implementing effective conservation strategies and safeguarding adaptive capacity. A range of DNA technologies are mature, though they require embedding, testing and refining through a pilot scheme before they could be integrated into a core scheme.

Malaise traps

Malaise traps offer the possibility to passively capture a wide variety of flying insects, and some non-flying insects, over long periods throughout the year (not observed by other methods). This method can provide quick estimates of diversity, and abundance of insects via biomass measurements, which have been shown to correlate well with both abundance and diversity of species in hoverflies. However, this method cannot provide absolute species abundance estimates. Further development, piloting and refinement is needed for standardising field methods across Europe, sample processing/storage and completion of DNA libraries before this method could be integrated into a core scheme.

1 Introduction

1.1 Policy context and background

1.1.1 EU Pollinators Initiative and A New Deal for Pollinators

The revision of the EU Pollinators Initiative: 'A New Deal for Pollinators' (COM(2023) 35 final) (European Commission, 2023), under 'Priority I: Improving knowledge of pollinator decline, its causes and consequences', called for the establishment of a comprehensive monitoring system. This requires a robust EU-wide monitoring scheme that provides regular and frequent information using standardised methods over a long time frame. The aim being to provide a rigorous measure of the trends in pollinator abundance and diversity, to be able to reliably assess progress towards reversing their decline. In addition, this also calls for the main threats to pollinator decline to be monitored, therefore requiring an integrated framework for monitoring pollinator decline, its causes and consequences, according to the DPSIR (drivers, pressures, state, impact and response) model of intervention, which would allow tracking the outputs and outcomes of relevant policy actions. The specific Actions towards the overarching goal of establishing a comprehensive monitoring system are:

1. The Commission and Member States should finalise the development and testing of a standardised methodology for an EU pollinator monitoring scheme (EU PoMS). The methodology will ensure delivery of annual datasets on the abundance and diversity of pollinator species, with adequate statistical power to assess whether the decline of pollinators has been reversed both at EU and at national level. Once the methodology is available, Member States should deploy the scheme on the ground.

2. The Commission will, with the support of Member States and the European Environment Agency, devise an integrated framework for monitoring pollinator decline, its causes and consequences. The Commission will continue supporting the systematic collection of data on major threats to pollinators, in particular through the EMBAL and INSIGNIA initiatives.

3. The Commission will develop indicators on the state of pollinator populations and the pressures they face and will explore options for developing indicators on the impacts of pollinators on ecosystem health, the economy and human wellbeing. These indicators will be developed with a view to contributing, among other things, to the evaluation of relevant policies, such as the common agricultural policy.

Based on this context, the key points informing the work under the second part of the STING project (STING2 hereafter) are to develop proposals for:

- Options for a **standardised approach** to collecting **annual data** on the **abundance and diversity of pollinator species** across ecosystems in each Member State, with data coming from an adequate number of sites to ensure representativeness across territories.

- The ability to measure changes in pollinator diversity and pollinator populations by 2030, and at least every six years thereafter, in each Member State.

- Identifying options to promote Citizen Science in the collection of monitoring data.

1.2 STING2: Science and Technology for Pollinating Insects 2

1.2.1 Objectives and approach

The STING2 expert group was established in June 2022, and comprises 26 international experts from 12 countries, with members being representatives of universities, research institutes and NGO's. The specific objectives of this group are:

1. **Provide technical assistance in implementing and fine-tuning the EU pollinator monitoring scheme (EU PoMS)**, which includes: updating power analysis; exploring pathways to integrate emerging technologies; revising cost estimates; ad-hoc support to conclude on a final methodology in the context of the EU biodiversity strategy to 2030; analysing links between the EU PoMS and other Citizen Science initiatives (e.g. eBMS); liaising with other in-situ monitoring of pressures on pollinators; exploring pathways to include genomic-level monitoring; tracking the development and proposing recommendation on pollinator taxonomic expertise; further develop the rare and threatened species module; and assessing options to develop a pollinator app as a tool for EU PoMS as well as for wider structured Citizen Science.
2. **Testing, refining and validating the proposals for pollinator indicators**, which includes: helping devise and refine a General Pollinator Indicator (GPI), and developing and testing options for Farmland Pollinator Indicator (FPI).
3. Developing options for data management/storage/access and models to process and harmonise pollinator data

JRC coordinated the work under the different tasks of the STING2 expert pool, and facilitated the dialogue between the experts and the relevant policy DGs, in particular DG ENV. Additionally, the JRC facilitated the liaison between the experts and the European Environmental Agency (EEA), for technical input on data management. JRC research staff also provided technical support for specific tasks (in particular computational support for the power analysis task), and specialised expertise when required by the experts (e.g. while for developing options for a farmland pollinator indicator). Furthermore, the JRC computed the preliminary analysis on the spatial distribution of sites in use by the EMBAL[2] and INSIGNIA[3] projects to inform options for monitoring pressures and site co-location. Lastly, after establishing a dedicated functional mailbox (jrc-poms@ec.europa.eu) the JRC served as helpdesk point to address, directly or after consulting relevant experts, specific questions about the STING project and EU PoMS. The same functional mailbox was used to communicate with named representatives from the Member States and non-governmental stakeholder groups, which were consulted on draft versions of this report.

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[2] https://wikis.ec.europa.eu/pages/viewpage.action?pageId=25560696#:~:text=EMBAL%20is%20a%20robust%20monitoring,landscapes%20in%20EU%20Member%20States

[3] https://www.insignia-bee.eu

The final report of the STING1 expert group (2019-2021) was published in 2021: "*Proposal for an EU Pollinator Monitoring Scheme*"[4] (Potts et al., 2021). See Annex 1 for summary of STING1 findings.

Since the publication of Potts et al. (2021) substantial advances in data, evidence and knowledge of pollinator monitoring has occurred. These includes large scale piloting of the methods through the SPRING project, multiple research and monitoring activities providing new data and knowledge on pollinator monitoring, advances in the development and testing of indicators, ongoing work by a number of Citizen Science and volunteer projects, in particular Butterfly Conservation Europe, as well as other preparatory actions helping develop human and taxonomic capacity for pollinator surveying and identification, such as SPRING, ORBIT and Taxo-Fly. Therefore, the key findings of the STING1 report (see Annex 1) must be considered as being the current state-of-the-art in 2021, after which considerable advances have been made through STING2 and a large number of linked projects.

The overall approach of the STING2 expert group is summarised in Figure 1.1. 1. The core work involved conducting a power analysis using the best available data to explore design options considering the methods, intensity of sampling, temporal and spatial replication needed to provide high quality species abundance data (as informed by the EU PI). The overall sampling design was developed in tandem with indicator options for both a general pollinator indicator and a farmland pollinator indicator. For each of the design options, the associated costs and taxonomic requirements, including human resources, were also assessed. The required data management requirements were explored, including the development of a dedicated app for the scheme. In addition to the core monitoring of bees, hoverflies and butterflies, options for monitoring moths using light traps, and tailored methods for monitoring rare and threatened species were also investigated. Finally, complementing the core scheme, options for the use of emerging technologies, genomic-level monitoring, and the monitoring of threats to pollinators were explored. The STING2 work benefited from many projects and initiatives, and in particular from data and insights from the SPRING, ORBIT, Taxo-Fly and European Butterfly Monitoring Scheme.

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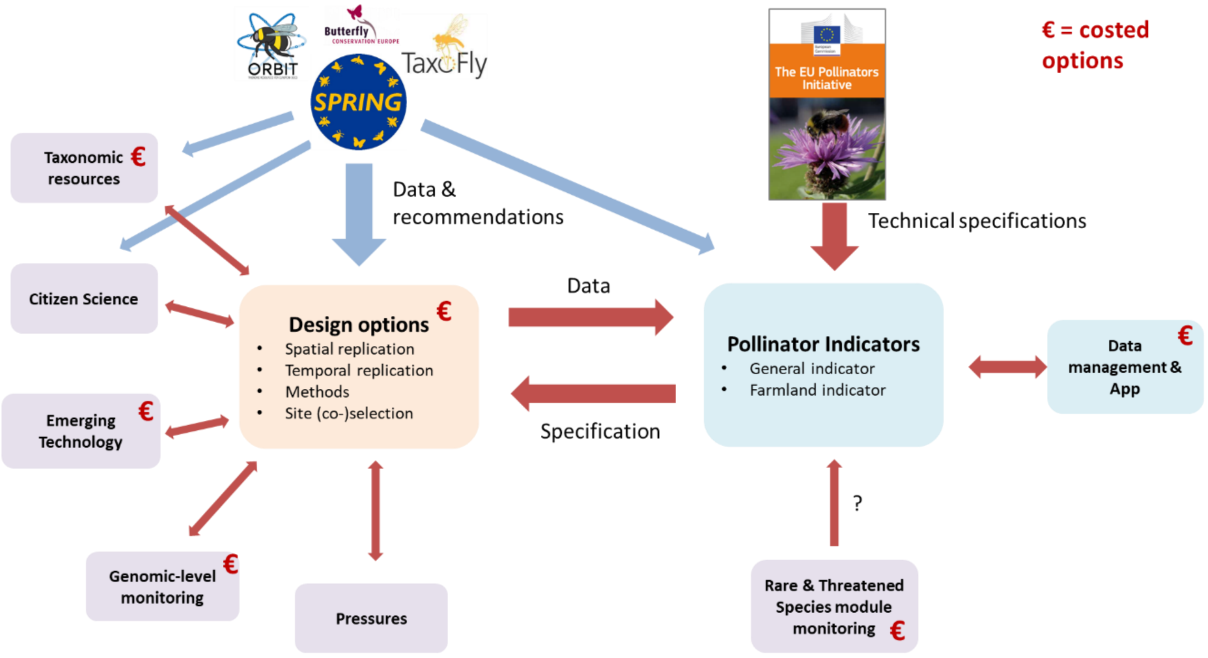
[4] Potts, S.G., Dauber, J., Hochkirch, A., Oteman, B., Roy, D.B., Ahrné, K., Biesmeijer, K., Breeze, T.D., Carvell, C., Ferreira, C., FitzPatrick, Ú., Isaac, N.J.B., Kuussaari, M., Ljubomirov, T., Maes, J., Ngo, H., Pardo, A., Polce, C., Quaranta, M., Settele, J., Sorg, M., Stefanescu, C., Vujić, A., *Proposal for an EU Pollinator Monitoring Scheme*, EUR 30416 EN, Publications Office of the European Union, Ispra, 2021, ISBN 978-92-76-23859-1, doi:10.2760/881843, JRC122225.

Figure 1.1. 1. Overview of the STING2 framework.



Source: Authors' elaboration.

1.2.2 STING2 deliverables

STING2 has two key deliverables:

- D.1: A report describing the contributions of the experts to Objective 1. This includes contributing to the further development of the EU PoMS, in particular fine-tuning the scheme in collaboration with SPRING.
- D.2: A report describing the contributions of the experts to Objective 2. This includes devising a General Pollinator Indicator (GPI) to support inter alia a potential legally binding target on reversing the pollinators decline, and also developing further options for a Farmland Pollinator Indicator (FPI), including analysing the methodology behind various CAP impact indicators and testing CAP indicator options.

This report combines both of these deliverables, covering all three objectives, into a single cohesive report.

1.3 Presentation of options for EU PoMS

This report provides the following options for the establishment of an integrated monitoring framework:

- **Main design options for EU PoMS** (Chapter 2), which provides a summary of the proposed EU PoMS, and explains the choice of methods (section 2.2), how change can be detected (section 2.3), the design options for the monitoring bees, hoverflies and butterflies, with scenarios for each Member State using reinforced transects (section 2.4) including costings (section 2.5) and taxonomic and human requirements (section 2.6), as well as options for building citizen capacity (section 2.7), rare and threatened species monitoring (section 2.8), moth monitoring (section 2.9) and pressure monitoring (section 2.10).
- **Indicator options** (Chapter 3) for a General Pollinator Indicator (section 3.1) and a Farmland Pollinator Indicator (section 3.2).
- **Data management options** (Chapter 4) including data management workflow (section 4.2), data standards (section 4.3), data acquisition (section 4.4), data preservation (section 4.5), web interfaces (section 4.6), and database structure (section 4.7).
- **Future scheme options** (Chapter 5), covering pan traps (section 5.1), emerging technologies (section 5.2), genomic-level monitoring (section 5.3), and Malaise traps (section 5.4).

Andrena clarkella, Axel Hochkirch

Annex 1. STING1: Science and Technology for Pollinating Insects 1

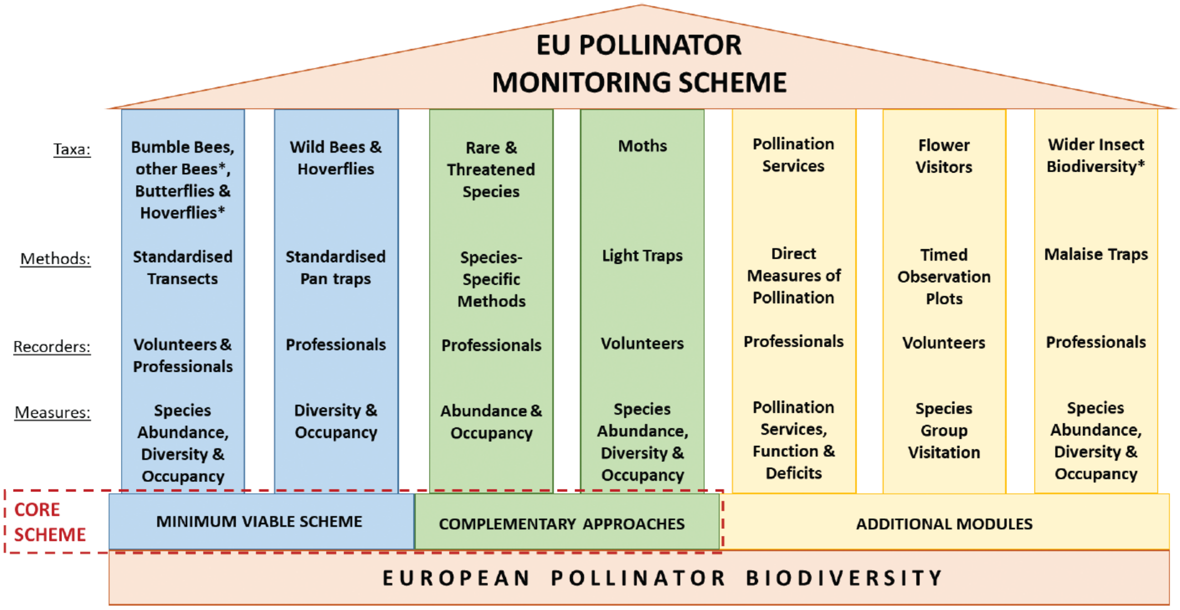
In 2019, the European Commission set up the STING1 (Science and Technology for Pollinating Insects) - technical expert group, comprising 21 individuals from 10 European countries plus representatives from JRC and the European Environment Agency (EEA). The remit of STING1 was to develop an initial proposal for a European pollinator monitoring scheme as part of Action 1 of the EU Pollinators Initiative. The specific objectives of the group were to:

1. Develop a cost-effective EU pollinator monitoring scheme (EU PoMS) to monitor pollinators with the following requirements: The scheme should include the most relevant taxa of pollinators (based on different criteria such as vulnerability to environmental pressures, Red List status, functional traits, relative importance for crop pollination, representativeness for biodiversity); The scheme should be able to detect changes in the status of pollinators; The scheme should consider the timing of the EU policy cycle (7 years); The scheme should include EU-wide coverage and should allow harmonised data collection at EU level, based on standardised sampling; The scheme should consider the current level of knowledge on pollinators in the EU Member States; The scheme could be based on professional monitoring, Citizen Science or a hybrid system; The scheme could have modular components; The scheme should indicate approximate costs according to the level of detection (e.g. short versus long-term perspective).
2. Assess if emerging technologies are fit for the purpose of sampling as an alternative method (e.g. remote sensing of habitats, DNA based sampling).
3. Make a proposal for a general indicator based on the monitoring scheme to assess status and trends of pollinators and specific sub-index tailored to measuring the status of pollinators in agricultural areas.
4. Assess for different options of the scheme: The costs for setting up a scheme, training experts, sampling, analysing and producing results, reporting and maintaining the data; The required taxonomical knowledge; The level of detection of change and its relative cost.
5. Present a list of options for the scheme to the Commission.

Main findings of STING1

The initial proposal is summarised in Figure A1. 1. STING1 proposed that the EU PoMS should comprise a ‘core scheme’, which includes the taxa that are essential to monitor across the EU: wild bees, butterflies, hoverflies, moths, including rare and threatened pollinator species. An overview of the proposed scheme is given in Figure A1. 1. The selection of taxa took into account: the proportion of a group, which are known pollinators, contributions to crop and wild flower pollination, representativeness of wider biodiversity, vulnerability to environmental change, taxonomic knowledge of the group, and conservation status. Honey bees were excluded from consideration as they are almost entirely managed in Europe, and are already being monitored through other initiatives and projects.

Figure A1. 1. Overview of the STING1 proposed EU pollinator monitoring scheme (EU PoMS). The overall scheme comprises a number of components: the **core scheme** are those taxa that are essential to monitor as part of an EU Pollinator Monitoring Scheme (i.e. wild bees, butterflies, moths, hoverflies, as well as rare and threatened pollinator species). Within the core scheme is a **minimum viable scheme** (MVS), which is feasible to implement in the short term and comprises two modules which use standardised transects and pan traps to provide species abundance, diversity and occupancy data on wild bees, butterflies and hoverflies. **Complementary approaches** are needed for moths, and for targeting rare and threatened species, which cannot otherwise be monitored through a large-scale standardised scheme. There are three **additional modules**, which are optional and could provide important measures of pollination services, flower visitors, and wider flying insect biodiversity. For each component of the EU PoMS the main target taxa, sampling methods, type of recorder, and output measures are given. * indicates that for these groups only a proportion would be identified to species; a number of important details and caveats for all elements presented in this overview are addressed in detail in Potts et al. (2021).



Source: Potts et al. (2021).

Alongside the MVS, and within the core scheme, two modules were proposed using ‘complementary approaches’ to monitor moths, and to monitor rare and threatened pollinator species (Figure A1. 1). The moth module would survey night active moths using light traps, and provide species abundance measures of an additional taxonomic group to the MVS; methods were reasonably well developed for this module but were seen to require fine-tuning and field validation. The rare and threatened species module would rely on species-specific field survey methods which is a fundamentally different approach to the MVS; this would be necessary as a standardised, large-scale pan-European monitoring scheme would be highly unlikely to sample rare species sufficiently to be able to detect changes in their status.

Finally, in addition to the core scheme (MVS plus complementary approaches) there are three additional modules proposed: pollination services, flower visitation, and wider flying insect biodiversity (Figure A1. 1).These three modules could provide important measures of biodiversity and ecosystem function/services not available through the core scheme, but required significant methodological development before they can be implemented at scale in a standardised manner.

Based on the available data and evidence at the time (i.e. up until 2021), for the MVS across the EU, it was estimated that a network of 2,000 to 3,000 sites is likely to provide power of >80% to detect changes of ~10% in abundance and species richness over 10 years for major groups (bees, butterflies and hoverflies), and changes of 30% for individual species that occur commonly across Europe. This estimate was based on expert opinion informed by a power analysis using the best available datasets (up to 2021), which were limited in number and geographically biased. To provide representative coverage, these sites should be allocated in proportion to the land area of Member States, and adjusted to ensure at least 10 sites per Member State (total sites = 2,102; sites per Member State, minimum = 10 and maximum = 238).

The estimate provided in 2021 needs to be updated based on the field data collected in the SPRING project. To date, not all individuals have been determined to species level. Therefore, the update of the power analysis will be undertaken in a follow-up project (STING+).Expert knowledge revealed a rich variety of taxonomic resources available in Europe, although the availability and quality vary markedly between Member States. For the MVS target taxa (bees, butterflies and hoverflies), the report provided a detailed stocktake for 2021 of the availability of national checklists, field guides, handbooks and identification keys, online identification tools, atlases, recording schemes, national Red Lists, internet fora, DNA-barcoding, experts, meetings and organisations.

Taxonomic capacity, in terms of both experts and resources, to support a MVS was assessed as highly variable across Europe and taxonomic groups. For bees and hoverflies, taxonomic knowledge and resources were generally better in northwest and central Europe, than in the south and east. For butterflies, taxonomic knowledge and resources are relatively good in nearly all countries; capacity for moths was not assessed.

A combination of volunteer recorders and professionals were proposed to run a cost-effective EU scheme, with each module within the EU PoMS requiring a different mix of these recorders (Figure A1. 1). The roles, levels of expertise and training requirements of these two groups of recorders were assessed, and guidance was provided on how to strengthen volunteer recruitment and retention.

The report of the STING1 expert group[5]:

Potts, S.G., Dauber, J., Hochkirch, A., Oteman, B., Roy, D.B., Ahrné, K., Biesmeijer, K., Breeze, T.D., Carvell, C., Ferreira, C., FitzPatrick, Ú., Isaac, N.J.B., Kuussaari, M., Ljubomirov, T., Maes, J., Ngo, H., Pardo, A., Polce, C., Quaranta, M., Settele, J., Sorg, M., Stefanescu, C., Vujić, A., *Proposal for an EU Pollinator Monitoring Scheme*, EUR 30416 EN, Publications Office of the European Union, Ispra, 2021, ISBN 978-92-76-23859-1, doi:10.2760/881843, JRC122225.

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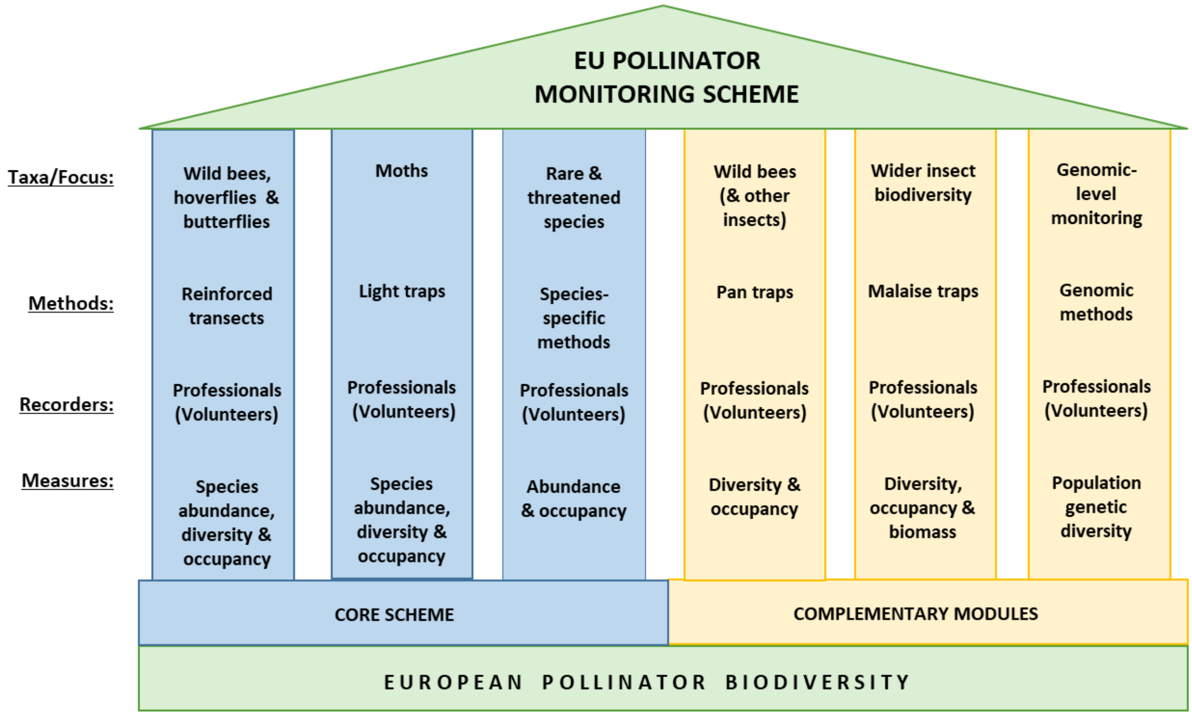
[5] https://publications.jrc.ec.europa.eu/repository/handle/JRC122225

2 Options for the EU PoMS design

2.1 Summary of options

Since the initial proposal from the STING1 expert group (Potts et al., 2021), the proposed framework has been refined in light of new data, analysis and expert opinion. The overall EU PoMS scheme is summarised in Figure 2.1. 1 and comprises two main components: the **core scheme** and **complementary modules**. The core scheme includes those taxa that are essential to monitor as part of an EU Pollinator Monitoring Scheme (i.e. wild bees, butterflies, hoverflies, moths, as well as rare and threatened species of pollinators).

Figure 2.1. 1. Summary of the revised EU pollinator monitoring scheme (EU PoMS). This consists of the **core scheme**, which includes methods that are ready to be used to monitor wild bees, hoverflies, butterflies (using reinforced transects), moths (using light traps) and rare and threatened species (using species-specific methods). In addition, there are three **complementary modules**, which still require further piloting and refinement, and these include pan traps, Malaise traps and genomic methods. For each component of the EU PoMS, the main target taxa, sampling methods, type of recorder, and output measures are given; a number of important details and caveats for all elements presented in this overview are addressed in detail in the following chapter. Recorders are expected to be professionals during the early stages of EU PoMS implementation, with the ambition to move towards an increasingly volunteer-led scheme in the longer-term (see section 2.6 for details).



Source: Authors' elaboration.

The first module of the core scheme uses standardised **reinforced transects** to survey wild bees, hoverflies and butterflies to provide species abundance data (see section 2.3 for details). The second module of the core scheme provides species abundance data for moths using standardised **light traps** (section 2.9). The third module of the core scheme uses **species-specific methods** to monitor rare and threatened species, which includes all pollinators (e.g. wasps, flies, beetles and other insects), in addition to bees, hoverflies, butterflies and moths (section 2.8). In the earlier version of the scheme design (Potts et al., 2021), methods for moths and rare and threatened species were assessed as not being sufficiently developed to include in the near term as part of the core scheme. However, significant technical and knowledge developments have occurred since the 2021 EU PoMS report, and now these two modules can be included in the core scheme.

There are three **complementary modules** which could provide important measures of: bee diversity (using **pan traps**, section 5.1), wider flying insect biodiversity (using **Malaise traps**, section 5.4), and genetic diversity of wild pollinator populations (using **genomic methods**, see section 5.3). These three complementary modules should be prioritised for further piloting and refinement to become part of a core scheme.

For all methods, it is expected that these will be primarily professional-led during the early roll out of EU PoMS, though the longer-term ambition is to shift to a hybrid model, with increasing proportions of volunteers trained to be able to implement the various methods in the field. Different Member States will have different starting conditions and capacities to involve volunteers, and these aspects are addressed in sections 2.6 and 2.7.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2.2 Choice of methods for the core scheme

The STING1 expert group proposed a minimum viable scheme (MVS) for bees, hoverflies and butterflies based on a combination of using standardised transect walks and pan traps (Potts et al., 2021). The STING2 experts have reassessed this proposal, in the light of analysing significant new data (from SPRING and other large scale projects), consulting a wide range of professionals and volunteers, and considering the expected requirements of the indicator(s) including the need for species level data as mandated by the EU Pollinators Initiative.

STING2 has concluded that for wild bees, hoverflies and butterflies that standardised transect walks are the most effective and efficient method for the core scheme. Pan traps have been dropped from the core scheme after careful assessment of the advantages and limitations; however, this method still offers important opportunities for understanding the diversity and occupancy of wild bees as well as wider insect biodiversity. The rationale for this decision is provided in section 2.2.1, with an overall summary in 2.2.1.5. Possible future options using pan traps are described in section 5.1. Here we present an overview of the rationale for retaining standardised transects as the sole method for the core scheme, and why pan traps were excluded.

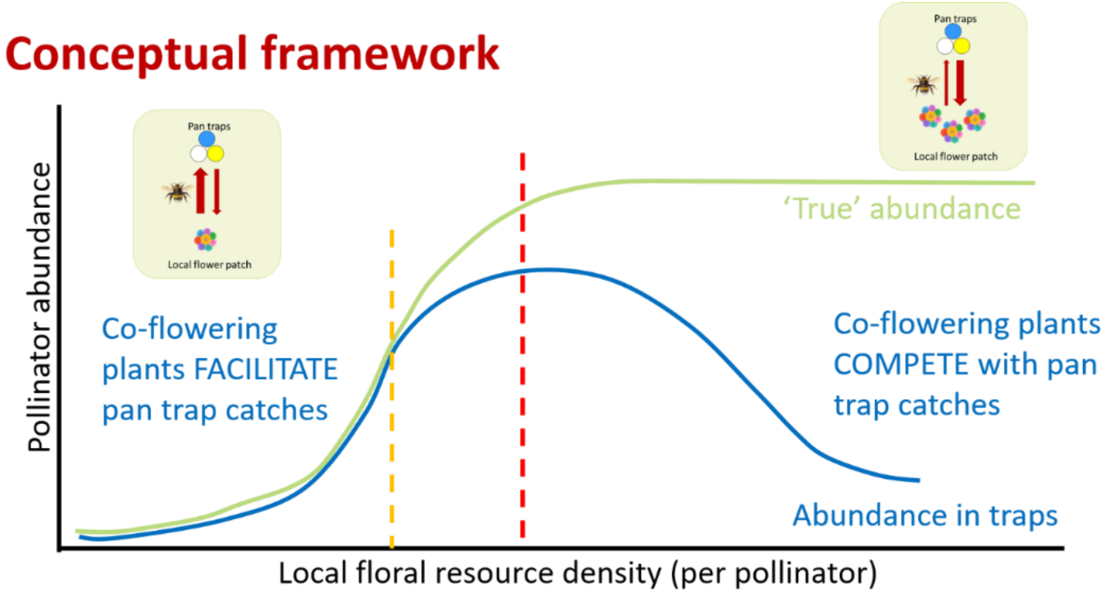
2.2.1 Assessment of the potential impact of floral resources on abundance estimates from pan traps in comparison with transect walks

European data from 11 datasets using pan traps, and 4 datasets using transect walks, were used to assess pollinator abundance in response to floral resources. The focus was on wild bees, since pan traps are commonly used for their assessment. Based on theory, it was expected that wild bees are attracted to pan traps when floral resources are scarce, while a dilution effect (due to a decreased detection chance) under high flower densities might lead to an underrepresentation of wild bees in pan traps. Assessments based on transects, on the other hand, are assumed to be less affected by pollinator attraction and dilution effects.

2.2.1.1 Conceptual framework

Floral resource availability is expected to potentially impact the assessment of pollinators and in particular their abundance from pan traps due to different mechanisms of attraction and ‘dilution’ of pollinator numbers, dependent on the abundance and diversity of flower resources within the vicinity of pan traps and in the broader landscape. Increased understanding of these mechanisms was achieved by analysing a comprehensive dataset on pollinator richness and abundance collected by pan traps and transect walks along gradients in local and landscape-level flower resource availability. Due to longer processing times of the SPRING samples, we started with datasets already available and complemented them with SPRING data. We contacted relevant data holders and, together with them, we developed a theory-based analytical approach (Figure 2.2. 1) during an online workshop (16 February 2022). The concept has been presented and discussed at the SPRING meeting in Barcelona (5 – 7 October 2022).

Figure 2.2. 1. Conceptual framework to assess impacts of flower resource density on assessments of pollinator abundance sampled with pan traps. Yellow dashed line: flower densities below which pollinator abundance might be expected to follow patterns of 'true' abundance. Red dashed line: flower densities beyond which significant deviations of 'true' pollinator abundances can be expected due to a 'dilution' effect.



Source: SPRING online workshop, 16/02/2022.

This conceptual framework assumes a sigmoidal response of 'true' pollinator abundance with increasing flower densities (green line in Figure 2.2. 1). Co-flowering plants at low densities are expected to facilitate pan trap catches, while high densities of co-flowering plants are expected to compete with pan traps. This leads to an initial match between 'true' abundances and assessments with pan traps, while at a certain point estimates from pan traps diverge from the expected 'true' pollinator abundances (blue line in Figure 2.2. 1). Note that other variables not considered here, such as species-specific behaviour, are also known to affect pan trap effectivity per species, but this factor is not analysed here.

2.2.1.2 Data and analysis

Based on provided meta-data, we identified 27 candidate studies covering eight European countries, about 1,000 sites with more than 26,000 spatio-temporal replicates providing data based on pan traps and transect walks. On this basis, we aimed to identify and quantify the potential impact of local and landscape-level flower resource densities on local pollinator abundance estimates and provide a framework to correct for such impacts and to inform the development of standardised assessments of local floral resources for inclusion in the core scheme.

From the 27 candidate studies, data were collated only from the 14 studies across Europe with suitable information. Those studies used pan traps, transects or both. After an initial screening of these 14 studies, 11 datasets remained (with 3 excluded) for pan traps (covering Spain, Greece, UK, and the Netherlands) and 4 for transects (covering Romania, the Netherlands, Greece, and UK; Table 2.2. 1). The transects have a fixed location in each site, with each 500m walk taking 30 minutes. Exclusion criteria for datasets were: (i) flower resources were provided in terms of percentage cover instead of density (flower unit per m^2), and (ii) low abundance, and in particular low variation across the samples. Since not all studies had information on the three focal groups of EU PoMS core scheme, we focused on wild bees for means of consistency and since transect walks are typically preferred over pan traps for butterflies and hoverflies.

To allow for a direct comparison across the different studies, pollinator and flower data were harmonised and adjusted for sampling effort. Spatial replicates of pan traps and transects were aggregated across the focal study site. Temporal replicates (sampling rounds) were not aggregated but considered as a separate data points. All studies had separate flower surveys for each sampling round. To account for differences in the number of pan traps and their operating time, we calculated wild bee abundance per trap and day. For transects, we used wild bee abundance per observation time (minutes). Flower densities are based on flower units, one flower unit is a cluster of flowers that can be reached without flying (e.g. *Compositae* or *Umbeliferae* inflorescences were counted as 1 unit of flower). Flower densities were either already provided as such or have been calculated based on the number of flower units and the size of the respective sampling plot.

Since average wild bee abundance differed considerably between locations in central/western Europe (median = 36 specimens) and southern Europe (median = 91 specimens), we split the dataset into two, a southern (Spain and Greece) and a central/western part (UK and the Netherlands). The distributions of the transect data were similar for southern and central/western locations (southern, Greece and Romania: median = 0.3 specimens; central/western, UK and the Netherlands: median = 0.4 specimens) which did not require a split for the identification and visualisation of the relationship with flower density. For the central/western pan trap dataset, we had 534 individual data points. The southern pan trap dataset comprised 346 data points, and the transect dataset had 659 data points (median abundance = 0.35 specimens).

To assess the relationships between wild bee abundance and flower density for pan traps and transects and to compare them with the expectations from our conceptual framework, we used local polynomial regression fitting (loess). This is a nonparametric technique for smoothing scattered data points, which is highly suitable to identify the shape of complex relationships. We identified the significance of the smoothed shape of the relationship against a null hypothesis of no relationship using a permutation test based on mean squared error (5,000 permutations).

Table 2.2. 1. Data sources and summary statistics. N: number of data points per study; Pan S: pan trap southern Europe; Pan C: pan traps central/western Europe; Trans: transects.

Study	Country	Method	N	Abundance mean (SD)	Flower mean (SD)
ALMOND[u]	Spain	Pan S	118	12.01 (12.32)	164.59 (242.34)
BIOPAIS[1]	Spain	Pan S	21	5.99 (3.63)	10.24 (5.92)
Landpolnet2[u]	Spain	Pan S	83	15.21 (8.22)	40.09 (61.06)
Landpolnet1[2]	Spain	Pan S	60	16.68 (10.92)	25.79 (34.25)
POLLOLE[3]	Spain	Pan S	22	5.64 (3.28)	0.19 (0.13)
Serapis[u]	Greece	Pan S	42	9.74 (8.32)	186.99 (154.39)
BHL[u]	Netherlands	Pan C	151	5.62 (6.22)	49.13 (79.15)
IPI_Crops[u]	UK	Pan C	85	4.41 (7.21)	714.4 (1185.45)
UKPoMS[u]	UK	Pan C	298	6.68 (8.07)	11.24 (22.71)

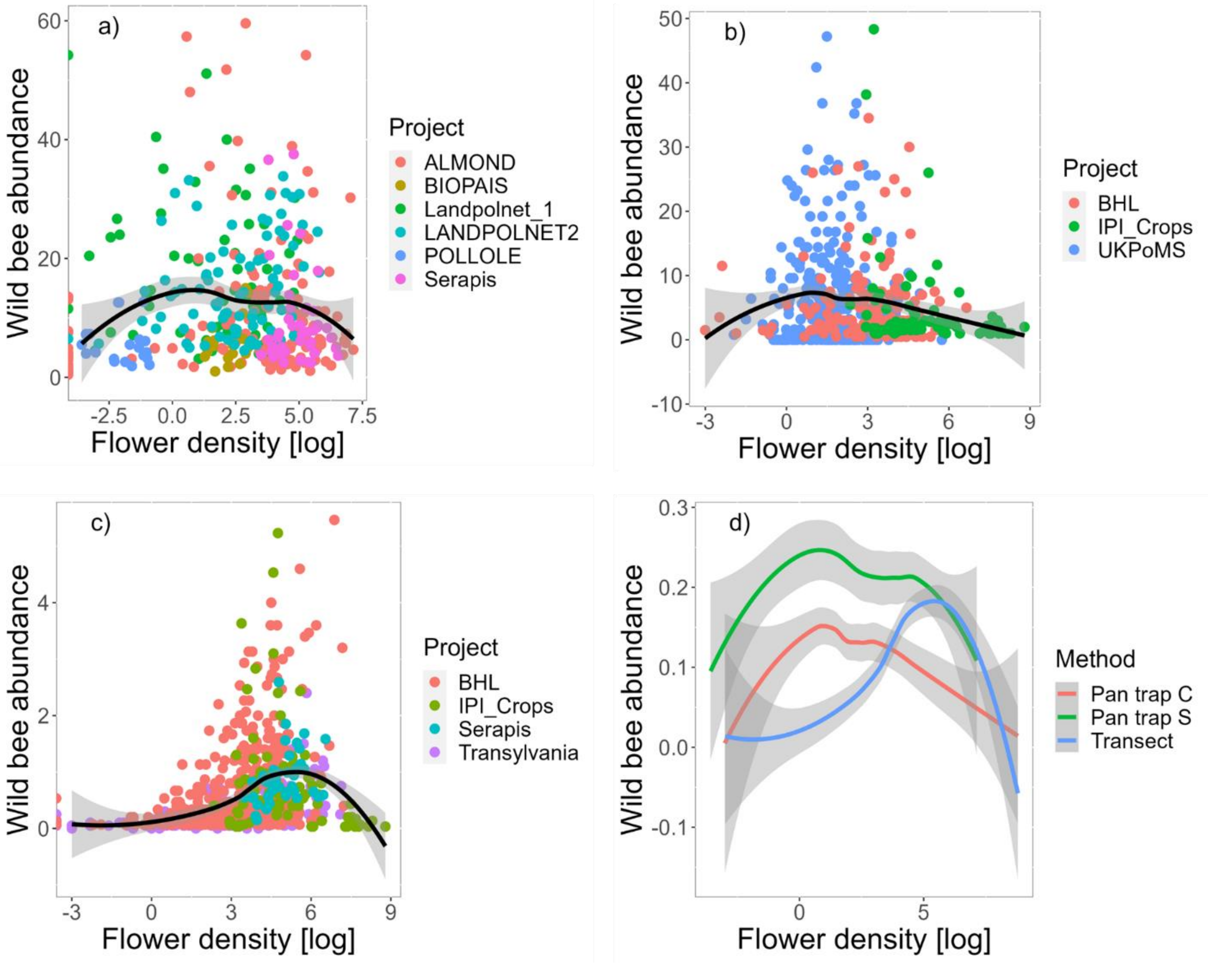
Study	Country	Method	N	Abundance mean (SD)	Flower mean (SD)
BHL[u]	Netherlands	Trans	351	0.76 (0.87)	72.71 (141.68)
IPI_Crops[u]	UK	Trans	84	0.77 (0.98)	647.41 (1138.88)
Serapis[u]	Greece	Trans	42	0.91 (0.48)	186.99 (154.39)
Transylvania[4]	Romania	Trans	182	0.31 (0.31)	100.91 (188.42)

Sources: [1]Hevia V, Bosch J, Azcárate FM, Fernández E, Rodrigo A, Barril-Graells H, González JA (2016) Bee diversity and abundance in a livestock drove road and its impact on pollination and seed set in adjacent sunflower fields. Agriculture Ecosystems & Environment 232: 336-344. [2]Torné-Noguera A, Rodrigo A, Arnan X, Osorio S, Barril-Graells H, da Rocha-Filho LC, Bosch J (2014) Determinants of Spatial Distribution in a Bee Community: Nesting Resources, Flower Resources, and Body Size. Plos One 9: e97255. [3]Hevia V, Carmona CP, Azcárate FM, Heredia R, González JA (2021) Role of floral strips and semi-natural habitats as enhancers of wild bee functional diversity in intensive agricultural landscapes. Agriculture, Ecosystems & Environment 319: 107544. [4]Kovács-Hostyánszki A, Földesi R, Mózes E, Szirák Á, Fischer J, Hanspach J, Báldi A (2016) Conservation of Pollinators in Traditional Agricultural Landscapes – New Challenges in Transylvania (Romania) Posed by EU Accession and Recommendations for Future Research. Plos One 11: e0151650. uUnpublished data.

2.2.1.3 Results

The loess smoothing was significant for all three cases (p-value pan traps central/west = 0.003; p-value pan traps south = 0.043; p-value transects < 0.001). The overlap in the ranges of covered gradients in flower density across the different studies was high for all three datasets, ensuring that the identified patterns are not driven by a single study (Figure 2.2. 2a, b, c). For both pan trap datasets and the transect dataset, wild bee abundance initially increased with increasing flower density, peaked at a certain point and decreased again thereafter. However, a considerable difference in the shape of the relationship and the flower densities at which the curves peaked was evident (Figure 2.2. 2d). The curves for both pan trap datasets were remarkably similar, except for an overall higher abundance level in southern Europe. For pan traps, wild bee abundance increased strongly with increasing flower density, deviating from an expected sigmoidal shape, and quickly reached its peak at a very low flower density of about 3 flower units per m^2. With further increasing flower density, abundance decreased, reached a plateau, and strongly decreased further on. In contrast to that, the shape of the response curve of wild bee abundance to increasing flower density, as assessed from transect data, followed the expected sigmoidal curve with an initial shallow relationship which got increasingly stronger at higher flower densities. Also in contrast to pan traps, wild bee abundance from transects reached a peak at a very high level of flower density of about 230 floral units per m^2. Beyond that, abundance decreased again.

Figure 2.2. 2. Relationship between wild bee abundance and flower density. Black line represents smoothing by a polynomial regression fitting (loess) for pan trap data from southern Europe (a), pan trap data from central/western Europe (b), transect data across Europe (c), and all three overlaid (d). Shaded grey areas are 95% confidence intervals. Different studies (Project) are colour-coded. Flower density is displayed at the logarithmic scale (peak of pan trap C and S is at about 3 flower units per m², peak of transect is at about 230 flower units per m²). Wild bee abundance in d) has been rescaled per Method to let the entire values range between 0 and 1 (by dividing the abundance values by the respective maximum value).

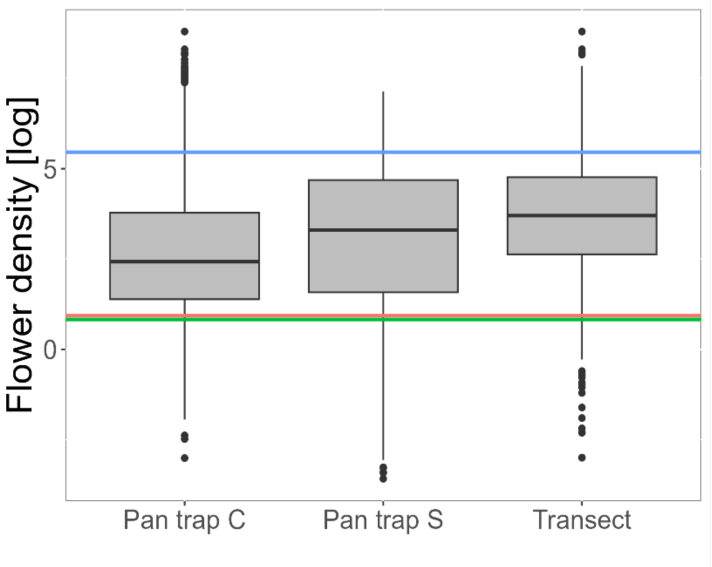


Source: Authors' elaboration based on the SPRING project.

2.2.1.4 Discussion and conclusions

Our results show a clear difference in the assessed relationship of wild bee abundance and flower density between monitoring methods based on pan traps or transect walks. Since this relationship for transect walks followed our expectation of a sigmoidal shape, transects seem to reliably reflect wild bee responses to changes in flower density across a large range. Transect walks thus highly qualify for the EU PoMS core scheme and other monitoring schemes. Only at very high flower densities, does this method come to its limits. However, such high densities (above 230 flower units per m², as might be found in mass flowering crops and some very florally rich semi-natural habitats such as chalk grasslands and Mediterranean scrub) represent a minority in our datasets (data points above the blue line in Figure 2.2. 3) and are usually not found in semi-natural areas but rather in mass flowering crops or fruit orchards. Whether the very flat relationship in cases of very low flower densities is caused by insufficient detection or reflects 'true' abundance conditions still needs to be identified or at least be considered in subsequent trend analysis (e.g. via including detection probabilities).

Figure 2.2. 3. Boxplot of flower density per method. Coloured horizontal lines indicate the wild bee abundance peaks in Figure 2.2. 2. Green: Pan trap S; orange: Pan trap C; blue: Transect.



Source: Authors' elaboration based on the SPRING project.

The consistency between the response curves based on pan traps from southern and central/western Europe indicates some general patterns. Response curves for pan traps deviated considerably from the expected 'true' pollinator abundance, but confirmed our expectations according to attraction and dilution effects. The consistently strong increase of wild bee abundance from very low to low flower densities and the deviation from an expected sigmoidal curve might indicate strong attraction of wild bees, for example from the surroundings or those just nesting at this location. This might lead to an actual overestimation of local pollinator abundances and consequently to an overly optimistic indication of success for limited management activities under such conditions. More worrying is the observed decline in wild bee abundance at flower densities higher than 3 flower units per m^2. This effect is likely caused by increased competition for attraction of pollinators by high flower densities. This means that abundance data based on pan traps are, if at all, only reliable for a minority of landscapes with low flower density (data points below the orange and green line in Figure 2.2. 3), while restoration activities that actually increase flower densities could be wrongly interpreted as leading to a decrease of pollinator abundance.

Based on the evident discrepancies between transect and pan trap methods, indicating strong effects of pollinator attraction and dilution of abundance estimates from pan traps, we strongly advocate that the EU PoMS core scheme and other pollinator monitoring schemes should focus on transect walks rather than using pan traps to ensure a reliable detection of pollinator trends.

2.2.1.5 Advantages and disadvantages of pan traps

In addition to the impacts of floral resources on pan traps, there are other important considerations. All pollinator surveying methods have associated advantages and limitations and these were reviewed in depth in the STING1 report (Potts et al., 2021). Similarly, there are a number of advantages and benefits of using pan traps and these are briefly outlined below, however the limitations and disadvantages overall are considered to outweigh these.

Potential benefits of using pan traps include:

- **Capture more bee species**. Based on the pilot work of SPRING, pan traps often detect more bee species than transects, including some small fast-flying ones, which may be under-sampled in transects (based on general consensus from bee experts in SPRING and STING, but with clear exceptions, especially in Mediterranean areas).
- **Easy to deploy**. Pan traps can be relatively easy to deploy by volunteers and allow multiple locations to be sampled in parallel.
- **Less affected by volunteer skills**. In some aspects, pan traps can be more readily standardised as they are a passive method and therefore volunteer skill level may have less influence on the samples captured.
- **Specimens kept.** All specimens are retained, which provides samples and (also bycatch) for longer-term additional identification and other purposes.
- **Additional information**. They can potentially provide additional information about species richness and occupancy, than transects alone can (see chapter 6.12 Potts et al. 2021, plus sections 3.1 and 5.1). The EU PoMS specification emphasises a diversity measure, which pan traps are well suited to provide (but see below discussion of abundance measures).

However, there are a number of disadvantages and limitations of using pan traps including:

- **Context dependent**. As is described in the analysis above this is a very severe limitation and bias in the samples collected and the interpretation of pollinator data.
- **Not suitable for abundance**. As a method depending on species activity levels, pan traps can only be used for occupancy and diversity, and not directly for abundance.
- **Costly**. It takes a large resource to deploy pan traps (both in terms of time and cost) compared to standardised transects. Indicative estimates are that more than half of total fieldwork and lab costs were allocated to pan traps for the SPRING pilot, and identification takes substantial time (at least as much as for transects), and for pan traps additional processing and preparation of wet specimen is needed before identification.
- **Taxonomic bias**. Pan traps are likely to have taxonomic/size biases, and SPRING and STING experts indicate there may be fewer bumble bees and large solitary bees, e.g. *Colletes* spp., collected by pans. Pans are also widely recognised to be poor for sampling butterflies and hoverflies, especially in southern Europe (though this may vary between countries).
- **Depletion of local fauna**. There are potential risks of long-term depletion of fauna if a site is intensively sampled with pan traps over a season and across years.
- **Kills specimens.** Volunteers are increasingly reluctant to use unselective lethal survey methods, which is a potential barrier to recruitment and retention of volunteers. This was highlighted in discussions with some of the SPRING field teams.

Given the critical issue of floral context dependence for pan traps combined with the other disadvantages, the conclusion of the STING2 expert group is to focus on only using transects for the core scheme. However, pan traps offer several other opportunities in terms of pollinator monitoring (see section 5.1 for options).

2.3 Detecting change

A robust experimental design is crucial to ensure the collected data are sufficient to reduce bias and to achieve enough statistical power to detect changes when those occur. Achieving an unbiased sampling design requires a randomized stratification of the sampling points, to ensure all biogeographical regions and target habitat types are representatively sampled within a Member State.

Further questions concern the minimal adequate sampling effort, in particular: (i) how many sampling points are needed, and (ii) how frequently they should be sampled. Answering these questions is the focus of the following paragraphs.

The statistical power of the sampling regime depends on:

1. The expected rate of change in the indicator per year (translated into a % rate per a 6-year period).
2. The variability of the data (how variable are natural pollinator populations across space and time).
3. The sample size (the number of sites, and the number of sampling rounds per site).

A power analysis can be done using data collected in similar conditions, so the intrinsic variability can be identified from the data, and the sampling effort needed for a given magnitude of change in the indicator can be estimated.

2.3.1 STING1 approach

Unfortunately, pilot data to run a classic power analysis did not exist at the time of STING1 (2019-2021). During STING1, using a compilation of available data to calculate natural variability across space and time, Potts et al. (2021) estimated that a minimum of 2,000-3,000 sites is needed across Europe, ranging from 10 to 238 by Member State depending on their area to detect 10 percent change over 10 years (i.e. a 1% change per year) in the indicator (abundance and species richness) for major groups (wild bees, hoverflies and butterflies). This calculation was based on 9 available datasets aiming to cover the range of bioclimatic regions of Europe, and that comprised more than 10 separate sampling sites, sampled for at least 2 years and more than once within each year. The SPRING project data was not available at that time.

2.3.2 STING2 approach

The STING1 estimates have certain limitations including: (i) strong reliance on untested assumptions, (ii) restricted spatial coverage of the available datasets impeding the consideration of different Member State contexts, and (iii) not being tested with modelling methods that maximize power. STING2 solves these limitations by: (i) developing their own data simulations, (ii) leveraging new data collected during SPRING project for each Member State, and (iii) using multispecies models with a high power.

A robust approach was employed based on building simulated data with similar properties as the ones expected from the EU PoMS monitoring. These properties are informed from the SPRING project data and recent studies on species distributions at the EU level. In particular, the SPRING project provides real world pilot data from >200 sites, collected in 2022-2023 using the initial Minimum Viable Scheme (MVS) protocols which were proposed by Potts et al. (2021), and included a combination of pan traps and transect walks. The revised proposal for the EU PoMS core scheme, uses reinforced transects without pan traps for wild bees, hoverflies and butterflies (see section 2.2).

2.3.3 How to interpret outputs

The power to detect a trend depends on the experimental design, on the analytical approach used, as well as on the nature of the data (expected effect sizes, sample size, and variability). In the absence of robust real world pilot data, informed data simulations can help us estimate how much sampling effort is required to have enough statistical power to detect a true trend given an experimental design and an analytical approach.

In addition to statistical modelling, the final decision on any proposed design should be informed by multiple sources of evidence including ecological first principles (i.e. processes underlying ecological phenomena such as spatial and temporal occurrence of species or local population dynamics), and expert knowledge, in order to overcome potential technical limitations. In the following section we describe how data simulations were built and tested, including key assumptions, what we learned from this process and how can we integrate the outputs of this analysis to determine recommended sampling effort for EU PoMS reinforced transects.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2.4 Design options for a bee, hoverfly and butterfly module (reinforced transects)

2.4.1 Summary

Building on the SPRING project protocols, we propose reinforced transect comprising a fixed 500m transect walked twice for butterflies and twice for bees and hoverflies together, taking a fixed amount of observation time. We use expert knowledge, practical experience from the SPRING pilots, data simulations and state of the art multispecies statistical models, to recommend a set of options for EU PoMS data that will ensure a high statistical power and that the data collected can directly flow into biodiversity indicators. We show that the proposed experimental design and statistical models have a high power for detecting a statistical trend, but due to the uncertainty introduced by the observation process, the power to precisely identify the strength of the trend, in terms of rates of change, is low. The analysis reveals that Member States with lower pollinator richness are not easier to model, indicating a similar number of sites may also be needed in these situations. However, we argue that our knowledge on the sampling effort required to properly monitor pollinators will increase as more data from the SPRING project is released (at the time of this report some specimens were still being identified), and data becomes available from the first years of the EU PoMS implementation, indicating that revisiting this approach in the future is important. We make a series of recommendations for next steps.

2.4.2 Background and context

The EU PoMS will generate valuable data on the status of pollinating insects across the European Union. The purpose of this section is to define the appropriate level of replication for detecting true pollinator species trends.

This report is built upon STING1 efforts and the SPRING project. However, assessing the power of an experimental design not yet deployed is a challenging task due to the many uncertainties on the nature of the final data collected. Hence, this exercise can provide an important guide on the minimum requirements the design options need, but cannot currently provide specific numbers. The next section details the methodology used and the main recommendations emerging from them.

2.4.3 Overall approach

We tested the power of an experimental design based on monitoring multiple sites per Member State, visited 6 to 8 times a year during the main pollinator activity season (i.e. the period where most taxa are active in each environmental conditions). Concentrating the sampling effort (number of rounds) on the main activity season for each Member State maximises the number of captures and is expected to increases the power to detect a general multispecies trend. Note that the focus of this sampling design is not assessing rare species (see section 2.8), but the general patterns in pollinator trends, which are mainly driven by relatively abundant species. In each visit, a reinforced transect, identifying all pollinators to species level (see section 2.2), is needed to detect enough specimens per site and visit to model species abundances with confidence.

We tested power using a statistical model (Generalized Linear Mixed Models: GLMM) based on estimating changes in abundance along time per species. Hence, only species detected in several sites and over multiple years can be modelled, but the obtained results are robust and generalizable. This modelling approach allows the calculation of different indexes, including an aggregated indicator of changes in abundance across species, as well as other metrics such as species richness and occupancy (see section 3.1 on General Pollinator Indicator options).

Finally, to evaluate the power of this modelling approach under this experimental design, we simulated the kind of data we expect to collect, informed by SPRING pilot study data. These simulations are simplified scenarios that allow us to: (i) test the performance of statistical models under known parameters representative of different Member States, and (ii) assess the power to detect true trends under imperfect detection. This second point is important because even the best experimental designs will not detect all species or specimens present at a site, and hence it is necessary to model this source of noise in our dataset. We ran simulations that cover the range of parameters expected across Member States and for different effect sizes (i.e. trends, or rates of change per year).

2.4.3.1 Basic design of reinforced transects

Following the SPRING project protocols and the lessons learned from modelling the statistical power of the proposed indicators, the proposed reinforced transect comprises a fixed 500m transect that is first walked to record butterflies, and then the same 500m transect is then walked to record wild bees plus hoverflies. This process is then repeated with a second butterfly, and a second bee plus hoverflies walk. Overall, the fixed 500m transect is walked on four occasions. The specific recording methodology is:

- Butterflies: for the 500m transect, all butterfly adults present are counted in an imaginary box of 2.5m to each side, 5m high and 5m ahead while walking at a constant, steady pace (a fixed amount of observation time to walk 500m). Repeated twice.
- Wild bees plus hoverflies: for the same 500m transect, all adult bees and hoverflies present are counted in an imaginary box of 1m to each side, 2m high and 2m ahead while walking at a constant, steady pace (a fixed amount of observation time to walk 500m). Repeated twice.

The four individual transects use a fixed amount of observation time each (for a total of 4 times the fixed amount) of effective sampling time (i.e. discounting insect collection handling time) and are walked in the same direction. Pollinators are recorded whether flower visiting or free flying.

The decision to combine wild bees and hoverflies into a single standardised transect was based upon inputs from SPRING and STING 2 experts; however additional insights from this group and from the wider expert community will be elicited during the STING+ process to evaluate whether the most efficient design would be to combine or separate these two groups. If they were to be separated, this would entail an additional two transects to be walked per site visit (up from a total of 4 to 6), which would have implications for human and financial resources required. These trade-offs will be analysed in STING+.

We assume sites follow a stratified random design, ensuring all habitats are well represented across the Member State geography. We assume all species are identified to the species level, either in the field or caught and retained for later identification in the lab.

Along the same 500m fixed transect flower abundance will also be recorded. While an estimate of flower richness and cover is not needed to estimate trends in pollinators, it will be highly informative in understanding the factors driving pollinator trends. Options for co-locating EU PoMS sites with those from existing biodiversity monitoring schemes, which record flower communities, are explored in section 2.10.

The final design of the reinforced transect will be determined under the next phase of STING (STING+).

2.4.4 Models

We use a Bayesian implementation of a Generalized Linear Mixed Models (GLMM). This modelling approach allows for testing if species abundances change over time, while accounting for species identity, and site location. Note that only species detected in at least three sites are included in this version, but this can be fine-tuned when real data are analysed (e.g. through STING+). The model is written in a general form but can be tailored for each Member State, for example by selecting which species to model and removing exotic or managed species.

2.4.5 Scenario building

Given the contrasting differences within the EU, we ran simulations that cover the parameter space found across Member States. Our approach was based on: (i) realistic simulations of local pollinator communities based on Member State representative parameters (see below), (ii) simulating the pollinator sampling process in a way which matches real-world observations based on the results of the SPRING project, and (iii) applying those simulations to different scenarios of monitoring effort and strength of trends in population change to assess the respective power under the different scenarios and to optimise the sampling design.

In particular, we simulate data based in the following workflow. First, we explore, for each Member State, sets of realistic species pools, and mean species occupancy (i.e. how widespread the species are). Second, we define a number of sites and link to each site a list of species found, based on the species occupancy rates and expected richness levels per site. Third, we assign to each species an abundance value (on the well-tested assumption that we observe in nature many dominant species and a few low abundance ones), a species' phenology and a probability of detecting it while sampling. Fourth, based on these parameters, we assign a true abundance per species and site for each sampling round. Finally, we mimic the sampling process by subsampling from this true abundance and obtaining observed abundances that include the sampling uncertainty. This is repeated by each site and year, assigning a declining trend with time. Overall, we explore a set of fixed parameters as informed by SPRING, and vary the number of sites, sampling rounds and declining trend in different simulations.

2.4.5.1 Fixed parameters

To build the simulations we used the following parameters per Member State: species pool representative, mean occupancy of pollinators, mean local species richness and its standard deviation, species abundance, mean peak and range in the phenology of pollinator species and their standard deviations, optimal start and end of sampling, mean variation in pollinator population size across years, and the fraction of individuals (and species) observed during a visit compared to the simulated overall number of individuals (and species) within a site (Table 2.4. 1).

- Species pools and occupancy: The number of expected species per Member State (species pool) was taken from Reverté et al. (2023) for wild bees and hoverflies; and from van Swaay et al. (2010) for butterflies. Occupancy was expressed as proportion of sites in which a pollinator species occurred in SPRING pan traps per Member State. Although pan traps might be less reliable in terms of estimating true abundances section 2.2), we assume that a potential effect on occupancy (in terms of presence/absence across all sampling rounds) is negligible.

- Expected richness per sampled site: Estimates of overall species richness per sampled sites were based on datasets with a comprehensive sampling campaign over several years from Germany (Frenzel et al., 2016) and Spain (Domínguez-Garcia et al., 2024) and estimated with extrapolated species accumulation curves. The fraction of local species richness compared to the number of species in the Member State-level pool was similar for Spain and Germany (5% and 3%, respectively) and the average (4% of national checklists) has been used to calculate average local species richness per sampled site for each Member State based on the respective species pools, i.e. each site represents 4% of the species richness of the country. The same approach was used for the standard deviation of local species richness (Spain: 0.4, Germany: 0.4, average: 0.4). Local abundances per species and Member State have been modelled based on well-known ecological principles assuming "Species Abundance Distributions" follow a log-normal distribution.
- Phenology: The peak and standard deviation of phenology (i.e. abundance dynamics within a year) and the optimal start and end month for sampling were obtained from the same datasets from Germany and Spain as used for calculating local species richness. In addition, a dataset with high temporal resolution based on pollinator camera traps (Bjerge et al., 2023) has been used for Denmark. To cover more extreme ends across Europe, estimates of peak phenology and start and end month have been made for Malta and Finland, informed by vegetation period data products of the Copernicus Land Monitoring Service. The mean range in phenology and its standard deviation as well as inter-annual variation in population size was also extracted from the above-mentioned datasets for Germany and Spain.
- Observation process uncertainty: To harmonise the simulated local number of occurring species and individuals with real-world conditions and to counterbalance potential uncertainties in these simulations, we calculated the parameter 'fraction observed' as the proportion of individuals observed in the Member State based on SPRING data relative to the simulated number per site and Member State. This parameter ranged between 1% and 7% (Table 2.4. 1) and was subsequently used for the simulation of the sampling process.

Note that data are not available for all Member States, but this data are sufficient to create representative scenarios. Occupancy values were available from SPRING for 19 Member States (Table 2.4. 1). The values for the remaining Member States have been interpolated based on statistical modelling ([Generalised] Linear Regression Models) relating occupancy to mean annual temperature, annual precipitation sum, human population density, and land area per Member State, considering quadratic terms and an interaction term for temperature and precipitation. The model has been simplified based on minimising AICc resulting in population density and land area as most important variables (Pseudo $R^2 = 0.59$). Similarly, mean peak phenology, standard deviation of mean phenology, optimal start and end month have been interpolated based on statistical models with high measures of goodness of fit (Pseudo $R^2 > 0.91$). The results have been checked for consistency and plausibility with vegetation period data products of the Copernicus Land Monitoring Service. Since the values for mean phenology range and its standard deviation, as well as the inter-annual variation in population size, were very similar for the German and Spanish datasets (phenology range: 40, 48; phenology standard deviation: 41, 41; inter-annual population size variation: 0.58, 0.52), mean values across both countries were assumed to apply to all Member States.

With these settings, representative of all EU Member States, we simulated the sampling process for each of these scenarios based on a six-years sampling period, which is deemed as the minimum number of years over which we can assess population changes.

Variable parameters: population change, number of sites, number of visits and number of transects

- Overall rates of population change: Across all the insect decline studies reviewed, the decline per year ranges between 0.3 and 5%, and is centred around a 1% per year. Hence, we tested potential effect sizes (i.e. declines per year) of 0.3%, 1% and 2% (larger declines 5% and 10% were considered but not shown here).
- Number of transects walked: Preliminary analysis indicated that a reinforced transect (i.e. two 500m transects) yield higher specimen counts per site needed to feed the statistical models; hence, only the reinforced transect option was further tested.
- Number of visits: 8 and 6.

This approach allows us to identify which factors influence statistical power across a set of realistic scenarios, and allow making robust general recommendations. Overall, we ran 12,000 simulations across 504 different scenarios.

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Table 2.4. 1. Member State-specific parameters for simulating realistic pollinator populations at EU PoMS sites. Pool, aggregated number of wild bee, hoverfly, and butterfly species per Member State; Occupancy, mean proportion of sites occupied by a species; Richness, mean local species richness per site (4% of the Member State pool); SD, standard deviation; Phenology, mean peak flight phenology across all species within a site; Start, End, optimal start and end month for sampling; Observed, fraction of observed individuals (from SPRING monitoring data) relative to the simulated overall number of individuals at a site and per sampling round. Cells in green indicate interpolated values based on (Generalised) Linear Regression Models. Values for mean phenology range, its standard deviation, and the inter-annual variation in population size have been set constant across all Member State (see text).

Member State	ISO2	Pool	Occupancy	Richness	Richness (SD)	Phenology	Phenology (SD)	Start	End	Observed
Austria	AT	1,342	0.47	54	21	220	19	5	9	0.01
Belgium	BE	819	0.33	33	13	160	25	4	8	0.02
Bulgaria	BG	1,427	0.29	57	22	134	27	3	7	0.01
Croatia	HR	1,148	0.33	46	18	126	27	3	7	0.03
Cyprus	CY	506	0.71	20	8	61	32	1	6	0.07
Czech Republic	CZ	1,101	0.32	44	17	204	21	4	8	0.02
Denmark	DK	614	0.37	25	10	217	6	5	8	0.02
Estonia	EE	634	0.59	25	10	238	6	6	9	0.01
Finland	FI	693	0.57	28	11	240	7	6	9	0.02
France	FR	1,745	0.13	70	27	130	27	3	7	0.02

Member State	ISO2	Pool	Occupancy	Richness	Richness (SD)	Phenology	Phenology (SD)	Start	End	Observed
Germany	DE	1,214	0.16	49	19	179	35	4	8	0.02
Greece	EL	1,840	0.28	74	29	67	32	2	6	0.01
Hungary	HU	1,230	0.31	49	19	155	26	4	8	0.01
Ireland	IE	314	0.4	13	5	167	25	4	8	0.02
Italy	IT	1,827	0.16	73	28	81	30	3	6	0.01
Latvia	LV	692	0.52	28	11	227	17	5	9	0.02
Lithuania	LT	714	0.47	29	11	222	18	5	9	0.02
Luxembourg	LU	626	0.6	25	10	182	24	4	8	0.02
Malta	MT	176	0.4	7	3	60	31	1	5	0.04
Netherlands	NL	750	0.33	30	12	168	25	4	8	0.02
Poland	PL	1,030	0.21	41	16	199	22	4	8	0.02
Portugal	PT	1,093	0.26	44	17	68	31	2	7	0.01
Romania	RO	1,362	0.37	54	21	179	24	4	8	0.02
Slovakia	SK	1,232	0.39	49	19	215	20	5	9	0.03

Member State	ISO2	Pool	Occupancy	Richness	Richness (SD)	Phenology	Phenology (SD)	Start	End	Observed
Slovenia	SI	1,105	0.64	44	17	177	24	4	8	0.01
Spain	ES	1,741	0.15	70	27	87	31	2	7	0.01
Sweden	SE	783	0.09	31	12	239	5	6	9	0.01

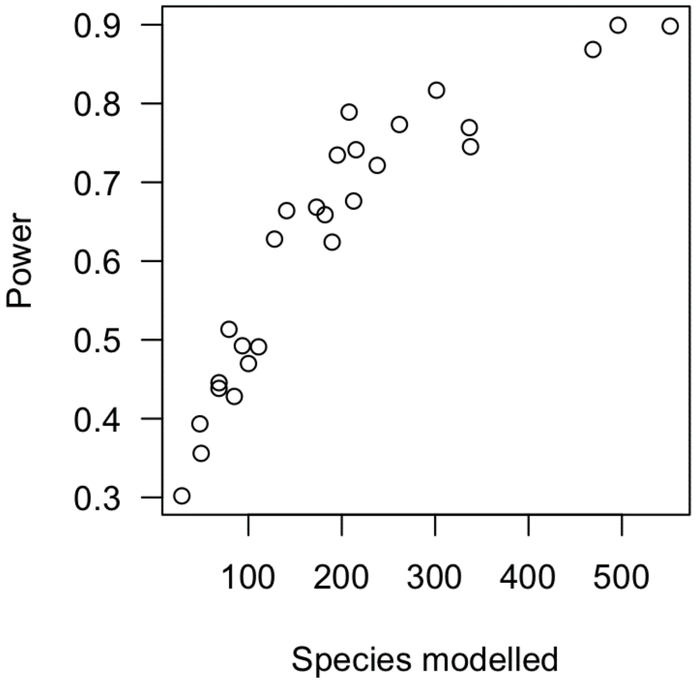
Source: Authors' elaboration based on SPRING monitoring data.

2.4.6 General findings

Overall, we have developed robust models to ensure a high power to detect a true trend of 1% decline per year (6% over a 6-year period). Below, we detail the main findings:

1. **To ensure that the specimens observed per round are enough to be modelled, we recommend using the reinforced transects** (i.e. two 500m transects) for each round. While modelling changes on species abundance ranging from 0-3 observations (typical from a single 500m transect) per round is really challenging, it is much easier modelling abundance ranging from 2-6 (achievable with two transects).
2. **We recommend using 8 rounds**, as reducing from 8 to 6 rounds requires on average 20% more sites, and the costs associated with increasing sites are larger than increasing rounds. Rounds should be concentrated in the peak season (i.e. the timing of maximum activity, which should be tailored to each taxon and environment) to maximize catches (see below).
3. **We recommend the relevant decline trend to be evaluated to be fixed at 1% per year**. Across all simulations, detecting higher declines is easy, as power is high, but realistically declines in aggregated species abundances should be expected around the 1% decline per year range according to literature. For example, we show that we have enough power to detect a 3% decline per year (18% for a 6-year period) at national level for >90% of simulations run regardless of Member State characteristics. This number is similar for a 2% decline (12% for a 6-year period; >80% of simulations), but drops drastically for a 1% decline (6% for a 6-year period). Exploring what factors define power at 1% is the focus of the following points.
4. **Simulations show that the most important variable to increase power is the number of species which can be modelled** (Figure 2.4. 1). Hence, ensuring that more than 200 species, occurring at least in 3 sites, are observed is important. This is easy for large countries with large species pools, high richness per site, and high species mean occupancy. However, it is challenging for species poor countries, or when occupancy is very low (and hence species show a large turnover across sites).
5. **Sampling design should maximize the number of species that can be modelled.** Options for this include, targeting good pollinator habitats (that is, not monitoring transects with no flowers) within natural and agricultural areas, and avoiding extreme habitats (e.g. dense urban, or known pollinator poor habitats). Focusing on the peak phenology when most pollinators are active is also important to maximize the number of species consistently detected. These options will be fully explored as part of the STING+ process of developing the final set of standardised protocols.

Figure 2.4. 1. Power as a function of species modelled.



Source: Authors' elaboration.

6. **Statistical models based on estimating the aggregated mean change in species abundances has a very high pure statistical power**. This is because we can leverage the information of different species. Hence, most of the uncertainty comes from the sampling process variability (see point 7 below). Note that our scenarios assume a consistent trend for all species and over all sites. Hence, more complex scenarios with a few winners and many looser species or with trends depending on the habitat monitored might be more difficult to detect, but the current statistical models can also be tailored to deal with these situations once known.
7. Overall, when we also account for process uncertainty, due to species imperfect detectability during sampling (i.e. different realizations of the simulation), power to detect a 1% decline per year reaches acceptable levels (~80% confidence) for Member States where more than 300 species can be modelled. Models can be tailored to maximize its power once real data are analysed, for example maximizing the number of species to be modelled. Defining which Member States can realistically observe 300 modellable species is unknown before starting the monitoring, but we envision moderate sized Member States, with a large pool of species and covering a single biogeographical region, will fit into that category. For larger countries covering several biogeographic regions (and hence with larger turnover of species across sites), or countries with small species pools, a larger number of sites will be needed.

The gist is that modelling the observed trend (pure statistical trend mentioned in point 6) is easier than modelling the true trend (trying to correct for unknowns in the sampling process). With long time series, the observed trend is often reliable, but with a few years of data, is especially important to account for the sampling process.

Note that we show that we can attain similar power using reinforced transects to previously reported values in STING1, which also included pan traps. Many strategies can be followed to maximize power. Combining methods (pan traps plus transects) is one way, but increasing the number of rounds during peak activity season and leveraging the information at the species level proved to be more cost-efficient. However, the main findings presented above will be systematically reviewed and refined, as part of the STING+ process.

2.4.7 Assumptions and next steps

Given the uncertainties we face, we recommend using these models with additional species-level data from SPRING (once available) and any other ongoing EU PoMS pilot work. At the time of preparing this report, SPRING data are still being processed. When processing will be completed, it will contain data on ~200 sites over the EU, with species-level identification mainly from pan traps[6]. Hence, the final power is complex to evaluate a priori. As stated above, when real data are provided, models can be optimized with the lessons learned here. Hence we are confident that the best decision is to some degree subjective, although informed by the data and models used.

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[6] https://www.ufz.de/export/data/498/268546_SPRING%20MVS%20Pilot%20Survey%20guidance_incl._recodring-forms_April%202022.pdf

2.5 Estimating the costs of EU PoMS options

2.5.1 Summary

We used information from participants in the SPRING project on pollinator monitoring to determine the likely costs of implementing the core reinforced transects in proposed pollinator monitoring scenarios, accounting for variation in wages, pollinator diversity, identification time and expenses between Member States. The costs of implementing the core reinforced transect monitoring scheme will be heavily influenced by the number of sites, the staff model and the number of individual specimens sampled and the complexity of identifying specimens.

2.5.2 Background and context

Biodiversity monitoring is often severely limited by available budgets and many monitoring schemes operate at an insufficient budget to achieve all their objectives. Understanding the real costs of pollinator monitoring is key to ensuring that any scheme is sufficiently resourced and facilitates capacity building. Previous assessments of the costs of pollinator monitoring have highlighted the significant role of species identification time, site numbers and relative wages as key factors driving costs (Breeze et al., 2021; Potts et al., 2021). However, the previous assessment of the EU PoMS costs (Potts et al., 2021) was constrained by limited available information on species catches, identification time in each Member State, leading to concerns that the time required for identification as too low in some Member States with large diverse pollinator pools. Furthermore, STING1 did not include aspects of the data workflow that are important to modelling and reporting the outcomes. Using data collected from the trial pollinator monitoring programme in the SPRING project and additional input from experts in the STING expert group, we have re-evaluated these costs to better reflect the variations between Member States and account for significant inflation since 2020.

2.5.3 Approach and methodology

This section outlines the approach to estimating the costs of EU PoMS options over a 10-year time frame, using the real **material** and **staff** costs collected from a survey of participants in the SPRING project. This approach is suitable for any site network structure; however, we do not present any specific sample network recommendations or associated costs in this section.

Costs are divided into two phases, **establishment costs,** which are incurred only infrequently such as long-lasting materials (e.g. nets) or irregular activities (e.g. site selection) and **annual costs**, which are incurred every year. Where it was necessary to convert currencies into €, we used average annual spot exchange rates from the year 2022 (European Central Bank, 2023). For the purposes of these cost estimations, we assume that all data collection and management is undertaken by professionals. We recognise that the ambition of EU PoMS is to grow the Citizen Science base and increase the proportion of volunteer recorders, which are expected to significantly reduce the costs of data collection, but should be accompanied with an appropriate increase of coordination (Breeze et al., 2023).

2.5.3.1 Material costs

A summary of material costs is given in Table 2.5. 1. These costs are averaged across all Member States, as prices for materials did not vary by much, although VAT is applied to each country individually. However, it should be noted that there are difficulties in sending some materials to some countries due to local customs regulations. When calculating costs we assume one team of two collectors is expected to cover 15 sites per year (based on feedback from the SPRING pilot and STING experts) so items only need to be purchased for every 15 (or part thereof) sites. Where an item's lifespan is expected to be less than 10 years, we included the cost multiple times to account for a replacement. Costs were estimated with VAT included.

Table 2.5. 1. Itemised breakdown for material costs (excluding VAT).

Item	Price/unit	Amount required	Stage	Lifespan	Costs
Insect net	€41.62 each	1 per collector	Establishment	5 years	€83.24/collector
100m Tape measure	€23.59 each	1 per collector	Establishment	10 years	€23.59/collector
Sampling tubes	€0.37 each	1 per specimen	Annual	1 use	€0.37/specimen
Ethanol	€4.51/l	20ml/specimen	Annual	1 use	€0.07/specimen

Source: Authors' elaboration.

Other material costs include **fuel** to each site. As site dispersal is not static, we used an average of 180km (round trip) in all Member States. This was chosen to allow for sufficient spatial distribution of sites in a professional scheme, with some sites requiring much greater travel distances than others. The fuel costs were drawn from the SPRING project survey, where respondents indicated their reimbursement rate. As such, these costs do not necessarily reflect the actual costs of fuel in many countries as some organizations reimburse only part of the rate, while in some Member States, reimbursement included vehicle depreciation premiums and was higher than the price of fuel.

Finally, material costs also include postage of samples from collectors to identifiers. Here, we used local postage rates of a 5kg box via tracked/recorded mail, sent within each country, using an average of process from the EU's Price comparison tool in January 2024 (European Commission, 2024). We assume that postage is required at establishment, to send items to collectors, and twice per sampling round to send specimens for identification. One collector is assumed not to send any items, reflecting the institution that will lead the scheme and identify specimens locally.

2.5.3.2 Staff costs

Staff costs used salary information provided in the survey of SPRING experts who undertook the pilot, for four groups of staff:

1. **Administrators**: An experienced administrator who can handle the coordination of collectors, data management, communications and other non-scientific work.
2. **Field Technicians**: Someone below postdoctoral level who would be expected to undertake the EU PoMS monitoring protocol independently.
3. **Specialists**: Someone who could be expected to identify specimens to species level and train staff e.g. a consultant, experienced ecologist, or postdoctoral researcher.

4. **Senior Researcher (Snr. Res)**: a lecturer, reader, senior research fellow or associate professor who would be expected to lead the scientific coordination.

2.5.3.3 Data collection

Following the recommendations of the experts, we base data collection costs on six 0.5FTE positions for every 15 sites in a Member State, with experts working in teams of two (see section 2.6.4). This was appropriate to the time to undertake each step of the protocol, using information from the SPRING project (Table 2.5. 2). These time estimates are based on actual numbers provided by national experts conducting fieldwork as part of the SPRING project. We recognise that there will be considerable variation around these average values reflecting the differences in the abundance and diversity of pollinators in different Member States, and in habitats with different levels of floral diversity and cover. As part of the STING+ project further analysis of time budgets and wider expert consultation will be undertaken to ensure that these values are field realistic and tailored to different Member States.

Table 2.5. 2. Itemised breakdown of staff time for executing the protocol. Travel time assumes a 180km round trip per site, at 60km/hr.

Activity	Time required	Regularity	Stage	Staff type
Site selection	2.0hrs	Once per site	Establishment	Senior Researcher
Transect description	1.0hr	Once per round	Annual	Specialist
Transect walk	1.3hrs	Once per round	Annual	Specialist
Sorting specimens	0.46hrs	Once per round	Annual	Specialist
Travel time	3.0hrs	Once per round	Annual	Specialist

Source: Authors' elaboration based on the SPRING project.

2.5.3.4 Identification costs

A major staff cost is the time taken to identify specimens (Table 2.5. 3). The number of insects that will need to be caught for identification and the time taken to identify specimens will increase with: (i) the overall diversity of species in the country, and (ii) fewer taxonomic resources available for identifiers. In the previous cost estimation (Potts et al., 2021), UK data on specimen catches and identification time was used as a proxy, but this is not accurate as the UK has particularly strong taxonomic resources and fewer cryptic species relative to most Member States. By contrast, Greece, the country with some of the highest identification time requirements, has a very high diversity of pollinators that span a wide range of biomes and are often very difficult to distinguish even by experienced taxonomists, and have limited taxonomic resources.

Here, we improve on this by using information on the species observations from the SPRING project, assuming that 10% of bees (excluding *Apis mellifera*) and 5% of hoverflies are caught for identification (see section 2.6.3). In southern European countries (Spain, Portugal, Italy, Malta, Greece, Croatia; following the United Nations Geoscheme for Europe, plus Cyprus; however, parts of some other countries, specifically Romania, France and Bulgaria, will a have higher pollinator diversity and may need more expert time) this was increased to 25% of bees and 10% of hoverflies.

We assume that experts are paid by the hour for this, and that the same experts involved in data collection would undertake the identification. The average time for a taxonomic expert to identify a specimen was collected from respondents to the SPRING Survey. It should be emphasised that these are average times across all captured specimens. Some species will be identified very quickly by an expert (e.g. a matter of seconds), while small, cryptic and rare species can take over a week to properly cross-reference (e.g. entailing visiting reference collections). As we did not receive expert responses from all countries, we use suitable near neighbour countries as proxies.

2.5.3.5 Training costs

All staff would receive training at the start of the monitoring effort from local experts. As the specific details of this will vary, we assume, based on the staff intake at the Pollinator Academy (see section 2.6.3), that staff are given a minimum 2 days of training with a senior researcher. As the staff participating in the SPRING project were largely experienced researchers already, on the advice of STING experts, we added a further **Initial phase** cost where the number of specimens caught was higher during the first three years of any scheme, as less experienced staff have to catch more specimens they are less familiar with. For this initial phase, included as an establishment cost, we assume that 25% of bees and 10% of hoverflies are caught on transects, increasing to 50% of bees and 20% hoverflies in southern Europe and add the additional identification time to the overall costs.

Table 2.5. 3. Species catch data and identification time by country. Asterisks (*) indicate that another Member State was used as proxy. These numbers were provided by national fieldwork experts participating in the SPRING project. There will be considerable variation around these values depending on various factors, such as the floral diversity and cover of a site. These figures will be further refined based on further analysis of SPRING data and wider consultation of experts as part of the STING+ project.

Member State	Bees		Hoverflies	
	Number caught per transect per round	Average time to identify one insect (hrs)	Number caught per transect per round	Average time to identify one insect (hrs)
AT	1.12	0.18*	0.36	0.05*
BE	1.03	0.15*	0.01	0.03*
BG	0.94	0.32*	0.48	0.07*
CY	10.47	0.24*	0.30	0.13*
CZ	1.23	0.32*	0.48	0.07*
DE	1.06	0.18	0.48	0.05
DK	1.16	0.18*	0.48	0.05*
ES	2.68	0.24	0.30	0.13
EE	0.36	0.18*	0.11	0.05*
FI	0.38	0.18*	0.26	0.05*
FR	1.28	0.24*	0.38	0.13*
EL	5.23	0.83	0.34	0.50
HR	5.69	0.32*	1.04	0.07*
HU	1.96	0.11	0.33	0.07*
IE	1.22	0.18	0.35	0.06

Member State	Bees		Hoverflies	
	Number caught per transect per round	Average time to identify one insect (hrs)	Number caught per transect per round	Average time to identify one insect (hrs)
IT	4.72	0.30	0.41	0.17
LT	1.58	0.18*	0.64	0.05*
LU	1.69	0.15	0.40	0.03
LV	1.47	0.18*	0.44	0.05*
MT	30.00	0.24*	1.05	0.13*
NL	1.40	0.15*	0.74	0.03*
PL	1.23	0.32	0.48	0.07
PT	1.99	0.30*	0.18	0.17*
RO	2.97	0.32*	0.72	0.07*
SK	1.07	0.32*	0.34	0.07*
SI	3.29	0.30*	0.19	0.17*
SE	0.17	0.18*	0.05	0.05*

Source: Authors' elaboration.

2.5.3.6 Workflow costs

After specimens have been collected, they need to be processed and analysed (Table 2.5. 4). This can consume significant time in itself, even when the data are harmonized and data handling is relatively consistent. Based on the data from the SPRING trials, we include the following staff costs to represent these workflow activities. For the purpose of this cost estimation, this is assumed to be part of the work done by the specialists that lead the field collection. These costs could be reduced by the development of standardised forms and Apps (see section 4.3).

Table 2.5. 4. Data management workflow costs.

Activity	Time required	Regularity	Stage	Staff type
Data validation	1.52hrs	Once per site	Annual	Consultant
Data handling	18.6hrs	Once per site	Annual	Specialist

Source: Authors' elaboration based on the SPRING project.

2.5.3.7 Coordination

Finally, the success of monitoring depends on stable coordination, which cannot be neglected. Existing biodiversity monitoring can have a variety of different coordination mechanisms, from governmental departments (e.g. Water framework Directive monitoring), regional initiatives linked to research organizations (e.g. HELCOM - the Baltic marine monitoring initiative) or NGOs (e.g. European Butterfly Monitoring Scheme; Birdlife Europe). Coordinators will need to handle work such as administration, acquiring site permits, reporting on findings and liaising with wider research organizations.

To account for this, we assume that each Member State has 1 full time administrator and 0.5FTE Senior Researcher who coordinate the core monitoring efforts. This is based on the management effort required by Butterfly Conservation Europe members (C.G. Sevilleja, S. Collins, A. Whitfield and S. Bonelli, personal communication, 2024) to develop and grow a Citizen Science oriented monitoring scheme. The time required will increase by 0.1FTE per 10 collectors, representing the increase in coordination effort with greater staff and site numbers and, in the future, volunteers. This time may be dispersed among many individuals and organizations, each handling separate tasks, but all should be based at an appropriate facility where they can engage with the wider biodiversity monitoring network, and Member States may need to employ different structures such as state-wide coordination or a single central coordinator. These are included as an annual cost.

2.5.3.8 Site numbers

The actual site numbers per Member State are still to be finalised, and once available, the methodology described here can be applied. However, to illustrate how these relative costs will change depending on the scale of the network, we projected the costs over a network of 15, 30, 60, 120, and 240 sites per Member State (representing 1, 2, 4, 8, and 16 teams of specialists per Member State). These are not intended as aspirational values, but only to illustrate how different cost components will scale.

2.5.3.9 Summary of Key assumptions

Throughout we have noted a number of key assumptions, which are summarised here for clarity. These are necessary to properly account for significant aspects of costs but may vary in practice.

1. **Travel time and fuel**: This is costed based on a 180km journey per sampling round (round trip) to reflect a realistic average distribution of sites (with some being closer and others being further away). In some Member States, sites may be much closer together while larger, more biologically diverse countries may have to disperse their sites further. This will depend on the specific requirements of site selection, and may be particularly high if specialist vehicle hire (e.g. boats, 4x4) is required to reach remote sites. STING+ will evaluate these costs in more depth, as well as the likely subsistence costs associated with them.
2. **Collectors**: It is assumed that there is one team of two collector per 15 sites, reflecting a realistic fieldwork load for staff over a 6-month period. This affects the quantity of materials purchased and the number of postage instances each year. More sites could be monitored if sites are less dispersed or greater if a collector only has limited site access.

3. **Specimens caught for lab identification**: Based on expert taxonomist feedback, we assume that 10% of bees and 5% of hoverflies are caught for lab identification on each transect round, and that in the more diverse southern European Region, this increases to 25%. These initial proportions reflect an average across many Member States, and so there will be variation around this number. We fully recognise that particularly in the Mediterranean the proportions of individuals that will need to be retained will be higher. Also in many cases individual experience shows that there are many more species that need to be retained, especially in flower-rich habitats; the final scheme design, however, will consist of sites that are both flower-rich and flower-poor, as they will be allocated to be fully representative of Member State ecosystems, and not just be selected on the basis of being flower-rich and therefore good in supporting a wide variety of pollinators. STING+ will reassess these proportions to ensure that they are realistic for the final protocols.
4. **Training**: We assume that staff are consistent for the whole scheme duration and require at least two days of training every 5 years. These costs are likely to be an underestimation for many southern European countries and will be further refined in STING+. We also assume that in the first three years, while collectors are learning the local fauna, they are likely to catch a greater number of specimens – 10% of hoverflies and 25% of bees, rising to 50% of bees in Southern Europe. This Initial phase, where taxonomist costs are high, is included as an establishment cost.
5. **Coordination**: Coordination is a significant component of any monitoring effort. A range of different, Member State-specific structures could be employed, but to account for these costs, we assume a single full-time administrator and 0.5FTE of Senior Researcher time are used to represent this in these cost calculations. These costs are assumed to increase by 0.1FTE of administrator and 0.05FTE of senior researcher time per 10 collectors.

2.5.3.10 Summary of differences in cost estimates relative to the first expert report

Between the data collected and the assumptions made, there are several differences that will affect the overall costs of the network, regardless of its size (Table 2.5. 5).

Table 2.5. 5. Overview of the main factors driving changes in costs since the first expert report (Potts et al., 2021) and this STING2 work.

Driver	Explanation
Inflation	The EU has seen an unprecedented degree of wage inflation since 2020 due to the impact of the pandemic and the war in Ukraine. As such, the salary costs used have increased significantly. Similarly, the costs of some materials have also increased. In particular, sampling nets, which increased significantly when factoring import taxes. We also did not include the costs of tape measures. However, for other items we were able to use bulk purchase values that were not previously available to the project team. Here, we update these costs with more recent data from the SPRING project and other academic partners.

Driver	Explanation
Citizen scientists	In the first expert report, we assumed that 50% of data collection would be undertaken by citizen scientists with associated postage and training costs. Here we assume 100% of sampling is done by professionals, but recognise that this is not the long-term ambition of the network.
Organizational overheads	In the original expert report, we did not have access to organizational overhead data. These are now included.
Data collection staff wages	In the first expert report, we assumed data were collected by staff at a field assistant wage on a per-hour basis. Here, we assume that higher paid, consultant grade staff do the data collection, on a full-time equivalent basis. This cost assumption is based on the need to retain staff by providing them with job security, which is a significant challenge for biodiversity monitoring (Breeze et al., 2023).
Specimens caught for identification per transect	In the first expert report, we used a flat value for specimens caught for identification based on double the number caught on a typical UK PoMS transect (0.86/transect, doubled to 1.72/transect) and did not include bees and hoverflies separately. However, the UK generally has a greater degree of taxonomic expertise in field (reducing the number of specimens caught) and has lower species diversity than many Member States but higher than a few others. Here we use a more accurate and up-to-date estimate of the number of individuals observed on a transect, as the basis for a country-specific estimate of the value of the numbers caught per Member State.
Identification time per specimen	In the first expert report, we did not have access to data on the time required for identifying specimens at a Member State level and used UK data (0.09hrs/specimen) as a proxy, and did not distinguish between bees and hoverflies. However, the UK has lower pollinator diversity and higher available resources than many EU Member States, making identification time per specimen faster. Here, we used more locally appropriate times for identifying specimens that reflect the current availability of resources and the overall diversity of pollinators in each Member State.
Initial phase	In the first expert assessment, we assumed that the sampling effort was constant and staff were experienced from the beginning. Here, we have added an “Initial phase” of learning where a greater number of specimens are caught for lab identification per transect.
Site selection and workflows	In the original expert report, we did not consider data entry, validation or site selection costs. Here, we include staff costs for these activities.

Driver	Explanation
Coordination	In the original expert report, we assumed only a single, central coordination effort was required, based in Belgium with 8 full time members of staff and 150% of their costs for overheads. Here, we use a more realistic model of national coordinators and do not include a central monitoring organization. This does not include the costs of EU agencies who would coordinate the scheme as a whole, as the structure of this is to be determined.

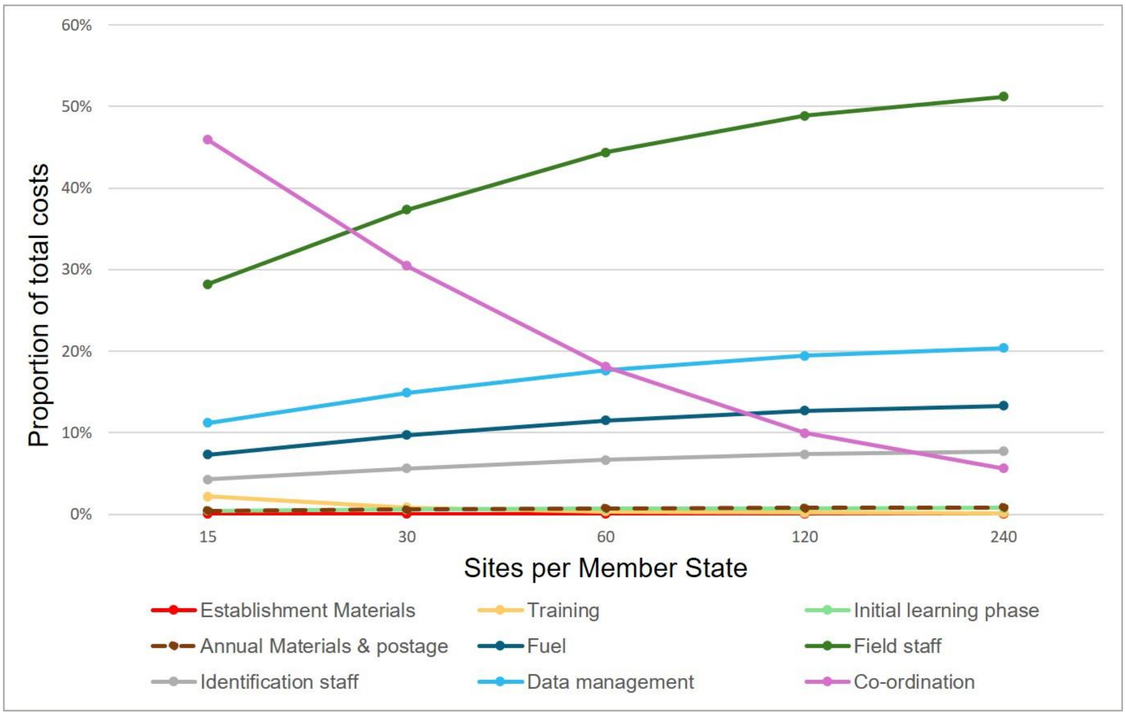
Source: Authors' elaboration.

2.5.4 Results

2.5.4.1 Distribution of overall costs

The main drivers of costs are the staff time to collect and manage data which collectively account for between 39% and 72% of the total network costs respectively (Figure 2.5. 1). Coordination is a very significant cost for smaller site numbers due to the fixed number of staff required to maintain the core of the scheme, but this will rapidly decrease as the scheme increases in scale. Fuel, identification and data management costs increase linearly as a proportion of the costs, but only by a very low amount. Establishment costs are only >1% in the two smallest networks.

Figure 2.5. 1. Distribution of overall costs for various cost components, for a range of illustrative site numbers (final site numbers per Member State are yet to be finalised). Data management and field staff costs are the total costs of full-time staff hired for the data collection, divided by the percentage of time they spend on field and data management tasks.



Source: Authors' elaboration.

2.5.5 Discussion

2.5.5.1 Overall costs

The major drivers of these costs are the level of intensive fieldwork required to sample pollinators on a regular basis. In both scenarios, establishment costs make up <3% of the whole network costs while annual field staff costs account for >50% of the total costs. By contrast, material costs are relatively low as lethal trapping is very limited, in turn reducing the overall costs of identification.

As material costs are relatively low, the number of collectors could be expanded relatively cheaply. This is ideal if sites could be co-located with existing monitoring efforts (see section 2.10), greatly reducing the travel time and fuel involved in visiting sites. Co-location is a significant cost-efficiency for biodiversity monitoring (Breeze et al., 2023) and can allow recorders to generate interconnected data that better explains wider biodiversity trends and the pressures that drive them. However, this would require those sites to be sampled very regularly already to maximise this benefit, for example, certain bird monitoring networks supported under Birdlife International or Natura2000 sites with established monitoring programmes. In this regard, EU PoMS also presents an opportunity to increase sample regularity in other networks, such as the European Vegetation Archive and the LUCAS Grassland module, without a significant increase in costs for those networks (section 2.10).

2.5.5.2 Distribution of costs

The costs of identification and data management then account for approximately 25% of the total costs. Data management is an often undervalued area of biodiversity monitoring and can be a considerable expense where data are not harmonized across recorders (Dobson et al., 2020). Effective data management technologies, such as easy to use data entry apps and standardised data and metadata protocols, can significantly reduce the time required to properly handle and manage data, especially when Citizen Science data are employed (see section 4).

2.5.5.3 Initial learning costs

Although it only amounts to 1.1% of the costs of the network over 10 years, the initial learning phase suggested by the STING2 expert group is still a notable additional cost when employing less experienced staff to collect data, and highlights the importance of capacity building in improving cost-efficiency. However, a major economic challenge for biodiversity monitoring organizations is often the retention of qualified staff due to low wages and limited job security (Breeze et al., 2023). If this staff turnover is repeated regularly then this initial phase where more specimens must be caught than would with an experienced recorder, will be extended. As such, it is crucial that Member States provide secure funding and appropriate wages to incentivise staff retention (see section 2.6.5).

2.5.5.4 Citizen science

As the material costs are relatively small, even if a large number of citizen scientists were to be supplied with materials, the reduction in staff costs would greatly outweigh this. However, this would require a sustained investment in coordination to support these volunteers as effective schemes require regular top-down engagement with members to build engagement (Breeze et al., 2023).

2.5.5.5 Coordination

Coordination costs cannot be ignored if monitoring is to be effective. Monitoring over larger numbers of sites, particularly in countries where there are restrictions on the lethal trapping of insects, can have a significant administrative burden, which risks squandering the skills of experts and reducing the overall quality of data collection. However, for a fully professional scheme, costs could be reduced through integration with existing biodiversity infrastructure or consultancies, and these estimates can be further refined through a better, more transparent understanding of each Member State's operating structure.

A much greater coordination effort will be required to manage and maintain a Citizen Science oriented scheme, however the costs savings compared to hiring professional staff are likely to be much greater.

2.5.5.6 Other costs

Although we have attempted to be as comprehensive as possible, there are some aspects of developing effective monitoring that are not included in these analyses: specimen storage and preparation of museum-grade collections, genetic archiving, the development of models, workflows, tools and materials which are all key to harmonization, the overall coordination of the EU PoMS network (through, e.g. the European Environment Agency), or the costs of data infrastructure required to undertake modelling and reporting. These costs are extremely difficult to estimate as they are often very bespoke, but we would recommend that at least €3M is allocated to supporting these activities at an EU level (e.g. through a COST Action project), based on the cost estimates for addressing biodiversity data needs in Liquete et al. (2024).

2.5.5.7 Further development

The cost methodology developed here is the most comprehensive method yet developed for assessing the costs of monitoring. However, they do not refer to the moth monitoring, which would require further field-testing to reach the level of depth available here, and the rare and threatened species monitoring, which will require highly variable efforts depending on the species. Furthermore, there are a number of further refinements, which would allow for more accurate estimates of costs under different scenarios:

1. **Site numbers**: Here we have used an illustrative set of values to explore how site numbers affect different cost components. Once the scheme design is finalised, it will be possible to use a series of actual site numbers, with a set of different detection scenarios. This would require a thorough power analyses based on data that meet a minimum criteria of site diversity.

2. **Indicator scenarios**: We have described the costs for a network designed to estimate a simple indicator metric (see section 3.1), however other indicators would require different data collection methods (e.g. light traps, rare and threatened species surveys). The relative value of information that each scenario provides (i.e. its quantitative contribution to the overall objectives to halt and reverse pollinator declines) could be assessed to provide an estimate of the benefits of the additional metrics.

3. **Novel technologies**: New technologies, such as visual identification of pollinators or DNA metabarcoding, will facilitate the effective collection of different types of data at lower costs than from traditional identification (see sections 5.2 and 5.3). We need to better understand the costs of these methods in the field, but also the potential upfront costs involved in their development. This can be achieved through direct engagement with projects that have developed and tested these technologies to identify material and time requirements.
4. **Workflow costs**: We have had to use assumed values for managing a workflow at a Member State level. In reality, these costs may vary depending on the size, scale and complexity of the Member States monitoring schemes (e.g. highly federalised Member States may have sub-national workflows that must be further amalgamated). Similarly, we do not account for the costs of development of workflows, particularly those which may need to combine different data types (e.g. transect data and photographic data). These costs are poorly recorded among biodiversity monitoring more broadly and would benefit from dedicated discussion sessions with experts from the wider monitoring community.
5. **Member-State specific species catches**: Here we have used blanket values to assume the numbers of species caught for each transect round for each Member State. However, the number of individuals that require identification could vary significantly within countries, particularly those such as Greece, Bulgaria and France that span a wide range of biomes. Developing more reliable estimates of the species catches, adjusted for recorder effort and experience, would help further refine out cost estimates.
6. **Benefits of recording materials**: The number of individuals requiring identification and the time required to identify individuals are heavily influenced by the quality of resources in each country and the experience of the recorders (section 2.6.4). If new materials are developed then these times will fall but the extent to which is unknown. A simple experimental phase, testing recorders with different skill levels using different materials could give a suitable estimate if the value of time saved from capacity building materials and activities.

2.5.6 Conclusions and recommendations

- Costs can be reduced through co-location with other monitoring networks. The costs of monitoring are driven by the sampling effort required. Reducing this effort through co-location with existing monitoring networks (e.g. eLTER, eBMS) could be a viable strategy for improving cost-effectiveness.
- Data management is a significant cost that can be reduced through careful planning. The effective, harmonized use of novel technologies and robust metadata standards will reduce the staff effort needed for data entry.
- Staff retention and training are crucial to long-term cost-effectiveness. The initial learning phase of many new recorders will result in higher initial costs. Staff retention is therefore key to both capacity building and cost-effectiveness.
- Coordination is an important investment in a stable monitoring scheme. The costs of coordination are substantial and are likely to increase with higher numbers of citizen scientists, but will maintain an effective monitoring network and capacity building.

2.6 Taxonomic and human resource requirements

2.6.1 Summary

The implementation of a thorough scheme for monitoring pollinators across the EU requires not only the necessary tools, protocols, parameters, but also standards to provide meaningful and harmonised results across Member States. More importantly, it demands expertise to be available to perform, analyse, coordinate the collection of specimens, and examine the outcomes of such an exercise. Human resources will be instrumental for the success of an EU pollinator monitoring scheme. We have identified the different categories of staff to be involved in the process, the current available experts, and the model to identify the gaps in expertise to be filled by Member States within the EU-27, as well as the requirements for effectively tooling them up through training and capacity building.

This section considers both the ***demand*** for expertise, in terms of resources required for the implementation of an EU pollinator monitoring scheme, and the ***supply*** of those resources either already available or to be built in the years to come. Any resulting ***shortfalls*** revealed (i.e. the difference between supply and demand) allow the identification of the level of effort necessary to effectively implement the overall scheme in each Member State. On the one hand, the data currently available on the supply of taxonomic and human resources should be further refined and complemented with the results of a harmonised and comprehensive survey launched across Europe. On the other hand, the number of sites and thus, the size and composition of teams to perform monitoring efforts still needs to be finalised and agreed upon. All these are essential to first quantitatively characterise, and then bridge, any expertise gaps. In the absence of a detailed assessment of both the supply and demand of taxonomic and human resources, we present a qualitative assessment of needs and requirements, and how they might be bridged in both the short- and long- terms.

2.6.2 Context and premises

EU PoMS requires reliable data on the status of the taxa groups to be analysed. That information is coupled to the expertise needed to interpret the data collected, with the latter supporting the former. While insect populations continue to decline, taxonomic expertise in Europe is currently at serious risk. A 2022 study commissioned by the European Union, the European Red List of Insect Taxonomists (RLT) (Hochkirch et al., 2022), confirms that the taxonomic capacity required for undertaking wide scale and stable biodiversity monitoring is under pressure and has undergone a long and persistent decline since the 1950s (Hopkins and Freckleton, 2002). This is due, among other things, to the scarcity of available positions for taxonomists, and/or to the decline of academic education in taxonomy, which together have resulted in a dramatic and progressive decline of properly trained taxonomists (i.e. experts who can distinguish and classify taxa according to explicit concepts and data-based hypotheses, name them respecting nomenclatural rules and check type specimens) (Engel et al., 2021). The RLT identified a clear shortage of insect taxonomists, which equated to a loss in an expertise that takes years to build.

Though specific taxa, often vertebrates, may attract great interest among new generations of scientists, insects in general and pollinators in particular, suffer of the dual stress, a combination of species decline (in population and diversity) and a shortage of taxonomic researchers on those taxa. The RLT already flagged that nearly half (41%) of the insect orders are not covered by a sufficient number of scientists.

The impact of such imbalance detected between the amount of data needed for effective, sound, and comprehensive understanding of biodiversity trends and the number of experts required to collect, interpret, and elaborate that data are huge, and may not have been properly considered for conservation planning and biodiversity monitoring.

In this section, the two sides of supply and demand, namely the current taxonomic capacity available (section 2.6.3) and the anticipated expertise required to support EU PoMS (section 2.6.4) respectively, are presented. We introduce how to compare them and analyse the possible shortfalls and imbalances (section 2.6.5), both in the European Union (EU-27) and more importantly, at the Member State level. We propose possible pathways and measures to overcome the potential gaps (section 2.6.5) and provide a set of recommendations to shape a framework to sustain taxonomic capacity over time (section 2.6.6).

2.6.3 Mapping current taxonomic capacity in Europe

Taxonomic knowledge is crucial to avoid errors in data interpretation. Taxonomic knowledge transfer includes thorough reviews of the species existing in each country (checklists, digital access to natural history collections data in museums), identification literature (field guides, keys, online tools, and mobile device applications), information on species' distribution (atlases) and threat assessments (Red Lists), and taxonomic training (courses and materials). However, the taxonomic expertise, albeit being fundamental notably for the identification of species (naming, describing, and classifying living organisms), both in the field and in the laboratory, has been relatively undervalued for decades.

This evaluation of taxonomic capacity in Europe is strongly based in the results obtained by the RLT (Hochkirch et al., 2022), to determine the number and allocation of insect experts across Europe.

The RLT extracted information from scientific articles published in the last decade, made queries to the most relevant databases, and reached out to the most important entities and networks linked to taxonomy, as well as using a tailored campaign to collect the most up to date information on insect taxonomists. A total number of 1,527 European insect taxonomists participated in a self-assessment survey to determine their expertise and analyse several features per individual (including age, affiliation, seniority, taxonomic group(s) of interest, and research outputs available).

These results bring consistency and amplifies the data collected under previous studies such as STING1 (Potts et al., 2021), and have been further refined and updated with information from the SPRING project.

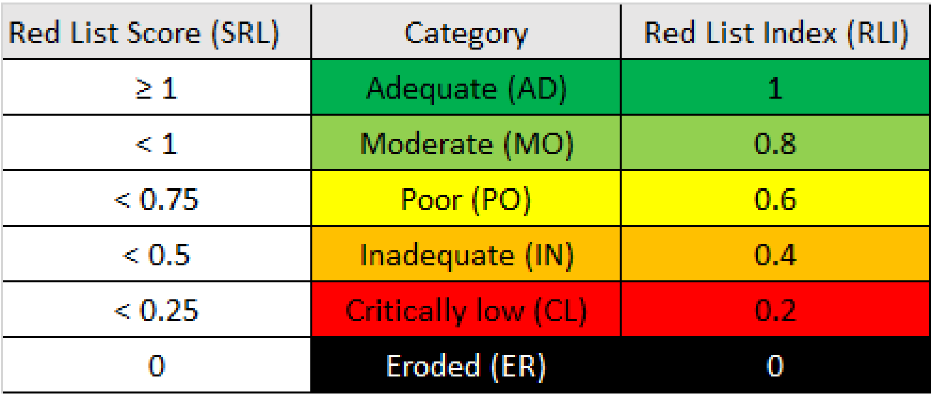
For this report, ***specialists and senior researchers***, otherwise known as ***Alpha Taxonomists***, are scientists specialized in taxonomy, the discipline of identifying, describing, and naming species, as responsible for the discovery and formal classification of species based on morphological (physical appearance), but also other characteristics (such as genetics). Their practice is pivotal for maintaining a standardized system of nomenclature in biology, a central dimension for accurately informing on biodiversity and thus for supporting the monitoring of species. They are affiliated to museums, Universities, and other biodiversity centres, producing critical information for taxonomy and many other disciplines, which on its own generally face significant challenges due to understaffing and inadequate infrastructure.

On the other hand, ***Para-taxonomists*** (that may fundamentally work as field ***technicians and assistants***) are trained personnel who work closely with taxonomists, but do not necessarily have formal academic training in taxonomy. Para-taxonomists often engage in the collection, preparation, and preliminary identification of specimens in the field. Mostly committed to biodiversity conservation and monitoring on a volunteer basis, their vital role may at the end require of experienced Alpha-taxonomists for final process the information, which is critical for certain taxa such as hoverflies and bees.

For better interpretation of outcomes in this section, to assess the availability of taxonomists across Europe, some basic assumptions have been made:

- Availability of experts refers to (alpha-)taxonomists.
- Experts may have dual or triple knowledge (combined expertise, on more than one taxonomic group), in which case they will count double or triple, as the case might be.
- With a final number of 219 experts allocated across EU-27, a correction factor (1.20) has been introduced to absorb the typical average response rate to surveys (between 10% and 30%), which indicates that around 44 experts conduct taxonomic research in Europe, although they have not (for different reasons) participated in surveys.
- The current taxonomic capacity availability, per MEMBER STATE is categorised following the classification made in the RLT which was based on the classification of threatened species used in the Red Lists of IUCN and then translated to experts (Figure 2.6. 1).
- A Red List Score (RLS) was derived for each taxon (i.e. insect order or family) by calculating the number of publications per 100 species in each taxonomic group (i.e. NPublications / (NSpecies*100)).

Figure 2.6. 1. Translation between Red List Score (SRL), Category, and Red List Index (RLI).



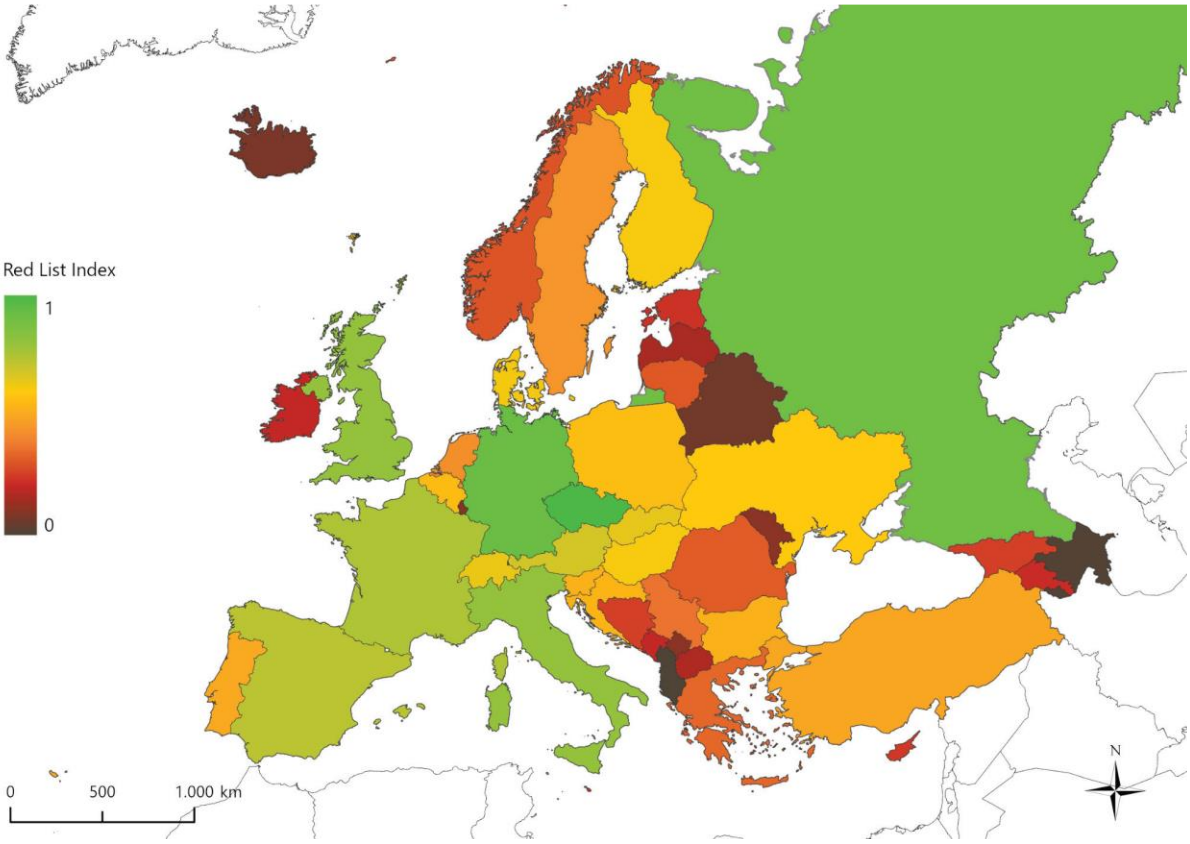
Red List Score (SRL)	Category	Red List Index (RLI)
≥ 1	Adequate (AD)	1
< 1	Moderate (MO)	0.8
< 0.75	Poor (PO)	0.6
< 0.5	Inadequate (IN)	0.4
< 0.25	Critically low (CL)	0.2
0	Eroded (ER)	0

Source: Authors' elaboration based on Hochkirch et al. (2022).

With these premises in mind, the mapping of taxonomic capacity in Europe reflects the current distribution of experts across Europe per Member State. This exercise will facilitate the ***baseline assessment*** of the current taxonomic capacity and taxonomic resources available so that the "taxonomic gap" can be quantified, and a plan of activities put in place in order to bridge it.

Geographical distribution. The insect taxonomists are not evenly distributed geographically and the overall capacity in Europe presents clear differences among countries and/or regions (Figure 2.6. 2).

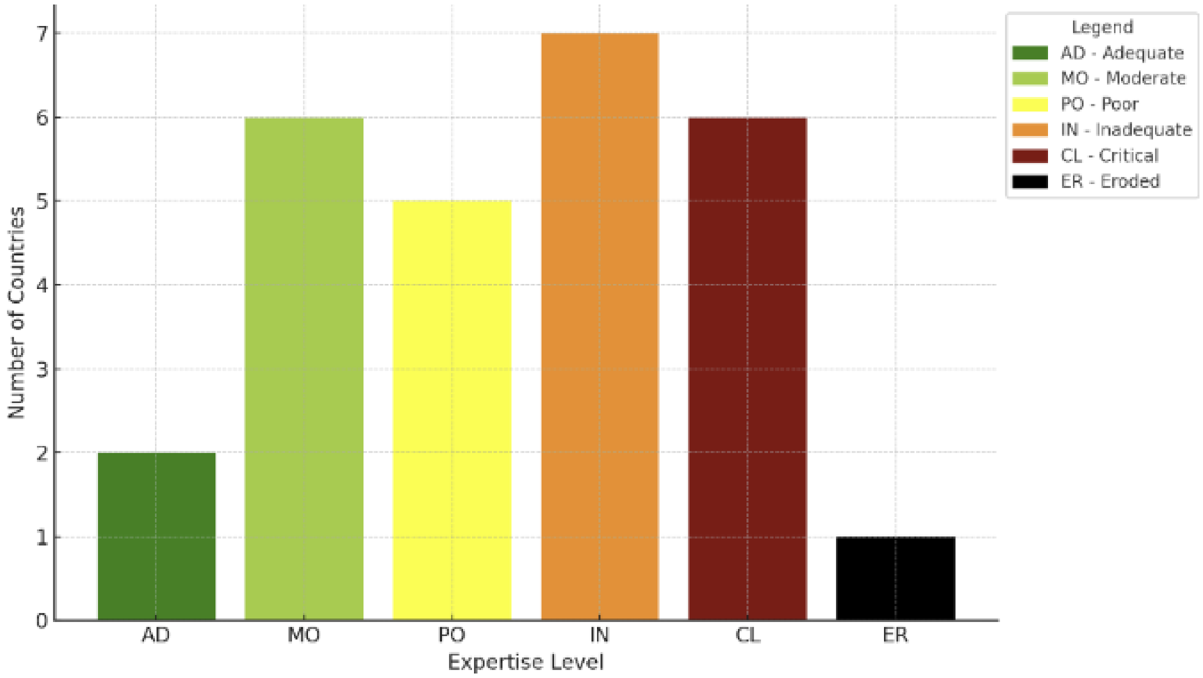
Figure 2.6. 2. Taxonomic capacity in Europe, as per European Red List of Insect Taxonomists Index (RLT Index), from eroded (value 0) to adequate (value 1) capacity.



Source: Hochkirch et al. (2022).

Level of expertise. The level to which taxonomists have expertise varies across countries (Figure 2.6. 3). This factor can be a key determinant for fostering mobility across borders, for taxonomists who can also monitor several areas.

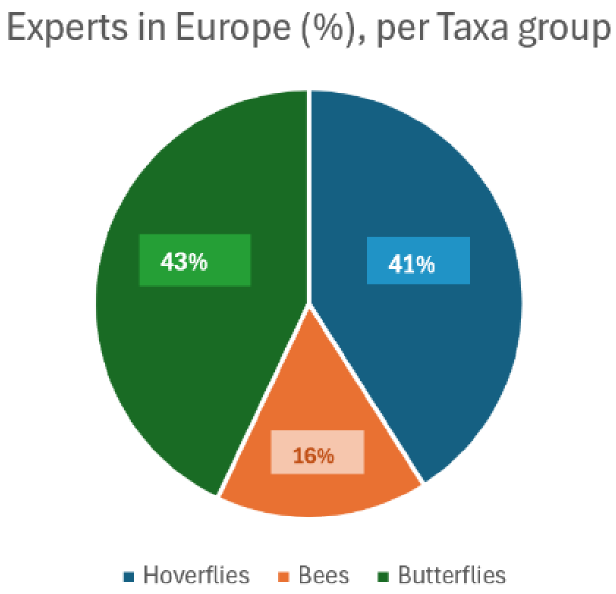
Figure 2.6. 3. Expert taxonomic capacity per Level, across EU-27.



Source: Hochkirch et al. (2022).

Expertise distribution, **per taxa group**. When differentiating expertise per taxa, we extracted aggregated data for the whole EU 27 (Figure 2.6. 4). As indicated in the RLT, the four largest insect orders were also the most studied orders from the survey (*Hymenoptera*, *Lepidoptera*, *Diptera* and *Coleoptera*, though noting that not all species within these orders are pollinators). For these groups, overall expertise was assessed to be at a very low level since they are categorised as either at Poor (PO) or at Moderate (MO) levels, due to the species richness and, in some cases, due to the species distribution across regions. Moreover, it does not implicitly mean that this expertise is evenly distributed per country, as we saw above. The RLT found that there was in general a strong linkage between taxonomic capacity and GDP, though with certain exceptions, such as Czech Republic and Poland where traditional taxonomy remains a recognized discipline. In other countries with higher GDP, taxonomy has been replaced by other research priorities.

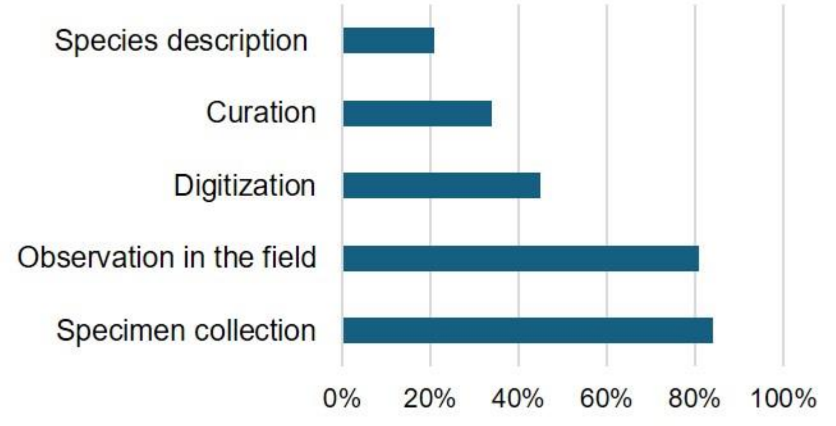
Figure 2.6. 4. Taxonomic capacity in Europe, for each taxon (percentage over the total capacity).



Source: Authors' elaboration.

Task priorities and experiences. Other results obtained from the RLT show that expertise demonstrated by taxonomists spread over several broad tasks (Figure 2.6. 5), mainly concentrated in collection and sampling (84%), and observation and identification of species in the field (81%). Additional work, including description, digitization and curation of specimens complement the taxonomic work and reinforce the expertise gained producing a flow of knowledge back to identification of species.

Figure 2.6. 5. Area of expertise (%) of all taxonomic capacity.



Source: Authors' elaboration.

Based on the RLT and SPRING project, in combination with extensive consultation with experts (including the STING2 expert group), it was concluded that the collections and identification by taxonomists of butterflies, and to some extent of hoverflies, can be done in the field, and resources necessary for performing these tasks can be achievable in the short- to medium-term. However, wild bees will require additional substantial investment in both development of resources and increase of taxonomic capacity.

The region of Southern Europe (only 8 countries out of 27, representing 27% of the entire territory) is most strongly affected by a shortage in available resources (near 70% of those countries have capacity ranging from poor to eroded) while it will face the highest level of pollinators identification demand. Together these two aspects indicate that a major effort is needed to enhance and harmonise capacities across Europe.

However, this preliminary analysis still needs to be made at a more granular level, with the integration of additional factors (such as status of resources available per country), to better understand the individual effort required at national level.

2.6.4 Addressing expertise requirements

Here we differentiate between ***human resources*** (section 2.6.4.1) and ***material resources*** (section 2.6.4.2). While in most cases the use of both is essential, taxonomic expertise of senior scientists and their knowledge can make up for the availability of other complementary means. However, the use of adequate tools can help improve taxonomic knowledge and contribute to overcoming shortfalls in species identifications (Murguía-Romero et al., 2021). Therefore, we analyse separately human resources, the taxonomists (at all levels of seniority and experience), and the materials to support the work undertaken by these taxonomists.

Following the outcomes of STING1 (Potts et al., 2021) and the work presented in this report, once the design of the EU PoMS is finalised to represent a harmonized and comprehensive scheme at the European level and at the Member State level, the taxonomic resources necessary for its implementation can be further refined.

Taxonomists work on biological specimens held in natural history collections, to study, curate and extract valuable information to create, improve and enlarge collections. They also collect new specimens as objects of new research. Besides the expertise gained over years by collecting samples and conducting research on top of the species under study, a wide array *of* ***tools, platforms and mechanisms*** can support their taxonomic work and facilitate comparison, checking and validation, as well as access to references (including images). Databasing the information extracted, curation and annotation of specimens collected in the field can then enhance current taxonomic knowledge and enlarge it with the identification of new species. These tools include checklists, field guides, atlases (printed and digital), handbooks or identifiers (ID) keys, and national Red Lists. Similarly, new technologies are increasingly being used for species identification both in the field (such as through Artificial Intelligence (AI) applications, for sound and image recognition, see section 5.2) and in the laboratories, with molecular and genomics-related techniques (e.g. DNA-barcoding methods, section 5.3).

For pollinator monitoring, sufficient taxonomists and material resources are critical to be available to perform high quality, efficient and cost-effective work. Where, how and to which extent the monitoring process should be undertaken are the factors that will lead to identify, categorise, and describe the specific taxonomic requirements needed for the implementation of EU PoMS, at the Member State level and under a harmonised EU programme.

A detailed assessment to comprehensively identifying the taxonomic requirements necessary for both human and material resources must be grounded in the following key criteria:

1. **Number of sites, per country**: The number of sites is yet to be finalised, however the design will be influenced by numerous critical factors, other than just a basic geographical size, and including abundance, richness and occupancy of species in the territory. Table 2.6. 1 provides the list of Member States, their surface area, in km^2 and the number of selected species to monitor (as identified in SPRING).
2. **Selection of sites per country**: Important considerations include the number of sites, their location, the distance among them, their accessibility, the available facilities, and the representativeness of the ecological features of the sites in relation to those of the country. These factors will determine whether a Member State can use single or multiple teams and mobilise them across the selected sites. The site locations could potentially also be coupled to specific areas (e.g. agricultural or protected areas), and existing facilities (e.g. national parks or biodiversity stations). All these criteria together would define the number and composition of teams required. The site-related algorithms are yet to be finalised and agreed upon, and will be the subject of a future analytical exercises beyond the STING2 outcomes.
3. **Number of iterations, per site**: the power analysis (section 2.4), identified that the threshold for taking enough samples and thus, collecting a sufficient number of species per site, should be 8 repetitions per site.
4. **Number of levels of detection to identify trends, per site.** The power analysis (section 2.4) recommends the relevant decline trend to be evaluated to be fixed at 1% per year, though other trend detection levels could be explored (0.5%, 1% and 2%), though these need to be finalised and agreed upon.
5. **Methods to collect species:** based on the analysis of SPRING data in conjunction with STING2 expert assessment, only reinforced transects will be used and not pan traps (see section 2.2 for full details). The standardised reinforced transect length is recommended to be of 500m. Transect walks will be then conducted 8 times per year, to identify in the field, or collect and identify later all bee, hoverfly, and butterfly specimens. Two other methods are also proposed for the core scheme: light traps for moths and species specific methods for rare and threatened species. Taxonomic requirements for both of these approaches should be included in the assessment of current capacity and future needs.
6. **Grouped sampling, per reinforced transect**: each reinforced transect will be walked by a professional to first record butterflies and then re-walked to record wild bees and hoverflies. This is considered the best time-effective procedure, since the teams of professionals will have expertise on the three taxa. This approach aims to make efficient use of time and facilitate interaction amongst the team for species identification and enhance “peer-review” on site, thereby lowering the identification load in the laboratory. Future development of EU PoMS is likely to increasingly use volunteers instead of professionals in the field, and a further assessment at this point will be needed to understand the extent to which volunteers can effectively monitor these three taxa on a reinforced transect walk. As described in section 2.5 above, the costing for these professionals will be based on the aggregation of their work summing 0.5FTE expert per site and visit, in each Member State.

Once the EU PoMS design is finalised and agreed upon, the next step is to identify the teams' composition and the right expertise required, considering the number of sites per Member State that will require taxonomic capacity, first per site and then, at national level.

Table 2.6. 1. List of Member States, size (land area in km^2) and estimated number of pollinator species (bees, hoverflies and butterflies) to monitor.

Member State		**Km^2**	**No species**
AT	Austria	82,519	1,342
BE	Belgium	30,452	819
BG	Bulgaria	110,001	1,427
CY	Cyprus	5,896	506
CZ	Czech Republic	77,212	1,101
DE	Germany	353,296	1,214
DK	Denmark	41,987	614
EE	Estonia	43,110	634
EL	Greece	130,048	1,840
ES	Spain	502,654	1,741
FI	Finland	304,316	693
FR	France	633,886	1,745
HR	Croatia	55,896	1,148
HU	Hungary	91,248	1,230
IE	Ireland	68,655	314
IT	Italy	297,825	1,827
LV	Latvia	63,290	692
LT	Lithuania	62,643	714
LU	Luxembourg	2,586	626
MT	Malta	313	176
NL	Netherlands	34,188	750
PL	Poland	30,7236	1,030

Member State		Km²	No species
PT	Portugal	90,996	1,093
RO	Romania	234,270	1,362
SE	Sweden	407,300	783
SI	Slovenia	20,145	1,105
SK	Slovakia	48,702	1,232
Sum		4,103,987	

Source: Authors' elaboration based on the SPRING project and Eurostat 2022[7].

2.6.4.1 Human resources

When considering taxonomic resources, we include both Alpha-taxonomists and Para-taxonomist (section 2.6.3). While Alpha-taxonomists are clearly identified with senior researchers, in this latter group of Para-taxonomists, we include a wide range of professionals, volunteers and interested citizens with a different gradient of taxonomic expertise, from basic familiarity with species collection and identification to highly experienced volunteers (Table 2.6. 2). We also consider technician and students in biology as included in this latter group.

We propose a two-step model for monitoring, starting in the (1) short-term (first year) with qualified experts (potentially supported by a part-time assistant to assist with specimen collection and storage for later identification work), and (2) increasingly moving towards a hybrid system in the long run, where both knowledge sources (experts and volunteers, at the proportion of 50% by 2030) could be combined to tackle different tasks and support jointly the identification of species. The use of assistants will strongly depend on the Member State available resources in the field (depending on the final allocation of the selected sites), and on the linked institutions where experts will conduct identifications such as universities, museums, and biodiversity centres.

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[7] https://ec.europa.eu/eurostat/databrowser/bookmark/e9572305-224b-4fa0-bf0f-a039d44e272e?lang=en

To identify the starting baseline, we will describe here the following dimensions and variables:

- The scope of the work to be developed by each team.
- The work distribution in the field and in the lab for quality review and validation, in general, and specifically for identification purposes in those cases (particularly for bees) where the species could not be readily identified in the field.
- The composition of the team, considering the short-term approach with a model expert taxonomist based.
- The area covered by each team, which is expected to significantly vary among countries.
- The geographic distribution of pollinators across EU-27.

Table 2.6. 2. Broad characteristics of Alpha and para-taxonomists with respect to their primary focus, work environment and scientific contributions.

Aspect	Alpha-taxonomists	Para-taxonomists
Primary Focus	Identification, description, and naming of new species, classification within the taxonomic hierarchy.	Collection, preparation and preliminary identification of species, often in support of biodiversity research and conservation efforts.
Work environment	Primarily in laboratories, museums or academic institutions, analysing species and conducting detailed taxonomic studies.	Mostly in the field, collecting specimens and data, or in community engagement related to biodiversity conservation.
Scientific contribution	Expanding scientific knowledge through the formal classification and naming of organisms, providing a foundation for biological research and conservation.	Bridging the gap between fieldwork and scientific research, facilitating the discovery and initial documentation of biodiversity, and engaging with local communities in conservation efforts.

Source: Authors' elaboration.

Scope of the team's work

Following the results obtained from the RLT, and wide consultation with experts, the expertise demonstrated by taxonomists spread over the main tasks to be developed (Figure 2.6. 5), is mainly concentrated in Collection and sampling (84%), and Observation and identification of species in the field (81%). Additional work, including description, digitization and curation of specimens complement the taxonomic work and reinforce the expertise gained producing a flow of knowledge back to identification of species.

Therefore, the team will focus on: reinforced transect walk; collection of samples; identification of species on site; identification in the lab, for those species which identification could not be done on-situ; and aggregation of data, databasing. Para-taxonomists identified as Field Technicians (below postdoctoral level, see section 2.6.5) can assist experts and will mostly focus on setting up the transect and collecting samples in the field, and possibly aggregating the data.

Other staff might be required for the following activities that need to be included as well, but are not included in the present section since those will be undertaken by technicians and administrators, outside the collection and identification of species: management of the data infrastructure (section 4); workflows maintenance for data supply (section 4); coordination of volunteers; reporting; communications; and other non-scientific work.

To tackle these tasks outside the specific taxonomic work, and specifically for costing purposes, it is proposed that the allocation applicable per Member State should be 1 FTE administrator plus 0.5 FTE senior researcher for coordination. Other staff are identified as Specialists and Field Technicians (see section 2.5 above, for costing).

Distributed work

Based on previous experiences by the expert communities (both within SPRING and STING, and other projects as ORBIT and Taxo-Fly), we can estimate that the highest workload in the laboratories will be happening in the case of bees and hoverflies, while the experts will be strongly occupied in the identification of butterflies in the field.

Identification of species will be done either on site or at the laboratory, the latter mostly in case of hoverflies and more importantly for wild bees. In this respect, proportions of bees, hoverflies and butterflies identified in the field is estimated in three different tranches:

- Bees: 75-90%, depending upon region and main habitats.
- Hoverflies: around 80-95%, depending on region and main habitats.
- Butterflies: near 100%.

As per SPRING results, only bees and hoverflies consistently require lab identification, however the number of individuals that require identification and the time it takes to identify one specimen, will vary greatly depending on the diversity of the fauna in the country. As a final statement, 5% of the hoverflies and 10% of bees (excluding *Apis mellifera*) would need to be caught for lab identification. However, in southern European countries (Spain, Portugal, Italy, Malta, Greece, Croatia, Cyprus, Slovenia, and also southern France), the number for bees that would need identification in the lab is estimated to be 25%. This percentage (and possibly even a higher value) may need to be applied to some Member States and sub-regions (such as southern France) in the first year of EU PoMS, to acquire base knowledge about the local fauna for both bees and hoverflies

These initial proportions reflect an average across many Member States, and so there will be variation around this number. We fully recognise that particularly in the Mediterranean the proportions of individuals that will need to be retained will be higher. Also in many cases individual experience shows that there are many more species that need to be retained, especially in flower-rich habitats. The final scheme design, however, will consist of sites that are both flower-rich and flower-poor, as they will be allocated to be fully representative of member state ecosystems, and not just be selected based on being flower-rich and therefore good in supporting a wide variety of pollinators. STING+ will reassess these proportions to ensure that they are realistic for the final protocols.

Table 2.6. 3 shows the number of species to be caught per transect per visit (round or iteration) and taken to the laboratory for further identification. It already considers the increases assigned to southern Europe.

When addressing each round of sampling per site, the time dedicated to field/lab work is expected as follows (costing of this time is included in section 2.5 above): in the field, the team will dedicate an average time per site per visit of 5.76 hours based on SPRING data: transect description (1 hr); transect walk (1.3 hrs); sorting specimens (0.46 hrs); and travel time to/from a site (3 hrs).

For the bee and hoverfly identification, time dedicated at the lab, as an average for the EU-27 and the entire set of species to identify varies:

— Total hours for bees: species identification (0.95 hrs) and data validation (1.52 hrs): 2.47 hrs.

— Total hours for hoverflies: species identification (1.90 hrs) and data validation (1.52 hrs): 3.42 hrs.

All these data should be considered when identifying the number of teams needed, and the time each one needs to dedicate to different tasks, both in the field and in the lab, per Member State. Other components of dedicated time will also be counted for additional tasks, such as data entry that will be carried out at the facilities where the identification is carried out (labs of museums or similar). Altogether, by aggregation, the final number of FTEs can be identified. It should be noted that creating stable teams would imply having full time dedication of staff to ensure their commitment and permanence over time, and to avoid repeating the learning curve every year if the staff is not fully engaged.

Additionally, it is worth noting that field assistants need to be procured. Most Member States are expected to rely mainly on professionals initially, until a larger volunteer community can be trained up in the longer-term. Therefore, a transition period is foreseen moving towards a higher proportion of volunteers in the longer-term. Yet, even with a strong volunteer component, some roles will only be feasible through professionals (e.g. some bee taxa).

Table 2.6. 3. Number of bees and hoverflies for identification in the lab per Member State. These numbers were provided by national fieldwork experts participating in the SPRING project, and there will be considerable variation around these depending on various factors, such as the floral diversity and cover of a site. These figures will be further refined based on further analysis of SPRING data and wider consultation of experts as part of the STING+ project.

Member State	Bee Numbers caught per transect per visit	Hoverfly Numbers caught per transect per visit
AT	1.12	0.36
BE	1.03	0.01
BG	0.94	0.48
CY	10.47	0.3
CZ	1.23	0.48
DE	1.06	0.48
DK	1.16	0.48
EE	0.36	0.11
EL	5.23	0.34

Member State	Bee Numbers caught per transect per visit	Hoverfly Numbers caught per transect per visit
ES	2.68	0.3
FI	0.38	0.26
FR	1.28	0.38
HR	5.69	1.04
HU	1.96	0.33
IE	1.22	0.35
IT	4.72	0.41
LT	1.58	0.64
LU	1.69	0.4
LV	1.47	0.44
MT	30	1.05
NL	1.4	0.74
PL	1.23	0.48
PT	1.99	0.18
RO	2.97	0.72
SE	0.17	0.05
SI	3.29	0.19
SK	1.07	0.34

Source: Authors' elaboration based on the SPRING project.

Composition of the team

Each team should be formed of 3 expert taxonomists (possibly 2 if they can cover both bees and hoverflies), supported by one assistant to help in the layout of the transects, the sampling collection and the information databasing.

Expert taxonomists will be dedicated to identification of species (in the field and/or the lab):

- Senior researcher: Someone senior who would be expected to be the scientific lead.
- Consultant/researcher: someone who could be expected to identify specimens to species level and train staff (usually a postdoctoral researcher or equivalent).

Assistants will majorly collaborate in the fieldwork:

- Field technician: who would be expected to collaborate with primarily the transect display and data collection but is not capable to fully identify species (students below postdoctoral level, experienced amateurs or equivalent).

The team is considered as an operational team that will run identification of species either directly on site or in the lab. Each one will visit the assigned sites, collect specimens and proceed with the species identification task (with the subsequent databasing of information). To complete the data circle, the team's activity should be supported by a central unit to organize, administer and finalize the process of documenting the monitoring scheme (for the period of time and the area assigned, which should be at national level, for cost-efficiency purposes).

Area covered by each team

Considering that each expert will operate on the basis of 0.5 FTE per team, based on SPRING and STING expert knowledge, each team could typically cover a minimum of 15 sites, and therefore each expert will be involved in 30 sites. Selection of the assigned sites could be based on parameters such as local knowledge and or distance (travel time) between the selected sites. In that latter regard, the distance between sites, for costing purposes, is considered to not exceed 90 km, which implies a typical round trip per visit of maximum 180 km (see section 2.5).

Number of teams

The estimate of number of teams needed per country (and therefore, the experts to be available for the implementation of the monitoring process) will necessarily follow the number of sites selected per Member State, along with all the above-mentioned premises (time dedication, distance between sites, etc.). In the short-term, before a work force of trained citizen scientists can be established, those professionals are expected to be expert taxonomists to maximise species identification and data validation on site. That will lead to cost efficiencies in the availability and use of resources.

Geographic distinctiveness

Monitoring efforts will be differentiated across biogeographical regions due to variations in pollinator richness. Mediterranean countries host the highest diversity of bees, while they show similar species richness of hoverflies to temperate countries (Reverté et al., 2023). The highest richness of butterflies is found in mountainous areas in southern Europe, mainly in the Pyrenees, the Alps and the mountains of Balkans (van Swaay et al., 2010). These geographical differences in pollinator diversity should be taken into account when planning the human resource requirements.

Gonepteryx rhamni, Alessandro Mari

2.6.4.2 Supporting material

As reported by the SPRING, ORBIT and Taxo-Fly projects, materials are unequally available across Member States in Europe. While field guides and keys appear to be the most accessible references, other references such as AI tools are scarce, or even absent, or non-harmonised, as the national validated reference collections for pollinators (both, physical or virtual). The TETTRIs project is currently building a roadmap to create those reference collections, which stand as a critical element to be used in identification of species.

Thanks to the developments made under projects such as ORBIT and Taxo-Fly, a wide set of tools and mechanisms to support taxonomic capacity have been developed, most of them accessible through the ***European Pollinators Academy***[8].

Briefly, ***ORBIT*** provides a centralised taxonomic facility that lays the groundwork for the identification of European wild bees. Such a baseline includes different tools for species identification and monitoring, to support further analysis of biodiversity patterns on how wild bee communities respond to environmental changes. Factsheets for each European wild bee species: these include descriptions, illustrations of morphological characters, macro-photographs made *in situ*, reference to DNA barcodes, and relevant information on their life histories, host-plant associations, and habitats.

Taxo-Fly has produced similar outcomes for hoverflies and has developed resources for European inventory and taxonomy of this taxa group. Factsheets for each European hoverfly species, include descriptions, illustrations of morphological characters, photographs, distribution maps and relevant information on the life histories, host-plant associations and habitat associations.

Both set of Factsheets are already included in the Pollinator Academy (developed under SPRING), along with other relevant information for butterflies such as regional (e.g. sub-national level) identification guides. To ensure improvement of this platform with additional resources (including courses and other supporting material) and its sustainability over time, the Pollinator Academy should be linked and inserted into the taxonomic community e-learning platform run by CETAF, namely the Distributed European School of Taxonomy (DEST)[9]. The overarching collaborative platform should be an open source, to collate specific taxonomic courses on pollinators at different levels, beginners, intermediate and advanced modules. In this learning environment, prepared by and for taxonomists, a multilingual tool is integrated and provides translation through DeepL[10] API to 24 languages.

For butterflies, the references, inventories and keys are well developed in many countries (such as those produced by Butterfly Conservation Europe[11] during the ABLE and SPRING projects). Comprehensive checklists have been updated, such as the National checklists and Red Lists of European Butterflies (Maes et al., 2019), the work produced by Wiemers at al. (2018) to update Fauna Europaea (de Jong et al., 2014).

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[8] https://pollinatoracademy.eu/

[9] https://cetaf.org/explore/dest-distributed-school-of-european-taxonomy/

[10] https://www.deepl.com/translator

[11] https://www.vlinderstichting.nl/butterfly-conservation-europe/

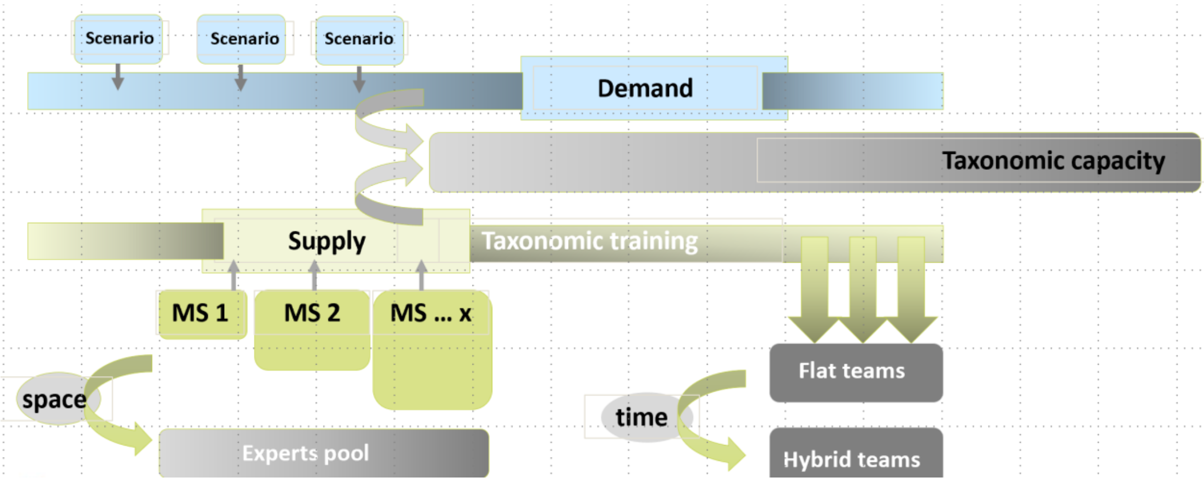
The project ABLE provided an extensive catalogue of field guides for butterflies in 11 European countries (Austria, Cyprus, Greece, Italy, Lithuania, Malta, Poland, Portugal, Slovenia, Slovakia and Spain), as well as many other relevant resources, including manuals for transects (translated into 13 different European languages), identification guides, and guidance booklets to record butterfly data.

Other resources might progressively be added as they are produced, such as inventories for images and sound records, poly-keys on the web, and outcomes supported by relational databases.

2.6.5 Bridging the gap

A plan is proposed to address the building of taxonomic capacity, considering the available resources in comparison to the requirements expected under the final agreed design of the EU PoMS (section 2.6.4). An overview on how the relationship between potential demand and current supply of taxonomic capacity for the various member states is summarised in Figure 2.6. 6.

Figure 2.6. 6. The relationship between key elements of taxonomic capacity building for EU PoMS. The gap between the anticipated demand of the monitoring scheme and the current supply of taxonomists and other resources can be bridged through establishing and training of teams of experts with various levels of expertise, which will depend upon the specific Member State conditions.



Source: Authors' elaboration.

By matching requirements towards existing capacity, the model envisaged for identifying needs of resources proposes three different Tiers based on the actual differences between the demand (requirements) and the supply (availability) at a certain time and per Member State. Such a difference or shortage may vary from 0 to 100% with specific thresholds suggested for:

- Tier 1: the estimated gap is over 70%.
- Tier 2: the estimated gap falls between 30 and 70%.
- Tier 3: the estimated gap counts less than 30%.

Tier 1: Substantial shortfall: the estimated gap is large, over 70%, and immediate and substantial measures need to be undertaken to ensure that EU PoMS can be implemented in timely manner and with the expected quality standards in terms of data gathered. Additional efforts should be allocated to effectively realising measures and integrating the results into the European aggregated scheme.

Tier 2: Moderate shortfall: the estimated difference, which falls between 30% and 70%, is likely to require a structured mechanism that tackles a diversity of factors including training and capacity building, attractive recruitment, additional funding, and collaboration between a variety of actors (from governments to academia, research institutions, biodiversity-related organizations, and citizens science initiatives). With adequate financial support, the implementation of the required measures should take up to 2 years, with a direct and visible impact on the increase of the taxonomic resources available.

Tier 3: No current shortfall: the estimated difference is less than 30% of what is required, are relatively easily to address. The actions required to overcome the gap are straightforward to implement (through pre-identified mechanisms), relatively low-cost to undertake, efficient in their implementation (target audiences and committed partners), quick to execute (less than 2 years), and with a direct and visible impact on the increase of the resources available.

Evaluating the evidence of the shortfalls should lead to policies and measures under a double approach to differentiate short-term and long-term perspectives. There are clear differences that drive such a distinction. First, the initial baseline requires an immediate action for grouping the necessary resources, making them available to the experts and implementing in situ the model in a systematic manner. Importantly, it needs to be robust and accurate to determine the starting data to which the evaluation of trends will be referred to over time. Such a challenge necessarily relies on the availability of existing resources plus short-term initiatives to complement them, with a very tight margin to create and solidify the needed components of the model (including human resources and tools).

This approach can be easily applied for Tiers 3 and 2 (provided critical measures are adopted in the latter case) and will require larger efforts for Tier 1. Immediate actions should be accompanied by a clear, structured, and harmonised model that will ensure expansion, sustainability and regularity of the efforts allocated for monitoring during the initial phase of EU PoMS and apply to all three Tiers.

With this approach in mind, it is critical to have comprehensive data from a survey launched at EU level to capture up-to-date national data regarding the actual capacity expertise available for monitoring. Those results will be instrumental to fine-tune and shape more precisely the actions to be undertaken for a comprehensive and consistent action in both the short and the long term.

2.6.5.1 Requirements for short-term action

As per the Tiers presented above, there is a significant effort needed to strengthen the taxonomic capacity that is required for the effective implementation of the monitoring of pollinators based on a harmonized and balanced system. Actions should address punctually what is needed in each Member State as to be able to form a skilled, trained and resourced team with the adequate tools and mechanisms to perform their work.

Two specific set of actions are envisaged. On one hand, mobilisation of experts that can act as trainers and tutors and could potentially train in countries in their proximity. On the other hand, training and e-learning will act as drivers for: (i) raising awareness across different communities of practitioners; (ii) crystalizing expertise capacity and engaging new generations of taxonomists; and (iii) form a solid foundation of taxonomic expertise.

Mobilisation of experts in punctual campaigns. To accommodate these needs to the specific national circumstances where implementation procedures may have already started and may involve contractual external agents. In case of a surplus of taxonomic expertise over the number required in certain Member State, they could easily act as trainers (in the model “train the trainers” approach) in proxy countries which may fall under other critical Tiers.

Training and capacity building. Several EU-funded projects and initiatives have developed or are developing material and courses that aim at providing professional training, including skills and competencies or the use the right tools, that will allow professionals to gain expertise to efficiently identify species either on site or at the lab, provided they can access to reliable material. The efforts in training should be focused on: (i) increasing taxonomic capacity among experts, professionals and non-academic practitioners, and (ii) providing access to the necessary tools, reference documents and collections and training material at large that tool-up the actors.

Increase taxonomic capacity. Two different categories of courses should be set up to ensure that capacity is available timely and with the standards required: a Harmonization module and a Skills and competencies modules.

Harmonization module: To ensure alignment across countries, allow equal access to centralised resources, and facilitate a shared understanding of objectives, mechanisms and expected outcomes. The target audience should be the entire set of teams involved in the process. It could adopt a blended format with an overarching workshop targeting European actors, and this followed by online module that could be reached by individuals at their best convenience:

- Targeted audience: expert taxonomists to be directly involved in EU PoMS.
- Format: online or physical workshop.
- Duration of the course: 3 hours.

Skills and competencies modules: a variety of courses should be made available centrally through the Pollinator Academy and CETAF-DEST platform where other initiatives (such as Transmitting Science, or ForBio[12]) are linked. The level of the courses should be accommodated to the needs at country level. In this respect:

Tier 3: They may require the teaching of Advanced Courses for better-trained personnel, specifically on the identification of bees, hoverflies, and butterflies:

- Targeted audience: PhD students and experienced professionals.
- Number of trainees, per course: 20 people.
- Duration of the course: 4 days online (4hrs each), plus 1 session (1 day) for fieldwork.
- Number of iterations, per country: as needed to cover the shortfall of skilled collaborators.

Some of these courses could be adapted for the different taxon groups (e.g. for butterflies, it is more valuable to have more field time than online).

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[12] https://www.forbio.uio.no/

Tier 2: Additional modules should be provided for intermediate levels, so that they can initiate the process to go from intermediate to advance levels in a period of 1-2 years.

- Targeted audience: Amateurs and Citizen Scientists (see section 2.7), and collectors in general of intermediate ability and/or with previous experience in the field.
- Number of trainees, per course: 20 people.
- Duration of the course: 4 days online (4hrs each), plus 1 session (1 day) for fieldwork.
- Number of iterations, per country: as needed to cover the shortfall of skilled collaborators, at least 1 per site per year (to ensure replacement in the number of iterations per site).

Tier 1: Specific effort should be dedicated to build capacity in these Member States where online training can be complemented with in-situ training, to build capacity. Other factors, such as capacity to retain trainees, progressive and consistent programmes, or trainers' availability might be more critical than just the possibility to access to instrumental courses. Collaboration with taxonomic facilities (as museums) will be essential at this stage to ensure access to collections and high-level experts.

Pollinator Citizen Science initiatives for monitoring are considered pivotal for the implementation of EU PoMS across Europe in the long run. As described in section 2.7, the most relevant aspects influencing Pollinator Citizen Science, including scientific, cultural and social are better established in northern and Western Europe while those tend to be scored as in embryonic or developing stages in Southern and Eastern countries. Still, critically for butterflies, embedding Pollinator Citizen Science as part of the monitoring scheme can greatly support the potential lack of other more experienced amateurs, especially in data collection and recording to which most of the Citizen Science projects are linked to (74% as per SPRING data).

While some of the Pollinator Citizen Science may fall under well trained categories of amateurs, their major role in supporting the role of experts is strongly linked to the use of technologies (e.g. image classification) and/or well-documented reference manuals (e.g. field guides). Despite other significant benefits of the Citizen Science involvement in environmental issues, their participation in monitoring schemes can be important to lower the costs of the human resources component, provided their commitment is stabilised and their skills upgrade is consistent and matches the needs for pollinators monitoring. Projects such as ABLE and SPRING have aimed at increasing the capacity of Pollinator Citizen Science to embed their participation in EU PoMS. Initial precautions and concerns in relation to their skills levels required for reliable species identification could be easily softened with a set of protocols and procedures, good validation processes (by experts), tooling them up adequately (with apps and other techniques), and training and capacity building actions.

Provide access to adequate resources. On top of what it is already available through the Pollinator Academy, an additional effort may be required to compile resources of any kind and typology, for different levels and for different targeted audiences. Apart from ORBIT, Taxo-Fly and Butterfly Conservation Europe, other related initiatives should be integrated, and outcomes should be classified and gathered when applicable to address pollinators monitoring. National endeavours need to be identified and integrated. Special considerations should be given to linkage with Citizen Scientist projects (by exploring links through the European Citizen Science Association-ECSA) to leverage on their objectives and benefit from existing results. Among others, reference collections from TETTRIs, the factsheets already compiled from the European Pollinators and field guides from Life4Pollinators project can be easily gathered in a centralised, fully accessible, open-source platform that can offer training material and a variety of resources adapted to the different actors involved in EU PoMS. In this respect, the building of (physical and virtual) reference collections at national level should be prioritised as a reliable, systematic and stable tool.

2.6.5.2 Model for long-term sustainability

Despite the urgent actions required to first implement EU PoMS and ensure a consistent and comprehensive European data collection for pollinator monitoring, a stable (harmonised with implementing protocols, standards and indicators), secured (with revisions agreed to improve the system), sustainable (in space and time) and well-supported model (organizationally, scientifically and financially) should be shaped and improved with results obtained from the first implementation round.

While in the short-term monitoring primarily is expected to be supported by highly skilled experts (professionally based), the system could move towards a ***hybrid (combined) format*** where professionals are assisted by volunteers whose competencies will increase over time, provided they are recognized, tool-up satisfactorily and guided efficiently.

Therefore, we distinguish actions directly tackling: (i) the development of taxonomic expertise in professionals, and (ii) the engagement and commitment of volunteers, notably Citizen Scientists (as defined in section 2.7).

Actions for taxonomic expertise capacity, towards strengthening and consolidation

Currently, taxonomists are usually linked to research institutions where biological collections are hosted. Those can be universities, museums, botanical gardens and biodiversity centres, and to a much lower extent, other facilities for which identification of biological material might be central (e.g. pharmaceutical industry). During the last decades shortage of these current positions is growing, since many positions are not being renewed (e.g. due to budget cuts), and European academic tracks are not giving significance to the discipline as to attract new generations of taxonomists. In this same scenario, the need for taxonomic knowledge has increased under the umbrella of strategic frameworks in Europe (the European Green Deal[13] and the EU Biodiversity Strategy for 2030 (European Commission, 2020)) and globally (Kunming-Montreal Global Biodiversity Framework-GBF, (Convention on Biological Diversity, 2022a)) that recognise the contribution of taxonomy as a fundamental pillar for biodiversity conservation, and more importantly to provide the baseline for tackling major challenges (see GBF Targets 1 to 8, under Chapter 1-Reducing threats to biodiversity).

Those two contradictory forces, the decline of experts and rise of taxonomic capacity requirements, are producing the shortfalls discussed in section 2.6.4, which need a long-term sustainable model to be overcome.

To ensure long-term stability and sustainability in building taxonomic capacity in Europe to meet the challenges imposed by the need of more, better and larger datasets on pollinators for their accurate and reliable monitoring, it appears essential to implement a multifaceted strategy that encompasses a variety of critical dimensions including funding, education, technology,

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[13] https://commission.europa.eu/strategy-and-policy/priorities-2019-2024/european-green-deal_en

collaboration, and policy integration. We present here some of the measures to facility monitoring implementation with a long-term perspective.

Recognition: Lack of recognition works as a pressure for taxonomic activity. Taxonomic research and its outcomes are often considered either “old-fashioned” or not significant or impactful enough. Therefore, specific actions should be implemented to recognise the role of taxonomists in tackling major challenges and their contributions should be highlighted to identify what to preserve, monitor and restore, wherever and whenever needed. Among the activities running under the TETTRIs project, the Taxonomy Recognition Day was launched (in 2024 for the first time) to raise awareness of this critical activity for halting biodiversity loss and preserving our natural resources.

Academic pathways: Attracting young students to the science of taxonomy necessitates its inclusion in the academic curricula from which it has progressively disappeared. Generally, biology only tackles taxonomy laterally during the Bachelor and Master programmes in most of the Universities across Europe. While taxonomy is referred to in many doctorate courses, it is only a fragment of the course content and never the core of the training. Only few specialised courses are taught specifically addressing taxonomy and most of the training addresses audiences formed by interested people rather than biologists or biology post-doc students (e.g. see Synthesys+ project[14] and its catalogue of training resources). This overall picture for taxonomic expertise applies equally to pollinators. Yet, to attract students, the academic curriculum should include this discipline and address the varied applied taxonomic research opportunities. In this respect, academic programmes should address taxonomy with an integral approach, where faunistic and molecular methods are combined, so that students can gain the necessary skills for undertaking better, expanded and reliable species identification. Graduates would then be able to choose to work at a university or a research institute, or access openly to a new array of opportunities, provided those employment opportunities exist in the labour market and offer a space for professional development. Some efforts are currently underway, such as the TETTRIs project which tackles specific academic certifications (for Master’s and Doctorate degrees) for taxonomy, and is building a roadmap for the European Taxonomic Agency where academia, private sector, scientific organizations, and policy makers can discuss mechanisms to improve taxonomic capacity in Europe. Other lateral factors such as taxonomic publishing should be revised and standards for taxonomic assessment reviewed in accordance to its relevance and impact.

Professional careers: New generations need to have future employment positions to build their professional careers, both scientifically and financially. Member States should become more aware of the shortfalls detected and make a firm commitment to support creation of new positions. Support should be targeted to:

- Consolidate taxonomy-related positions in research institutions.
- Integrate taxonomic expertise in policymaking processes, through governmental agencies (in public health, civil planning, agriculture, wildlife management and forestry).
- Facilitate and foster linkage with private sector (such as agricultural processors and pharmaceutical companies).

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[14] https://www.synthesys.info/about-synthesys/deliverables.html

- Endorse scientific protocols for monitoring process, making this implementation binding (as for the environmental impact assessments).
- Promote the implementation of taxonomic practices across actors. In this context, the TETTRIs project has created the programme “Taxonomists in Residence” that aims to associate the practice and transfer the knowledge of taxonomists from taxonomy to other different disciplines and fields.

Actions for volunteers, towards engagement and commitment

It is expected that the majority of Member States will use professionals for sampling identification at the start of EU PoMS; however, the transition to a more volunteer focused approach poses important opportunities and challenges. Linkage with Citizen Science initiatives (see section 2.7) and in situ practitioners (including farmers and protected areas managers) will be essential to build a coherent and sustained model for pollinators monitoring.

Participation of citizens with voluntary contributions to the implementation of the EU PoMS in the long run will require the creation, development and continuous training of stable groups raised locally, to efficiently move from a flat towards a hybrid format (with non-professionals potentially contributing up to 50% of the workforce). It should be noted that the non-professionals, in most cases, should concentrate their efforts in one single site, close to their residences, deeply known by means of repeat visits and strongly linked to their particular interests.

While Pollinator Citizen Science is well anchored in the societal structures in northern Europe, where important initiatives support their work very efficiently (such as national portals and global initiative such as eBird and iNaturalist), most of the countries in southern Europe may need additional efforts to create these structures. In both cases, across the entirety of Europe, to fully integrate Pollinator Citizen Science into EU PoMS in the long run, several dimensions should be tackled in a multifaceted effort:

- Involvement of enlarged numbers of volunteers. Apart from naturalists, there are several target groups that could be involved, based on shared interests and impacts: gardeners, practitioners linked to forestry, citizens engaged in outdoor activities, beekeepers, farmers, and other members of agricultural communities. In this context, local governments are critical to reach these groups and engage them through communication campaigns and raising awareness of the importance of the citizen’s contribution to preserve natural resources of the community.
- Commitment and stability. These potential groups of interest need to be organised in communities that form stable structures that can be easily reachable. For this, local governmental bodies and other institutional entities (such as local museum, botanic gardens, parks and similar) could facilitate the creation of these informally as stable structures to gather people’s interests and enhance commitment.

- Resources provision to communities. Adequate tools should be provided to enable communities to become meaningful collaborators. Access to keys, field guides, atlases, Apps, and web-based tools should be granted free of charge, and the communities should be trained in their use. Leveraging on outcomes from projects such as TETTRIs and SPRING, facilitating benchmarking, promoting school camps, and enabling exchange of information and networking (across localities, at national level, and when feasible also beyond country borders), and other similar initiatives should be provided. On top of those local efforts, centralised training (in both online and blended formats with practise in the field) should be created and promoted through a central hub, at European level. National authorities should finance necessary translation and provision of expert trainers.
- Structural recognition. All actors involved in these activities should be engaged with the recognition of those supporting communities. Through publications, awards, organization of events, integration in institutional websites and social media, and many other initiatives could be put in place to recognise the extremely important role of citizens in the implementation of EU PoMS.

Maniola jurtina, eBMS transect at JRC Ispra

2.6.6 General recommendations

We consider that the implementation of EU PoMS needs to rely on a holistic approach that encompasses social, technical, and financial facets. This comprehensive strategy could contribute to ensuring the longevity and effectiveness of the scheme across Member States under the umbrella of a harmonised mechanism at the European level. Strategic support for monitoring implies the design of a resilient and adaptive framework for taxonomic capacity, capable of evolving and improving in response to the national requirements across the EU-27. We present here some key recommendations that may guide the design of a comprehensive scheme for building taxonomic capacity critical to run EU PoMS with a long-term perspective. These recommendations require the integration of European and national commitments.

2.6.6.1 Social infrastructure

The social component is extremely pivotal, since no strategy for pollinator monitoring would be successful without the necessary dedicated expertise and the engagement of various actors. Building taxonomic capacity requires a concerted effort from academia and educational institutions, research entities, non-governmental organizations, and government bodies. Key options should include:

Education and training:

- Launch educational programmes (from primary schools) to raise interest and consciousness about taxonomy and its role in preserving a healthy environment for the future.
- Establish targeted training programmes and integrate them in the formal education systems, in collaboration with academia and existing training initiatives for taxonomy.
- Facilitate the certification and validation of non-formal training programmes provided by recognised entities that ensure expertise of tutors and quality of contents.

Workforce Development:

- Create clear career paths for taxonomists, including roles in academia, government agencies, NGOs, and the private sector, ensuring job diversity and security.
- Foster mentorship programs that connect emerging taxonomists with experienced professionals, encouraging knowledge transfer and skill development.
- Facilitate the integration of taxonomists in a wider multidisciplinary environment (e.g. through initiatives such as “Taxonomists in Residence”), to underline the richness and applicability of taxonomic knowledge.

Collaboration and partnerships:

- Validate the role of European networks on taxonomy (as CETAF) that can foster collaboration among institutions, researchers, and practitioners, facilitating the sharing of knowledge, resources, and best practices.
- Strengthen international partnerships to leverage global expertise and resources, and alignment with sister initiatives at international level.

Policies integration and coordination:

- Integrate taxonomic knowledge and expertise into European environmental policy and decision-making processes, recognizing the importance of taxonomy in addressing biodiversity loss, and support among others, pollinator monitoring.
- Support the community participation through existing hubs of experts that can act as direct interlocutors and coordinators of actions.

2.6.6.2 Technical infrastructure

Parallel to the social infrastructure, the development of a robust technical infrastructure is essential. This encompasses the deployment of tools and mechanisms that support the intricacies of taxonomic work for pollinator monitoring. Those include digital libraries and reference collections, to provide accessible, accurate, and comprehensive taxonomic information. Equally, the provision of tools and mechanisms to ease the gathering, interpretation, and analysis of data in the field to facilitate the work of practitioners at all levels, from enthusiasts and volunteers to managers, professionals and experienced amateurs, and also the taxonomic experts located at the end of the knowledge creation and data validation chains. Multilingual aspects and customisation to national specificities should be considered. Key actions should include:

- Establish and coordinate national units where the main tasks will be conducted for monitoring (identification and databasing).
- Support the development of comprehensive digital databases (as virtual reference collections) and online platforms (e.g. DEST and the Pollinators Academy) that facilitate the sharing of taxonomic data on pollinators and resources across Europe, and globally.
- Implement policies that sustain the building and conservation of taxonomic reference collections at national level (physical and virtual), encompassing larger taxa, ensuring they are well maintained, updated, and made accessible for future research. Achieving this goal necessitates a concerted effort to foster both staffing levels and the technical infrastructure within natural history museums and other taxonomic facilities.
- Link to a coordination hub, and allocate a central platform at European level (e.g. under the Pollinator Information Hive) to gather available protocols, standards, indicators and other different policies that are intrinsically linked to pollinators monitoring. Specific pages per country could be integrated.
- Ensure that adequate pipelines are implemented to secure uploading data from the teams working in the monitoring, quality checks and validation mechanisms. Workflows should made available in the central hub.
- Invest and promote the integration of advanced technologies, such as AI, machine learning, and genetic sequencing, to foster integrative taxonomic research.

2.6.6.3 Financial infrastructure

The financial infrastructure necessarily plays a critical role in underpinning the other components and ensuring that the overall system works efficiently. Sustained longer-term funding for taxonomic work at both national and European levels is vital. This entails not only securing government allocations but also exploring diverse funding streams notably public-private partnerships. Financial resources are required not only for the direct costs associated with research and fieldwork, but also for supporting the development and maintenance of technical infrastructure, and for facilitating capacity-building activities. This financial structure also needs to consider aspects such as equity and inclusiveness to compensate for differences between northern and southern regions, the former being better developed currently, while the latter has higher pollinators' richness. Key actions should include:

- Create and implement a sustainable funding model to cover the implementation of EU PoMS: (i) a centralised hub for harmonisation of the scheme, its standards, protocols and indicators; and (ii) a distributed mechanism supported by national governments, with a diversified mechanisms for funding (national grants, private sector partnerships, grants from environmental and scientific foundations, and crowd-sourced initiatives).
- Create a robust mechanism to ensure efficiency in the use of resources, effectiveness in the implementation of measures and adaptability to overcome new challenges and detected bottlenecks. In that regard, the use of adaptive models such as the OECD evaluation model (OECD, 2021) could be customised and applied (Figure 2.6. 7).
- Establish dedicated endowments for taxonomy to ensure long-term financial stability: EU-level support through calls and subsidies specifically earmarked for taxonomic research and taxonomy-related infrastructures, emphasizing the critical role of taxonomy in biodiversity conservation (and environmental policy at large).

Figure 2.6. 7. The OECD evaluation model framework, which could be adapted to ensure the effective implementation of financial measures.

Source: OECD (2021).

2.7 Options for building Citizen Science capacity for EU PoMS

2.7.1 Summary

Europe has a long and rich tradition of Citizen Science and its innovation. This has provided a wealth of data and knowledge alongside the benefit of engaging people with science and nature. Recognising this value, Citizen Science has become increasingly prevalent within European Union funding programmes such as Horizon Europe, BiodivERsA, COST Actions and LIFE projects, and recognised by European institutions (De Rijck et al., 2020). In this chapter, we evaluate the potential of Citizen Science as an integral element of an EU pollinator monitoring scheme.

We summarise the current state and capacity of Citizen Science networks in EU countries using results from the SPRING project, notably a questionnaire receiving over 320 responses on the current status of Pollinator Citizen Science. The mean score for most countries placed factors (i.e. aspects influencing Pollinator Citizen Science) as either developing or establishing, indicating that there is support and potential for Pollinator Citizen Science across all countries. There was a general trend for most factors being more established in northern and western Europe. Factors in southern and eastern Europe tended to be scored as in embryonic or developing stages, aligned with our expectation that these regions pose the greatest challenge to embed Pollinator Citizen Science as integral part of EU PoMS.

Although Pollinator Citizen Science encompasses a range of approaches, SPRING results showed that data collection projects fall into one of three types based on broad ecological scope: most projects (74%) focus on recording organisms that are pollinators; one quarter (25%) collect data on the process of pollination, typically plant-pollinator interactions; and only a very small number (1%) examines the outcomes of pollination through measuring attributes like seed-set.

We review the potential of involving a range of new audiences in Pollinator Citizen Science, beyond established networks of people interested in recording species. We provide an overview of options for Pollinator Citizen Science in a farmland context given the importance of agriculture in Europe. Farmers and other members of agricultural communities are an important audience as they engage regularly with data collection sites and can adapt their farming practices as a direct response to the results of data collection on their own land.

We identify opportunities provided by Citizen Science across the range of EU PoMS proposed monitoring approaches, including core scheme sampling via reinforced transects, moth monitoring, rare and threatened species surveys, and wider insect diversity monitoring. While the early phase of the implementation of EU PoMS is expected to be primarily professional-led, the longer-term ambition is to increase the role of volunteers in the scheme as it matures. We note that the extent and rate of this shift to a more hybrid approach will depend very much upon the starting conditions and resources available for each Member State. In particular, Citizen Science has a potentially important future role in reinforced transects, one of the core methods of EU PoMS. This includes data collection by experienced naturalists for some groups and specialists for other groups and for training and engagement. Transects involving Citizen Science has potential to integrate with existing schemes, particularly Butterfly Monitoring Schemes and place-based monitoring (e.g. Nature Reserves).

The barriers and opportunities for successful Citizen Science are increasingly being recognised and we provide recommendations of key consideration when implementing new initiatives, including for farmland, and as an important component of EU PoMS and wider initiatives to protect and restore biodiversity in the EU.

2.7.2 Overview of current Citizen Science activities

Citizen Science can be defined as “the involvement of the non-academic public in the process of scientific research – whether community-driven research or global investigations”[15]. As might be expected from this broad definition, there are a wide variety of related terms (e.g. participatory action research, civic science, amateur science, community science, crowdsourced science) which are either synonymous with Citizen Science or overlap in scope. In the context of biodiversity, Citizen Science has a long and rich history (e.g. Pocock et al., 2015; Silvertown, 2009) and has been used in a wide variety of research (e.g. Hochachka et al., 2012) and applied contexts (e.g. McKinley et al., 2017), including biodiversity monitoring (Chandler et al., 2017). Citizen Science is increasingly recognised as a cost-effective approach to monitoring (Breeze et al., 2021) and has grown and diversified as an approach, often through the use of technology (Pocock et al., 2017).

Although now a global phenomenon (Requier et al., 2020), Europe benefits from being home to a long and rich tradition of Citizen Science and its innovation. As well as providing a wealth of data and knowledge, environmental Citizen Science has the additional benefit of engaging people with science and nature, so supporting trust in science, pro-environmental behaviour and better natural resource management. Often, volunteers are engaged in data collection within Citizen Science projects, with expert volunteers also involved in the classification and quality-assurance of records (e.g. providing identification of photographed animals and plants). Volunteers can also be integral to the design and reporting of Citizen Science projects, working with researchers to co-design an approach and interpret results. Involving people in the process (not just the outputs) of scientific research can support informal learning and scientific awareness, enhance public engagement with science and support the development of public policy (McKinley et al., 2017; Tulloch et al., 2013).

Implementation of the EU PoMS could benefit from involvement of citizen scientists, as volunteer participants and alongside professional researchers, data analysts and taxonomic experts, although the extent to which might vary over time and between regions of Europe. Differences in circumstance mean that Member States will be at different points along a gradient ranging from professional-dominated through to Citizen Science-dominated approaches to implementing the scheme. Although there are proven examples of Citizen Science involvement in pollinator monitoring in parts of Europe (e.g. Billaud et al., 2021), there are considerable challenges to strengthening Citizen Science capacity across the whole of the EU (Johnston et al., 2023; Richter et al., 2021). For example, butterfly monitoring through volunteers has over 40-year tradition in parts of Europe (e.g. the UK, the Netherlands, Catalonia, Finland) and has been undergoing a phase of expansion since mid-2000s (e.g. Germany, France, Luxembourg, Spain) with new schemes being established in the past few years (e.g. Italy, Portugal, Hungary). The recent expansion has been supported by EU funding through the ABLE project and the SPRING project. As part of the expansion and diversification of Citizen Science across environmental science, a range of approaches has been developed to assess pollinating insects beyond butterflies (Falk et al., 2019; H. E. Roy et al., 2016), and pollination services (Birkin and Goulson, 2015; Bloom and Crowder, 2020; Garratt et al., 2019). This includes reaching new audiences, such as Citizen Science involving farmers, which has been shown to be successful in relating biodiversity trends to agricultural practices (https://www.greatsunflower.org/ (Billaud et al., 2021), though the majority of Citizen Science

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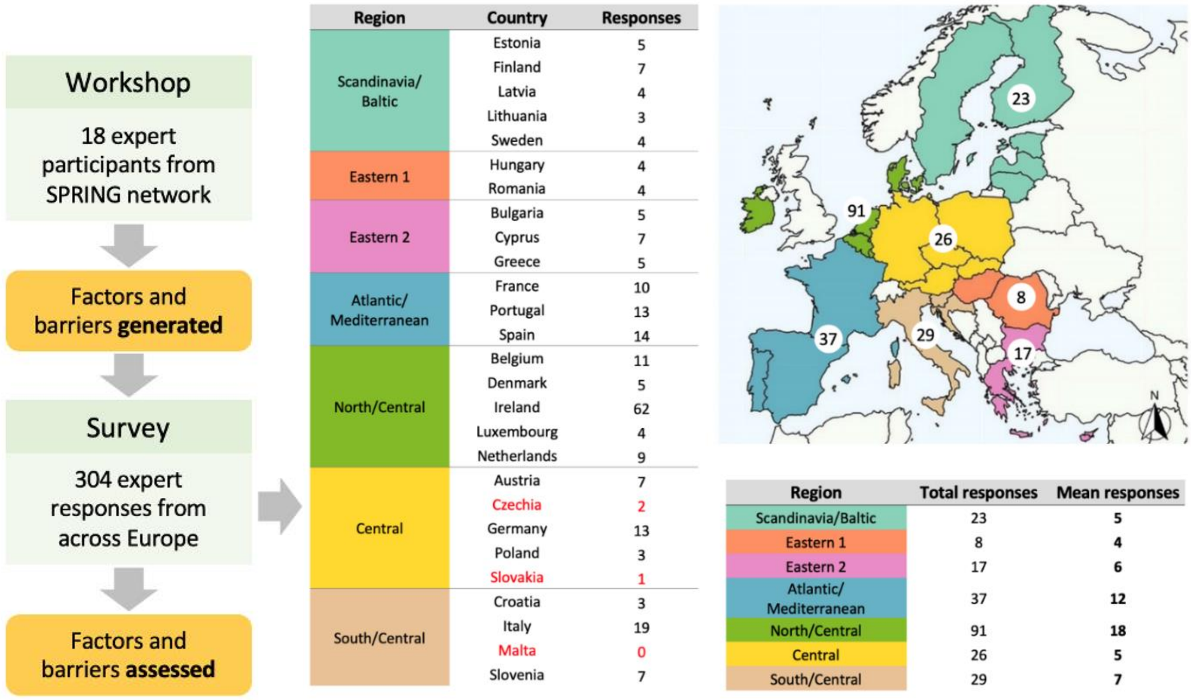
[15] https://citizenscience.org/

initiatives on farmland leaves farmers out of the picture (Ebitu et al., 2021; Garratt et al., 2019; Ruck et al., 2023).

This report expands on previous Pollinator Citizen Science. The first part is based on work undertaken during the SPRING project (Pocock and Bane in prep). During the first year of the SPRING project (2022), the current state and capacity of Citizen Science networks in EU countries were assessed using expert consultation, through a workshop, and via an online survey. A preliminary workshop was held on the 6th of December 2021 with experts to collaboratively develop criteria for the prioritisation of Pollinator Citizen Science across different regions. Eighteen experts from across the EU attended and all participants completed a pre-workshop task: identifying factors that enable successful Pollinator Citizen Science and Citizen Science more generally. These factors were finalised, and a set of barriers to Pollinator Citizen Science were identified in the workshop.

Key aspects identified in the workshop were used to create a questionnaire. This was sent out to stakeholders across the EU to assess the existing capacity for Pollinator Citizen Science. The survey was live for 3 weeks and was widely promoted through the SPRING network, other pollinator research networks and on X (formerly Twitter). The survey was completed by 321 participants from across Europe, representing 37 different countries and all EU Member States (Figure 2.7. 1**Figure 2.7. 1**). Response rates varied greatly across countries, with 62 responses from Ireland, none from Malta and a median response rate of 5 per country.

Figure 2.7. 1. Schematic method for the assessment of Pollinator Citizen Science across the EU, showing the number of responses per country and region on the right. The minimum of 3 responses was achieved for all but 3 countries (Czechia, Slovakia and Malta). All regional targets were achieved (>5), and greatly surpassed in some cases. Overall, the response rate was sufficient for our analysis.



Region	Country	Responses
Scandinavia/ Baltic	Estonia	5
	Finland	7
	Latvia	4
	Lithuania	3
	Sweden	4
Eastern 1	Hungary	4
	Romania	4
Eastern 2	Bulgaria	5
	Cyprus	7
	Greece	5
Atlantic/ Mediterranean	France	10
	Portugal	13
	Spain	14
North/Central	Belgium	11
	Denmark	5
	Ireland	62
	Luxembourg	4
	Netherlands	9
Central	Austria	7
	Czechia	2
	Germany	13
	Poland	3
	Slovakia	1
South/Central	Croatia	3
	Italy	19
	Malta	0
	Slovenia	7

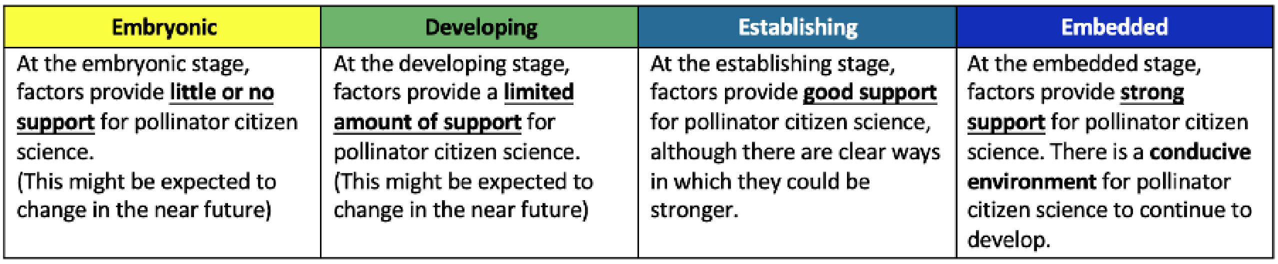
Region	Total responses	Mean responses
Scandinavia/Baltic	23	**5**
Eastern 1	8	**4**
Eastern 2	17	**6**
Atlantic/ Mediterranean	37	**12**
North/Central	91	**18**
Central	26	**5**
South/Central	29	**7**

Source: Authors' elaboration based on the SPRING project.

2.7.3 Current state of Pollinator Citizen Science

Twelve key factors that enable successful Pollinator Citizen Science were identified and their current status evaluated in countries across Europe (Figure 2.7. 3). Factors were evaluated according to our EDEE scale (Embryonic, Developing, Establishing and Embedded; Figure 2.7. 2). Overall, the mean score for most countries placed factors as either developing or establishing, indicating that there is support and potential for Pollinator Citizen Science across all countries.

Figure 2.7. 2. Embryonic, Developing, Establishing and Embedded scale (EDEE scale) for evaluating factors that enable Pollinator Citizen Science. Based on the EDGE scale[16] used to evaluate public engagement ('Embryonic', 'Developing', 'Establishing' and 'Embedded').



Embryonic	Developing	Establishing	Embedded
At the embryonic stage, factors provide **little or no support** for pollinator citizen science. (This might be expected to change in the near future)	At the developing stage, factors provide a **limited amount of support** for pollinator citizen science. (This might be expected to change in the near future)	At the establishing stage, factors provide **good support** for pollinator citizen science, although there are clear ways in which they could be stronger.	At the embedded stage, factors provide **strong support** for pollinator citizen science. There is a **conducive environment** for pollinator citizen science to continue to develop.

Source: Authors' elaboration.

There was a general trend for most 'factors' (i.e. aspects influencing Pollinator Citizen Science) being more established in northern and western Europe. Factors in southern and eastern Europe tended to be scored as in embryonic or developing stages. This trend is aligned with our expectation based on previous discussions with experts and indicates that the greatest challenge for EU PoMS to embed Pollinator Citizen Science would be in southern and eastern Europe.

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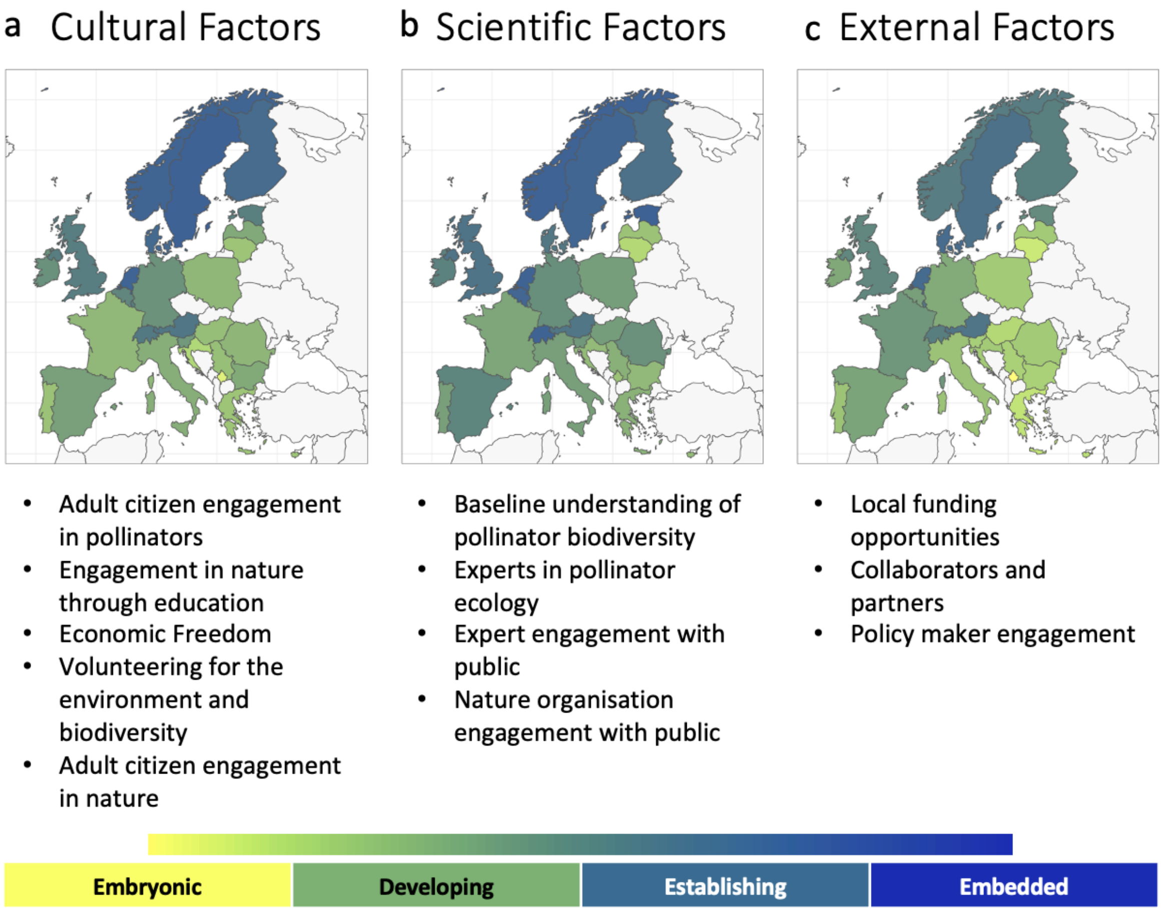
[16] https://www.publicengagement.ac.uk/support-engagement/strategy-and-planning/edge-tool

Figure 2.7. 3. The overall state of Pollinator Citizen Science, grouped into a) cultural factors, b) scientific factors and c) external factors.



a Cultural Factors

- Adult citizen engagement in pollinators
- Engagement in nature through education
- Economic Freedom
- Volunteering for the environment and biodiversity
- Adult citizen engagement in nature

b Scientific Factors

- Baseline understanding of pollinator biodiversity
- Experts in pollinator ecology
- Expert engagement with public
- Nature organisation engagement with public

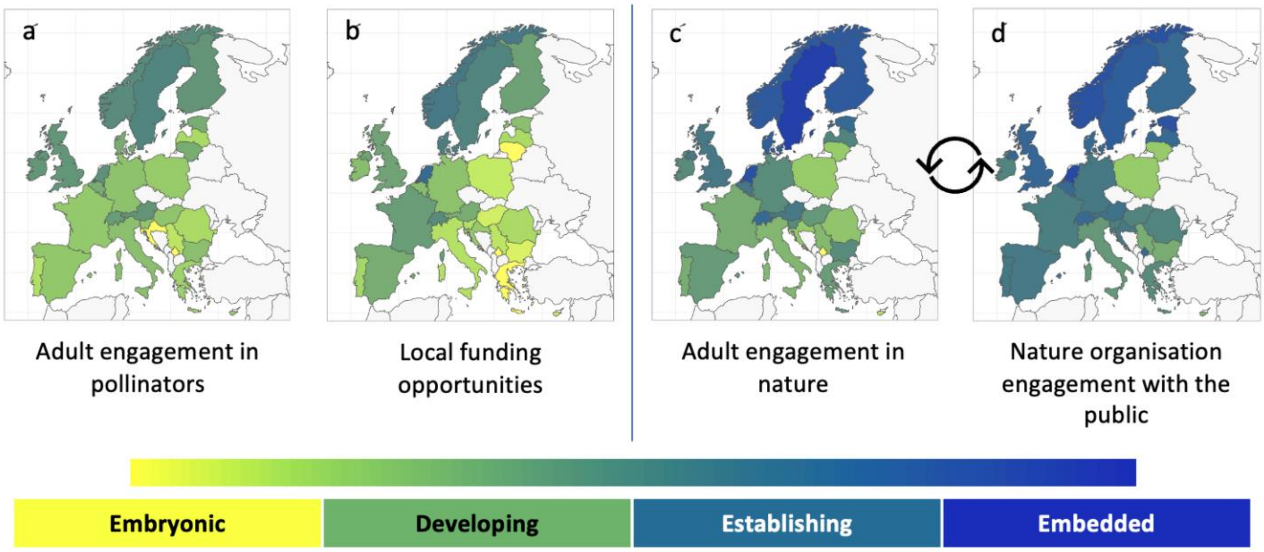
c External Factors

- Local funding opportunities
- Collaborators and partners
- Policy maker engagement

Source: Authors' elaboration based on the SPRING project.

The greatest barriers for Pollinator Citizen Science, notably across southern and eastern Europe, identified by SPRING and in line with Richter et al. (2021), are the extent to which there is 'adult engagement with pollinators' and availability of (local) funding (Figure 2.7. 4). On the other hand, it was reported that adult citizens tend to be well engaged with nature, and that nature organisations facilitate public engagement in biodiversity (Figure 2.7. 4). It is logical to assume that these two factors are highly interlinked, with engaging nature organisations improving adults' engagement in nature and interested adults creating an active audience and demand for nature organisations to cater to. There are likely to be other important factors affecting Pollinator Citizen Science development that have not been assessed here; lack of trust in government and institutions, including those promoting or organising Citizen Science may be a barrier in some situations, for example.

Figure 2.7. 4. The factors that scored lowest across Europe were a) 'Adult citizen engagement in pollinators', and b) 'Local funding opportunities'. These were also identified as being the greatest barriers to successful Citizen Science. At the other end of the spectrum were c) 'Adult engagement in nature' and d) 'Nature organisation engagement with the public'.

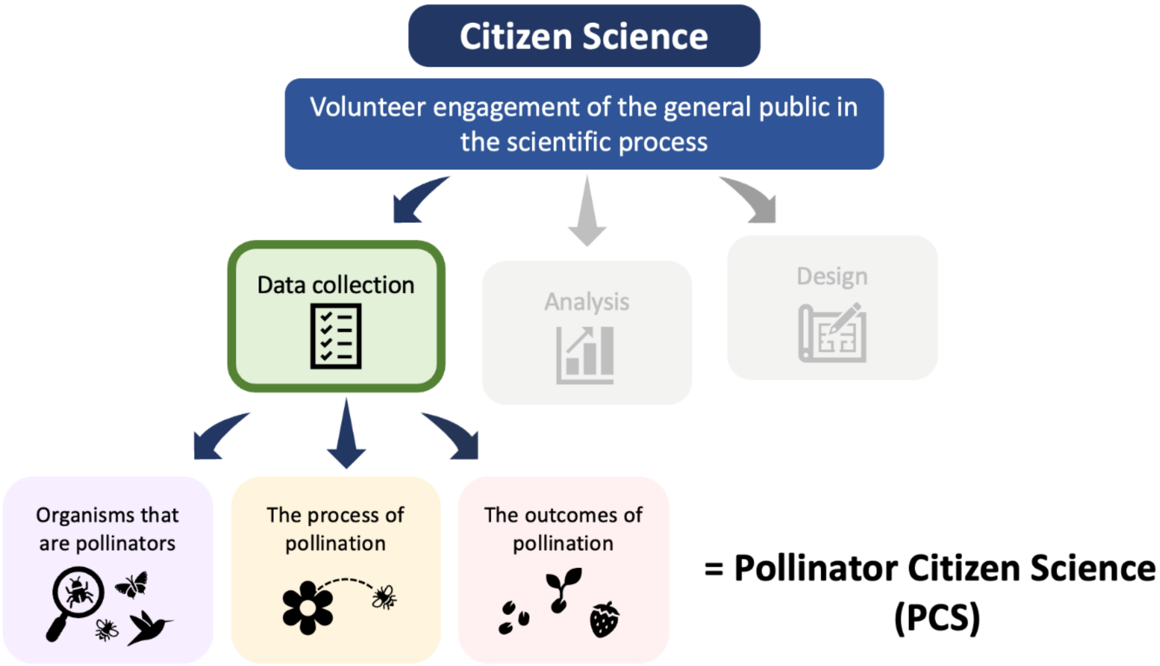


Source: Authors' elaboration based on the SPRING project.

2.7.4 Pollinator Citizen Science approaches

Pollinator research is broad and rich in its scope. Similarly, Pollinator Citizen Science covers a myriad of different foci and approaches. The SPRING project undertook a review of Pollinator Citizen Science projects from across the world, but with a focus on Europe. The review focussed on data collection projects, but some also include citizen scientist involvement in project design and data analysis (Figure 2.7. 5). This analysis provided a 'state of play' of Pollinator Citizen Science globally as per Pocock et al. (2017) for Citizen Science more generally. It did not assess 'success' of the projects, because this is difficult to do without a clear understanding of the projects' aims. A database of circa 250 projects was constructed, with a systematic approach for scoring project attributes.

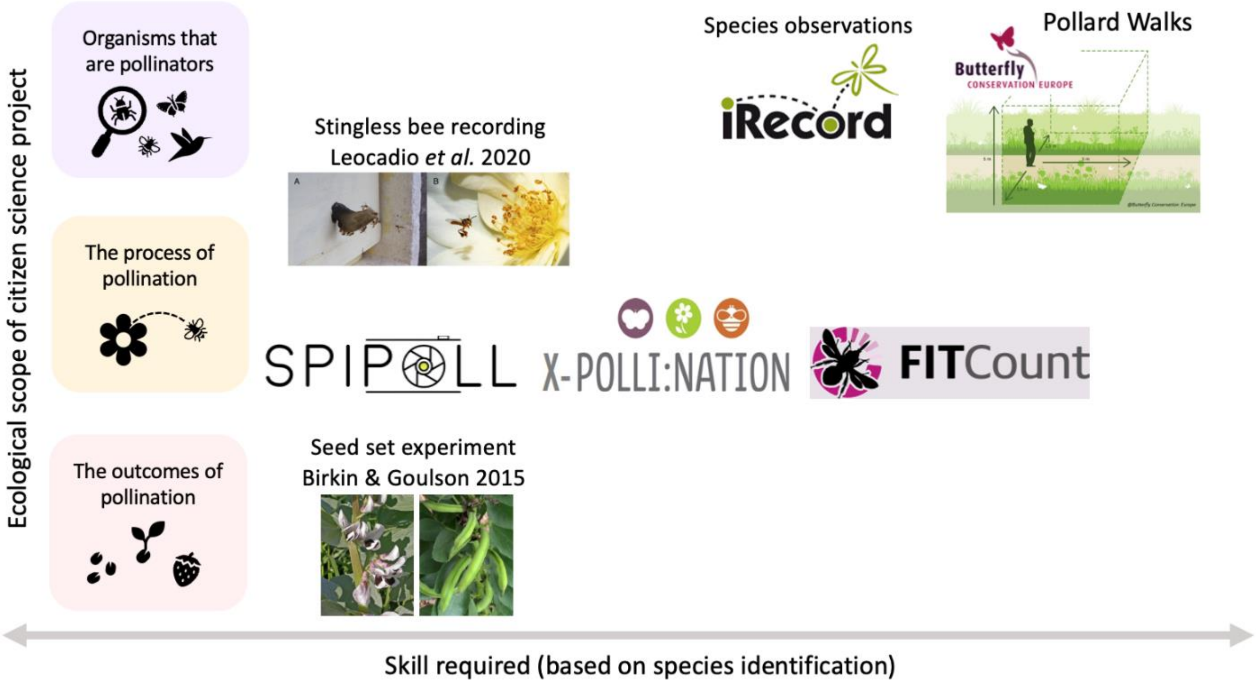
Figure 2.7. 5. Pollinator Citizen Science is made up of Citizen Science projects that collect data on organisms that are pollinators, the process of pollination and the outcomes of pollination. Data analysis and project design are also valuable Citizen Science approaches but are not the focus of the SPRING review.



Source: Authors' elaboration based on the SPRING project.

The results showed that data collection Pollinator Citizen Science projects fall into one of three types based on broad ecological scope. Most Pollinator Citizen Science projects (74%) focus on recording organisms that are pollinators. One quarter (25%) collect data on the process of pollination, typically plant-pollinator interactions. Only a very small number (1%) examines the outcomes of pollination through measuring attributes like seed-set. There is huge diversity in the projects across many different attributes such as target audience, complexity, data type, data quality and time required. One particular attribute, the 'skill level required' was subject to much discussion in the expert workshop in connection with concerns over the ability of citizens to identify species and provide reliable data. Thus, we provide examples to illustrate the diversity of projects with respect to 'skill level required' and the three types of ecological scope, demonstrating that such concerns can be overcome through appropriate project design.

Figure 2.7. 6. Illustrating the diversity of Pollinator Citizen Science projects according to the skill required (based on species identification) and the ecological scope of projects. This is a simple representation (prior to formal analysis) and projects requiring greater identification skills in the field are towards the right of the figure. Links to ongoing projects named in figure: Spipoll[17]; X-Polli:Nation[18]; FITCount[19]; iRecord[20]; European Butterfly Monitoring Scheme[21].



Source: Authors' elaboration based on the SPRING project.

The SPRING report brings out that it is a common misconception for Pollinator Citizen Science that all citizen scientists must be able to identify pollinator species reliably. For some projects, such as the Pollard transect walks used by Butterfly Conservation Europe to record species abundance, this is a prerequisite and therefore only citizens with such skills (or those willing to learn them) can participate. Projects such as FIT counts run by the UK Pollinator Monitoring Scheme focus on plant-pollinator interactions and only require identification to broad species groups. SPIPOLL and X-Polli:nation take this a step further and utilise AI and expert identification of photographs to soften the requirement for identification from those collecting the data in the field. Projects that focus on measuring the outcomes of pollination such as seed set do not require insect identification skills (but may require other skills), because the data comes from counting or assessing seeds and fruit from a given plant. Therefore, a variety of approaches with different target audiences can be used to maximise Pollinator Citizen Science project uptake and data collection (Figure 2.7. 6).

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[17] https://spipoll.org/

[18] https://xpollination.org/

[19] https://ukpoms.org.uk/fit-counts

[20] https://irecord.org.uk/

[21] https://butterfly-monitoring.net/

2.7.5 Developing EU pollinator Citizen Science

As the above already indicates, there are many ways of doing Citizen Science, and Citizen Science itself is only one family of participatory approaches that relies on voluntary contributions in the context of environmental monitoring or management (others being e.g. collaborative management, community-based management, monitoring under adaptive management). Citizen Science itself is differently imagined and defined (e.g. Eitzel et al., 2017) and has become a catch phrase that suits a large set of activities and circumstances. In reality very different forms of Citizen Science are practised, each with their own logics; and importantly for EU PoMS, connecting to different layers of society and working from different structures, principles and interests (see also Bryn et al., 2023; Land-Zandstra et al., 2021)

2.7.5.1 Target audiences

One of the reasons why environmental Citizen Science has been able to come up so rapidly as 'method' is that it has appropriated well-anchored structures in the western world to do with interests in species. The success of environmental-based Citizen Science activities therefore must be considered in relation to the long-term tradition of biological recording (Pocock et al., 2015). The most prevalent form of Citizen Science therefore goes far back, and the combination of deep environmental concern and digitisation has lifted the level at which traditional species recording and naturalist societies worked at to a global enterprise of digital biological recording communities - scaffolded by science itself (Larson et al., submitted) - of which the two giants, eBird[22] and iNaturalist[23], have become the image of environmental Citizen Science and what it can achieve. EU PoMS arguably works from and with that image and could connect to voluntary recorders from the (now digitally operating) biological recording world, i.e. naturalists, many of which hold rich knowledge and skill of the kind that EU PoMS values (i.e. species identification & field observation skills) (see section 4.4). Motivations of naturalists to contribute to Citizen Science initiatives are relatively well understood (e.g. Charvolin, 2022; Merenlender et al., 2016) and concern learning, attachment to nature and others, and sharing observations, while species identification is an important means for enacting their relationship with nature (Ellis, 2011). Attracting already-engaged participants would bring years of experience and networks of contacts (Everett and Geoghegan, 2016).

Environmental Citizen Science connects to many other specific audiences than naturalists, be it generally at a far smaller scale. Typical audiences are hunters, fishers and gardeners, each grouping around a specific interest and with structures (e.g. national, regional and local organisations, communication channels) that allow initiators (from within or out with those 'worlds') to reach potential volunteers. For EU PoMS, gardeners could be of interest, and their motivations are also relatively well understood (e.g. Sharma et al., 2019), centring on 'learning' and 'helping' (species, conservation and science). Another potentially relevant interest group, given the paucity of pollinator data from wooded landscapes, could be those connected to forestry. Less obvious but nevertheless potentially relevant interest groups could be those engaged in outdoor activities (e.g. walkers, bikers, climbers, orienteers, canoers and beekeepers), given some form well-structured and thus reachable communities. Beekeepers are a further potential group, already involved in Citizen

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[22] https://ebird.org/home

[23] https://www.inaturalist.org/

Science (e.g. INSIGNIA project) (Woodcock et al., 2022) and with a potential interest in, and expertise in, ‘wild’ pollinating insects. A major interest group for EU PoMS would be farmers and other members of agricultural communities (e.g. commercial beekeepers), hence covering those more extensively in the below. What most of these interest groups have in common is that potential volunteers therefrom hold deep understanding and relevant knowledge, but likely of different kinds from those we may expect due to differences in perspectives, experiences and worldviews; and as we will see in the below, their motivations may therefore differ too.

2.7.5.2 Involving farmers

Because of the importance of agriculture, farmers and other members of agricultural communities would be a natural target of EU PoMS - were it to include Citizen Science - for two reasons. First, they are well placed to participate in such monitoring given their proximity to and daily engagement with what would be their data collection sites (Ruck et al., 2023). Second, in terms of engagement and (for pollinators positive) change, farmers are a particularly important audience, given that they usually have at least some degree of agency to adapt their farming practices as a direct response to the results of data collection on their own land (Billaud et al., 2021). Ruck et al. (2023) reviewed existing Citizen Science approaches involving biodiversity monitoring on farmland, resulting in a typology of eight programme types unfolding along distinctions in types of data collected and nature of volunteer involvement. Their reflection on respective strengths and limitations is of considerable importance to EU PoMS and the different modes it may consider employing monitoring across Member States. Fundamentally, they point to two principal routes towards increasing the amount of volunteer-based biodiversity monitoring on farmland: 1) attract existing (naturalist) volunteers to new sites, i.e. on farmland, and 2) engage new groups of people that are already spending a lot of time on farmland, for example farmers, in the monitoring. Five key findings relevant to EU PoMS are:

1. While all identified types of Citizen Science can make substantial contributions to farmland biodiversity monitoring, there is considerable scope for their further development, particularly through increased engagement of farmers (see also Ebitu et al., 2021) and the use of technologies to reduce technical barriers to participation (e.g. using image classifiers to support the identification of species).
2. When developing farmland-specific programmes, the pool of potential volunteers is considerably reduced, making it yet more important to reflect on likely motivations of potential volunteers. With this in mind, naturalists may not be particularly attracted to farmland sites, while potential new volunteers from outside naturalist communities may be more attracted to programmes with methods where it is clear when a meaningful contribution (to e.g. science, contributing to greater knowledge on farmland biodiversity) is made. In many cases, highly prescribed programmes could be executed by professionals, although the costs would be higher. One can question whether it is ethical to engage volunteers if merely to reduce costs, particularly when a strongly structured (top-down) approach can regiment participants, thus limiting the influence of (for example) farmers on which biodiversity-related questions to address. It could also be safer to rely on professionals than on volunteers to ensure the long-term viability of the data collection.
3. When using, or planning to use, Citizen Science as a way to monitor farmland biodiversity, it is important to be aware of the main strengths and limitations of the different types of programmes identified here, including those related to their respective primary audiences (see also Bloom and Crowder, 2020). Different types of monitoring programmes are useful

for different purposes and attract different participants. See Annex 2.7 for likely dimensions to include in reflections.

4. Building links between Citizen Science and agricultural communities might be characterised as bridging the gaps between two distinct 'communities of practice' (e.g. Oswald, 2020; Sbrocchi et al., 2022). While bringing certain groups of people together through a common purpose or interest, such communities can also unwittingly create boundaries that make it challenging for those from outside that community to participate. This risk of such un-intended consequences should be evaluated when building Citizen Science approaches to connect agricultural communities with citizen science practitioners.
5. Finally, projects with higher levels of participation may not necessarily be 'better' than those where volunteers' participation is limited to data collection and submission. "Deep learning is possible in any project, as participants learn differently and engage with the project in unplanned ways" (Van De Gevel et al., 2020; p. 35).

2.7.5.3 Casting the net wide

A third and final type of target audience could also be of relevance to EU PoMS, which are untrained (with respect to the tasks at hand) and/or less specific audiences. A common approach in Citizen Science is to involve school children, sometimes for the purpose of data collection but mostly for engagement (with nature and scientific methodology) or education reasons – perennial dimensions of Citizen Science (Bonney and Dickinson, 2012). School structures allow for access, but mostly to classes at lower grades as at higher grades competition with fixed curricula intensifies. Reaching broad audiences can also be done through digital Citizen Science. Some of the World's largest Citizen Science programmes fall in this category. Zooniverse is the flagship example, which has generated over half a billion classification by registered volunteers so far. EU PoMS has opportunities here, within the Zooniverse ecosystem, or via more specialised approaches (e.g. X-Polli:nation[24], FITCounts[25]), through crowdsourcing, were it to employ networks of volunteers or new tools that generate a lot of images in need of species identification. Increasingly, such tasks are in the hands of automated species recognition software, which comes with opportunities and difficulties (Trulong and van der Wal, in review). Although such crowdsourcing can bring valuable data to scientists and rich experiences to participants, it is important to be aware of the risk of extractive processes, notably when also gamification comes in (Kreitmair and Magnus, 2019), exploiting people and their time without giving much in return (Ponti et al., 2018).

2.7.6 Opportunities provided by Citizen Science in the EU PoMS proposed monitoring approaches

As described above, Citizen Science has provided a wealth of data and knowledge on the status of pollinating insects in Europe, alongside the benefit of engaging people with science and nature. This section reviews the opportunities for Citizen Science to support the EU Pollinator Monitoring Scheme as the approaches are finalised. These opportunities include support for field sampling components as well as wider engagement and capacity building for pollinator monitoring.

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[24] https://xpollination.org/

[25] https://fitcount.ceh.ac.uk/

The EU Pollinator Monitoring Scheme as initially designed (Potts et al., 2021) comprised seven modules: a Minimum Viable Scheme (MVS, two modules), complementary approaches (two modules) and optional, additional modules (three modules). The revised design proposed in this report has two parts (see Figure 2.2.1 in section 2.1): the core scheme and complementary modules. The core scheme has 3 modules:

- Reinforced transects for monitoring bees, hoverflies and butterflies.
- Light traps for moths.
- Rare and threatened species using tailored methods depending upon the target species.

Transects can be conducted by engaged volunteers if the protocols are sufficiently clear; they do not have to be skilled naturalists, but need to be trained such that the sampling is done in an ecologically sensible way. Identifying what is caught, however, requires reasonable (butterflies, some bees) to high (many other bees, hoverflies) skills, and hence select for either naturalists or professionals.

Were the EU PoMS to transition to include a higher proportion of volunteer recording, then this would increase the need for Citizen Science capacity building, i.e. interest in pollinators and learning to identify pollinators. Here, naturalist societies and species group-centred organisations (e.g. BBCT[26], Vlinderstichting[27]) can play a key role, through hands-on in-person training and promoting digital systems (e.g. X:polli-Nation). Collaboration of EU PoMS with digital operators such as iNaturalist[28] and notably Observation.org[29] (who cater specifically for Europe) could be of value, as would reaching out to other target audiences that are relatively easy to contact through stakeholder organisations (e.g. hunters, foresters, farmers, beekeepers, outdoor recreationists of various kind).

The general principle of Citizen Science approaches are applicable to the core and complementary modules of the EU PoMS. We summarise the potential contributions from naturalist and other target audiences for Citizen Science approaches (Table 2.7. 1).

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[26] https://www.bumblebeeconservation.org/

[27] https://www.vlinderstichting.nl/

[28] https://www.inaturalist.org/

[29] https://observation.org/

Table 2.7. 1. Overview of the potential for Citizen Science approaches to support modules of an EU pollinator monitoring scheme.

EU PoMS module	**Naturalists**	**Other target audiences**	**Broader approaches**
Core scheme: Reinforced transects module	Experienced naturalists for some groups; specialists for other.	Training and engagement. Integrate with existing schemes – particularly Butterfly Monitoring Schemes.	Integrate with existing structured such as NGOs, specialist taxon-focused groups, and local place-based monitoring (e.g. Nature Reserves). Ethical considerations of destructive sampling.
Core scheme: Moths module	Generalists: trap placement and processing. Specialists: species identification supported by AI image classification.	Trap placement and processing by target communities, notably farmers, foresters, hunters, outdoor recreation enthusiasts; and wider publics (including gardeners, green space managers).	Broad recruitment activities. Potential to engage with farmers (as citizen scientists) as has proved successful for schemes in the Netherlands and Ireland.
Core scheme: Rare & threatened species module	Specialists on specific species or narrow taxonomic groups.	Outdoor enthusiasts scouting for certain species to broaden chances of encounter.	Launch annual call for focal species together with (digital and wider) biological recording organisations. Citizen Science could have a role depending on target species.

EU PoMS module	Naturalists	Other target audiences	Broader approaches
Complementary module: Pan traps module	Generalists: trap placement and processing. Specialists: species identification.	Trap placement and processing by target communities, notably farmers, foresters, hunters, outdoor recreation enthusiasts.	Ample opportunities for training interested audiences; good focus for creating interest (and attracting new volunteers) together with country specific interest groups. Adaptable to participants. Could be combined with other protocols. Ethical considerations of destructive sampling.
Complementary module: Wider insect diversity module	Specialists for trap placement, sample processing and species identification.	Trap placement and processing by target communities, notably nature reserve volunteers working alongside paid staff.	Combined with molecular approaches for species identification.

Source: Authors' elaboration.

2.7.7 Conclusions and recommendations

Europe has a long and rich tradition in Citizen Science. This includes world-leading monitoring of pollinating insects through long-established Butterfly Monitoring Schemes in several EU Member States. Schemes of this kind point to the value Citizen Science monitoring can bring to the EU PoMS – for extending e.g. butterfly monitoring to cover all EU Member States and to develop and promote Citizen Science approaches to encompass all pollinating insect groups. While the opportunity is there, our evaluation also draws out that it is not without challenge and requires careful preparation, relationship building and coordination. Hence, we expect that EU PoMS will initially rely strongly on professional recorders, but that over time Member States might increasingly transition to higher proportions of volunteer recorders over the longer-term. The barriers and opportunities for successful Citizen Science are increasingly being recognised and are important to consider when considering new initiatives (Annex 2.7.A), including for farmland (Annex 2.7.B), as a component of EU PoMS and wider initiatives to protect and restore biodiversity in the EU.

We recommend:

1. Support coordination and development of Citizen Science in all Member States as a long-term goal of capacity building to support an EU pollinator monitoring scheme. Resources

invested in Citizen Science should provide incentives and rewards for participants who given their time, e.g. provision of training, community-building events and regular feedback.

2. Adopt proven Citizen Science methods such as Butterfly Monitoring Schemes in all Member States, to enable the collection of data to support assessment of trends in pollinating insects and development of biodiversity indicators.
3. Evaluate Citizen Science methods that enable wide participation without requiring high levels of expertise in species identification, and which can be supported by new technologies such as image recognition and mobile applications.
4. Engage with the farming community at Member State and EU levels to evaluate the potential of their involvement in Citizen Science to improve knowledge of biodiversity on farmland.
5. Build collaborations between Citizen Science practitioners and social scientists to understand motivation of volunteers and overcoming barriers to participation, particularly for regions of Europe with less of a tradition for Citizen Science (e.g. Southern and Eastern Europe).

Pollinator citizen scientists, eBMS transect at JRC Ispra

Annex 2.7. Thinking tools for future capacity building of Pollinator Citizen Science

2.7.A. How to get Citizen Science 'right'. Were Citizen Science to become part of EU PoMS, instigators may benefit from asking four fundamental and conceptually-related questions: 1) ***why*** to embark on an initiative (i.e. well-identified motivations); ***what*** should be achieved (i.e. setting and communicating clear aims, such as engagement or empower participants with actionable data to support the conservation of pollinating insects); ***who*** to involve (i.e. considered audience selection, there is no 'general' public when it comes to specific interests); and ***how*** to go about, thereby ascertaining that participants are not mere data providers but participants in their own right with valuable knowledge and expertise, whose involvement requires built-in opportunities for learning where possible shaping initiatives' processes and outcomes. Here, considering feedback is important.

2.7.B. Dimensions of Pollinator Citizen Science on farmland. While using the above diagram, various dimensions may need reflection on when launching, modifying or promoting a Pollinator Citizen Science initiative. The list below are dimensions that were identified as part of the process of reviewing Citizen Science approaches intersecting with farmland (Ruck et al., 2023):

- Volume of data
- Accounting for farmland
- Spatial coverage
- Number of participants
- Skill levels (including attraction of 'high quality' volunteers)
- Ease to get started/record
- Species identification learning resource
- Data quality
- Long running/longitudinal data (including commitment pull)

- Standardized methods and efforts
- Consistency of sites (longitudinal data)
- Farmland specific data
- Data from new sites
- Volunteer-professional engagement
- Farmer involvement/volunteer engagement
- Relevance of data

Papilio machaon, Ana Montero

2.8 Design options for a rare and threatened species (RaTS) module

2.8.1 Summary and recommendations

Many insect species are rare, geographically localised or ecologically highly specialised. A standardised, large-scale pan-European pollinator monitoring scheme such as EU PoMS is extremely unlikely to sample these species sufficiently to detect changes in their status. The goals of the rare and threatened species module are: (i) to provide better data for assessing the conservation status of pollinators with the aim to reduce the number of Data Deficient and Not Evaluated species on the IUCN Red List and improve the data basis for threatened species; and (ii) to develop tailored recommendations to inform conservation management and future monitoring for each species or set of species in order to reverse declines of pollinator species.

Prioritisation should focus on those species with the highest extinction risk (based upon the IUCN Red List) and lowest data availability. A formula for prioritisation is proposed based on: the IUCN Red List Score, date of last record, date of last survey and survey intensity. Priority lists should be co-developed between the European level and Member States, considering both EU and Member State priority species. Collaboration with non-EU countries should also be sought whenever priority species occur outside the EU. For each priority species, a list of potentially co-occurring rare species should be created to cover a maximum of species during each survey.

Monitoring methods should focus on the most important information needed according to the current status of the species and may include presence-absence data, population size, density, timed counts, transect counts, phenology, host plant distribution or threats. Decisions about the monitoring methods should be based upon two primary questions: (i) what is the most important information needed to update the IUCN Red List assessment of the species and inform conservation action to improve the status of the species? (ii) which method should deliver the best (and most cost-effective) data to close respective knowledge gaps? After an initial survey, recommendations for long-time monitoring and management should be developed. Later monitoring should thus provide data to assess the efficacy of conservation action.

Two indicators are proposed to measure the trends of rare and threatened species: (i) The IUCN Red List of Threatened Species, and (ii) the IUCN Green Status of Species. The IUCN Red List status can be used to calculate a Red List Index, which serves as a long-term indicator for biodiversity trends. The IUCN Green Status of Species provides a more rapid and more differentiated assessment of species recovery, and can be standardized across many different taxa and methods. Monitoring rare and threatened species requires good communication between the European level, EU Member States as well as interested NGOs, species experts and interested citizen scientists/naturalists.

Lycaena helle, Axel Hochkirch

2.8.2 Introduction

Many insect species are rare, geographically localised or ecologically highly specialised. A standardised, large-scale pan-European pollinator monitoring scheme is extremely unlikely to sample these species sufficiently to be able to detect any meaningful changes in their status (D. Roy et al., 2020; van Swaay et al., 2008). However, data on their population status is important to measure biodiversity trends as rare and threatened species have a higher extinction risk than common species. The IUCN (International Union for Conservation of Nature) Red List of Threatened Species^{TM} is the most important tool providing information on the conservation status of species and can be considered a “barometer of life” (Stuart et al., 2010). It provides valuable data for measuring progress towards international biodiversity targets, such as the Convention on Biological Diversity (CBD, e.g. Global Biodiversity Framework (GBF) target 4) and the Sustainable Development Goals (e.g. SDGs 14 and 15). Assessing the IUCN Red List status of species is based upon five different criteria, but good knowledge of the distribution, population status and trend as well as the threats is required to provide robust assessments. Simply increasing the sampling effort of standardised monitoring approaches is not sufficient to provide reliable data on the population trends of rare species, as these schemes are designed to be representative of the landscape (not the taxon), and therefore unavoidably biased towards more common and widespread species (Potts et al., 2021). However, rare and threatened species often represent national and European endemics for which the European Union has a high responsibility in order to reach internationally agreed conservation targets. The chronic lack of data on distribution, population trends, ecology and threats to those insect species is a major obstacle to assessing their conservation status and to monitoring overall biodiversity trends (Hochkirch et al., 2021). This is illustrated by the first European Red List of Bees (Nieto et al., 2014), where 56% of the bee species occurring in the EU were found to be Data Deficient and where their population trend was classified as “unknown” for

79% of the species. Based upon experience from the European Butterfly Monitoring Scheme (eBMS) and expert opinion, it is estimated that ca. 40% of all insect species are too rare to be detected by a standardised monitoring scheme (Kuhn et al., 2022; Settele and Vujić pers. comm.). Consequently, specific monitoring approaches are needed for those species, tailored to the specific ecology and biology of the target species. The rare and threatened species module of EU PoMS has been developed to close this knowledge gap and focus on the least known and most highly threatened species with the ultimate goal to avoid any 'silent' extinctions.

2.8.3 Aim of a rare and threatened species module

The primary goal of the rare and threatened species module is to provide better data for assessing the conservation status of pollinators with the aim to reduce the number of Data Deficient and Not Evaluated species on the IUCN Red List and improve the data basis for threatened species. A second important goal is to provide tailored recommendations to inform conservation management and future monitoring for each species or set of species in order to reverse declines of pollinator species.

Priority lists of rare and threatened pollinator monitoring should be created at the European level in collaboration with EU Member States. For each priority species, EU Member States should first conduct an initial survey to fill knowledge gaps and set the basis for future monitoring of the species in question. Member States should be encouraged to add their own priority species to the list of European priority species (particularly for Member States with low numbers of European-wide priority species), but the European priority list should always be ranked higher. National priorities should focus on species listed in national Red Lists but may also include umbrella species or indicators of threatened habitat types. Collaboration with non-EU countries should also be sought whenever priority species occur outside the EU.

During the first years of the implementation of the rare and threatened species module, the date of the last record will be of higher importance for prioritisation than the IUCN Red List status as the number of Data Deficient species is relatively high in insects (Hochkirch et al., 2021). The data recorded during monitoring can then help to update IUCN Red List assessments and over the years, the reduced time since the last records and last surveys will result in a stronger importance of the IUCN Red List status in informing the prioritisation process (see formula below). However, it also needs to be considered that IUCN Red List assessments are not updated regularly and may be outdated. Therefore, a proper management of the priority list is required, using published and unpublished information from species experts. Priority lists need to be developed, maintained and updated regularly at European level. A European coordination of the rare and threatened species module across the European Union would be ideal, as this would also facilitate EU-wide analyses. The priority list, current state of monitoring as well as the results should be made publicly available in order to inform conservation practitioners and engage citizen scientists.

For each priority species, a list of potentially co-occurring rare species for its locations should be created to cover a maximum of species during each survey. After the initial surveys, future monitoring recommendations need to be developed for each species or species group based upon the results (including monitoring frequency and method). These recommendations should be drafted in collaboration with other Member States hosting populations of the target species. Furthermore, management recommendations would be devised based upon the monitoring results. These recommendations should be drafted in collaboration with relevant stakeholders and aim at reversing pollinator declines by mitigating the major threats to each species. After each monitoring round, the monitoring and management recommendations should be updated. This approach would help to maximise the number of species monitored and ensure that Member States take accountability for the status of pollinator species. This in turn would also help to improve the conservation status of rare and threatened species and reach the target of halting the loss of pollinators. While moderately rare species might still be partly neglected by this approach, falling in the gap between the standardised monitoring of EU PoMS and the rare and threatened species module, they should be included in the list of co-occurring species as far as possible. Otherwise, they would fall into the focus of the rare and threatened species module only when their status changes into a threatened category of the IUCN Red List.

2.8.4 Prioritisation of species for inclusion in the rare and threatened species module

The number of rare and threatened pollinator species is very large and a complete coverage of all taxa is impossible, given that the majority of insect species has not even been scientifically described (X. Li and Wiens, 2023). Furthermore, our knowledge regarding the pollination function and efficacy of insect species as well as their ecological interactions is still at its infancy for many species. Therefore, a precautionary approach needs to be followed when deciding which species require targeted monitoring. A prioritisation mechanism is required, focusing on those species with the highest extinction risk (based upon the IUCN Red List) and lowest data availability. However, most insect species have not been assessed for the IUCN Red List so far, and even among the assessed species, there is often a lack of data regarding distribution, population trends, ecological requirements or threats (Hochkirch et al., 2021). While species in the threatened categories (i.e. Critically Endangered, Endangered, Vulnerable) (IUCN Species Survival Commission, 2001) should have the highest priority for monitoring in order to inform conservation action, Data Deficient or Not Evaluated species may also be at a high risk of extinction (Borgelt et al., 2022; Liu et al., 2022) and thus require similar attention, especially since lack/limited data may stem from their rarity, which further supports their prioritization.

Rediscovering “lost species” (species that have not been recorded for many years) should be a key task of the rare and threatened species module. The date of the last record and information on past survey efforts provide, therefore, additional layers for prioritisation. Obtaining data on the population status of species that have not been recorded for decades will help to assess or reassess their Red List status and provide the basis for future prioritisation. Furthermore, spatial overlap of several target species and less rare species needs to be considered in the prioritisation process in order to use the scarce resources as efficiently as possible by focusing on areas with overlapping occurrences of rare species. Other prioritisation mechanisms, which are sometimes used in nature conservation (e.g. ecological functionality, evolutionary distinctiveness) are here not considered, as biodiversity, ecological interactions and evolutionary relationships are still far from completely understood, but future development of a rare and threatened species module could consider these eventually. Moreover, recent evolutionary radiations may also be considered of high conservation value due to their high evolutionary future potential. In fact, conservation legislation (including the CBD) often highlights the intrinsic value of species, irrespective of their beauty, economic value, ecological role or evolutionary distinctiveness. Targets to achieve an increasing trend for pollinator populations can only be reached by obtaining data for a wide range of potential pollinators. Even pollinator groups, which are currently not selected as target groups for European legislation need to be considered. This also includes often-neglected pollinator taxa, such as many fly families (e.g. *Bombyliidae*, *Mydidae*, *Phoridae*, *Conopidae*, *Muscidae*, *Calliphoridae*), beetle families (e.g. *Buprestidae*, *Oedemeridae*, *Meloidae*, *Mordellidae*), hymenoptera families (e.g.

Pompilidae, Vespidae), thrips (*Thysanoptera*), flower bugs (*Anthocoridae*), bush-crickets (*Tettigoniidae*) or ectobiid cockroaches (*Ectobiidae*).

2.8.4.1 Prioritisation formula

At the start of the rare and threatened species monitoring scheme, the following formula (Equation 2.8. 1) is proposed to prioritise species for monitoring:

$$Priority(P) = S_{RL} + S_{DR} + (S_{LS} + S_{SI})$$

Equation 2.8. 1. Prioritisation formula for rare and threatened species monitoring.

where

S_{RL} = Red List Score (Critically Endangered - Possibly Extinct = 1.0, Critically Endangered = 0.8, Endangered = 0.6, Vulnerable = 0.4, Near Threatened = 0.2, Least Concern = 0.1, Data Deficient = 1.0, Not Evaluated = 1.0)

S_{DR} = Date of Last Record Score (Years since last record / 100)

S_{LS} = Date of Last Survey Score (Years since last survey / 100)

S_{SI} = Survey Intensity Score (comprehensive survey = 0, very high intensity = 0.2, high intensity = 0.4, medium intensity = 0.6, low intensity = 0.8, insufficient intensity = 1.0)

S_{RL} is derived from the Red List Index (Butchart et al., 2007), but the calculations are inverse (to give species with a higher extinction risk a higher score) and slightly adapted (including a special score for possibly extinct taxa, data deficient taxa and not evaluated taxa. The S_{SI} values would need to be scored in collaboration with experts for the species group and/or the researchers who conducted the surveys. All data available should be used to calculate P, including unpublished information from species experts (e.g. adjusting S_{RL} if a Critically Endangered - Possible Extinct (CR-PE) species has meanwhile been rediscovered; information on last surveys and survey intensity). For S_{DR}, records on Citizen Science platforms should be considered, but (in case of doubts) carefully cross-checked with species experts. Final priorities should be discussed with species experts and adjusted if necessary. All priority scores should be entered (together with the known distribution) into a GIS, so that overlap analyses can be made to identify regions with occurrence of several priority species. After some years, the formula can be simplified by focusing on the Red List Score alone, because the scores for the date and intensity of the last survey will become close to zero after the onset of monitoring. In case of unsuccessful monitoring attempts of a lost species, extinction probability needs to be modelled and the chances of successful future monitoring rounds assessed (see Thompson et al., 2017). Ultimately, some species will be assessed as Extinct as a result of the monitoring efforts and removed from the priority list. These species should nevertheless be kept on a vigilance list for surveyors targeting other species in their region of occurrence.

2.8.5 Monitoring methods

The data required from the targeted monitoring may differ among species and should be adjusted to the most important information needed according to the current status of the species. For some species simple presence-absence may be sufficient to reconfirm their presence at a given site, for others more detailed data on the population size, density, host plant distribution or threats may be required. The methods used to survey each species will depend upon the ecology and biology of the species and may entail visual or acoustic surveys, pheromone traps, bait or light traps, mark-recapture studies, transect walks, timed counts, counts of nests, eggs, larvae or adults, environmental DNA etc. Decisions about the methods should be based upon two primary questions: (i) what is the most important information needed to update the IUCN Red List assessment of the species and inform conservation action to improve the status of the species (e.g. population size, population trend, range size, number of locations, threats)? (ii) which method will deliver the best (and most cost-effective) data to close respective knowledge gaps?

All data collected must be spatially explicit in order to inform any spatial planning efforts and should be made available with open access (except for sensitive data). The following data will be particularly important:

- **Distribution**: Distribution data are the most basic and fundamental data for biodiversity conservation. They are not only crucial for Red List assessments (IUCN Red List criteria B and D2), but also important for identifying Key Biodiversity Areas (KBAs), Key Pollinator Areas or other areas important for biodiversity, to inform strategic conservation planning and to implement appropriate conservation action. However, distribution information is usually incomplete or outdated for insects. Therefore, collecting up-to-date distribution data has the highest priority in the targeted monitoring for rare and threatened species. For species with a lack of recent records, targeted searches should be conducted based upon the records available in the literature, museum material and databases to reconfirm their presence. For species with presumably incomplete distribution data, the known occurrences as well as similar habitats in the vicinity of known records (or based upon species distribution modelling) should be surveyed so that the most comprehensive and up-to-date distribution data possible is obtained. For species that are easy to identify, Citizen Science approaches may be applied, while for elusive or highly cryptic species the use of more sophisticated methods (e.g. eDNA) may be prioritised (considering all life stages of the target species, i.e. eggs, juveniles (larvae, nymphs, pupae) and adults). Spatial data needs to be made available with open access, wherever possible (but protecting species which may be targeted by collectors etc.) to facilitate conservation practice (i.e. Red List assessors, national and regional authorities, NGOs, Protected Area managers) and encourage cross-sectoral collaboration, which is critical for successful conservation practice.
- **Population**: Population data are crucial to assess the extinction risk of species (IUCN Red List criteria A, C and D), identify populations with high conservation value and instigate conservation action timely. Estimating population trends is, therefore, a key element of species monitoring. To obtain data on population trends of rare and threatened species, it is important to use a standardised (but species-specific) method over time to measure or estimate population sizes or abundances. Methods to assess population sizes depend on several factors (detectability, habitat, phenology, life cycle, daily activity pattern) and, therefore, can vary strongly among species. They may include standardised trapping/recording on plots or transects or more sophisticated methods, such as mark-recapture (for species with small populations). Each survey aims to acquire robust data, allowing us to estimate or infer population trends of the respective species at a given site. To standardise methods as far as possible, monitoring guidelines should be developed at the European level and be regularly updated.

- **Ecology**: Information on the habitat preferences of rare and/or threatened species is crucial for identifying and assessing the effects of potential threats (like habitat loss and fragmentation), and improving conservation planning and habitat management. Therefore, habitat variables considered relevant for the respective species should be recorded during each survey. These data will also help to improve future targeted searches for this species and improve distribution data. Important habitat parameters to consider are, for example, host plants, vegetation structure, nesting sites, microclimate, soil parameters etc. (depending upon the species under study). Habitat data should have to be stored alongside distribution and population data in an online, open access database so that this information can be used to inform Red List assessments and conservation action. These habitat data should follow a standardised habitat reference system, but additionally provide information in free text format to be able to cover any peculiar habitat requirements.
- **Threats**: Halting biodiversity decline is only possible by mitigating threats to species. While some general information on threats to European biodiversity is available, conservation action requires much more specific information on the major threats to each species at a given location. Therefore, actual or potential threats to the species under study should be recorded at each site. These may include details on known threats such as agricultural practices (e.g. type and density of livestock, crop type, use of pesticides and fertilisers, date and type of mowing, ploughing, rolling, drainage, irrigation), forestry (e.g. type, age and structure of forest, dominating tree species, use of liming, pesticides and fertilisers, type and number of roads and logging trails, use of heavy machines and other management practices), land abandonment, urbanisation and infrastructure, aquaculture, wildfires, drainage, damming, canalisation of lotic waters, mining, invasive species, biological resource use, direct human disturbance, pollution or effects of climate change. A clear scoring system of the severity of each threat, like the one offered by the IUCN Red List, should be applied so that the most pressing drivers of biodiversity decline as well as potential future drivers can be addressed. This information will be critical to improve habitat management and facilitate conservation action.

2.8.6 Data storage, analysis and indicators

All data obtained from the rare and threatened species module need to be validated at the national level and submitted or shared by the Member States in a standardised form via an online platform to a European data platform. National monitoring facilities should have their own interfaces to submit or correct data from the respective country. Each step of data entry, correction and validation, needs to be thoroughly documented. All data should be open access (CC0 or CC BY-NC licence) at capture resolution (but might be provided with lower resolution if sensitive data are included, such as species with high threat status). All data should be mirrored on several servers to avoid any loss of data. Data from Citizen Science should be submitted via an own gateway and incorporated in the database after validation by experts. Whenever possible, the data can be submitted via an App, but flexibility is required as different type of data may be submitted and different methods may be used. These data should be stored in the central database, but should be entered through the web portal.

All data can be analysed by the Member States as well as on European level. The type of data required will be clarified during prioritisation and in the monitoring recommendations. The following key variables need to be analysed (depending on the status of each species):

- **Distribution**: Spatially explicit information on occurrence of rare and threatened species is key to inform conservation management. Maintenance of a GIS database is, therefore, crucial. These data can be used, among others, to calculate (a) the number of populations, (b) the area of occupancy (AOO), (c) the extent of occurrence (EOO), and (d) the degree of population fragmentation. These measures, which are clearly defined by IUCN[30], are important to conduct Red List assessments under IUCN Red List criterion B and D2.

- **Population status**: In most cases, it will not be possible to estimate the exact number of individuals of any insect population. However, population estimates can be obtained from mark-recapture studies and population trends can also be calculated from standardised monitoring on transects, timed counts or trapping. Calculating population reduction is particularly important for assessing the IUCN Red List status under criterion A, but data on population trends also inform assessments under IUCN Red List criteria B and C ("continuing decline", "extreme fluctuations"). Good population estimates (in terms of number of mature individuals) are required for IUCN Red List criteria C and D. Assessments of population viability can help to estimate the severity of population fragmentation (see IUCN Standards and Petitions Committee, 2024) and inform conservation planning processes.

- **Threats**: Information on the existence, importance and spatial distribution of threats is important to guide conservation planning and management. Threat information is also required for IUCN Red List assessments, including the estimation of the "number of locations" (as defined by IUCN Standards and Petitions Committee, 2024) under IUCN Red List criterion B as well as assessments under IUCN Red List criterion D2 ("restricted distribution with a plausible future threat that could drive the taxon to CR or EX in a very short time").

- **Ecology**: Information on the habitat requirements of species is key to derive suitable conservation action. However, the habitat requirements of many insect species are still unknown. Therefore, it will be important to identify key gaps in ecological knowledge of each species and collect data to close those knowledge gaps. Data on habitat affiliation can help to guide searches to discover potentially unknown populations of threatened insect species or discover suitable, but unoccupied habitats, which may be suitable for any future reintroductions. Habitat data can also be used to infer population trends of species in case of highly specialised but elusive species.

2.8.6.1 Indicators

Two major indicators are proposed to measure the trends of rare and threatened species: (i) The IUCN Red List of Threatened Species, and (ii) The IUCN Green Status of Species. Using the data obtained from the rare and threatened species module monitoring, re-assessments of the IUCN Red List status could be made for each species. The assessments should always be made on the geographic level at which the inclusion of the species in the RaTS priority list was based upon (i.e. if a species has been included because of a high European Red List Score, the European Red List status should be used, while if a species has been added as a national priority, the national Red List score should be chosen).

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[30] https://portals.iucn.org/library/node/10315

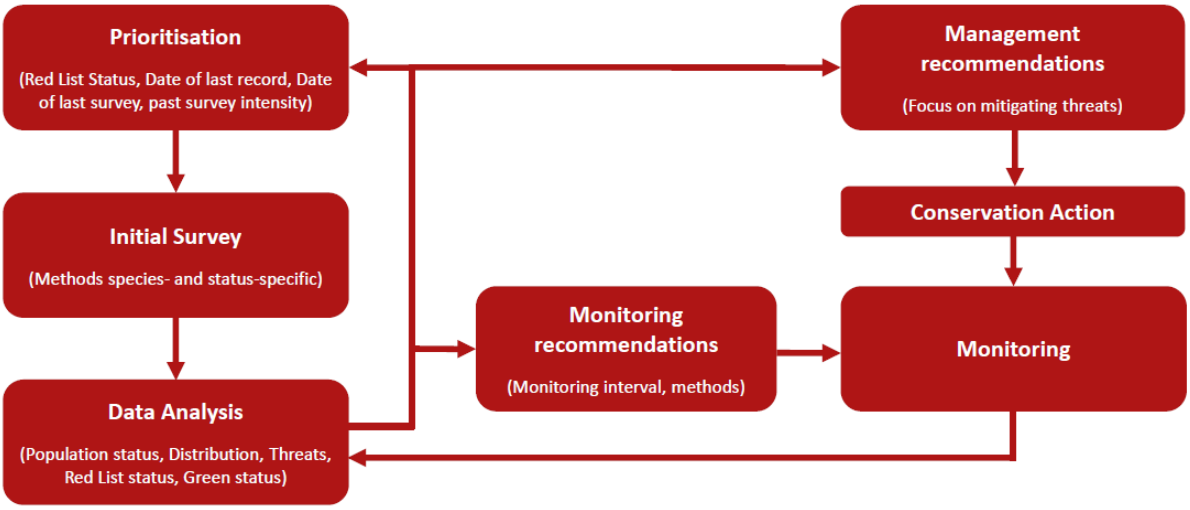
The IUCN Red List status can be used to calculate a Red List Index (RLI, Butchart et al., 2007), which serves as a long-term indicator for biodiversity trends (Stuart et al., 2010). However, IUCN Red List assessments have a strong inertia due to the methodological requirements and downlisting procedures (e.g. the 5-year rule, which regulates movements of taxa to a lower threat category "when none of the criteria of the higher threat category has been met for five years or more") (IUCN Standards and Petitions Committee, 2024).

The IUCN Green Status of Species provides a more rapid and more differentiated assessment of species recovery. It entails four different metrics (for details, see Akçakaya et al., 2018): (i) Conservation Legacy, which captures the impact of past conservation interventions on the status of the species (measured by a "Recovery Score", which ranges from 0% = extinct, to 100% = fully recovered), (ii) Conservation Dependence, which captures what is expected to happen over the next ten years if current conservation actions were to cease, (iii) Conservation Gain, which captures the change in status expected to occur within the next ten years resulting from planned conservation actions, and (iv) Recovery Potential, which is the maximum recovery that can be potentially reached given the state of the world today. A species is considered fully recovered "if it is viable and ecologically functional in each part of its indigenous and projected range" (Akçakaya et al., 2018). Changes in the Recovery Score could be a suitable indicator to measure progress in the conservation of rare and threatened species. The proposed Red List Index and Green Status of Species indicators are complementary to the general pollinator indicators linked to EU PoMS (see section 3.1).

2.8.7 The rare and threatened species module monitoring framework

Monitoring rare and threatened species requires good communication between the EU Member States, the EU as well as interested NGOs, species experts and interested citizen scientists or naturalists (Figure 2.8. 1). Prioritization needs to be done at the European level (creating, maintaining and updating the priority list of species), either by a European coordinating body or a coordination mechanism between national authorities. All other steps should be conducted at the Member State level. This includes the initial survey or first monitoring round, analysing all monitoring data and devising monitoring recommendations. National and local authorities need to be involved in co-developing management recommendations and are also responsible for the implementation, including both implementation of conservation action and further monitoring.

Figure 2.8. 1. Proposed framework for the rare and threatened species module.



Source: Authors' elaboration.

Spatially explicit data from both conservation actions and monitoring should be submitted to the European database. Ideally, there would also be a European-wide analysis of the data, update the priority list, re-assessment of the Red List status. All data, including the priority list, monitoring recommendations, management recommendations and monitoring data, should be made publicly available online in order to benefit from Citizen Science engagement. Information on priority species and monitoring results should be spread via reports and the social media to encourage citizen scientists to engage. Data from Citizen Science should be incorporated in the data management process by creating a platform to submit own monitoring data (ideally a sub-platform of existing Citizen Science platforms). There should be a particular focus on engaging citizen scientists in the search for lost species. For each species in the priority list, recommended monitoring methods minimum requirements for data submission should be provided. Information from other monitoring schemes, Citizen Science platforms, scientific research and other sources should be incorporated whenever possible.

2.8.8 Budget and timelines

At Member State level, the coordination, prioritisation and data management of the rare and threatened species module would require at least two full-time staff (1 coordinator, 1 database manager/data miner) as well as a budget to fund fieldwork. As most highly threatened or lost insect species have small geographic ranges and often a short activity period, the targeted the rare and threatened species module monitoring fieldwork does not require large funds. The funding required will differ among species (or species group), depending on their distribution, monitoring methods and effort, but is expected to be usually less than €10,000 per species (or area). For instance, a fixed budget of €500,000 per year would thus allow surveying >50 species (or areas with multiple species) per year. Member States may thus hire species experts, consultants or organisations to conduct the initial surveys of priority species (or sets of species) following the monitoring protocols. Here are some illustrative examples for monitoring recommendations in different circumstances:

- A Data Deficient wild bee species is only known from type material collected several decades ago. The most important information is to confirm its occurrence at the type locality or areas close to it. In case of unknown habitat preferences, information from related taxa should be considered. An initial survey would include targeted searches in the area close to the type locality during the most likely season of adult appearance. This would involve some travel costs (for traveling to and between different study sites): ca. €1,500, staff time (e.g. 10 days x 8 hours x 2 staff = 160 h): ca. €8,000, consumables (e.g. vials, liquids): ca. €500; Total = €10,000.
- An Endangered hoverfly species is known from three localities. The species is difficult to detect, but may be recorded by using eDNA from tree sap. This would involve some travel costs (for collecting tree saps): ca. €2,000, staff time (e.g. 10 days x 8 hours x 1 staff) = €4,000, eDNA analysis and barcoding (100 samples x 30 €) = €3,000; Total = €9,000.
- A Critically Endangered butterfly species is only known from a single locality. The species is easy to find and catch, mark-recapture is recommended as the most suitable method to estimate population size. This would involve travel costs (for travelling to the study site and conduct the mark recapture study over 3 weeks) = €3,000, staff time (20 days x 3 hours x 2 staff) = €6,000, consumables (coating pens, nets) = €500; Total = €9,500.

Epeolus tarsalis, ©NJ Vereecken

2.9 Design options for a moths module (light traps)

2.9.1 Summary and recommendations

There is increasing evidence of the importance of nocturnal pollination, and moths are major contributors, hence monitoring moths is increasingly gaining attention. Moths can look very similar and there are over 8,000 species in Europe, thus moth monitoring was traditionally done by experts as identification can be complex.

In recent years, the development of image recognition has made moth identification much easier (see section 5.2.4). Image recognition allows volunteers to quickly identify moths without extensive prior knowledge. An image recognition-based moth monitoring system has been developed to the point where it could potentially be quickly and widely deployed as part of a pollinator monitoring system. This system consists of a small light trap that can be placed out in the evening, and trap placement takes about 30 seconds. In the morning the trap is emptied by a volunteer (or professional), all moths are photographed using an already available App. After being photographed, the moths are released.

This system has been tested in several European countries and, although adaptations had to be made to adjust for local circumstances, the results are very promising. By implementing this approach, moths could become one of the easiest pollinator groups to monitor and contribute greatly to our knowledge and insights into night pollination by collecting data on moth occurrence and abundance.

To further develop this monitoring network to the EU scale we recommend the following actions:

- Appoint and fund a full time EU coordinator of the recognition-based moth monitoring system, and funding should be provided for national coordinators. The role of the European coordinator would be to support, motivate and help the Member State coordinators. The national coordinators would handle the contact with the local volunteers and manage the scheme on a national level. This approach reflects the European Butterfly Monitoring Scheme (eBMS), where this structure has worked well.
- Build and financially support a network of validators to give feedback to volunteers. This would rapidly collect additional training data for the image recognition system, allowing it to develop further.
- Create and translate supporting materials. These would be user-friendly moth information and identification materials to increase volunteer enthusiasm as well as user-friendly protocol descriptions. Although it is not necessary for volunteers to learn moth identification, being able to recognize some species and learning about them greatly increases enthusiasm, which in turn can increase volunteer retention.

- Extend the existing IT infrastructure (see Chapter 4). The European Butterfly Monitoring Scheme[31] (eBMS) IT system already fully supports moth recording via a mobile app using image recognition. However, a pan European system would increase the pressure on the databases, portals and image recognition systems; hence, the IT infrastructure needs to be expanded. Additionally, the system needs dedicated support (e.g. respond to queries from users).
- Continue development of statistical analyses to produce trends and indicators for moths. The first results will be mostly based on data from countries where this scheme is already running (such as the Netherlands) but having the processing tools available could encourage countries to join.

Autographa gamma, Axel Hochkirch

2.9.2 Background and context

Many pollinators are difficult to recognize and image recognition can support volunteers by aiding with identification. Especially when combining image recognition systems with a structured monitoring network. There are over 8,000 moth species in Europe, and evidence of their importance as pollinators is mounting (Alison et al., 2022; Anderson et al., 2023; Walton et al., 2020) especially in agricultural systems (e.g. for strawberries, Fijen et al. (2023)). Until recently, monitoring moths was restricted to a select group of experts who could correctly identify these moth species. Image

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[31] https://butterfly-monitoring.net/

recognition now enables volunteers to quickly identify a large proportion of moth species without having to study moths for several years. At present, the average identification accuracy of the automatic identification is estimated at 94% for the macro-moths in north-western Europe, although it is important to note that this accuracy strongly depends on the exact selection in the validation data (e.g. which species are included, which regions; L. Hogeweg, lead designer of the Image Recognition System behind ObsIdentify, personal communication, 2024). This enables monitoring by non-experts, for example by volunteers or farmers, which has led to a rapid growth of the moth monitoring networks.

As part of the SPRING project, the potential for moth monitoring with non-lethal LED based traps using image recognition was tested in five European countries (Netherlands, Sweden, Hungary, Spain and Germany). The trap is placed by a volunteer in the evening and emptied in the morning. When emptying the trap each moth is photographed and released. These photographs are automatically identified by image recognition software. Both the images and identification results are transmitted to a server and stored.

Not all species are caught, as not all moth species are attracted by light. However, trends across years can be established because of the ease of identification and the standardisation of the effort and frequency of the monitoring. Photos of the moths can also be stored for later verification and further improvement of the identification algorithm. Note that the attractive nature of this trap is unlikely to cause a statistical problem as it is not competing with naturally occurring landscape features; i.e. the effectiveness of the trap is based on light, which does not depend on changing local landscape characteristics such as flower richness, though other sources of light must be considered when locating traps. This attractiveness will differ between landscape types (the attractive range will be smaller in a forest than in an open area). However, our aim is to calculate trends (analyse data on a location over multiple years). As the effect of landscape does not differ between years, the deployment across different landscape types does not affect our ability to calculate trends.

The TRL (Technology Readiness Level) of this technique in north-western Europe is estimated to be 8, the technique is ready for deployment in this region, but algorithms need further development to improve performance outside of north-western Europe. To achieve this, more validated images need to be collected of south-eastern European species. It is therefore important to include human validators in the EU-wide deployment of this monitoring scheme.

This monitoring method has the potential to be upscaled as part of a pan-European monitoring system capable of delivering high quality species abundance data. It relies on non-lethal sampling and requires very limited knowledge to participate, making it attractive to volunteers. Once tested and refined for southern and eastern Europe, this method could have, with support, the potential to be a component of EU PoMS and deliver data suitable for moth trend analyses.

2.9.3 SPRING field trial

As part of the SPRING project, the potential for moth monitoring using image recognition was tested in 2022-2023 in five European countries (Netherlands, Sweden, Hungary, Spain and Germany), which led to the development of standardised monitoring protocols. This standardised monitoring protocol relied on traps that attract moths with LED lights (Figure 2.9. 1), the trap is placed by a volunteer in the evening and emptied in the morning. The moths are photographed and released in the morning. The moths are generally docile and easy to photograph, although in warmer climates they become more active early in the morning. This can be addressed by using a mosquito net, or in extreme cases a killing agent. Once specimens are photographed, they are automatically identified by image recognition software.

Figure 2.9. 1. Examples of the moth traps tested in the SPRING project.

Source: SPRING project.

Fieldwork was undertaken in 253 locations. In Sweden, Hungary and the Netherlands extra datapoints were added over the 125 that were originally planned. In total in 3,006 light traps were set out in the SPRING project (1,586 in 2022 and 1,420 in 2023).

2.9.3.1 Protocols

Three protocols to guide volunteers were produced by SPRING:

- How to build your own LED moth trap[32]. Although for monitoring purposes is not needed to use exactly the same trap on every location (as long as the trap remains the same in time), the LED traps are a relatively cheap and versatile method to trap moths.

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[32] https://butterfly-monitoring.net/sites/default/files/Pdf/moth monitorin/Self-made your LEDmoth Trap.pdf

- How to set up and use a LED trap[33]. Also available in Spanish[34] , Italian[35], German[36], Dutch[37] and Swedish[38].
- How to register moth trap samples on eBMS website.

More information can be found on BMS methods page[39].

The protocols were specifically designed to guide citizen scientists in placing the LED trap. The ButterflyCount app (available on Google Playstore and Apple Appstore) is designed to make entering data as simple as possible for volunteers. This app is fully developed, and already widely used. Not only does it make entering data easy and quick, but it also has a built-in moth identification via the ObsIdentify image recognition, which has been developed by the SPRING partner Naturalis.

At the end of the SPRING project, extra attention was given to the validation of moth photos that have been entered using the ButterflyCount App. These photos can further improve the quality of the image recognition, as this algorithm is trained on a regular basis (usually once a year).

2.9.3.2 Analysis and findings

In total 69,426 moths of 1,506 species were reported, with a mean of 23.1 moths per trap per night (median 9 moths per trap per night). In 2022, most moths were trapped in Spain with a mean of more than 80 moths per trap per night for weeks 35-40 (Figure 2.9. 2). The lowest numbers were counted in the Netherlands. In 2023, Spain again had the highest number of moths per trap, however in August (between weeks 30 and 35) Hungary took over. Except for Spain, where numbers were comparable, mean number of moths in the investigated traps were higher in 2023 than in 2022.

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[33] https://butterfly-monitoring.net/sites/default/files/Pdf/moth%20monitorin/Manual%20Ledtraps%20English%20Feb2022%20-%202%20pages.pdf

[34] https://butterfly-monitoring.net/sites/default/files/Pdf/moth%20monitorin/Manual%20Ledtrap%20Spanish%20Feb2022%20-%202pages.pdf

[35] https://butterfly-monitoring.net/sites/default/files/Pdf/moth%20monitorin/Manual%20Ledtraps%20Italian%20Feb2022%20-%202%20pages.pdf

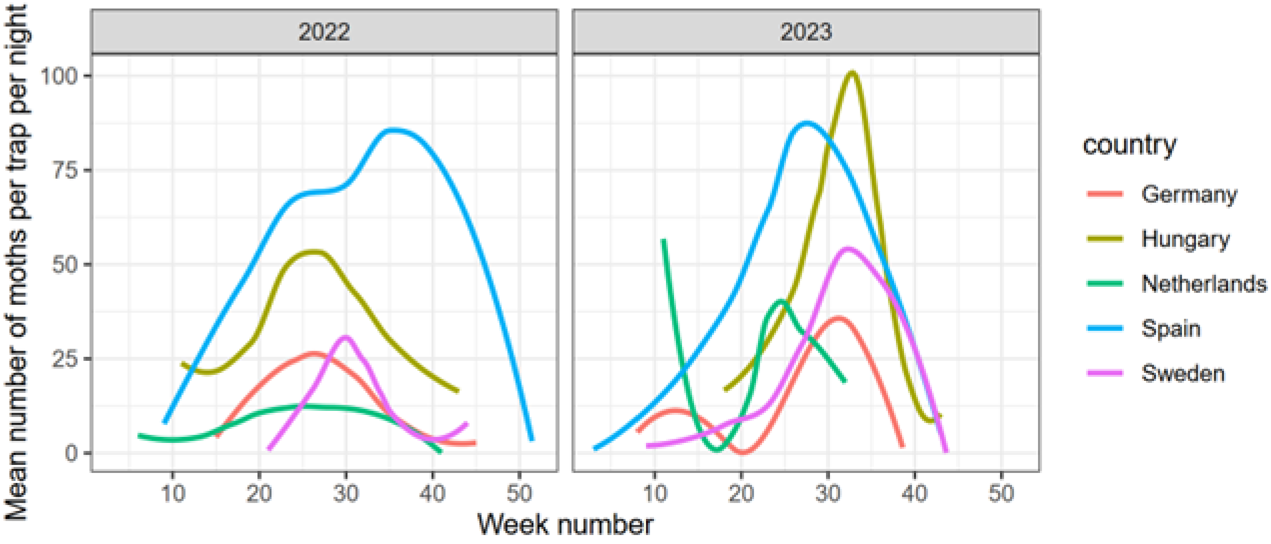
[36] https://butterfly-monitoring.net/sites/default/files/Pdf/moth monitorin/Manual LedEmmers German March 2022.pdf

[37] https://butterfly-monitoring.net/sites/default/files/Pdf/moth monitorin/Manual Ledtraps Dutch.pdf

[38] https://butterfly-monitoring.net/sites/default/files/Pdf/moth monitorin/Manual LedEmmers Swedish maart 2022.pdf

[39] https://butterfly-monitoring.net/bms-methods

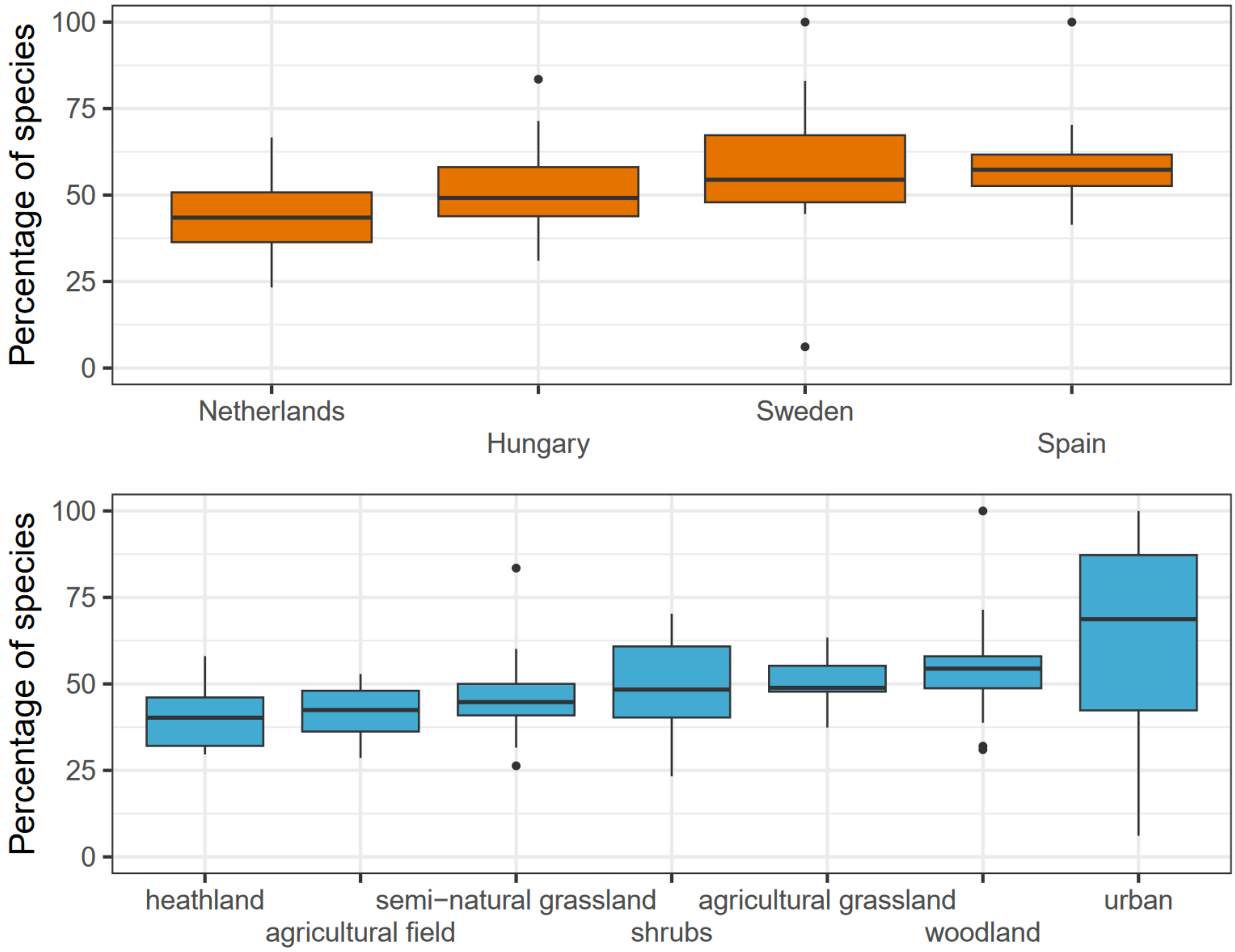
Figure 2.9. 2. Mean number of moths per trap per night per country, in 2022 and 2023.



Source: Authors' elaboration based on the SPRING project.

The traps are deployed in clusters of 5, each single trap caught close to 50% of the total number of species observed in all 5 traps, for most of the countries and habitats (Figure 2.9. 3). Only in traps in urban areas, is this percentage clearly higher, indicating a more homogeneous moth fauna in cities and villages.

Figure 2.9. 3. For each country (top, orange) and habitat (bottom, blue) the distribution of the percentage of the species of a cluster per trap is given.



Source: Authors' elaboration based on the SPRING project.

2.9.4 Current status and development opportunities

Currently the image identification works best in north-western Europe. Further development is required to improve the moth recognition in the rest of Europe. This development is currently ongoing but is constrained by low image availability for rare species or species occurring in parts of Europe with limited monitoring activity. By starting the monitoring scheme with additional experts to validate images of underrepresented species, the availability of training data should rapidly increase, allowing the algorithms to be improved.

The advantages of including additional sensors that record local conditions (such as sound or light levels) are currently being investigated; however, this would make the trap more expensive.

The data requirements of this tool are similar to other image recognition-based techniques: large datasets (preferably several hundred images per species) of validated images, even more if multiple forms, phenotypes or angles of the same species are to be recognised. Access to high performance computation resources is usually required to develop and update these algorithms.

2.9.4.1 Advantages and limitations

This method does not depend on lethal sampling, gives immediate results, and both deploying the trap and emptying it can be done without much effort and require no special expertise. This makes the method highly suitable for volunteers in addition to professionals. The technology has already been developed to the point where it can be deployed widely and the first international field tests were successful. A power analysis in the Netherlands shows that the method produces data of sufficient quality to allow for trend monitoring and also indicates that the costs are low, even if the scheme was entirely operated by experts (see 2.9.4 and 2.9.5).

The effectiveness of the trap will change when the environment becomes lighter (e.g. additional street lighting being placed), this would have to be noted and potentially the trap has to be moved. The light dependency of this trap means that it will perform poorly in northern countries where in summer the nights are very light. However, as this effect is stable through time, this should not affect our ability to calculate a trend, but it will affect our ability to measure both species richness and abundance. In southern European countries the opposite problem occurs, where species become active early in the morning, and become difficult to photograph. This can be counteracted with a mosquito net or by using a killing agent.

The effective range of these traps depends on the local landscape, e.g. the light will have a smaller range in a forest. This is not an issue if trend calculations only focus on a comparison between years. However, this would be a significant problem if these data were to be used to compare species richness between different habitat types; and it is important to note local changes in circumstances, such as habitat structure or light pollution.

The LED trap is primarily focused on moths, as few other pollinators are attracted to light. Not all moth species can be monitored using light traps, as not all moth species are attracted to light. In general, macro-moths are more attracted to light than micro-moths. For these two groups combined, experts estimate that roughly 80% of species can be monitored using light trapping on a European scale.

2.9.4.2 Estimated costs

The LED traps are currently being sold at ~€100 for monitoring purposes, and for ~€150 to interested individuals not part of a monitoring scheme (excluding shipping costs). A detailed DIY guide is available, so anyone can easily produce these traps. Having an expert deploy and emptying a single trap costs €75 per sampling event. These costs were calculated by previous STING1 group (Potts et al., 2021). Hence, operating a single trap for a year (assuming 6 visits per year) costs €450. Based on the power analysis in section 2.9.5, in the Netherlands ~40 traps would produce a power of 80%. Therefore, starting the monitoring scheme would cost €4,000 (assuming €100 per trap). The yearly operational costs of the entire moth monitoring network, solely based on experts, would cost about €18,000. This does not include travel expenses, coordination, (image) data storage and data processing. This is an example based on a relatively small country with a low diversity of habitat types, but it indicates that compared to other monitoring techniques and species groups, moth monitoring can be done at relatively low costs.

2.9.5 Feasibility for inclusion of moth monitoring in EU PoMS

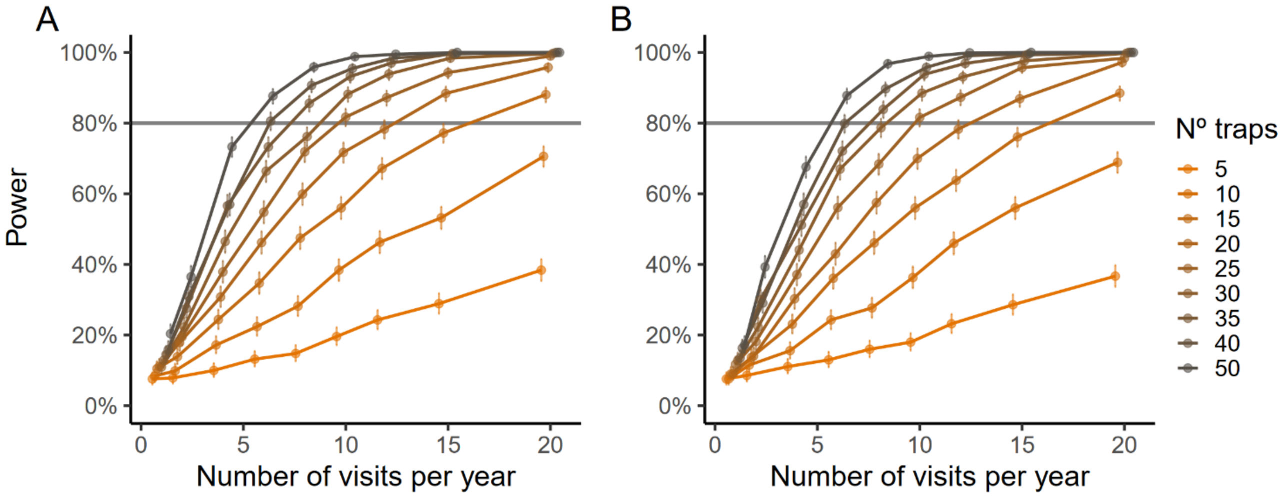
As part of the SPRING project, successful moth monitoring was conducted in five European countries (Sweden, Netherlands, Germany, Hungary and Spain), which led to minor adjustments to the existing well-established, standardized, monitoring protocols. These adjustments ensure that established field methods should also be feasible in other European countries. This standardized monitoring protocol relies on led traps that attract moths with LED lights. Although not all species are caught, most species can be. What is important, though, is that trends across years can be established because of the ease of identification and the standardization of the effort and frequency of the monitoring. Photos of the moths can also be stored for later verification.

To determine the required monitoring effort to get reliable five-year trend estimates of macro moths as a group (not a trend per species), model-based power analyses were conducted for different combinations of number of traps and visits per trap per year (with each visit consisting of one night). The effect size was estimated from the data in the Dutch moth monitoring scheme. Figure 2.9. 4 shows the power for different combinations of number of traps and number of visits per trap. For a power of ~80%, one could use 40 LED traps that are visited six times a year. As can be seen in Figure 2.9. 4, other combinations are also possible, for example 25 traps visited ten times a year. This exact number of sites strongly depends on the spatial distribution of sites and on how well they represent main habitat types. As well as the number of main habitat types present in a country. This example is based on a small country with a relatively limited number of habitat types. However, it clearly shows the potential of this approach.

In the SPRING project, data are acquired from traps in spatially close clusters in different countries (for this purpose analysed: Hungary, Sweden, Spain, and the Netherlands). This dataset shows that there is little overlap in macro-moth counts (total number of macro-moths) between these spatially close traps.

Species composition showed little commonality between traps that are spatially close. Hence placing several traps on a single sampling site seems a good strategy to place the required number of traps without a drastic increase in sampling effort.

Figure 2.9. 4. Power to detect changes in moth abundance for different combinations of visits per trap and number of traps (different coloured lines) for all observations of macro moths in all habitats in the Dutch moth monitoring scheme. The horizontal grey line indicates a threshold of 80%. (A) Power analysis results for a generalized linear mixed model, with year as an ordered factor and polynomial contrasts. (B) Same as (A), but with year as factor with repeated contrasts.

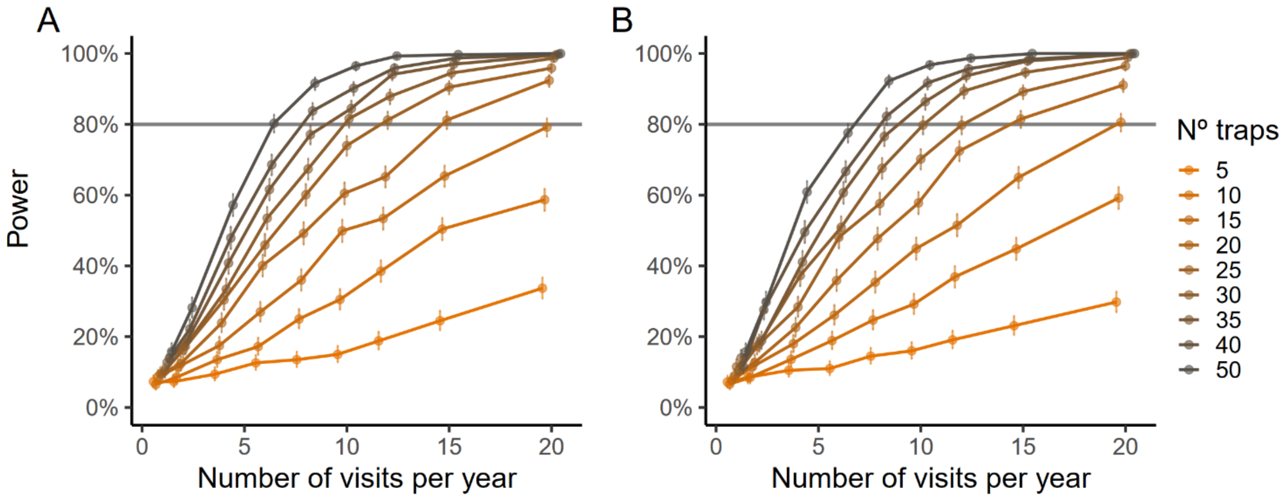


Source: Authors' elaboration based on the SPRING project.

Given the smaller number of moths present in intensive agricultural areas in the Netherlands and their importance for pollination in these areas (Fijen et al., 2023), power analyses were also conducted only on agricultural monitoring sites (Figure 2.9. 5). We found that a solely agricultural landscape will require a slightly higher sampling effort, but differences are minimal.

It is important to stress that for placing and emptying the traps, no moth-identification skills are needed. Simply making photos of all moths inside the trap, and identifying them either via AI or later via an expert, makes it possible for every interested farmer, warden or nature lover to participate in the monitoring of moths, making this one of the monitoring methods which can be relatively easily deployed with the help of volunteers. This can help in reducing the costs for moth monitoring.

Figure 2.9. 5. Power for different combinations of visits per trap and number of traps (different lines) for observations of macro moths in agricultural areas in the Dutch moth monitoring scheme. The horizontal grey line indicates a threshold of 80%. (A) Power analysis results for a generalized linear mixed model, with year as an ordered factor and polynomial contrasts. (B) Same as (A), but with year as factor with repeated contrasts.



Source: Authors' elaboration based on the SPRING project.

Well-established and standardized protocols for the monitoring of moths are used already in eight European countries (Belgium (Flanders), Estonia, Finland, Ireland, Hungary, the Netherlands, the United Kingdom, and Portugal). These protocols, together with the monitoring effort here determined, provide a feasible method to monitor and estimate reliable trends of macro moths across the European Union. This can be done in habitats rich in pollinators but could also be sufficient for trend estimates in areas with lower insect densities like intensively used agricultural areas as in north-western Europe. Due to the relative ease of identifying moths and clear protocols for monitoring, monitoring moths in more European countries could provide reliable trends as indicator of changes in pollinators in Europe.

In the Netherlands, establishing a monitoring system that allows us to detect a significant change over five years requires 40 traps deployed once a month in the season (six times per year). However, as the Netherlands has a volunteer-based moth monitoring scheme running many more sites already, extra costs would be minimal. This also applies to the other countries where moth monitoring schemes are already underway.

2.9.6 Future steps

The standardised protocols described here provide a strong basis for further refinement for inclusion in EU PoMS, and this will be addressed in STING+. The image recognition system could be expanded to include all European moth species. This is already underway but still requires significant work. By piloting and testing the monitoring system, additional images can be quickly be collected. During the testing of this technique in the SPRING project, we had reports of large numbers of moths being captured in south-eastern Europe, and these moths were reported to become active early in the morning. This can be addressed by using a weaker LED light, combined with a mosquito net or a stunning/killing agent. Local and regional differences in species richness and diversity throughout Europe would likely require further small adaptations; several datasets and information sources have already been offered to support further fine-tuning of this method. However, these regional differences should not introduce a bias in the trend calculations, as a location is studied through time. If a European moth monitoring scheme is properly supported, and the method is further tested and refined in southern and eastern Europe, it could potentially grow into a prominent component of the EU PoMS.

Based on the experiences of the European Butterfly Monitoring Scheme with setting up such a network, we recommend the following steps:

- Appoint and fund a full time European coordinator of a European moth monitoring scheme, as well as national coordinators. This would boost the growth rate of the volunteer network.
- Build and financially support a network of validators to ensure quality of moth identification and ensure validated input for the AI system. Validators would target species where image classification success is lowest, in order to make the greatest contribution to ongoing development of image classification models.
- To further lower the threshold for volunteers to get started, supporting materials should be created and translated. These could be user-friendly moth information and identification materials as well as user-friendly protocol descriptions.
- Extend the existing IT infrastructure. The eBMS IT system already fully supports moth recording using image recognition, but the system would need to be expanded. A pan-European scheme would increase the pressure on the databases, portals and image recognition systems.
- Continue development of statistical analyses to produce trends and indicators for moths (see modelling and indicator development in section 3.1). In particular, this would need to include southern and eastern Member States. The first results are likely to be mostly based on data from countries where this scheme is already running (such as the Netherlands) but having the processing tools available could encourage other countries to join.

2.10 Options for monitoring pressures and site co-location

2.10.1 Summary and recommendations

Five candidate schemes potentially suitable for co-locating the EU PoMS site network have been identified: Land Use and Cover Area frame Survey (LUCAS); the European Monitoring of Biodiversity in Agricultural Landscapes (EMBAL); the Monitoring of Environmental Pollution using Honey Bees (INSIGNIA); the Integrated European Long-Term Ecosystem, critical zone and socio-ecological Research Infrastructure (eLTER RI); and the EU Farm Sustainability Data Network (FSDN).

There is no single ‘one-size-fits-all’ monitoring scheme with which EU PoMS is best aligned with. This is because of limitations due to: (i) limited environmental information (LUCAS, INSIGNIA, eLTER, FSDN), (ii) non-representative coverage of the land cover across the EU (LUCAS Grassland, EMBAL, FSDN), or (iii) an insufficient number of observation sites (INSIGNIA, eLTER).

Since EU PoMS should representatively cover the land cover and habitat types across the EU Member States, there can only be partial alignment with one or multiple other monitoring initiatives, i.e. a subset of EU PoMS sites is aligned to selected monitoring scheme(s), while the other part is (stratified) randomly distributed. For the (stratified) random sampling, the LUCAS Master grid is proposed. However, for a subset of EU PoMS sites to be co-located with INSIGNIA, eLTER or FSDN sites, some flexibility to allow for deviations of the gridded approach would be needed. It is likely that aligning with more than one initiative might be challenging in terms of agreements and coordination.

We recommend the design of EU PoMS is prioritised, and that EMBAL (or maybe LUCAS Grassland) and INSIGNIA co-locate to EU PoMS sites. INSIGNIA could further aim to increase the number of sampling sites considerably and seek options for a more spatially constant sampling design.

2.10.2 Introduction

Potts et al. (2021, section 5.2.3) proposed a systematic random or stratified-random process to determine the location of EU PoMS sampling sites to ensure pollinator monitoring is not overly biased towards specific regions, habitats or location of recorders. They further recommended that sites should be co-located with other EU monitoring initiatives to make use of synergistic effects. These effects include:

- Obtaining additional data on environmental factors and thus optimising the interpretation of pollinator monitoring data, e.g. when set into different environmental contexts.
- Enabling the identification of critical drivers of decline, or the quantification of different restoration interventions.
- Fostering the development of explanatory and, moreover, predictive modelling for a spatially-explicit risk assessment and further guidance for targeted mitigation and restoration.
- Utilising an existing network of surveyors familiar with the sites and potentially available to undertake pollinator monitoring.
- Gaining access to a wider knowledge-exchange network including (online) infrastructure and stakeholders to aid promotion of survey activities.

Here we provide an overview of other in situ EU monitoring initiatives potentially suitable for co-locating the EU PoMS site network; and assess opportunities and barriers to co-locating EU PoMS sites with other schemes.

2.10.3 Potential monitoring schemes for site co-location

Five candidate schemes have been identified:

- Land Use and Cover Area frame Survey[40] (LUCAS)
- European Monitoring of Biodiversity in Agricultural Landscapes[41] (EMBAL)
- Monitoring of Environmental Pollution using Honey Bees[42] (INSIGNIA)
- Integrated European Long-Term Ecosystem, critical zone and socio-ecological Research Infrastructure[43] (eLTER RI)
- EU Farm Sustainability Data Network[44] (FSDN)

2.10.3.1 LUCAS: Land Use and Cover Area frame Survey

Based on a decision by the European Parliament, a collection of data on land cover and land use is organised by the European Statistical Office (EUROSTAT), in close cooperation with DG AGRI and supported by the JRC, across all 27 EU Member States. Data collection started in 2009 and is repeated every third year. It is based on the intersection points of a regular 2 km grid including more than 1 million points across EU 27. The latest LUCAS survey took place in 2022. Out of the 1 million points, 400,000 points were observed based on a stratified random sub-sampling. Half of them were monitored directly in the field (within a radius of 1.5 m) and the other half through photointerpretation (when they cannot be accessed[45]). Each survey round (every third year), a different subset is selected, and each sample location is visited once per round. Within this so-called Master sample or grid, information on land cover (74 classes) and socio-economic land use (40 classes) is collected at the spot. Surveyors also take pictures of the point and in all cardinal directions. In addition to the Master sample, five different modules exist which are based on subsamples of the Master sample (Soil, Grassland, Extended Grassland, Landscape Features, Copernicus) of which the Grassland module can be of particular relevance for EU PoMS. This module was piloted in 2018 with 3734 sites and repeated in 2022 with 20,000 sites selected as a subset of the Master sample. Grassland type and quality is monitored via a transect of 20 m in length and 2.5 m in width, giving a total surveyed area of 50 m². The following variables are surveyed: Habitat type (e.g. EUNIS type, presence of structural species), Environmental conditions (e.g. slope in degrees, orientation, heterogeneity of soil surface), Age of grassland (estimated based on visible evidence), Use type (e.g. type of grazing animal, evidence of abandonment, presence of agroforestry), Use intensity (derived from type of vigour, height of vegetation, indicated fertilization, indicated irrigation, mono-structured vegetation), Structure of vegetation (e.g. heights and coverages of different elements of vegetation layers), Biodiversity value (e.g. presence of indicator species, balance of elements of herb layer), Pollinator value (e.g. number of flowering species, flower density) (Sutcliffe et al., 2019).

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[40] https://esdac.jrc.ec.europa.eu/projects/lucas

[41] https://wikis.ec.europa.eu/pages/viewpage.action?pageId=25560696

[42] https://www.insignia-bee.eu/

[43] https://elter-ri.eu/

[44] https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=COM:2022:296:FIN

[45] https://ec.europa.eu/eurostat/web/products-statistical-working-papers/-/ks-tc-22-005

2.10.3.2 EMBAL: European Monitoring of Biodiversity in Agricultural Landscapes

EMBAL was launched by the European Commission DG ENV to provide a harmonised pan-European overview of the state and changes of biodiversity in agricultural landscapes and with the particular aim to contribute to the EU Pollinators Initiative (amongst others). It started with a pilot in 2020 at 250 plots and to rollout in 2022 (3,000 plots), continuing in 2023 at the same plots. Based on simulation studies and respective power analyses, a range between 5,000 and 40,000 plots has been recommended when being fully operational, depending on different scenario settings (including a rolling design). Its design is based on and fully harmonised with LUCAS, i.e. the same 2 km x 2 km grid (1 million points) and the subset of the Master sample. Whether the sample locations will be spatially fixed or will be based on a rolling design has not been decided yet. The locations are visited once per year, but within a vegetation phenology-optimised time window. The survey is restricted to areas under agricultural use (arable land, permanent grassland, permanent pasture, permanent crops), while non-agricultural elements are only basically classified. It is based on plots of 500 m x 500 m (25 ha) with a condition of having at least 10% agricultural land as a selection criterion. The surveys cover three spatial levels: (i) plots; (ii) parcels and landscape elements; and (iii) vegetation transects. At the plot level (500 m x 500 m), information from the parcels and landscape elements is aggregated and includes landscape structure, land cover (8 broader categories, 81 finer categories), land-use intensity, and structural diversity. At the parcel and landscape element level, the elements are digitised yielding relevant structural metrics, in addition to information on the stage of the vegetation, use intensity (crop coverage vs wild plant coverage, irrigation, vigour of grassland, graminoid vs forb coverage) and pollinator value (flower density, number of flowering colours). Across the plots, nine transects are placed (5 within agricultural fields, 4 at the field border) covering 20 m in length and 2.5 m in width (according to the LUCAS grassland module design). On the transects, all former mentioned measures are taken and additional information on EUNIS grassland type, land use intensity (grassland fertilisation, height of arable crop), and pollinator value (number of flowering forb species, type and number of plant indicator species) is obtained.

2.10.3.3 INSIGNIA: Monitoring of Environmental Pollution using honey bees

Based on a proposal by the European Parliament, INSIGNIA aims to use the honey bee (*Apis mellifera*) as a bioindicator for the monitoring of environmental pollutants. In a pilot project (2018-2021) focusing on pesticides, relevant methods have been identified and tested and respective protocols have been developed. During a Preparatory Action (2022-2023), more than 600 apiaries were sampled across all EU Member States and the focus will be expanded to other environmental pollutants such as heavy metals, air pollutants, microplastics, veterinary products. The sampling design is based on a Citizen Science approach, where participating beekeepers are asked to sample beehive matrices (e.g. pollen) and deploy non-biological passive samplers, both of which will be sent to laboratories for residue analyses. The selection of apiary locations is intended to be stratified according to country size, land use type (agricultural, artificial, forest, natural), and land use diversity (high, medium, low).

2.10.3.4 eLTER-RI: Integrated European Long-Term Ecosystem, critical zone and socio-ecological Research Infrastructure

The Integrated European Long-Term Ecosystem, critical zone and socio-ecological Research Infrastructure follows a “whole system research” philosophy to facilitate research on impacts of climate change, biodiversity loss, soil degradation, pollution, and unsustainable resource use. eLTER is now in the preparatory phase on the way to becoming a fully-fledged European Research Infrastructure. It covers a broad range of European ecosystems and with the eLTER facilities also socio-ecological systems, and it provides access to over 500 sites and more than 50 larger eLTER facilities. Because of the bottom-up evolution of the networks, the sites vary considerably in size and in the monitoring focus and methodological monitoring approaches. However, a number of Standard Observations (76) have been proposed, which shall be made at all sites finally constituting the Research Infrastructure (Zacharias et al., 2021). These Standard Observations cover six fields: abiotic heterogeneity (17 variables), water budget (12), matter budget (10), energy budget (5), socio-ecology (24), and, most relevant for pollinators, biotic diversity (8, e.g. flying insects [Malaise traps], habitat structure [remote sensing], birds [amongst other groups, voice recognition], and plant phenology [video recognition]).

2.10.3.5 FSDN: EU Farm Sustainability Data Network

The EU Farm Sustainability Data Network (FSDN) is based on the EU Farm Accountancy Data Network (FADN). A proposal to convert FADN into FSDN was adopted by the European Commission on 22 June 2022[46]. Respective amendments have been negotiated[47] and a provisional agreement between the European Parliament and the Council was reached on 29 June 2023[48]. The aim of this conversion is to better reflect the goals of the 'farm to fork' strategy and to improve the sustainability of the EU's food systems through an enhanced data collection process. In addition to the already collected microeconomic and accountancy data, environmental and social data (to be specified) will be collected. In particular, FSDN also aims to **improve links with other data collection initiatives, making them useful for research and policy-making. Collected data shall be representative** for all agricultural holdings in the EU of at least 1 hectare, but Member States had established their own selection plans not to sample all farms but a representative subsample. To account for the immense heterogeneity across the EU, a stratification approach is used for selection, based on region, economic size classes and type of farming. Guided by this stratification, a random subsampling is done on an annual basis. However, since the participation of farmers is on a voluntary basis, full randomisation cannot always be reached. Currently, FADN is based on a network of 80,000 farms (representing ~5 million farms in the EU and ~90% of the agricultural area and production). The final FSDN will include detailed data on microeconomies and farm production (also including innovation and market position), environmental variables relevant for assessing natural resource, nutrient, and pesticide use and management, emissions, energy use and production, biodiversity, and social aspects such as working conditions, social inclusion, and generational renewal.

2.10.4 Summary of suitability across initiatives

Options for co-location are assessed based on two hierarchical criteria (Table 2.10. 1). ***Implementation*** covers the *phase of implementation* (regulatory basis, preparatory, rollout, fully operational) and mode of *co-location (alignment)* where the respective monitoring initiative can/should align with EU PoMS or EU PoMS needs to align with the initiative. The ***spatial design*** includes *spatial coverage* (in terms of number of EU Member States); the *design*, i.e. whether sample locations are grid-based, opportunistic or placed randomly; the *number of sample locations* (spatial points); *spatial constancy*, i.e. whether the sample locations are constant through time or variable; and the *spatial extent* of the sampling activity. The ***temporal design*** provides information on the *inter- and intra-annual sampling design*. The criterion ***environmental variables*** informs about the measured *environmental conditions* and *whether the information is spatially explicit* or not. ***Co-benefits*** covers information on additional *biodiversity* aspects and *ecosystem* properties. ***Socio-economy*** indicates whether additional information on *microeconomics*, *agricultural production*, and *economically relevant land use* is available.

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[46] https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=CELEX%3A52022PC0296

[47] https://data.consilium.europa.eu/doc/document/ST-9067-2023-INIT/en/pdf

[48] https://www.consilium.europa.eu/en/press/press-releases/2023/06/29/farm-sustainability-data-network-council-and-parliament-reach-provisional-political-agreement/

Table 2.10. 1. Suitability of other monitoring initiatives for co-locating EU PoMS sites. For combined co-location with multiple initiatives (EMBAL-FSDN; EMBAL-FSDN-eLTER), the best colour code per criterion is given: Green, optimal; Yellow, with restrictions; Orange, suboptimal; Grey, not yet decided.

Criterion I	Criterion II	LUCAS Master	LUCAS Grassland	EMBAL	INSIGNIA	eLTER-RI	FSDN	EMBAL FSDN	EMBAL FSDN eLTER
Implementation	Phase	Operational	Operational	Rollout (2022)	Preparatory (2022-2023)	Implementation (2021) Operational in 2026	Regulation adopted 2023		
	Alignment	With EU PoMS	With EU PoMS	With EU PoMS	EU PoMS should align	EU PoMS should align	EU PoMS should align		
Spatial design	Spatial coverage	EU-27	EU-27	EU-27	EU-27	19 Member State	EU-27		
	Spatial design	Grid	Grid	Grid	Opportunistic	Opportunistic	Random		
	Sample points	400,000	20,000	5,000 - 40,000	>600	>500	80,000		
	Spatial constancy	Yes	Yes	Yes	No	Yes	Yes		
	Spatial extent	7m²	50 m²	25 ha	5 km²	Varying	Varying		
Temporal design	Inter-annual	Triannual	Triannual	Not decided	Not decided	Varying	Annual		
	Intra-annual	Once	Once	Once	9 rounds	Varying	Once		
Environmental variables	Spatially explicit	Yes	Yes	Yes	Yes	Yes	No		
	Land cover	74 classes	74 classes	81 classes	No	Yes	No		
	Use intensity	No	Yes	Yes	No	Yes	Detailed		

Criterion I	**Criterion II**	**LUCAS Master**	**LUCAS Grassland**	**EMBAL**	**INSIGNIA**	**eLTER-RI**	**FSDN**	**EMBAL FSDN**	**EMBAL FSDN eLTER**
	Pesticides	No	No	No	Exposure	No	Application		
	Restricted to habitat type	No	Grasslands	Agricultural	No	No	Agricultural		
	Habitat type	Yes	Yes	Yes	No	Yes	Agricultural		
	Habitat quality	No	Yes	Yes	No	No	Agricultural		
	Vegetation	No	Yes	Yes	No	No	No		
	Pollinator value	No	Yes, less detailed	Yes, more detailed	No	No	No		
	Terrain	No	Yes	Yes	No	No	No		
Co-benefits	Biodiversity	No	No	No	No	Yes	Limited		
	Ecosystem	No	No	No	No	Yes	Limited		
Socio-economy	Microeconomies	No	No	No	No	Partly	Yes		
	Production	No	No	No	No	Partly	Yes		
	Land use	40 classes	40 classes	No (LUCAS)	No	Yes	Yes		

Source: Authors' elaboration.

2.10.5 Assessment of opportunities and barriers to co-locating EU PoMS sites with other schemes

Opportunities and potential barriers of co-locating EU PoMS sites with the identified monitoring schemes depend on agreed priorities, i.e. which kind of synergies are most desired. Each of the schemes has its particular benefits and shortcomings for co-location with EU PoMS sites, covering aspects of implementation (and timing), the spatial and temporal design, type, number and quality of assessed environmental variables, potential co-benefits with other biodiversity and ecosystem measures, and the coverage of socio-economic factors (Table 2.10. 1).

2.10.5.1 LUCAS

Pros: LUCAS, and in particular the LUCAS Grassland module, is fully operational and covers all EU 27 Member State. The spatial design along a 2 km grid and a stratified random subsampling provides an objective, un-biased, and sufficient number of candidate points for alignment with EU PoMS. Both LUCAS and the LUCAS Grassland module provide basic land cover and habitat information. Particularly valuable for EU PoMS is the assessment of pollinator value variables, providing important information on the local context.

Cons: A particular drawback of both schemes is the limited spatial extent of the sampling (7 m^2 for LUCAS, 50 m^2 for the Grassland module) and the triannual sampling frequency. A much larger extent would be needed for EU PoMS reinforced transects (proposed 1km^2, as a compromise to consider foraging ranges of both small and large pollinators) and to relate them to LUCAS measurements. In addition, information on an annual basis would be desirable to match EU PoMS sampling and to identify relationships between pollinator trends and the landscape, habitat or local flower resources, particularly in the first years of EU PoMS with limited power to detect trends. While LUCAS covers a representative sample of all EU habitat types, the Grassland module, which is in principle more beneficial for EU PoMS, is restricted to grasslands. However, this restriction does not match with the aim of EU PoMS to be representative across all habitat types of the EU. Finally, both schemes do not allow to link results from EU PoMS to other measures of biodiversity or ecosystem-relevant variables, for the assessment of potential co-benefits, or to (detailed) socio-economic conditions with final relevance for policy-making.

Conclusion: The main benefit of a link to the LUCAS site network is that it provides the grid structure that allows for a stratified random selection of EU PoMS survey sites. However, the sampling protocols within LUCAS offer relatively limited direct benefit for EU PoMS. Any EU PoMS activity would have to be set up independently from the LUCAS work, will benefit only very little from LUCAS point information, and will not benefit from LUCAS survey infrastructure.

2.10.5.2 EMBAL

Pros: Since EMBAL builds upon the LUCAS sampling scheme, it has all its benefits but adds more. The multi-scale approach (from 50 m^2 to 25 ha) allows for potentially perfect alignment with EU PoMS sites. In addition to matching spatial scales, EMBAL provides detailed information on local and landscape-level floral resources enabling assessments of pollinator value metrics, to set the monitoring results from EU PoMS into local context.

Cons: At this time, EMBAL is not fully implemented yet and respective synergistic effects will depend on the timing of the rollout phase. In addition, the final number of sampling points has not been decided yet, and the suggestions (between 5,000 and 40,000 sites across the EU) and the potential degree of possible alignment with EU PoMS sites would need to be considered. In addition, EMBAL is restricted to agricultural landscapes, which is not in line with an unbiased representation of EU PoMS sites, but can provide highly relevant additional information for the Farmland Pollinator Indicator. Same as LUCAS, EMBAL does not allow to link results from EU PoMS to other measures of biodiversity or ecosystem-relevant variables, for the assessment of potential co-benefits, or to (detailed) socio-economic conditions with final relevance for policy-making.

Conclusion: EMBAL combines the benefits of LUCAS and additionally provides (i) a better matching with EU PoMS in terms of spatial coverage, and (ii) more detailed information on local flower resources and thus qualifies well for co-location with EU PoMS sites. The fact that the final design is not decided yet, in terms of number of sites and sampling frequency (annual, multi-annual, rolling), might provide options for a better coordination between the two schemes and a tighter link is recommended. However, EMBAL is restricted to agricultural areas. To avoid a biased distribution sample locations towards agricultural land, EMBAL cannot be the only source for co-location.

2.10.5.3 INSIGNIA

Pros: INSIGNIA covers all EU 27 Member States and provides some critical information on environmental pollutants, including pesticides. Approximated by the average flight range of the honey bees, it covers an area of about 5 km^2 which is sufficient for placing EU PoMS reinforced transects. Direct measures of exposure to chemicals can be related to pollinator trend analyses and thus represent valuable information that is lacking in most of the other monitoring schemes.

Cons: The current number of INSIGNIA sites (about 600) provides only limited opportunities for co-locating EU PoMS sites. Moreover, the locations of most of the apiaries can be expected to vary across and even within the years, particularly if professional beekeepers are involved as they usually move the hives to optimise honey production. Such high spatial dynamics challenge co-location with EU PoMS sites, since trend analyses on spatially fixed sites might be more reliable and less questionable. However, a certain level of spatial stability might be expected, e.g. for orchards and private beekeepers, but for a limited number of apiaries. Same as for LUCAS and EMBAL, INSIGNIA does not provide information on other measures of biodiversity or ecosystem-relevant variables, or on socio-economic conditions.

Conclusion: Information on environmental pollutants (including pesticides) is highly relevant as they represent major drivers of pollinator declines and are not provided by most of the other monitoring schemes. However, current low numbers of participating beekeepers and an expected high proportion of spatial dynamics in the site locations challenge co-location with EU PoMS sites. Depending on the final number of participating beekeepers once the scheme has been fully rolled out, a fraction of stable locations (we recommend an alignment with EMBAL and/or EU PoMS sites) might be considered for co-location with EU PoMS sites but INSIGNIA cannot be the only source for co-location.

2.10.5.4 eLTER-RI

Pros: Once fully operational, the eLTER-RI provides infrastructure which can be utilised by EU PoMS together with a vast amount of standardised background data, in particular on other biodiversity measures, ecosystem variables and partly on socio-economic conditions. This information is unique compared to the schemes discussed before, and particularly helpful for the assessment of co-benefits, e.g. with respect to successful pollinator restoration interventions, and to set changing pollinator trends into a socio-economic context. In addition, mutual benefits for eLTER would emerge from aligning EU PoMS sites to eLTER. Despite the coverage of multiple species groups and ecosystem variables, pollinators are not explicitly considered in the set of standard observations, although they will be (partly) covered by catches from Malaise traps which will be analysed through metabarcoding (see also section 5.4). However, an additional targeted measure of pollinator abundance and diversity would also enrich the set of eLTER standard observations.

Cons: Not all EU 27 Member States are covered and the locations of the sites are a result of a naturally evolving network and are thus less representative of the overall landscape of the EU Member States. In addition, similar to INSIGNIA, the number of sites (about 500) is low compared to the likely requirements of EU PoMS (see section 2.4). In addition, detailed information on habitat quality, particularly on pollinator value (i.e. floral resource density and diversity) is lacking and socio-economic variables are collected on a smaller subset only.

Conclusion: The largest benefit of aligning EU PoMS sites with eLTER sites would be the link to co-benefits in terms of other biodiversity aspects and ecosystem variables. However, the low number of sites and the only partial coverage of the EU Member States, limits the options for co-location.

2.10.5.5 FSDN

Pros: Linking with FSDN would provide clear benefits for gaining the most detailed information on land use intensity, in particular on pesticide applications, in contrast to INSIGNIA, which provides pesticide exposure, and on socio-economics, especially on microeconomics and agricultural production, which makes it unique compared to all other schemes. FSDN covers all EU 27 Member States; it is based on a stratified random sampling and a more than sufficient number of participating holdings. In contrast to all other schemes, FSDN data are collected annually which eases a direct link to EU PoMS data and allows to identify respective relationships within a shorter time period. Aligning with FSDN would also enable a direct link to the EU Common Agricultural Policy (CAP) via information on direct payments and rural development and thus to assess the contribution of the CAP to the European Green Deal.

Cons: The information collected by FSDN is not spatially explicit, but refers to the participating agricultural holdings, which complicates the link between FSDN data and the EU PoMS indicators obtained at a particular site. However, at higher aggregation levels, e.g. Member States or region, such links can be established. FSDN holds highly sensitive data such as personalised financial data and information on management practices and resulting yields. Although improved links with other **collection initiatives and usability for research and policy-making are envisaged, access options for such sensitive data are still not clarified.** In addition, same as EMBAL and LUCAS Grassland, FSDN information does not represent the full range of land cover across the EU but is restricted to land under agricultural use. Finally, it does not provide information on pollinator value, e.g. such as EMBAL.

Conclusion: FSDN would provide the most detailed information on land use intensity and the socio-economic context, allowing links to the CAP, but access conditions to the highly sensitive data need to be clarified. Furthermore, due to the sectoral focus on farm conditions, FSDN cannot be the only source for co-location with EU PoMS sites.

2.10.6 Conclusions and recommendations

There is no single ‘one-size-fits-all’ monitoring scheme with which EU PoMS is best aligned with. This is because of limitations due to: (i) limited environmental information (LUCAS, INSIGNIA, eLTER, FSDN); (ii) non-representative coverage of the land cover across the EU (LUCAS Grassland, EMBAL, FSDN); or (iii) an insufficient number of observation sites (INSIGNIA, eLTER).

Since EU PoMS needs to representatively cover the land cover and habitat types across the EU Member States, there can only be partial alignment with one or multiple other monitoring initiatives, i.e. a subset of EU PoMS sites is aligned to selected monitoring scheme(s), while the other part is (stratified) randomly distributed. For the (stratified) random sampling, the LUCAS Master grid is proposed. However, for a subset of EU PoMS sites to be co-located with INSIGNIA, eLTER or FSDN sites, some flexibility to allow for deviations of the gridded approach would be needed.

Therefore, if a decision is taken to align with only one scheme, a prioritisation process is needed, depending on the preferred synergism. In short, LUCAS Grassland and more so EMBAL could provide detailed information on local context, i.e. flower abundance and distribution, in addition to coarser land cover and intensity measures. EMBAL might be preferred over LUCAS Grassland because of its better matching of the spatial scale needed for EU PoMS. INSIGNIA provides information on pesticide exposure, while FSDN collects detailed information on pesticide application in addition to CAP-relevant socio-economics data. Here, FSDN might be preferred over INSIGNIA because of the low number of the sample sites, which may be spatially varying, of the latter and the additional socio-economic information of FSDN. All these initiatives have a strong bias towards agricultural land, therefore options for aligning these with a potential Farmland Pollinator Indicator (see section 3.2) should be considered. In all cases, data access needs to be clarified. If the focus should be on co-benefits with other biodiversity and ecosystem aspects, then eLTER-RI might be chosen, but keeping the low number of sample sites in mind.

Partial alignment with a combination of other monitoring initiatives would optimise synergistic effects. A combination of EMBAL and FSDN, for instance, would increase the amount of valuable information considerably, and adding eLTER sites would provide most detailed information on almost all of the analysed criteria, i.e. covering: (i) environmental variables at the landscape and local scale, including information on pollinator value and land use intensity; (ii) co-benefits, including biodiversity and ecosystem aspects; and (iii) the socio-economic context with high policy relevance (Table 2.10. 1).

An option we recommend is to prioritise the design of EU PoMS, and that EMBAL (or maybe LUCAS Grassland) and INSIGNIA co-locate to EU PoMS sites. INSIGNIA could further aim to increase the number of sampling sites considerably and seek options for a more spatially constant sampling design. Since EMBAL, LUCAS and INSIGNIA do not cover all land cover types across the EU, EU PoMS sites can only partly be co-located with these schemes. The final EU PoMS design should ensure a representative coverage of all relevant land cover types for which we recommend using the LUCAS Master grid, but also allowing some flexibility to align some EU PoMS sites with less flexible initiatives such as FSDN and eLTER. To utilise comprehensive information on land use intensity and the socio-economic context from FSDN, we recommend establishing agreements regulating the access to these data.

3 Options for pollinator indicators

3.1 Options for a General Pollinator Indicator

3.1.1 Summary

We define a set of options for converting EU PoMS data into pollinator biodiversity indicators, and how these indicators can be used to assess whether there has been a reverse in the decline of pollinators (i.e. a trend should be shifted from a declining to an increasing one), using annually collected data, assessed over a standardised time interval of 6 years, at the Member State level by a given date. Based on the EU PI, and STING expert consensus, we recommend species abundance as the core metric for assessing trends. We describe a set of metrics that could be derived from EU PoMS and some options for statistical models to fit them. We demonstrate how indicators of the state of pollinator diversity might be used, potentially in combination, to assess targets for whether there has been a reverse in the decline of pollinators. We make a series of recommendations for next steps.

3.1.2 Background and context

The EU PoMS will generate valuable data on the state of pollinating insects across the European Union. The purpose of this section is to define options for converting these data into useful information, including biodiversity indicators.

This report is written in five sections. Section 3.1.3 defines the principles and assumptions that have guided the development of this work. Section 3.1.4 identifies the range of biodiversity metrics that can be derived from the data in the core scheme. Section 3.1.5 outlines a set of statistical models to estimate these metrics and present them as biodiversity indicators. Section 3.1.6 considers options for assessing these indicators against targets with different time horizons. Finally, in section 3.1.7, these issues are brought together into a series of recommendations.

3.1.3 Principles and assumptions

- Reporting is at the Member State level, so it is at Member State level that we need indicator(s). Further stratification by biogeographic region, ecosystem level and Natura 2000 or habitat type (farmland vs semi-natural) within a Member State is desirable but not considered here.
- We seek indicators that can be calculated annually, but the assessment of trends would only be undertaken towards 2030, and thereafter every 6 years.
- The primary data source consists of counts of individual pollinators from reinforced transect walks (section 2.2). The aim is that counts are resolved at species level. It is recognised that this will require swift and adequate investment in taxonomic capacity building in all Member States (see section 2.6).
- Regardless of the taxonomic level of recording, we assume that it will be possible to harmonise the transect data for each Member State to a common set of taxa for reporting. Any variability within Member State in taxonomic resolution, either among sites or over time, would incur a cost in terms of data management and potentially also in terms of statistical power.
- The scheme design and protocols are not discussed here.

- The indicator is intended to measure changes in wild pollinators, so honey bees and other intensively managed species should be excluded.

Sphaerophoria scripta, Axel Hochkirch

3.1.4 Metric options

Biodiversity is multi-faceted and multi-scale in nature. For this reason, there are many biodiversity metrics in use, none of which can adequately represent all facets.

It is useful to think about the potential metrics in terms of Essential Biodiversity Variables (EBVs). EBVs provide a framework for harmonizing the collection and reporting of biodiversity data. In particular, the 21 EBV types, arranged into six classes, provide a way to reduce the complexity of biodiversity into a few key axes. In the context of the EU PI, the most relevant are four EBV types in the Species Populations or Community Composition classes.

3.1.4.1 Species Population: Species Abundance

Species abundance is an essential metric for reporting biodiversity change. Reporting on changes in species abundance is a central requirement of the EU PoMS scheme. Species abundance is a highly valued metric because it is considered more responsive to environmental change than other metrics, and because it is directly related to species' probability of extinction.

High quality data on species abundance can be relatively costly to collect and can present numerous challenges for modelling. The most acute of these challenges occurs when abundance fluctuates markedly from one year to another. Extreme fluctuations are commonly observed in insect populations, arising from a capacity for rapid population growth, strong density dependence and the fact that population counts reflect not just abundance but also activity, which is primarily a function of weather conditions. For this reason, indicators of insect population abundance are unlikely to show meaningful patterns over short time periods (White, 2019). One solution to population fluctuations is to apply some kind of statistical smoothing, the aim of which is to reveal the multi-year trajectory underlying the interannual variation. Thus, a question for EU PoMS is whether it is possible to detect change in a smoothed index of abundance within a six-year assessment window. Note that the power analysis (section 2.3) was conducted on the basis of measuring linear trends in species abundance over a six-year period.

Calculating an indicator of species abundance typically involves two stages of analysis (Gregory et al., 2005). The data for each species are first converted into a national index of abundance for each year, using a statistical model. These species index values are then combined in a second step, using the geometric mean, and finally scaled to have a value of 100 in the baseline year. The geometric mean is preferred over other metrics because it has a number of desirable properties for measuring change over time (Buckland et al., 2005, 2011). One or both calculation stages might involve smoothing the data to remove interannual fluctuations. Many well-known indicators of species abundance follow this general recipe, including the UK Farmland Bird Index[49], the Common bird index in Europe[50], the European Grassland Butterfly indicator[51] and the Living Planet Index[52].

3.1.4.2 Species Population: Species Distribution

Species distributions can be conceptualised in many ways, including the Extent of Occurrence and Area of Occupancy, both of which are used for IUCN Red List assessments (see IUCN criteria[53] for definitions of these terms). For annual indicators, the most appropriate measure of species' distribution size is occupancy (i.e. the proportion of occupied sites). Indicators of occupancy, such as the UK indicator of Pollinating insects[54] are now gaining popularity. As with an abundance index, the workflow typically involves a separate analysis to calculate national trends for each species, which are then combined (Boyd et al., 2023).

Metrics based on species' occupancy are slower to respond to environmental change than species abundance, but contain fewer challenges for modelling and interpretation. An occupancy indicator would provide a valuable complement to an abundance indicator.

3.1.4.3 Community Composition: Taxonomic diversity

The Taxonomic diversity EBV includes a broad suite of biodiversity metrics. The simplest of these is species richness, i.e. the number of species present at each site.

Note that taxonomic diversity is dependent upon the scale at which it is measured. Diversity at individual sites is referred to alpha diversity, whereas diversity at large scale, such as a Member State, is referred to as gamma diversity. Indicators based on gamma diversity are not recommended, because they would be extremely insensitive to change.

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[49] https://www.bto.org/our-science/publications/developing-bird-indicators#farmland

[50] https://www.eea.europa.eu/en/analysis/indicators/common-bird-index-in-europe

[51] https://www.eea.europa.eu/data-and-maps/figures/european-grassland-butterfly-indicator

[52] https://www.livingplanetindex.org/latest_results

[53] https://portals.iucn.org/library/node/10315

[54] https://jncc.gov.uk/our-work/ukbi-d1c-pollinating-insects/

If an index of taxonomic diversity were chosen, it would be important to develop rules for which species would be included and excluded among the pool of potential species, in order to avoid perverse consequences. For example, we recommend excluding any invasive alien species, but including species that colonize naturally from neighbouring countries, perhaps in response to climate change.

Many other biodiversity metrics could conceivably be reported under the Taxonomic diversity EBV. In particular, two families of metrics are worth considering. The first family is the set of alpha diversity metrics that include information about species abundance and evenness (i.e. how abundance is distributed between species). The best known of these metrics are Shannon's index and Simpson's index. The second family of metrics capture how community composition varies across sites: these are known as beta diversity metrics. A decrease in beta diversity over time would indicate that sites are becoming more similar to one another (i.e. biotic homogenisation).

Metrics capturing taxonomic diversity would provide useful information that is complementary to an indicator of species abundance. An index based on species richness (e.g. the geometric mean across monitored sites) would have similar properties to an index of species occupancy, since both are based upon changes in species presence-absence across sites.

3.1.4.4 Community Composition: Taxon-aggregated abundance

The total abundance of all species within a community is seen as being relevant to the potential delivery of ecosystem services (Purvis, 2020). The key distinction between indicators of taxon-aggregated abundance and species abundance (section 3.1.4.1) is that changes in the former reflect trends among common species, whereas in indicators of species abundance each species is weighted equally.

For insects, taxon abundance would be expected to fluctuate substantially from year to year, in the same way as species average, so a degree of smoothing would be appropriate. The Biodiversity Intactness Index[55] is conceptualised as a measure of taxon abundance. The UK Pollinator Monitoring Scheme is developing an index of taxon-aggregated abundance.

An index of taxon-aggregated abundance is not consistent with the primary focus of EU PoMS but could be a useful complement to an indicator of species abundance. In particular, taxon-aggregated abundance is seen as a good indicator of the provision of ecosystem services.

3.1.5 Models for pollinator indicators

3.1.5.1 The need for models

Ecological monitoring data are extremely noisy, even for schemes with rigorous survey design and protocols. This noisiness arises from a number of unavoidable hard facts. First, it is simply impossible to observe all of the species present on a site, let alone count all of the individuals. This is known as imperfect detection. Second, the detectability of many species, especially for

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[55] https://www.nhm.ac.uk/our-science/data/biodiversity-indicators/biodiversity-intactness-index-data?future-scenario=ssp2_rcp4p5_message_globiom&georegion=001&min-year=1970&max-year=2050&georegion-compare=null&future-scenario-compare=null&show-uncertainty=true&min-biigraph-y-axis=0&max-biigraph-y-axis=100&min-factorgraph-y-axis=0&max-factorgraph-y-axis=100&underlying-factor=crp

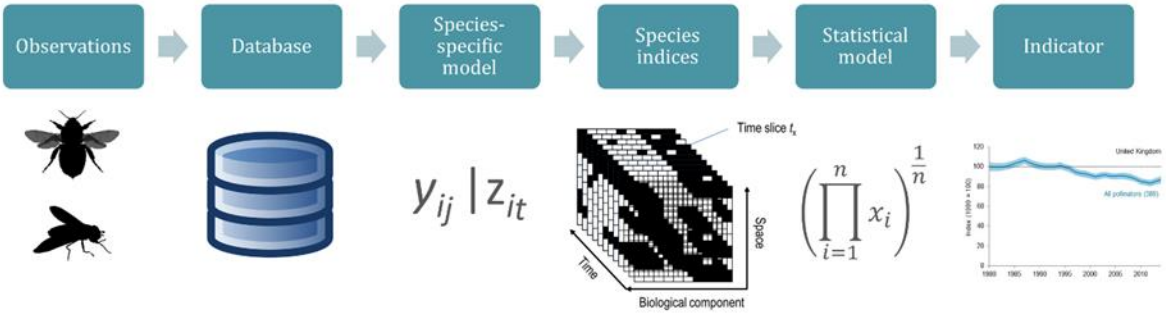
pollinating insects on transects, varies with the weather: it is typically much higher on warm sunny days than when it is cold, overcast, or in windy conditions. Third, the population size for many organisms is highly seasonal. This is especially true of pollinating insects, many of which live as adults for just a few weeks. As a result, the actual number of organisms that are available for detection changes throughout the year. Fourth, not every planned survey actually takes place, because of either equipment failures, bad weather or illness among the survey team. This creates missingness in the resulting datasets.

For these reasons, it is not possible to derive indicators directly from raw data without advanced statistical processing. Fortunately, ecological statisticians have created a rich set of modelling tools for estimating metrics of interest using models.

3.1.5.2 Generalised indicator workflow

As mentioned previously, biodiversity indicators are the product of multiple stages of data processing and analysis, typically involving more than one statistical model. Collectively, these steps are referred to as a workflows (Boyd et al., 2023; Kissling et al., 2018). Figure 3.1. 1 defines a generalised workflow for species-based indicators of the state of biodiversity, modelled on the UK Wild Bird Indicators[56] and the English species abundance index[57] (which was developed by Nick Isaac and will be used to assess a legally binding target to halt the loss of species abundance). This approach would be appropriate for metrics in the Species Populations EBV class (i.e. species abundance or occupancy): slight variations would be required for Community Composition metrics.

Figure 3.1. 1. Generalised workflow for biodiversity indicators.



Source: Authors' elaboration.

The first steps in a biodiversity workflow are to (i) collect data in the field and (ii) input these into a database (Figure 3.1. 1). The data ingestion step would include checks to validate and verify the data: these aspects of EU PoMS are described elsewhere (section 4.6). Once the data have been assembled, the third step is to fit a statistical model to the data for each species to create national indexes for each year for the metric of interest (e.g. abundance). Not every species has sufficient data to derive reliable index values, so there is a need for rules to determine which species should

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[56] https://www.bto.org/our-science/publications/developing-bird-indicators

[57] https://www.gov.uk/government/statistics/indicators-of-species-abundance-in-england/indicators-of-species-abundance-in-england

be included. Options for which statistical models to use for EU PoMS data are described in more detail in the next section. The fourth step is to aggregate the results from these species-specific models into a database. This "data product" is sometimes described as an "EBV data-cube" (Kissling et al., 2018). The fifth stage is to combine the species-level data into a multispecies aggregate. This could be a simple summary, such as a geometric mean. More typically, the structure of the data demands a statistical model (Freeman et al., 2021) to create the multispecies summary.

In the context of EU PoMS, this workflow would be performed separately for each biodiversity metric (species abundance, distribution, taxonomic diversity, taxon-aggregated abundance) for each taxonomic group (bees, hoverflies, butterflies) and for each Member State.


Lycaena phlaeas, Axel Hochkirch

3.1.5.3 Options for models

The STING1 report contained a series of modelling options. In that report, the key question defining the model options was whether the data from the transect data are at species level or not. Here we focus on the modelling approaches that would be appropriate for the different metrics from transect data only. We present brief summaries of the various modelling options, rather than provide detailed equations. Further development of these models is expected to be a major focus of STING+.

Species abundance model

This refers to a separate model for the abundance of each species:

$$N_{it} \sim site_i + year_t$$

Equation 3.1. 1. Species abundance model.

In Equation 3.1. 1, N_{it} refers to species abundance at site *i* in year *t*. Abundance is modelled on the log scale, reflecting that population growth is a multiplicative process. The year effects of this model can be interpreted as the national index of log(abundance) of the species in question for each year.

The simple version of this model contains a term for the site identity, reflecting the fact that sites vary in abundance, and year. The year effects from the model capture change over time and can be interpreted as the national index of log(abundance) of the species in question for each year. These index values are what is passed onto the next step of the indicator workflow, in which an indicator of species abundance would be calculated as the geometric mean value of N_{it} for each year (Buckland et al., 2005, 2011).

The year effect could be modelled either as a categorical effect or, more likely, as a smoothed function. Note that the power analysis implemented a version of this model in which the year effect was modelled as a linear change: this was appropriate given the aims of the power analysis, but would not be appropriate for a real indicator of change over time. To make the model suitable for noisy ecological data, it would also be appropriate to include terms in this model for seasonal variation and potentially also weather conditions at the time of the survey (Müller et al. 2023).

Status: This type of model is routinely applied to existing monitoring data, including most Butterfly Monitoring Schemes (Dennis et al., 2016), so there would be relatively little development work required for use on EU PoMS. The main area for development would be to derive rules for when there is enough data to fit a model and to determine the appropriate degree of smoothing.

Advantages: Provides data that is consistent with established indicators, following standard methods.

Disadvantages: Sufficient data are usually available for only the widespread and common species.

Richness and Occupancy

Indicators of species occupancy (the proportion of sites that are occupied by a particular species) are produced in several nations using species-specific occupancy models (Boyd et al., 2023).

$$Z_{it} \sim site_i + year_t$$

Equation 3.1. 2. Species-specific occupancy model.

In Equation 3.1. 2, Z_{it} represents a binary presence-absence state at site *i* in year *t*. Occupancy is modelled on the logit scale, which converts numbers bounded between zero and one onto an unbounded scale, which is convenient for linear modelling. An indicator of species occupancy would be calculated by first aggregating across sites to derive the proportion of occupied sites for each species in each year, then averaging across species for each year (Figure 3.1. 2).

As with the abundance model described above, a species-specific occupancy model from EU PoMS data should be augmented to account for variation in detection across the year and across sites, and for survey-specific weather conditions.

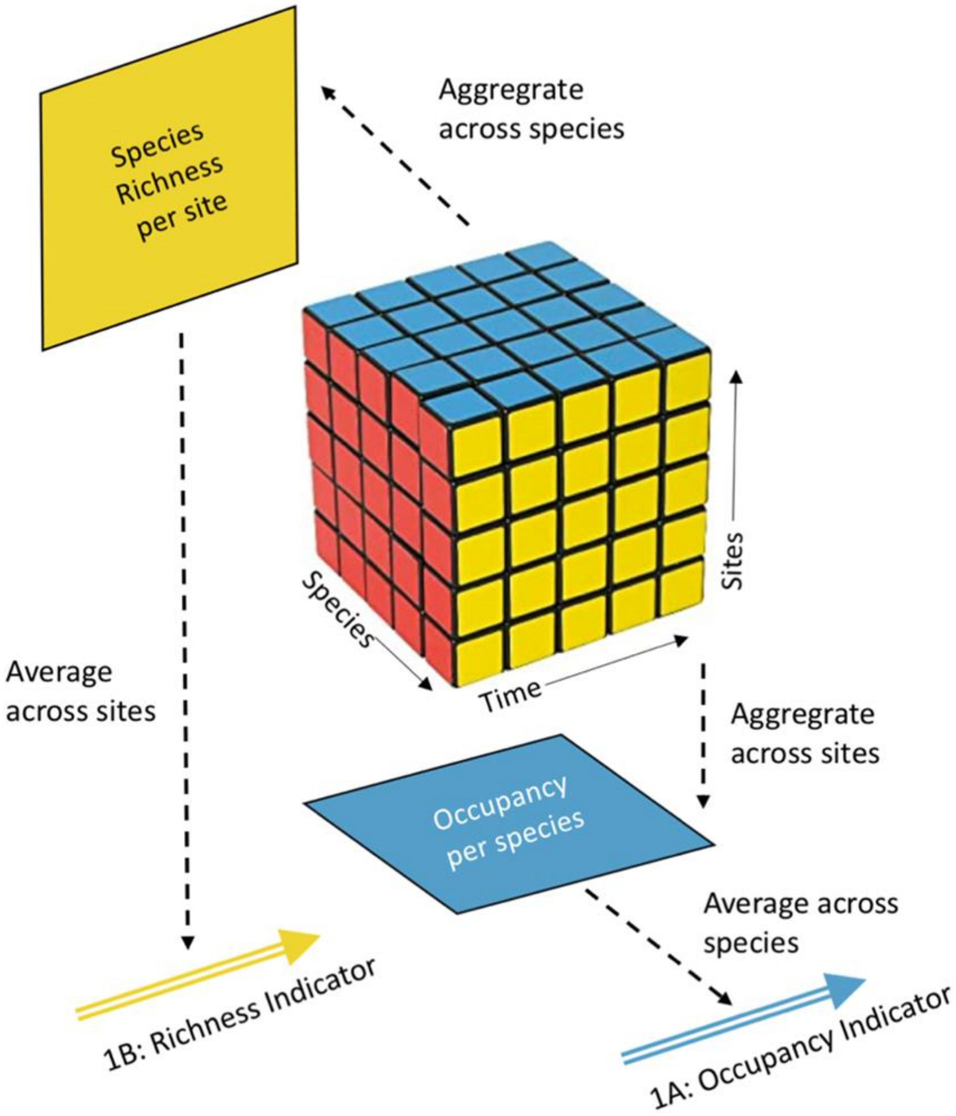
Whilst species-specific occupancy models are already used for biodiversity indicators elsewhere, there are several arguments for using a multispecies approach.

$$Z_{ijt} \sim site_i + year_{jt}$$

Equation 3.1. 3. Multispecies model.

In Equation 3.1. 3, the year effects reflect the multispecies average, i.e. a single model would capture steps 4-6 of the workflow in Figure 3.1. 1 in a single step. A second advantage of the multispecies model is that trends in the occupancy of individual species could be modelled at the same time as trends in the species richness of sites, since these are complementary summaries of the Z_{ijt} matrix (Figure 3.1. 2).

Figure 3.1. 2. Deriving complementary indicators from the species-space-time cube of occupancy. The individual cell indicates whether the site in question was occupied by the focal species in a particular year, i.e. the Z_{ijt} of Equation 3.1. 3. Indicators of species occupancy and species richness are both derived as alternative ways of summarising this cube.



Source: Authors' elaboration.

Status: occupancy modelling is a mature approach in statistical ecology (MacKenzie et al., 2006), including multispecies variants. As with the abundance models above, there would need to be some development to data thresholds, especially for the single-species variant. The multispecies model would need to be tested extensively to test for sensitivity to rarely observed species.

Advantages: Produces indicators and metrics of both richness and occupancy in a single model.

Disadvantages: Multispecies variant would need to be tested thoroughly.

Community Diversity

Community diversity derives from measures of each species at each site in each year. This is best conceptualised as a multispecies abundance model.

$$N_{ijt} \sim site_i + year_{jt}$$

Equation 3.1. 4. Multispecies abundance model.

Trends in measures of community diversity (e.g. Shannon's Index) could be derived as a summary of the three-dimensional N_{ijt} matrix. As with previous models, it would be appropriate to include terms to account for seasonality and weather.

An indicator of community diversity could be derived as the annual mean value of the site-specific Shannon's Index values (or other metric).

Status: Not a standard product from existing monitoring schemes. Would need to be developed and tested thoroughly.

Advantages: This model captures elements of both species abundance and richness, so it could be used to estimate all metrics of interest. If imperfect detection were modelled properly then no need to have rules for the inclusion of species in the model.

Disadvantages: Diversity indices are more difficult to communicate than other metrics.

Group abundance model

The total abundance at the group level (either all pollinating insects or for each group separately) could emerge as a simple summation of the N_{ijt} matrix in Equation 4. A simpler alternative would be to aggregate the data to groups first, and then fit an abundance model as in Equation 1.

An indicator of group abundance would be derived by first summing the abundances for each site:year combination, then calculating the annual average across sites.

Status: A similar approach is being developed for the UK Pollinator Monitoring Scheme.

Advantages: Straightforward to model: the multispecies trend emerges from a simple model.

Disadvantages: Potentially complicated to communicate, especially in conjunction with species abundance. In addition, this metric is unlikely to be sensitive to change.

3.1.6 Assessing the target

To assess a reverse in the decline of pollinators (by a given date) means that the trend should be shifted from a declining to an increasing one. In the context of biodiversity indicators that measure the state of some biodiversity metric each year, the target would be met if the first derivative (the change from one year to the next, or growth rate) of this indicator line would be greater than zero.

In this section, we discuss some of the issues associated with assessment of targets using indicators, and the pros and cons of different metrics as indicators (recognising that the EU PoMS design makes it possible to estimate several metrics – see above).

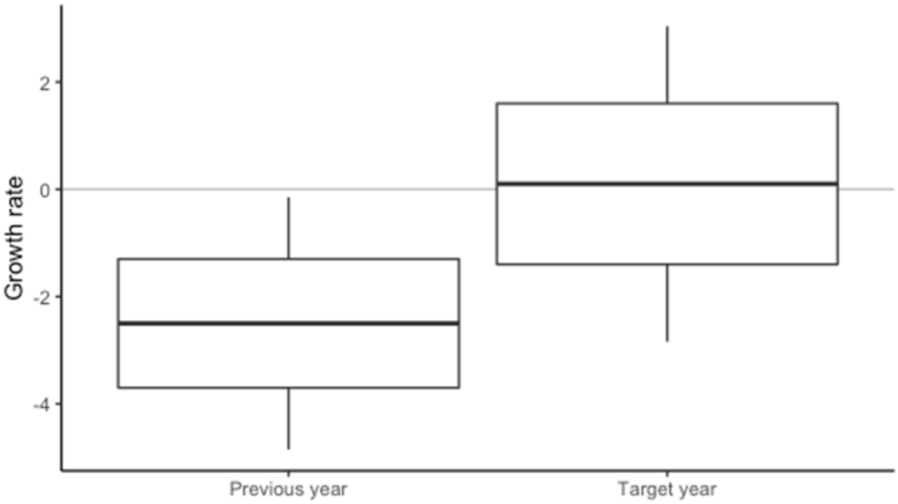
3.1.6.1 Bayesian vs Classical; qualitative vs quantitative assessment

Traditional metrics are assessed using classical inference, based on null hypothesis significance testing (NHST). One attraction is that the result is expressed as a binary outcome: either the null is rejected or not. However, this does not translate into an unambiguous test of whether the target has been met (i.e. whether the trend in pollinators has shifted from negative to positive). This is because the power to reject this null hypothesis is strongly influenced by the confidence intervals around the quantity being estimated: if these are wide then it creates a strong bias toward detecting “no overall change” (i.e. failing to reject the null hypothesis). Thus, a classical NHST has the potential to create ambiguous results about whether the target has been achieved. It’s possible to conceive a situation in which the “best” estimate of the first derivative is positive, but also that it is not significantly different from the previous year in which the best estimate was negative (Figure 3.1.3).

Bayesian statistics present a potential solution to this problem. Whereas in classical statistics, the confidence intervals define the probability of the data given the parameter values, in Bayesian statistics the credible intervals can be interpreted as in terms of the probability that the true value lies within this range. Therefore, if the results in Figure 3.1. 3 were derived from a Bayesian model, we might conclude that there is 99% confidence that the indicator declined in the previous year, and 51% confident that it increased during the target year (noting that confidence can never be lower than 50%).

This makes it possible to define the assessment of a target in probabilistic terms, by setting a threshold level for the confidence required in order to pass. It is perhaps easier to think of these thresholds in terms of an odds ratio: e.g. if we set the threshold to 75%, it would be stating that the weight of evidence for an increase was three times greater than the evidence for a decline (75:25). Similarly, a 90% threshold would be stating that the ratio of evidence for an increase was at least 9 times the evidence for a decline (i.e. 90:10). Framing the assessment in this way is consistent with a recent proposal by Leung and Gonzalez (2024) to assess biodiversity targets in a risk-based context, considering both the magnitude and probability of change.

Figure 3.1. 3. Illustration of problems associated with assessing the target by null-hypothesis significance testing. The data show hypothetical parameter estimates for two years: the year in which the target is assessed (right hand side) and the year before. The y-axis shows the growth rate, i.e. the annual change in the metric being assessed. The horizontal bar shows the "best" estimate, the box delimits ±1 standard error, and the vertical bars extend to the 95% confidence limits. Achieving the target requires this growth rate should be positive. In this example, the growth rate in the target year is slightly above zero, following a period in which the metric has been in decline (significantly negative growth rates). In this instance, the trajectory of the indicator has clearly improved, but it is ambiguous whether this is enough to meet the target. Specifically, we cannot conclude that the index has declined, nor that it has increased, nor whether the growth rate has changed from the previous year (during which there was a significant negative decline).



Source: Authors' elaboration.

3.1.6.2 Risks and perverse outcomes associated with particular metrics

As described in section 3.1.5, the candidate metrics for reporting in indicators (for the 2030 target and beyond) have a range of properties that should be carefully considered when deciding which to use.

There are specific risks associated with the short time window between the start of the EU PoMS in 2026 and assessment in 2030. This is only a five-year window, thus the metric for assessment must have the potential to show a change during this period. This has two components: (i) is the metric likely to have changed over a five-year period, and (ii) if the metric does change, are we likely to detect it? Both conditions must be met in order for the metric to be useful. The choice between alternate metrics is complicated by the fact that there is a trade-off between these two components: metrics that are likely to meet the criteria for the first component are more likely to fail the second, and *vice versa*.

To illustrate this in more detail, let us first consider compositional-based metrics, i.e. species richness, occupancy and Sørensen's index of beta diversity. In order for these metrics to change, entire populations need to be lost (for a decrease) or new sites colonized (for an increase). These changes happen relatively rarely, so the plausible effect size over five years is rather small. However, changes in richness and occupancy should be fairly easy to detect, given the spatially-replicated design of EU PoMS.

By contrast, abundance of insects (including Group or Total abundance) is likely to be far more responsive to environmental change (either positive or negative). However, insect populations tend to fluctuate markedly from year to year, in part because the number of insects counted on transects reflects not just abundance but also activity, which is a function of weather conditions. This means that insect abundance time-series insects tend to be very noisy and require smoothing before assessment. Smoothing will dampen out these fluctuations, but make it more difficult to detect changes in the trajectory of the indicator. Basing the assessment solely on an abundance-based metric would run the risk of ambiguous results in all Member States (i.e. high uncertainty and/or a bias towards "no overall change").

Itis possible that community metrics, such as Shannon's index, might be more sensitive to change than compositional metrics whilst also less noisy than simple abundance metrics. However, this would need to be tested formally using simulations (e.g. an extension of the power analysis).

Whatever the metric chosen, some careful attention would need to be given to which species should be included, and which should be excluded. If no stipulation were applied then the metric could be "gamed" by promoting the spread of introduced species, including invasive aliens. Given that climate change is already causing the many species to shift their ranges (Chen et al., 2011), it would be appropriate to allow natural colonists to be included. However, species classed as anthropogenic introductions (i.e. alien invasive species) should not.

Note that, apart from taxon-level abundance, all of the metric proposed in section 3.1.4 require species-level data. Although it is the stated aim that all observation on EU PoMS will be identified to species level, there is not yet the taxonomic capacity to achieve this in many Member States. Thus, unless taxon-level abundance is included in the suite of metrics for assessment, there is a risk that data collected under EU PoMS will not be fit for evaluating the target.

Andrena haemorrhoa, Axel Hochkirch

3.1.6.3 Options for assessing targets

Option A: assess based on a single metric from the above

The simplest approach would be to select one metric and assess based on this. The only real advantage of this approach is that it is simple and clear. There are several disadvantages. One is that choosing any one metric would capture only a partial picture of how biodiversity is changing. Another is that the metric may have to be decided before the data become available. Species abundance is often seen as the gold standard, but there are risks that an index solely based on species abundance would deliver ambiguous results.

Option B: Alternative metrics

A second option is to make the assessment based on the trajectory of multiple metrics, e.g. species abundance and richness. Each metric would have a separate indicator, but the assessment of the target would be based on both. There are several ways in which this could be achieved, depending on whether the test was conducted as NHST or using Bayesian methods.

An assessment with NHST would deliver a traffic-light measure for each metric: green for increasing, red for decreasing and amber for no overall change. The target would then be assessed according to some vote counting approach, e.g. the target might require that there are more green lights than red. However, as noted previously, the “no overall change” category is problematic, and potentially reflects lack of power rather than genuine evidence for stability. Setting these thresholds should be informed by an augmented power analysis.

If Bayesian methods were used, then it becomes possible to construct a more sophisticated test using the confidence (or probability) that the true trend is increasing. One possibility one could convert each confidence score into an odds ratio and calculating the product across all available metrics. For example, consider that a trend has been assessed for three separate metrics: for total abundance there is weak evidence for an increase (60% confidence); for occupancy, there is strong evidence for an increase (80% confidence) and for species abundance there is weak evidence for a decrease (33% confidence of increase vs 67% confidence of a decrease). Converting these into odds ratios we get 60/40 = 1.5, 80/20 = 4 and 33/67 = 0.5, so the product across all three metrics is 3, which corresponds to a 75% confidence in an overall increase across metrics.

If the combination of Bayesian confidence scores were adopted, this approach could also be used to combine metrics for bees, hoverflies and butterflies into a single composite assessment for each Member State.

The assessment could be made more sophisticated by weighting the metrics according to some pre-defined values (e.g. if the species abundance was considered more important than other metrics). Weighting the probabilities is mathematically trivial, but weights would be difficult to justify as objective, and the outcome would be highly sensitive to the weighting chosen.

One advantage of this approach is that it makes full use of the breadth of biodiversity metrics that could be estimated from EU PoMS. It also reduces the risks associated with option A. For these reasons, this is our recommended approach.

3.1.7 Recommendations

- Refine and test statistical models for species abundance, a multispecies model for richness and occupancy, for taxon-level abundance and potentially also a multispecies abundance model. Test the sensitivity of these models to data from rarely observed species and develop data-driven thresholds for which species to include. Test the statistical properties of these models and the resultant multispecies indicators in the context of their ability to detect changes over a six-year window.
- Fit these models in a Bayesian context to facilitate assessment of the target within a risk-based framework.
- Develop tests for the target based on combining indicators from multiple biodiversity metrics. Evaluate the power of these tests to correctly diagnose biodiversity trends within Member States, using an extended version of the power analysis.

Bombus pratorum, Axel Hochkirch

3.2 Options for a Farmland Pollinator Indicator

3.2.1 Summary

Pollinators are of great importance for agriculture as they make a major contribution to food security, farmer's income through seed production, fruit production, and agricultural production in general, as well as maintaining plant diversity. It should therefore be in the interests of agriculture to protect and promote pollinators. The EU Common Agricultural Policy (CAP) plays an important role in this context, as the CAP defines the framework for action for the Member States and thus plays a key role in shaping agricultural landscapes within the EU, with close to 90% of the utilised agricultural area being covered by CAP policy.

EU PoMS provides an opportunity for monitoring pollinators in agricultural landscapes. To achieve this, we suggest a two-stage monitoring approach to cope with the complex interplay of site characteristics, land use history, different production branches and forms of management and policy interventions, such as CAP measures. The monitoring approach consists of either surveillance monitoring and monitoring under adaptive management, so that medium- and long-term statements on development of farmland pollinators can be made, and the impact of different types and levels of CAP implementations can be assessed using State and Impact indicators. While the trend monitoring is based on the sampling methods and the sample set of the EU PoMS core scheme, a Citizen Science-based approach with farmers is proposed for the monitoring under adaptive management approach. This is because farmers decide where and when which CAP measures are implemented and make it possible to evaluate them at farm level in the best possible way. To ensure that the proposed indicators for farmland pollinators are functional and can be reported in the future, we recommend conducting a pilot study in selected EU agricultural landscapes to test and further develop the conceptual approaches presented here.

3.2.2 Background and context

Around 38% of the land in Europe is used for agriculture purpose (European Commission Eurostat, 2022). Hence, agricultural land makes an important contribution to open-land habitats of pollinators. The quality of those habitats is to a considerable extent driven by policy-induced interventions such as CAP measures. The purpose of this chapter is therefore, to outline potential monitoring approaches and indicators for reporting agriculture-related trends of pollinators, and also assessing effects of different types and different levels of policy induced land and land use change inter alia related to implementation of CAP.

The chapter is divided into two parts: The first part is dedicated to the need for a Farmland Pollinator Indicator (section 3.2.3) and which insights for its development can be drawn from existing indicators, such as the Farmland Bird Indicator and the Grassland Butterfly Indicator (section 3.2.4). In addition, the potential of existing CAP indicators with regard to their suitability as surrogate indicators for an interim evaluation of the CAP is assessed (section 3.2.5). Based on the insights gained, conclusions are drawn for developing options for a Farmland Pollinator Indicator (sections 3.2.6 and 3.2.7). The second part of the chapter deals with conceptual considerations of a Europe-wide Farmland Pollinator Indicator. Section 3.2.9 formulates the demands on its design considering the political (CAP) context. As the design of the core scheme is unsuitable for a farmland specific focus, an optional two-stage monitoring approach with a selection of possible state and impact indicators is presented (3.2.10) and evaluated regarding their potential informative value (3.2.11). The chapter ends with recommendations for the next steps that are considered necessary, towards developing a Europe-wide Farmland Pollinator Indicator (3.2.12).

3.2.3 Why a Farmland Pollinator Indicator is useful and what can be learned from other existing farmland indicators

The European Parliament, in its resolution of 23 November 2023 on the revised Pollinators Initiative, agreed that pollinator decline poses a threat to agricultural productivity and food security, hence to human well-being. It further emphasised that crop pollination mediated by wild and domesticated animals is an essential agricultural input and is a crucial and endangered ecosystem service. Despite the importance of pollinators for agriculture, intensive agriculture is one of the most pressing drivers of pollinator decline (IPBES, 2016). Decline of pollinators in farmland across the EU is putting this agricultural input of pollinators at risk.

Within agricultural landscapes, the destruction of suitable natural and semi-natural habitats and degradation of habitat quality in terms of high regional flower cover and nest-site availability are considered to be among the main drivers of pollinator decline across Europe (Nieto et al., 2014; Ockermüller et al., 2023). Habitat loss and habitat degradation are driven by a syndrome of factors linked to the development of farming practices, including the spatially inclusive and comprehensive use of agrochemicals, high nitrogen input as well as herbicide and insecticide application in particular. A high input of nitrogen fertilizers results in nitrophilous plant communities with low plant species diversity, resulting in a monotonous diet for bees (Kleijn et al., 2009) and decreased survival of *Lepidoptera* larvae due to excessive dietary nitrogen content (Kurze et al., 2018), especially within managed grasslands. The use of insecticides in the crops, and the drift of these insecticides into adjacent semi-natural habitats can cause sublethal or lethal effects on pollinators (Chmiel et al., 2020; Tosi and Nieh, 2019). Although the use of pesticides is highly regulated, chronic or toxic effects of insecticides on pollinators under commercial field conditions still remain largely unknown (Arce et al., 2018; Tosi et al., 2022; Tosi and Nieh, 2019; Woodcock et al., 2016). Low crop diversity with a high percentage of wind pollinated or self-pollinating plants, along with use of herbicides resulting in a low diversity of the arable weed communities, impact bees indirectly by diminishing resource availability (Bretagnolle and Gaba, 2015). Such simplified crop rotations combined with large field size and loss of semi-natural habitats such as hedgerows, fallows or road and field margins have led to homogeneous landscapes with very few structures of ecological value for pollinators (Stoate et al., 2001; Tscharntke et al., 2002). The combination of these stressors, together with competition with introduced species, the spread of parasites and diseases, as well as climate change is likely to have harmful consequences for pollinators (Goulson et al., 2015; Potts et al., 2010).

Therefore, with about 40% of land in the EU covered by agriculture (European Commission Eurostat, 2022), farmers and other open-land users in the EU play an essential role of maintaining habitats for pollinators and fostering sustainable agricultural practices that prioritise the well-being of pollinators and contribute to their preservation and the preservation of habitats and resources those require. There is evidence that mitigation measures such as some agri-environment schemes can benefit pollinators in agricultural landscapes, in particular those measures increasing floral and nesting resource (Ammann et al., 2024; Bishop et al., 2024; Image et al., 2022).

Given our understanding of the principal pressure and mitigation factors affecting pollinators in agricultural land, the application of a DPSIR-approach in farmland pollinator monitoring would facilitate the evaluation of national and/or regional pollinator protection strategies and of the common agriculture policy (CAP) strategic plans. In addition to the monitoring of the state (species richness and abundance) of pollinators, trends on the development of pressure and mitigation factors could provide insights in the potential success of the strategies, way before the state of the pollinators may respond to the measures applied.

In the following we look at what we can learn from existing state indicators of other farmland taxa (i.e. farmland birds and grassland butterflies) for farmland pollinator monitoring and indicators and which existing environmental and land use indicators may serve as pressure/mitigation indicators in an integrated farmland pollinator monitoring. First, we provide a short overview of the DPSIR-approach.

3.2.4 The DPSIR model

The Driver-Pressure-State-Impact-Response (DPSIR) framework was developed by the European Environment Agency (EEA) in 1999[58]. It was built upon several existing environmental reporting frameworks, like the Pressure-State-Response (PSR) framework developed by the Organization for Economic Co-operation and Development (OECD) in 1993. The DPSIR model has been adopted as the most appropriate way to structure environmental information by most Member States of the European Union and by international organisations dealing with environmental information, such as Eurostat, the European Environment Agency (EEA), and (since the early 1990s, as PSR model) by the OECD.

From the policy point of view, there is a need for clear and specific information on:

- Driving forces and
- the resulting environmental *Pressures*, on
- the *State* of the Environment and
- *Impacts* resulting from changes in environmental quality and on
- the societal *Response* to these changes in the environment (Figure 3.2. 1).

Due to pressure on the environment, the state of the environment changes. These changes then have impacts on the functions of the environment, such as human and ecosystem health, resources availability, losses of manufactured capital, and biodiversity. Impact indicators are used to describe changes in these conditions (Gabrielsen and Bosch, 2003).

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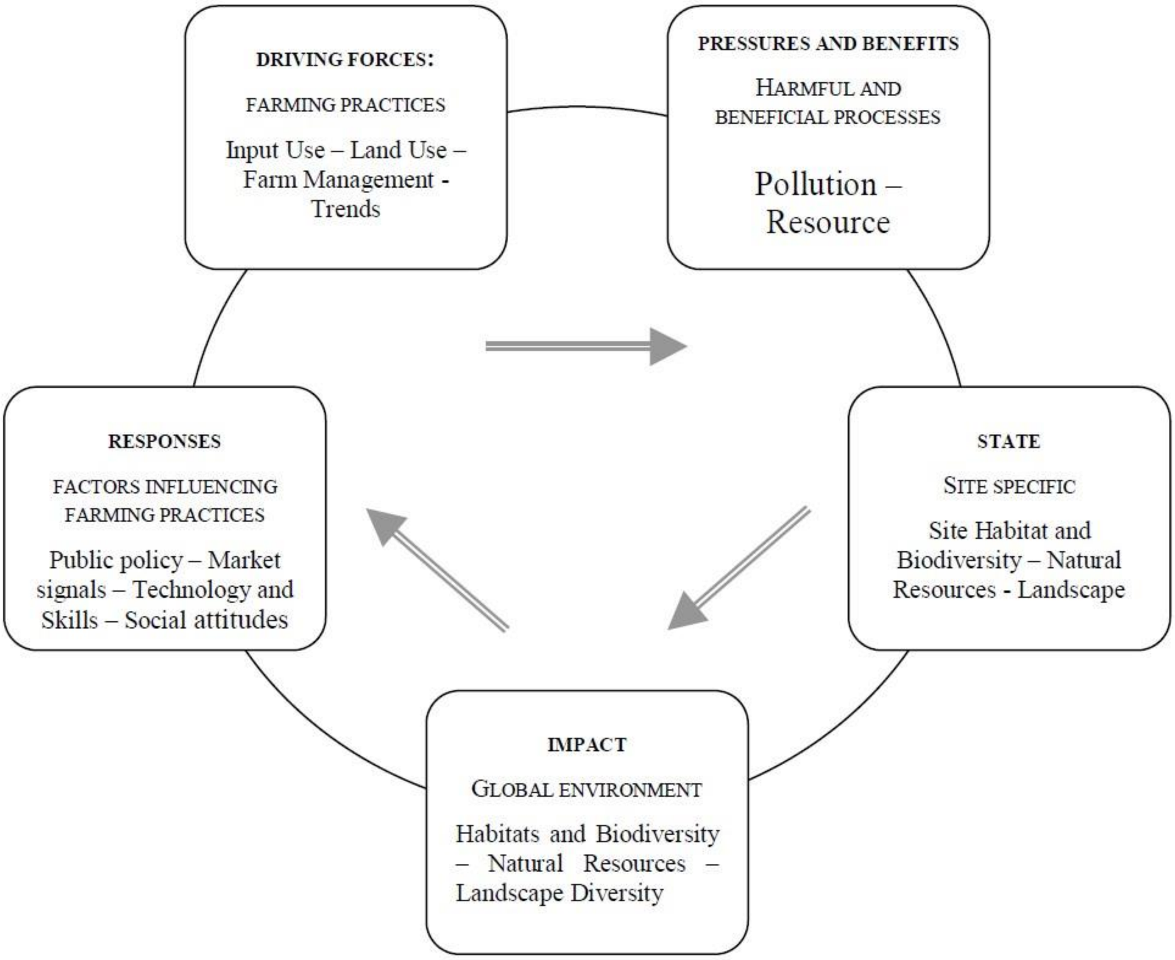
[58] https://www.eea.europa.eu/publications/TEC25

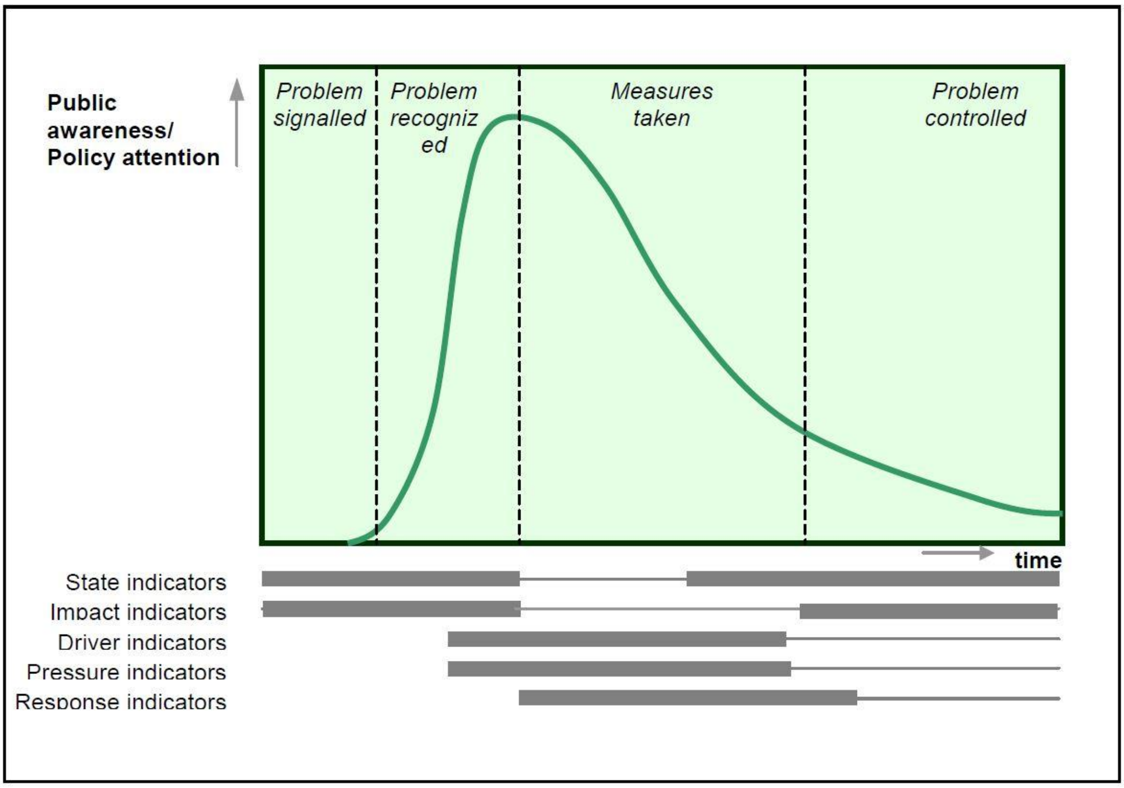
Figure 3.2. 1. The agricultural DPSIR model.



Source: European Commission (2000).

Indicators from different parts of the DPSIR framework have more or less relevance to policy makers depending on what stage the policy life cycle has reached (Figure 3.2. 2). For problems that are in the beginning of their policy life cycle, that is, in the stage of problem identification, indicators on the *state* of the environment and on *impacts* play a major role. Once the problem is politically accepted and measures are being designed, the attention shifts to *pressure* and *driving force* indicators. In the next and longer stages of the policy cycle - from formulation of policy responses to implementation of measures and control - policy-makers focus on what they can influence, the driving forces through volume measures, the pressures with technical measures and educational projects. *Performance* indicators on changes in driving forces and pressures are the most used. In the last stage - the control phase of the policy cycle - *state* and *impact* indicators become important again to watch the recovery of the environment and a limited number of these indicators will be used to continuously monitor the state of the environment (Gabrielsen and Bosch, 2003).

Figure 3.2. 2. DPSIR indicators use in the policy life cycle.



Source: Gabrielsen and Bosch (2003).

3.2.5 Learning from the farmland bird indicator and the grassland butterfly indicator

3.2.5.1 Farmland Bird Indicator

The Farmland Bird Indicator is based on data of large-scale and mostly long-term national Citizen Science breeding bird-monitoring programs that are often coordinated nationally by professional organisations. Annually, around fifteen thousand fieldworkers count breeding birds using standardized protocols in 28 European countries. The original purpose of the national monitoring schemes was simply to obtain information about the population trends of birds.

The Farmland Bird Index (as well as other continental bird indices) is calculated by the Pan-European Common Bird Monitoring Scheme (PECBMS[59]), a project that started in 2002 as a joint initiative of the European Bird Census Council (EBCC) and BirdLife International. Over the years, the UK Royal Society for the Protection of Birds, Statistics Netherlands, the European Commission, the Czech Society for Ornithology, the British Trust for Ornithology, the Dutch Organisation for Field Ornithology and L'Institut Català d'Ornitologia have been important partners of the project. The main objective of the PECBMS is to use common birds as indicators of the general state of nature

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[59] https://pecbms.info/

using large-scale and long-term monitoring data on changes in breeding populations across Europe. The PECBMS produces annual updates of the between-year and long-term changes of widespread and common bird species breeding in Europe.

The data underlying the Farmland Bird Indicator represent population trends of 39 species that are dependent on farmland for feeding and nesting and are not able to thrive in other habitats. They were chosen from a list of common EU species; no rare species are included in EU species selection. Since not all 39 species occur in each country in sufficient numbers to reliably estimate population trends, countries supply trends for the subset of species that are relevant to them. In each country, modelled population trends are derived from the counts of individual bird species at census sites. Population trends are expressed as an index that indicates population size in a certain year relative to a reference year (2000; which is set at 100%). Indices are first calculated for each species independently at the national level. Then for each species, the national indices are combined into a supranational index. To do this, they are weighted by estimates of national population sizes because this allows for the fact that different countries hold different proportions of the European population of each species. In a third step, the supranational indices for each species are combined on a geometric scale to create a multispecies aggregate index at the European level.

The data underlying the national species trends of birds are annually collected by volunteers. Survey methodologies differ between countries (Brlík et al., 2021), but generally fall into one of three methods or combinations of these: point count transect, line transect, or territory or spot mapping (Vorisek et al., 2008). National monitoring schemes use either random, stratified random, systematic selection, or allow a free choice by the volunteers for the selection of sampling plots. Stratified random selection generally uses a predefined stratum such as a region with similar attributes. These might be proportions of habitat types, altitude bands, bird abundance, accessibility of survey sites or volunteer density, depending on the local circumstances (Brlík et al., 2021). Systematic selection predefines a spatial grid for sampling plot selection while free choice enables volunteers to select their study areas without restrictions. The use of a free choice, or stratified random selection of sampling plots, may result in a biased sampling of specific habitat types (typically species-rich habitats) and regions (remote areas poorly covered), but post-hoc stratification and weighting procedures are generally used to correct for unequal sampling and reduce sampling bias as long as the number of plots per stratum is sufficient. Moreover, national coordinators provide volunteers with recommendations or oversee the study plot selection to prevent oversampling of specific habitat types and regions.

In addition to being an impact and context indicator in the Performance Monitoring and Evaluation Framework (PMEF) of the CAP, the Farmland Bird Index is currently being used as an agro-environmental indicator (AEI 25: Population trends of farmland birds) and it is also used by Eurostat on the SDG monitoring framework under the "Common bird index by type of species - EU aggregate (sdg_15_60)"[60]. It is considered a proxy for the biodiversity status of agricultural landscapes in Europe; therefore, it is used formally as well as informally by national governments and (inter)national NGO's. Out of the ex post evaluation reports on the Rural Development Programmes (RDP), 37% of the evaluations suggest that the RDPs have positively contributed to reaching targets related to the Farmland Bird Index, whereas 21% of the reports stated that the programmes had limited impact or no impact (ECORYS and IfLS, 2018).

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[60] https://ec.europa.eu/eurostat/cache/metadata/en/sdg_15_60_esmsip2.htm

The Farmland Bird Index is without a doubt the single most comprehensive and reliable biodiversity indicator that currently exists in the EU. It uses primary biodiversity data collected by an impressively large number of citizen scientists that covers extensive areas in many European countries. However, the distribution of the sampling plots does not consider farm management. Individual sampling plots may cover a variety of land use types such as (combinations of) different farms and management types, public space and protected areas. The cover of each land use type in each sampling plot could be quantified using existing databases, although this would be an arduous task because both management and land use change over time.

In the context of its use as impact indicator in the PMEF, it is considered that the main pressures for the farmland bird populations are farm management and that in Europe farm management decisions are CAP policy driven, hence they should represent indicators for the impact of the overall policy on biodiversity. Given the plethora of impacts on farmland bird populations that are independent from CAP policy, this consideration is highly questionable. Beyond the indication of overall policy impacts, there is a desire to use the FBI data for an evaluation of CAP measures.

However, the spatial coverage of the Farmland Bird Index sampling plots is rarely dense enough to allow the identification of the impact on birds of a particular component of the CAP, such as the implementation of agri-environment and climate schemes. A reliable assessment of the impact of a specific type of CAP measure would entail comparing the trends of the Farmland Birds Index in a large number of plots where that specific type of CAP measure is implemented with those in plots where it is not present. This comparison should ensure that the plots share similar environmental conditions and management practices (counterfactual approach). Experience teaches that such requirements are generally too demanding for a general monitoring scheme, even for the most extensive ones such as those implemented in the United Kingdom or the Netherlands. An additional complication is that, because agriculture is one of the key drivers of biodiversity decline, bird numbers are generally low in agricultural areas and many species will be absent from a significant proportion of the plots. This generally means that a larger sample size is required before reliable statements can be made about impact of the CAP or other policy interventions in farmland. From this, it can be deduced that a farmland pollinator indicator and monitoring would also benefit from a sufficient number of sampling sites distributed across the various agricultural landscapes and farming types within the Member States (see section 3.2.9).

3.2.5.2 European Grassland Butterfly Indicator

Butterfly Monitoring Schemes are present in a growing number of countries and new ones are being initiated in many places, but long time-series are currently only available for a limited number of countries. The data sampling for the butterfly indicators is based on the fieldwork of trained professional and volunteer recorders. More than 10,000 transects are scattered across Europe, with transects ideally being best selected in a grid, random or stratified random manner. In most schemes, however, transects were selected by free choice of observers, which in some cases has led to the overrepresentation of protected sites in natural areas and the under-sampling of the wider countryside and urban areas, but this is not the case in all countries. Standardised conditions provide high-quality data that are suitable to assess species status and trends and national coordinators collect the data and perform the first quality control (van Swaay et al., 2022).

The Grassland Butterfly Indicator is the combined population trend of 17 selected grassland species monitored across Europe. The indicator can be calculated from population trends estimated for the whole European region or restricted to the 27 EU Member States. Species' trends are combined by calculating the geometric mean of the species' collated annual indices, which is considered a measure of biodiversity change, with 1990 as base year (van Swaay et al., 2022).

In the last ten years, the indicator shows a linear decline of 32% in the EU27 and 36% in Europe. The main reasons for the decline are agricultural intensification, land abandonment (van Swaay et al., 2022) and nitrogen deposition in nature reserves (WallisDeVries and van Swaay, 2017), especially in NW Europe. In some parts of Europe climate warming led to an increase in the numbers of some of the widespread generalist butterflies (van Swaay et al., 2020). However, the recent accumulation of extremely hot and dry summers has reversed this trend leading to new declines. Overall, disentangling effects of climate change from effects of land use change in agricultural landscapes may be a challenge for connecting the butterfly indicators to concrete impacts of CAP interventions. With respect to evaluating specific CAP measures, the European Grassland Butterfly indicator share many of the limitations mentioned for the Farmland Bird index. Nevertheless, a recent study conducted with data from the German butterfly monitoring showed that indicators related to grassland management intensity based on livestock distribution data can provide insight into processes and spatial diversity patterns of butterflies at the national level (Kasiske et al., 2023). Nevertheless, a higher number of sampling sites and a higher cover of different farming types would support evaluation efforts of policy interventions from a farmland pollinator monitoring (see section 3.2.9).

Gonepteryx rhamni, Axel Hochkirch

3.2.6 Potential of existing CAP Indicators as pressure and benefit indicators for pollinators

The Better Regulation Guidelines set out the principles that the European Commission follows when preparing new initiatives and proposals, and when managing and evaluating existing legislation. The guidelines apply to each phase of the law-making cycle (European Commission, 2021a, 2021b).

Since the programming period 2014-2020 of the Common agricultural policy (CAP), for the first time the monitoring and evaluation framework covered the whole CAP (both pillars). CAP is the EU's single unified policy on agriculture, comprising subsidies and a range of other measures to guarantee food security, ensure a fair standard of living for the EU's farmers, promote rural development and protect the environment. A new monitoring and evaluation framework (the Common Monitoring and Evaluation Framework - CMEF) was set up. It provided to administrations, and to all those interested in agriculture and rural development, key information on the CAP implementation, on its results and on its impacts. It quantified the actions in the different Member States, described their achievements, highlighted which instruments are most efficient and verified how well objectives have been reached (European Commission Directorate-General for Agriculture and Rural Development, 2015).

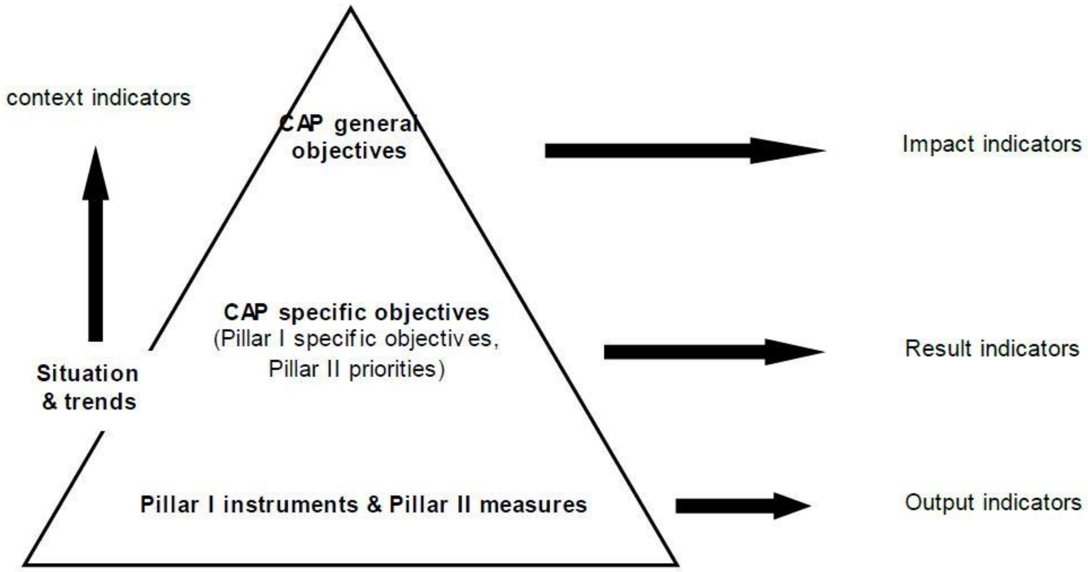
Each policy initiative relies on a *logic of intervention*, which plays a central role in guiding its development, implementation, monitoring, and evaluation. The intervention logic can also help in identifying the supporting evidence needed in each phase of the policy cycle. In particular, the monitoring and evaluation phases may benefit from a careful data and evidence planning so that the effectiveness of EU legislation can be properly assessed (European Commission, 2021a, 2021b). The intervention logic is the logical link between the problem that needs to be tackled (or the objective that needs to be pursued), the underlying drivers of the problem, and the available policy options (or the EU actions actually taken) to address the problem or achieve the objective (European Commission Directorate-General for Agriculture and Rural Development, 2017).

The performance of the CAP is measured at different levels with the help of three types of indicators (Figure 3.2.3):

- *Output* indicators give the direct 'product' of the measure (e.g. 50 energy-saving investments funded through a measure).
- *Result* indicators give the direct, immediate effect of the measure/programme (e.g. 500 jobs created as a result of the investment measure).
- *Impact* indicators go beyond the direct, immediate effect but look at the longer term (e.g. rural unemployment rate).

Overall, impact indicators are linked to the general objectives of the CAP, result indicators to the specific objectives and output indicators to individual policy interventions. Finally, there is a set of context indicators, which provide information on general trends of economy, state of the environment, general climate indicators, agricultural and rural statistics, etc. Together the indicators can be considered as the 'dashboard' of the CAP policy, giving a set of essential information.

Figure 3.2. 3. CAP indicator levels and hierarchy.



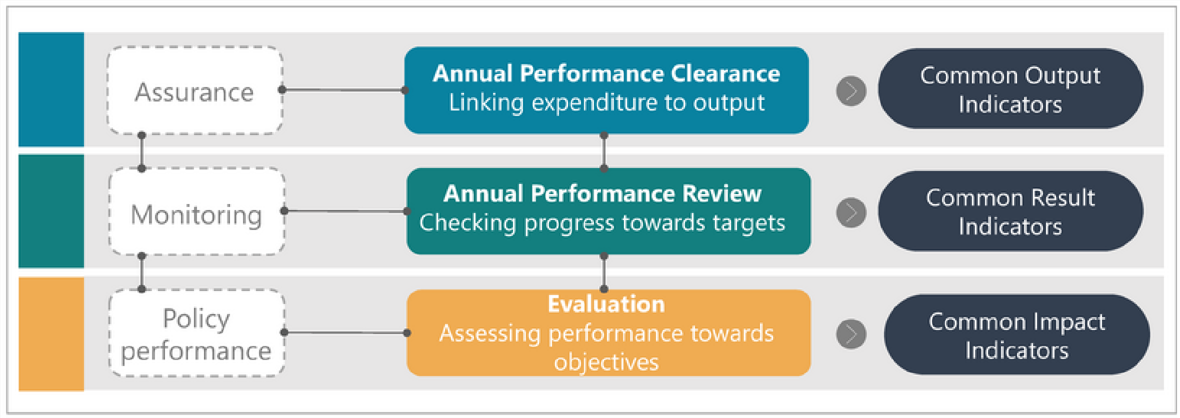
Source: European Commission Directorate-General for Agriculture and Rural Development (2017).

In an impact assessment process, the term *impact* describes all the changes which are expected to happen due to the implementation and application of a given policy option/intervention. Such impacts may occur over different timescales, affect different actors and be relevant at different scales (local, regional, national and EU). In an evaluation context, impact refers to the changes associated with a particular intervention, which occur over the longer term (European Commission, 2017).

A new Performance Monitoring and Evaluation Framework (PMEF) is proposed for the programming period 2023-2027. It covers the performance of all instruments of the CAP and is an evolution of the 2014–2020 CMEF. The PMEF of the CAP Strategic Plan Regulation (SPR) supports the shift in policy focus from compliance with rules to performance and results. The PMEF is organised around the following principles (Figure 3.2. 4):

- *Context* indicators remain pertinent in the intervention logic set up and follow up.
- Common *output* indicators will annually link expenditure with the performance implementation (performance clearance).
- A set of *result* indicators will be used to reflect whether the supported interventions contribute to achieving the EU specific objectives.
- Annual performance follow-up will rely on a limited, but more targeted, list of common *result* indicators (performance review). It is currently supposed the use of only one indicator for each EU specific objective.
- Multiannual assessment of the overall policy is proposed based on common *impact* indicators (evaluation).

Figure 3.2. 4. Multiannual programming approach within the Performance Monitoring and Evaluation Framework.



Source: Cagliero et al. (2021).

The output and result indicators are usually applied at measure level, e.g. at the level of agri-environmental schemes (AES). The impact indicators in contrast aim at measuring the environmental (as well as socio-economic) effects of the whole programme. The evaluation of the extent to which a programme has achieved the objectives of its strategy, is built up from the outputs and results of individual measures at the hierarchy level of CAP specific objectives, which are assessed against the impact indicators at programme level (Morkvenas and Schwarz, 2012). All impact indicators listed for the specific objective to contribute to halting and reversing biodiversity loss, enhance ecosystem services and preserve habitats and landscapes, are also context indicators. As context indicators aim at providing information on general trends, the same necessarily applies for the impact indicators.

3.2.6.1 CAP impact indicators potentially relevant for the development of a farmland pollinator indicator

Out of the currently existing list of context/impact indicators of the PMEF[61], we have selected 4 indicators (I.18, I.20 – I.22) which are linked to the objective "to contribute to halting and reversing biodiversity loss, enhance ecosystem services and preserve habitats and landscapes" (Table 3.2. 1). These indicators may have the potential to function as pressure and benefit indicators on farmland pollinators.

To assess whether these indicators could serve as examples for pressure and benefit indicators in the context of farmland pollinator indicators, we looked at the problem framing, design, data requirements, implementation and revision of these indicators. The question is whether the underlying methodologies of these indicators may be instructive for the development of indicators to be used for relating trends in pollinators to changes in agricultural landscapes (see section 3.2.10, Option 1b) or as surrogate indicators for an initial evaluation of CAP interventions. Our analysis is based on the following questions:

- On which data do the indicators rely and how are those data generated in time and space?
- Are data actively sampled (for the original purpose of the indicator) or does the indicator rely on pre-existing data (generated for a different purpose)?

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[61] https://agriculture.ec.europa.eu/common-agricultural-policy/cap-overview/cmef_en#towardsthepmef

- Who is sampling the data? Is it a professional sampling or is it based on volunteers?
- How high is the level of standardisation across the EU?
- Are Member State or regional specific subsets of data generated?
- In which time intervals are the data recorded (timeliness)?
- Are the data recorded on selected sampling sites or at a national level?
- Are national indices compiled by each Member State and which is the level of standardisation?
- How standardised is the design and implementation of the indicator across Member States?

Table 3.2. 1. Impact indicators of the PMEF and other indicators selected for analyses of potential use as farmland pollinator pressure and benefit indicators.

PMEF: Impact (I) and Context (C)	Name of the indicator
I.18 C.49	Sustainable and reduced use of pesticides
I.20 C.37	Enhancing biodiversity protection
I.21 C.21	Enhancing provision of ecosystem services
I.22 C.22	Increasing agro-biodiversity in farming system

Source: Authors' elaboration.

3.2.6.2 Overview of selected impact indicators

I.18: Sustainable and reduced use of pesticides

This indicator should inform about the risk, use and impacts of pesticides and consists of 3 specific indicators:

- Sales of pesticides.
- The Harmonised Risk Indicator.
- Sales of more hazardous pesticides.

Sales of pesticides is understood as a proxy of pesticides use in agriculture, and harmonized risk is based on annual quantities of active substances placed on the market in the form of plant protection products multiplied by the relevant weights, based on the regulatory status of the active substances under Regulation (EC) No 1107/2009. Hence, this indicator provides only a very coarse proxy of pesticide applications in space and time and is therefore not suitable for making any inferences about concrete risks and impacts on pollinating insects within farming regions of the Member States. For this, concrete and spatially fine scaled information about the application and concentration of pesticides, the active substances and combination of pesticides within agricultural landscapes would be required.

I.20: Enhancing biodiversity protection

This indicator assesses the conservation status trends of those habitats and species of Community interest, i.e. listed in the relevant Habitats Directive annexes that are considered to be strongly linked to agro-ecosystems. In addition, it should explicitly provide the conservation status trends specifically for pollinators. Hence, there may be two sub-indicators:

1. Percentage of species and habitats of Community interest related to agriculture with stable or increasing trends.
2. Percentage of pollinator species of Community interest related to agriculture with stable or increasing trends.

Species and habitats of Community interest are those in danger of disappearance in their natural range, rare or endemic, or characteristic of one or more of the EU biogeographical regions; these species and habitats are listed in the annexes of the Habitats Directive. For pollinators, the indicator should build on a subset of the same species lists, i.e. the relevant species among the 38 butterflies listed in the Habitats Directive under Annex II and Annex IV. Other groups of pollinating insects are not well represented in those lists and hence I.20 may have a bias towards butterflies. However, butterfly species from Habitats Directive Annex II and IV could be too rare for most practical indicator applications.

The Member States should report every six years, taking the developments over the six-year period into consideration, but a caveat to this may be that there can be a variable time lag between changes in agricultural practices pattern and the impact on habitats and species. Nevertheless, those data are too coarse in spatial and temporal resolution to provide a useful pressure/mitigation indicator. This indicator may provide complementary information about pollinators in agricultural habitats but as such could not serve as a Farmland Pollinator Indicator.

I.21: Enhancing provision of ecosystem services

Hidden behind this indicator on ecosystem service provisioning is the share of agricultural land covered with landscape features. The idea for using landscape features as a proxy for ecosystem services is based on the understanding that such landscape features provide benefits to agro-ecosystems and the wider environment, including habitat provision, mitigation of soil erosion, improvement of soil fertility, water flow regulation, water courses protection, climate change mitigation and adaptation.

This indicator aims to estimate the area covered by landscape features in the agricultural land. Landscape features may include linear elements (e.g. hedgerows) and patches (e.g. trees, woodland, etc.), water and wet spots (ponds, water bodies, streams, etc.); moderately managed areas (e.g. field margins), etc. The indicator should consist of two specific sub-indicators:

- The share of agricultural land covered with landscape features.
- An elaborated index of landscape element’s structure, which is currently under development.

The data source for this indicator should be remote sensing data from the Copernicus Land Monitoring Service fed with LPIS/IACS data and land use/cover data from the LUCAS-landscape features module. It is seen as a challenge to find a combination of features that can be mapped reliably to be valid in all EU countries, considering the diversity of landscapes, biogeographic and socio-economic conditions. This indicator is anticipated to provide a valuable proxy, although not a precise measurement of all relevant landscape features in farming landscapes.

Although there may be abundant literature on the relationship between landscape features and biodiversity and certain ecosystem services, the question remains open, whether the information about the share of landscape features in agricultural land alone would be sufficient for drawing any conclusions on biodiversity and ecosystem service provision. Landscape structure represents only one dimension of agricultural intensity. Therefore, land use (e.g. crop diversity, crop rotations, farm specialisation) and field management (e.g. soil management, fertilization, pesticide application) would have to be included to get a full picture of potential supply and demand of ecosystem services (Firbank et al., 2007). At least, it would be important to consider how this indicator could be closely connected to the indicators I.18 and I.22 to create a more consistent picture of agriculture and its potential impacts on biodiversity and ecosystem services.

Impacts of landscape features on pollinators and pollination depend on the type and quality of such features (Fijen et al., 2022; Garratt et al., 2017). The benefit of hedgerows for example, as a habitat for functionally important taxa such as wild bees, depends on hedgerow quality and management practices and is further moderated by management intensity at landscape-scale (Garratt et al., 2017).

Thus, if only trends of the share or extent of landscape features were reported, lacking information about the quality of the respective features, this may not proof helpful for making any inferences about their impacts on pollinators and pollination. The state and extent of the provision of ecosystem services, such as pollination, likely varies greatly across the different rural environments across the EU, with different types of landscape features having different impacts in different landscape contexts. Given such heterogeneity, flexible evaluation frameworks using a mix of different methods and a broad suite of indicators, adapted to the respective context may be required (Mortimer et al., 2010).

For the indicator I.21, the lack of robust data about quantity and quality of landscape features, therefore, impede its usefulness as a sound Farmland Pollinator Indicator.

I.22: Increasing agro-biodiversity in farming system: Crop diversity

This indicator comprises two sub-indicators:

1. Crop diversity on farm (number of farms by number of crops and size):
   - Number and percentage of farms by number of crops (1, 2, 3, and >3).
   - Number and percentage of farms by size of arable land (arable land < 10 ha; 10 ha < arable land < 30 ha; 30 ha < 100 ha; arable land > 100 ha), at NUTS 2 level.
2. Crop diversity in a region:
   - Average number of crops grown on a holding at NUTS 2 level as one.
   - Average number of crops grown on a holding at NUTS 2 level, broken down by arable land size classes (arable land < 10 ha; 10 ha < arable land < 30 ha; arable land > 30 ha).

The sub-indicators and measurement protocol/methods seem consistent, but there are differences between Member States in the frequency in which sampling and census are being conducted.

— The indicators we found are straightforward and based on data that can be collected also by remote sensing (aerial/satellite). This will likely improve the cost-efficiency of these indicators.

- The indicators used provide a good framework for monitoring pollinators as well, but some adjustments and refining are needed to better match agriculture land classification to pollinators' resource requirements. We suggest a tier classification based first on cultivated/non-cultivated classification, and within each category to further classify based on resources provided to pollinators (relative density of floral resources and duration of bloom along the activity season) and pollination-dependency of crops.
- Since the use of pesticides varies considerably between different types of crops, this aspect should also be integrated into the classification of different agricultural land uses.
- Standards that should be avoided – based on points 2 and 3 – a mere assessment of the diversity of different types of agriculture on the farm or region level may be misleading, if for example agriculture types do not provide resources for pollinators or can expose them to high doses of pesticides.

The indicator I.22 can provide a basis for estimating the availability of food and nesting resources to sustain pollinator populations. As current crops are, however, grouped into four categories (arable land, permanent grasslands, permanent crops, kitchen gardens) that do not provide information about their nutritional potential for pollinators, we recommend re-sorting the groups reflecting nutritional potential and flowering time. For example: spring/summer mass flowering industrial crops (high/low value); spring permanent grasslands (medium/low value); spring/summer fodder crops/grass/meadows.

Eristalis arbustorum, Axel Hochkirch

3.2.7 Lessons learned from the existing indicators for a future farmland pollinator indicator

Options and limitations learned for designing pressure and benefit indicators in the context of a farmland pollinator indicator

Given that agricultural landscapes vary greatly within the EU Member States, adaptive and flexible evaluation frameworks may be required. Therefore, we recommend more flexibility in the selection of appropriate pressure indicators to address spatially explicit environmental problems and objectives on the one hand and variations in the implementation of agri-environmental interventions on the other hand.

From the HNV farmland indicator we can learn that even region-specific indicators can be used in aggregated form for describing common trends at national and EU level. To make indicators like the Enhancing provision of ecosystem services more meaningful, the quality of landscape features with regard to their potential as nesting site and food resources, but also their exposure to pesticides should be considered. Nevertheless, to meaningfully use pressure and benefit indicators of national monitoring programs within a farmland pollinator monitoring, we may also have to improve our knowledge on local pollinator species, their ecological traits and their environmental requirements (Albertazzi et al., 2021).

Ex post evaluation reports had to be completed two years after the end of the funding period (see the Learning Portal - Ex post evaluation of the RDPs 2014-2022 for information on ex post evaluation)[62]. Evaluators could often not make use of the latest values of output and result indicators, as these were made available by the Managing Authorities too late to be taken into consideration in the evaluation.

For some of the indicators which are based on annex species and habitats and those based on agricultural census data, the timeline of reporting may not match the evaluation timeline resulting in data coming too late to be included in the respective evaluations. Hence, suitable pressure and benefit indicators may be helpful for the evaluation of policy strategies.

Options and limitations learned for designing state indicators in the context of a farmland pollinator indicator

The Farmland Bird Indicator and the Grassland Butterfly Indicator have been developed to describe and report changes in population trends at national and European scale. Due to the mismatch between the spatially fixed design of long-term monitoring programs and the dynamic, small-scale spatio-temporal farm management decisions, trend monitoring approaches are suitable to assess the state of those taxa but rarely the impact of the CAP resulting from mitigation of pressures. In specific cases and on an ad-hoc basis it may be possible to use data from standard monitoring programs to evaluate the impact of specific components of the CAP (e.g. Breeuwer et al., 2009; Kleijn and van Zuijlen, 2004).

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[62] https://eu-cap-network.ec.europa.eu/training/evaluation-learning-portal/learning-portal-ex-post-evaluation-rdps-2014-2022_en

We can learn from the successfully established bird and butterfly monitoring schemes in Europe that thanks to a huge number of volunteers and the validation of these Citizen Science data, a sound data basis for trend analyses, and therewith also for the corresponding indicators, is available.

Impact indicators recorded in areas targeted by rural development policy can most likely illustrate medium- and long- term trends. Evaluation reports, however, have to be reported during the CAP period or shortly afterwards. It is questionable whether the impact indicators would already depict any effects of CAP interventions on pollinating insects two years after the implementation of the first CAP measures or one to two years after the end of a funding period. There may be a mismatch between the response of organisms to the (ongoing and previous) CAP interventions or any other policy interventions and the defined evaluation timeline.

3.2.8 Conclusions based on existing farmland indicators

In contrast to the Farmland Bird Indicator and the Butterfly Grassland Indicator, which were not specifically designed for the purpose of serving as farmland or CAP impact indicators, there is now an opportunity to develop a Farmland Pollinator Indicator, and to design it purposefully to fulfil the demands of evaluating the CAP and other policy strategies. Therefore, the EU PoMS core scheme should be complemented by additional sampling sites within agricultural landscapes reflecting the impacts of the respective policy interventions and thus allow making inferences about their potential impacts. The site selection would either have to be grid-based (e.g. LUCAS grid, see section 2.10) or informed by regional specific differences in the implementation of intervention measures to embrace the variability of interventions within and across Member States. Sampling by trained volunteers may be possible but even then, data on pollinating insects would be available only late during the evaluation period. For an earlier and more rapid assessment of impacts, a further set of indicators (pressure/mitigation) could be harnessed, which would aim at reporting changes in the quantity and quality of habitats and habitat conditions for pollinating insects in agricultural landscapes. Those indicators could be based on the conflation and interpretation of remote sensing data, IACS data and spatially explicit data of pesticide use (not sales). Habitat suitability models could be calculated based on information provided about the implementation of CAP measures, changes in crop rotations and crop diversity together with parameters of landscape structure and quality of landscape features. To get an even faster data flow and to mitigate the time lag caused by processing time of IACS and remote sensing data, engaging farmers as volunteers for data gathering may be an additional option.

3.2.9 Policy context for developing a farmland pollinator monitoring and indicator(s)

The Common Agricultural Policy largely determines how agricultural land is utilised in the European Union. The CAP defines the scope of action for the Member States, while farmers play a decisive role in shaping our agricultural landscapes with their decisions on production branches, types of farming, forms of management and the implementation of CAP interventions. Their decisions are influenced by site characteristics and by (global) market prices for agricultural products. Consequently, agriculture in its complexity has an important role to play in preserving and promoting biodiversity.

The EU currently supports agriculture with around one third of its budget. In addition to the direct payments of the first pillar, which are primarily aimed at securing income and strengthening competition among farmers, the second pillar focuses on social benefits. These include the preservation of cultural landscapes and the associated biodiversity, sustainable and environmentally friendly farming, animal welfare and the development of rural areas. Each Member State has developed a national strategy plan for the current CAP period to realise the overarching objectives of the CAP. To this end, each Member State has formulated specific targets that are to be achieved through corresponding measures. In comparison to previous CAP periods, the Member States are given greater responsibility and therefore also for the implementation and realisation of the Green Deal. It can be assumed that the effects of the CAP on land use and land management will vary greatly between the Member States because of this Member State-oriented approach. It is therefore to be expected that the impact of CAP policy on biodiversity, including pollinators, will also vary from one Member State to another.

The current design of the CAP and its control and evaluation mechanisms at different times – within and after/before a CAP period – pose major challenges for assessing potential impacts of the CAP on pollinators. This is because it requires two consecutive steps: in a first step, a monitoring approach needs to be conceptualised that captures CAP measures in a sufficient spatial coverage to enable statistically validated statements about changes in populations; in a subsequent step, an evaluation of possible effects of the CAP on pollinators within a period (of seven years) is required. To meet these challenges, an optional two-stage monitoring approach with a selection of state and impact indicators according to the DPSIR model (section 3.2.4) is proposed. This would allow us to describe trends of pollinators in agricultural landscapes at EU, national and sub-national level and to assess possible effects of CAP measures in interaction with environmental factors.

3.2.10 Monitoring approaches and indicators - assessing state and trends of farmland pollinators and possible impacts of CAP policy.

The drivers and their interactions that change and shape our agricultural landscapes are complex and multi-layered. It is therefore difficult to single out individual drivers, such as the CAP with its diverse interventions and associated measures, and to consider their effects on pollinators in isolation. This is because site characteristics, habitat diversity, the spatial heterogeneity of habitats, the prevailing forms of agricultural utilisation and management practices interact with the measures implemented. In addition, the effects of measures from the previous CAP period can outweigh the effects of current measures. Therefore, an, ideally, two-stage monitoring approach is recommended. The first stage encompasses a surveillance monitoring that allows the description of trends of pollinators and links them to land use and landscape structures, including CAP measures, depending on the commitment. The second stage involves a monitoring under adaptive management realized by farmers. Because they decide where and which measures are implemented in the field, this approach makes it possible to evaluate different types and levels of CAP measures and thus derive recommendations to improve habitats for pollinators in agricultural landscapes.

The optional two-stage Farmland Pollinator Monitoring presented here pursues four overarching objectives that are aligned with the environmental goals of the CAP and of the New Deal for Pollinators:

- Create a scientifically robust data basis to describe state and trends of farmland pollinators in the form of state indicators (S-indicators) at EU level.

- Describe the links between the development of pollinators and pollination and the shape of agricultural landscapes, including CAP interventions (at EU, national and, where appropriate, sub-national level) (impact indicators, pressure and benefit indicators).
- Identify possible options for evaluating CAP interventions in terms of their effects on pollinators (EU, national and regional scale) and thus verify the formulated target achievement of the CAP and national strategic plans of the Member States (pressure and benefit indicators).
- Use the findings from the Farmland Pollinator Monitoring to make CAP interventions and their biodiversity-enhancement measures (more) effective for pollinator conservation.

The following section presents the optional two-stage Farmland Pollinator Monitoring and the indicators that can be derived from it and their significance.

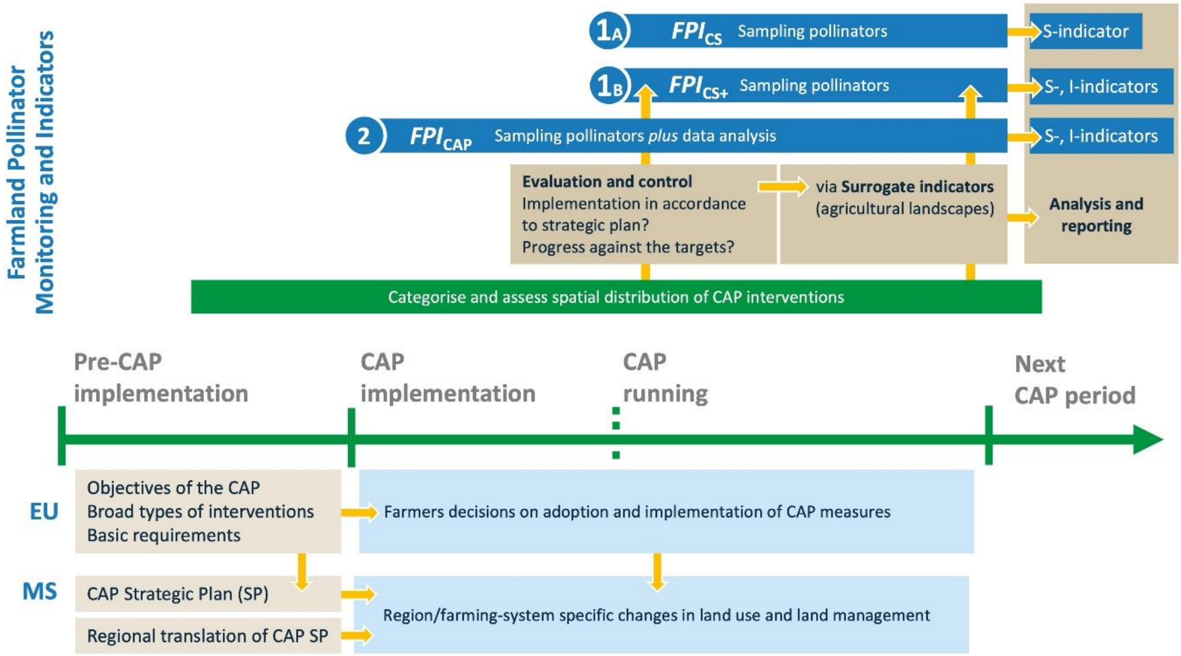
3.2.10.1 Defining agricultural landscapes within Member States and describing agricultural diversity in the EU

The pronounced north-south gradient in Europe and the associated biogeographical regions form the basis for diverse agricultural production systems and forms of cultivation. To make EU-wide statements about the status and development of pollinators, it is necessary to define the agricultural landscape of each Member State and translate it into data. The agricultural landscape identified in this way then forms the basis for classifying monitoring plots of the core scheme as agricultural monitoring plots (Hellwig et al., 2024). For this purpose, a threshold of at least 10% agricultural land within agriculturally classified monitoring plots is proposed, based on the European Monitoring of Biodiversity in Agricultural Landscapes (EMBAL) (Oppermann et al., 2017).

3.2.10.2 An optional two-stage Farmland Pollinator Monitoring – the basis for state and impact indicators

An optional two-stage Farmland Pollinator Monitoring is proposed as an extension of the EU PoMS Core scheme: A surveillance monitoring to describe (agricultural-related) trends of farmland pollinators and a monitoring under adaptive management to assess effects of different types and levels of CAP measures (Figure 3.2. 5).

Figure 3.2. 5. Overview of workflows and the optional two-stage Farmland Pollinator Monitoring for the current CAP period. FPI_{CS}: Surveillance monitoring, Option 1a (Trends of farmland pollinators); FPI_{CS+}: Surveillance monitoring, Option 1b (Relating trends of farmland pollinators to characteristics of agricultural landscapes, including CAP measures); FPI_{CAP}: Monitoring under adaptive management - assessing effects of different types and levels of CAP measures. MS: Member State.



Source: Authors' elaboration.

Option 1a: Trends of farmland pollinators [FPI_{CS}]

This monitoring approach focusses on recording the status of pollinators and describing their trends in agricultural landscapes at EU level. For this purpose, all those sites of the core scheme are selected that are located in agricultural landscapes and contain at least 10 % agricultural land. The pollinators recorded on the agricultural sites form the data basis for the following state indicators. The indicators presented here are sub-indicators of the S-indicators of the core scheme. Due to the limited number of agricultural sites, the calculated trends are subject to greater uncertainties, thus changes can be detected only with lower probabilities compared to those of the core scheme. The data on species richness and abundance will be used to calculate the following Farmland Pollinator State indicators (see chapter 3.1 on indicators in this report):

Farmland Pollinator State-(sub)Indicators

Option 1a is based on the same set of S-Indicators of the core scheme as there are:

- Species abundances
- Species distribution
- Taxonomic diversity
- Taxon-aggregated abundance

In line with the core scheme, the same metrics should be used for calculating the State-(sub)Indicators (see section 3.1).

Possible applications and policy fields of actions: The proposed S-(sub)Indicators should make it possible to identify changes in farmland pollinators at EU level.

Option 1b: Relating trends of farmland pollinators to characteristics of agricultural landscapes [FPI_{CS+}]

Like $\mathrm{FPI}_{\mathrm{CS}}$, this monitoring approach aims to provide information on the trends of pollinators in agricultural landscapes. However, this approach is conceptualized in a way that trends can be interpreted independently of the core scheme and thus, trends may reflect agriculture-related changes, including CAP measures, in pollinator populations. For this to be possible, the number of sites in agricultural landscapes must be increased to the total number of sites of the core scheme per Member State (random sampling design according to the core scheme). In addition, data are needed to depict agricultural landscapes, in particular land use and landscape structure, and to indicate changes in habitat quality, habitat quantity and connectivity. Based on remote sensing and IACS data, the following metrics (or pressure and benefit indicators) should complement the data on pollinators and be calculated for the agricultural sites. These metrics can also be used as surrogate indicators for an initial evaluation of CAP interventions at the beginning of the CAP period (see sections 3.2.2 - 3.2.8 and Figure 3.2. 5).

Diversity of land use (DivLandUse): The diversity of agricultural land use has a direct influence on species diversity, which varies in strength and expression depending on the species/organism group. The indicator describes the composition of land use based on the area shares of individual agricultural utilisation classes (Equation 3.2. 1). The available and commonly used classification of land use classes for each Member State serves as the basis for the calculation. The area share of the land use classes is calculated in relation to the total area of agricultural land within the monitoring site (Klein et al., 2024).

$$DivLandUse = pLF_i = \frac{a_i}{A_{FL}}\{(0|1)\}$$

Equation 3.2. 1. Diversity of land use.

where DivLandUse stands for diversity/composition of land use, pLF_i for utilised agricultural area, a_i for area of land use class, A_{FL} for proportion of agricultural area.

CAP interventions (CAPInt): The first and second pillars of the CAP support a wide variety of measures from which pollinators can also benefit, e.g. through the (temporary) provision of food resources and nesting resources.
The indicator reports the subsidised area (%) per site on which CAP interventions are implemented. If several measures have been implemented on the same area, this area is only considered once. There could be sub-indicators on, for example, the proportion of subsidised area with pollinator-friendly CAP interventions or the proportion of subsidised area with first/second pillar measures (Klein et al., 2024).

The spatial and temporal information on CAP measures can be extracted from IACS data, provided that the data are available for the Member States. The classification scheme developed by the JRC to report and describe interventions defined in the Member States CAP Strategic Plans by farming practices could be helpful for aggregating similar interventions relevant for pollinators across different Member States and different CAP areas (European Commission Joint Research Centre et al., 2024). As discussed in section 2.10.5, co-locating EU PoMS additional FPI sites with other farmland specific monitoring schemes (e.g. EMBAL) may also support sourcing of relevant land use and land management data. Furthermore, useful data on land use and landscape structures may also be derived from remote sensing data (e.g. Frank et al., 2024).

The metric proposed here only considers whether CAP measures (1st and 2nd pillar) are present in a site, regardless of, for example, the duration and quality of a measure. The reason for this is that the design of this monitoring approach only allows an assessment of the potential impact of CAP measures in interaction with land use, landscape structures and site characteristics on pollinator trends. To account for the complexity and multi-layered nature of interventions and their measures, a differently designed approach is required, as for example outlined in the following section.

Habitat diversity (HabDiv): Diversity of habitat types present in an agricultural site, including linear habitat types, considering both the number of habitat types and their relative proportions in the total area of the site (Equation 3.2. 2). The unit of measurement is the Shannon index, which has a value of zero if only a single habitat type is present in the monitoring plot (no diversity) and increases with increasing diversity of habitats, especially if their proportion of the habitat area is similar (Bailey et al., 2012).

$$HabDiv = -\sum_{i=1}^{N} A_i(lnA_i)$$

Equation 3.2. 2. Habitat diversity.

where HabDiv is habitat diversity, N is the number of habitat types within the site and A_i is the proportion of the monitoring plot of habitat type *i*.

Length of linear habitats*:* The total length of hedges, rows of trees and shrubs, green strips between fields, streams, rivers, stone walls, and terrace walls in kilometres per site.

Spatial heterogeneity of habitat types*:* Increasing structural richness in agricultural landscapes also increases the likelihood that organisms, including pollinators, will find all required habitat requirements they need to maintain and increase populations.

Therefore, the calculation of the mean Hix-index per site based on Meier et al. (2021) and Fjellstad et al. (2001) is recommended here. For this purpose, each site is covered with a 50m grid. Using a so-called moving window, the habitat type of each grid is compared with the neighbouring maximum of eight habitat types. Only grid cells located in agricultural landscapes are considered. If the habitat type in the centre corresponds to the neighbouring habitat type, this relationship is assigned a value of zero. If this is not the case, the relationship is assigned a value of one. The mean value of these relationships is then calculated for each grid cell, which can therefore have values between 0 (all neighbouring habitat types the same) and 1 (all neighbouring habitat types different). A high Hix-index therefore means that different habitat types are found in the monitoring plot in question on a relatively small scale.

The pollinator survey follows the core scheme method and allows calculating the following state and impact indicators being in line with those of the core scheme (see chapter 6 in Potts et al. (2021)):

- Farmland Pollinator State-Indicators:
    - Species abundance

  - Species distribution
  - Taxonomic diversity
  - Taxon-aggregated abundance
  - Functional diversity (supplementary data sources on functional pollinator traits are needed)

- Farmland Pollinator Impact Indicators as a proxy for indirect pollination:
  - Species abundance of major (crop) pollinating species. Classification in (crop) pollinating species can be realised by additional data sources on EU crops and their pollinators
  - Taxonomic diversity of crop pollinators
  - Functional diversity of (crop) pollinators

Combining the S-Indicators with those focusing on functional diversity and (crop) pollinating species may be helpful for the interpretation of the trends observed and may thus provide insights about the situation of e.g. habitat specialists or pollination potential (Powney et al., 2019)

Possible applications and policy fields of actions: The proposed Farmland Pollinator S- and I-indicators are stand-alone indicators that can be reported independently of those of the core scheme. This allows the reporting of agricultural landscape-related trends of pollinators and initial insights for possible changes and adjustments to CAP measures and their implementation at regional level. The sample size makes it possible to consider trends at different spatial scales: from the EU level to the national and possibly sub-national level (depending on the sample size per Member State).

The proposed Farmland Pollinator Indicators could be included as future performance indicators in the CAP's Performance Monitoring and Evaluation Framework and used as indicators for the EU PI. In addition, the indicators are suitable for checking formulated targets in national pollinator action plans and insect conservation programs.

Option 2: Assessing effects of CAP interventions [FPI_{CAP}]

Various factors interact in agricultural landscapes, making it difficult to consider possible effects of CAP in isolation. While surveillance monitoring approaches can be used to report medium and long-term trends in farmland pollinators, other monitoring approaches are required to check whether the targets formulated in the national strategic plans have been achieved through interventions and their associated measures. For doing so, monitoring approaches under adaptive management (after Reynolds et al. (2016)) are required to estimate the impact of (aggregated) measures and derive information for the next action(s) to take. For this to succeed, clearly a priori formulated questions and hypotheses are required *before* the monitoring is implemented.

Another challenge for the evaluation of the CAP – from an entomological and scientific perspective - is the short duration of a CAP period of seven years on average. This makes it almost impossible to obtain EU-wide information on where and in which year which CAP measures are being implemented at the start of a CAP funding period. We therefore recommend a Citizen Science-based monitoring approach to evaluate CAP interventions and their measures, which is carried out by farmers, by the decision-makers themselves, who implement the measures and bring them to the field. This approach makes it possible to implement the necessary monitoring approaches, including before and after controls, and creates the conditions for reviewing the targets formulated in the national strategic plans of the Member States. The concrete design of the monitoring depends upon a close match between the strategic plan with its regionalized targets and the adoption of the measures by farmers. As about 90% of the agricultural area in the EU is covered by the CAP, it is unlikely to carry out controls based on comparisons between agricultural areas without and with CAP measures. Instead, it will be more realistic to assess the effects of different types and different levels of CAP implementations on pollinators (Potts et al., 2021). The fact that specifically designed monitoring approaches and indicators are required to address the question of possible impacts of CAP policy on biological diversity, show that the currently used performance indicators (e.g. bird indicator) of the CAP PMEF fail to do so.

The future Farm Sustainability Data Network (FSDN) of the European Commission[63] is recommended as a potential backdrop for this 'monitoring under adaptive management'. However, the FSDN is not spatially explicit, and only represents coarse spatial resolution. To address this point, the FSDN could be complemented by national networks of farms or incentives for farmers to survey pollinators (and pollination) themselves and thus evaluate the measures they have implemented. In this way, the EU could recognise pollinator monitoring as an integral part of the Ecoschemes obligations. If such a network of farms is large enough and covers a representative share of the agricultural area of a Member State, the conditions could be created to evaluate various interventions and related measures. Realising a monitoring under adaptive management by farmers could also provide opportunities to gain additional information for example on land use intensity and land use history, including spatial and temporal information on the implementation of previous CAP measures. This could make analyses more meaningful, but also serve as a basis for P-indicators.

While experts record the selected pollinator groups in the core scheme, the evaluation of the CAP measures by farmers requires recording approaches that (where possible) provide observer-independent and high-quality data. One success story, for example, is the moth monitoring with farmers in Ireland, which is based on a non-lethal image recognition based system[64]. A similar moth monitoring system has been developed and piloted in the SPRING project and has finally been integrated in the core scheme (see section 2.9). Therefore, it would be conceivable to use this moth monitoring approach for the citizen science-based evaluation of CAP measures and, if possible, to calculate the same S- and I-Indicators of the optional two-stage Farmland Pollinator Monitoring.

Possible applications and policy fields of actions: The potential of the Citizen Science monitoring approach with farmers is promising, even if additional coordinating structures, such as contact persons for queries and support for farmers, would be necessary. On the one hand, involving farmers in pollinator monitoring can help to raise awareness of the underlying relationship between the design of agricultural landscapes and pollinators. On the other hand, this approach enables an understanding of the impact of different types and levels of CAP measures on pollinators, and thus it creates the prerequisites for designing effective measures. Depending on the aggregation level of CAP measures, this approach could be used to review the formulated

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[63] https://agriculture.ec.europa.eu/data-and-analysis/farm-structures-and-economics/fadn_en

[64] https://biodiversityireland.ie/projects/farmer-moth-monitoring-project/

overarching objectives of the CAP and the national strategic plans at EU, national and regional level.

3.2.11 Farmland pollinator monitoring: an optional two-stage approach

Pollinators are of particular importance for agriculture and make an important contribution to food security. Therefore, both medium and long-term statements on trends at EU and Member State level are important, as well as short-term assessments of the effectiveness of measures to promote pollinators and therewith biodiversity. For this reason, an optional two-stage Farmland Pollinator Monitoring is proposed, in which surveillance monitoring and monitoring under adaptive management complement each other. The latter approach can be carried out by farmers, with two advantages: firstly, farmers themselves decide where and when to introduce which CAP measures into the field. Secondly, Citizen Science approaches based on image recognition based surveys allow pollinator data to be available for data analyses as soon as CAP measures are implemented (see Figure 3.2. 1). This means that evaluation results of measures could already be available during the CAP funding period and the knowledge gained could be incorporated into the planning for the next CAP period. In contrast, trend monitoring approaches take more time - from data collection to species identification and data analysis, especially if additional environmental data must first be made available and processed (see Figure 3.2. 1).

3.2.12 Recommendations

Agricultural landscapes are significantly shaped by the complex interplay of various drivers at EU and Member State level as well as by the individual decisions of farmers. As a result, it is difficult to assess the impact of the CAP on biodiversity. The indicators used so far in the PMEF are not suitable for this, as they were originally designed for other purposes and therefore do not cope with the described complexity acting in agricultural landscapes.

We therefore recommend a two-stage monitoring approach (FPI_{OPT}). This should enable the assessment of medium and long-term trends of pollinators in agricultural landscapes, as well as the possible impacts of different types and levels of CAP measures on pollinators, using S- and I-indicators. For the surveillance monitoring approach, we recommend option 1b FPI_{CS+}. This option makes it possible to relate changes in pollinator populations to characteristics of and changes in agricultural landscapes – both at EU and Member State level.

Before the monitoring approach (FPI_{OPT}) proposed here and the associated indicators can be implemented, the following aspects for the individual components of FPI_{OPT} need to be tested, further developed and, if necessary, clarified:

FPI_{CS+}

- Define the agricultural landscapes for each Member State.
- Carry out power analyses to estimate the number of monitoring plots required for robust data analyses at EU and Member State level.
- Test whether the proposed surrogate indicators are suitable for:
    - Detecting changes in the CAP policy between two CAP funding periods.

  - Deriving statements on habitat quality, habitat quantity as well as connectivity of potential pollinator habitats.

- Analyse possible effects on the informative value of the surrogate indicators depending on the data sources used (EU-wide vs national data sources).
- Assess in which Member State IACS data can be used for FPICS+ and within which timeframe IACS data can be made available to the analysing institutions.

FPI_{CAP}

- Define possible pollinator groups suitable for assessing the impact of CAP interventions based on specific traits.
- Select standardised recording approaches that:
  - Allow farmers to record pollinators easily and with little time expenditure.
  - Allow the collection of observer-independent and high-quality data.
  - Are based on image recognition systems.
- Categorise CAP measures into 1st pillar, 2nd pillar and pollinator-friendly ones.
- Develop a sampling design that allows the assessment of the impact of different types and levels of CAP measures.

For the development of functional FPI_{OPT}, we recommend a four-year pilot study in which:

- SPRING data in combination with remote sensing datasets are used for the calculation of surrogate indicators to test the validity of the proposed FPI_{CS+}.
- In selected agricultural landscapes in the EU (mapping the gradient), promising Citizen Science-based monitoring approaches, such as moth monitoring (see section 2.9), or possibly the monitoring of cavity-nesting wild bees could be trialled together with farmers from the Farm Sustainability Data Network. Noting however, that the information collected by FSDN is not spatially explicit, but refers to the participating agricultural holdings, which may complicate the link between FSDN data and the EU PoMS indicators obtained at a particular site. However, at higher aggregation levels, (e.g. Member State or region), such links can be established. The data collected from the FSDN could be used to calculate S-, I- and P-indicators.
- Proposals are developed on how:
  - Possible workflows and infrastructure required to implement the FPI_{OPT}, in particular the FPI_{CAP}, could/should be designed.
  - Farmers could be financially compensated for the implementation of monitoring under the CAP.

4 Options for EU PoMS data management

4.1 Summary

Europe supports a rich diversity of wild pollinators, which provide a wide range of benefits to society. There is increasing evidence that many European pollinating species are declining. However, major gaps remain in our knowledge regarding the status and trends of pollinating insects, especially in a continental scale. Therefore, a proposal for an EU pollinator monitoring scheme (EU PoMS) comes on the heels of a July 2020 report by the European Court of Auditors (ECA) (European Court of Auditors, 2020), aim to overcome outstanding knowledge gaps and to provide high quality data on pollinator and pollination trends. These data will be analysed and modelled for designing and implementing effective policy and management response options across governance levels.

The complexity of European pollinator monitoring data arises from the diversity of pollinator species, spatial and temporal variations, quality assurance, large data volumes, data integration challenges, and the need for long-term preservation. Addressing these complexities requires interdisciplinary collaboration, standardized protocols, advanced data management systems, and robust analytical approaches. Building upon the initial proposal in Potts et al. (2021) and drawing upon relevant initiatives such as the H2020 EuropaBON project[65] and existing monitoring schemes, we aim to design an optimal workflow for data management throughout the entire data life cycle following the FAIR (Findable, Accessible, Interoperable, Reusable) data principle (Wilkinson et al., 2016). Management requirements and methodology recommendations are presented for data acquisition, data documentation, data validation, data preservation with versioning, data integration, as well as data publishing providing open access.

Considering the requirements of relevant end-users and stakeholders including, but not limited to EU PoMS staff, EEA, DG ENV and other Commission and Member State entities, NGOs, researchers and conservation practitioners, this document proposes suitable server infrastructure and software architecture including a recommended user interface. It lists a set of options for the existing data management solutions, including detailed description of its functionalities and configuration, for consideration, review and assessment by the EEA and the DG ENV coordinators of the Initiative.

Our key recommendations for data management workflow of EU PoMS are outline as follows:

- 8 groups of stakeholders should be recruited/contributed to actively updating EU PoMS database (section 4.6.1).
- A unified central hardware infrastructure should be implemented for the EU PoMS database, including a primary server, a mirror server, a test server, and a backup system (section 4.5.1).
- Data management solutions should be based on existing software and be further developed based on specific need of EU PoMS (section 4.5.2).
- Both develop a new app and cooperate with existing apps are recommended to maximize the impact of EU PoMS (section 4.4.1).

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[65] https://europabon.org/

- 2 levels of validation procedure are advised to guarantee the quality of data (section 4.7.3).
- The EU PoMS database should establish a species referencing table for standardizing nomenclature to ensure data consistency and accuracy (section 4.7.2).
- Publish annual monitoring data with open access and assign citable DOIs, offering flexibility for the download of accumulated multi-year datasets as well as data specific to spatial, temporal and taxonomic contexts (section 4.7.4).
- Data publication policy should be openly accessible and be made very clear to volunteers prior to them participating in EU PoMS (section 4.3.5).

A glossary to all the technical terms used in this chapter can be found in Annex 4. A.

4.2 Data management workflow

Effective management of research data throughout the data life cycle, from data generation to knowledge creation to policy making, is crucial to the success of the EU Pollinator Monitoring Scheme (EU PoMS) (Potts et al., 2021). Our goal is to ensure that the management of monitoring data aligns with the principles of findability, accessibility, interoperability, and reusability (FAIR principle, (Wilkinson et al., 2016)). A clear and structured data management workflow within the EU PoMS could significantly improve management efficiency, preservation continuity, and reproducibility of monitoring data (Boyd et al., 2023; Harjes et al., 2020). Therefore, a well-organised data management workflow is essential to the success of this project. Such a workflow provides stakeholders with an understanding of their roles and responsibilities, enhancing productivity and resource allocation. Moreover, it enables streamlined quality control mechanisms and supports decision-making by offering clear biodiversity indicators.

Drawing upon the well-established 8-step data life cycle framework (plan, collect, assure, describe, preserve, discover, integrate, analyse) proposed by DataOne[66] (Michener et al., 2011) and the biodiversity-specific 10-step data life cycle framework (plan, collect, assure, describe, submit, preserve, discover, integrate, analyse, publish) adapted by GFBio[67] (Grobe et al., 2019), and further considering the unique characteristics of monitoring data, we have devised a comprehensive workflow comprising 15 distinct milestones illustrated in Figure 4.2. 1.

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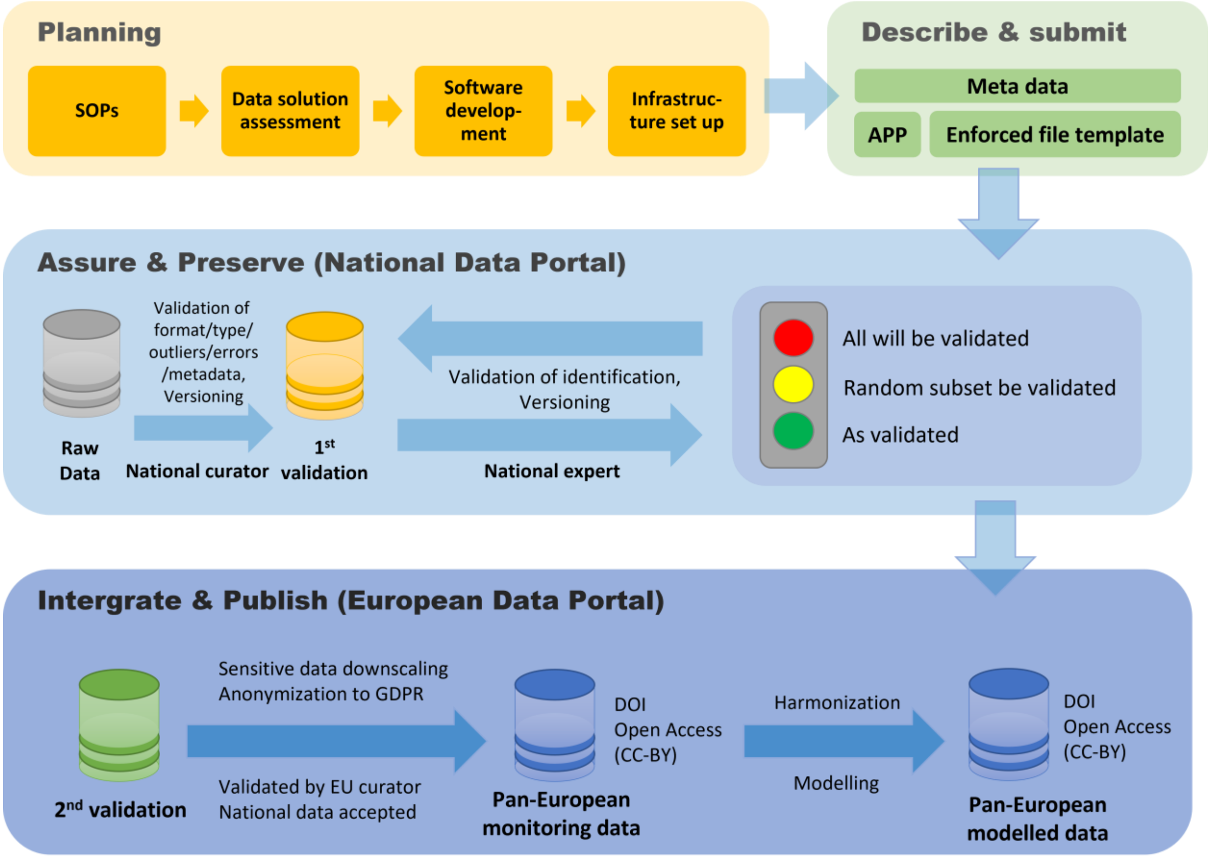
[66] https://www.dataone.org

[67] https://www.gfbio.org

Figure 4.2. 1. Devised data management workflow for EU PoMS.



Source: Authors' elaboration.

The detailed descriptions of the 15 milestones along with corresponding stakeholders (roles of different stakeholder groups are documented in section 4.6.1 User management) are listed as follows:

1. Set up Standard Operating Procedures (SOPs) of data acquisition, documentation, validation procedure, sensitivity downscaling, and publication (whole consortium).
2. Software (app, database) option assessment (EU hosting facilities, EU data coordinator).
3. Software development of app and database to customize existing data solution for specific requirements of EU PoMS (EU data coordinator, EU software developers).
4. Hardware set up and maintenance including primary server, mirror server, testing server, backup plan, and scalability plan (EU data coordinator, EU software developers).
5. Database online, documentation offered in all languages, training offered, user registration, dissemination (EU data coordinator, national data coordinators).
6. Monitoring data and metadata submission (national taxonomic experts, national volunteers, national data coordinators).
7. Largely automated first level validation including error, outlier, missing data detection (national data curators, national data coordinators).

8. Second level validation including species identification (national taxonomic experts).
9. Automated sensitive data downscaling, anonymization aligns to General Data Protection Regulation[68] (GDPR), translation into universal language adapted by EU data tables (national data curators, national data coordinators).
10. Final validation and acceptance of national data (EU data coordinator).
11. Data extracted, consolidated, and exported into CSV format with metadata, published annually with yearly DOI under Creative Commons license (EU data coordinator).
12. Data modelling and visualization (EU model experts).
13. Modelled data documentation and submission to database (EU model experts).
14. Annual data report (EU data coordinator, EU model experts).
15. Dissemination of results (EU data coordinator, EU model experts, national data coordinators).

This streamlined data management strategy is an investment that potentially yields significant cost savings across various stages of EU PoMS. It reduces the duplication of infrastructure costs and maintenance efforts, improves the scalability of data systems, and minimizes the efforts required for data acquisition and entry into databases. By implementing a robust data scheme, it enhances data harmonization, and through semi-automated validation procedures, it improves data quality in a cost-effective way. Additionally, it reduces training costs by providing standardized procedures (SOPs) and comprehensive documentation.

4.3 Data standard

To assure high quality monitoring data, a European cyberinfrastructure needs to be set up for data acquisition, validation, storage, integration, modelling, and visualization. Given the inherent heterogeneity across Member States in terms of language, data standards and formats, expertise and capacities, and data sharing practices, it is crucial to meticulously document and widely disseminate Standardized Operating Procedures (SOPs) for the entire data management cycle. These SOPs should be made publicly available via the EU PoMS web portal. This approach aims to facilitate seamless collaboration and accessibility for all stakeholders involved.

4.3.1 Standard data acquisition and submission

In order to maintain the quality and reliability of collected data, it is essential to establish standardized data acquisition protocols once standardized sampling methods have been implemented. Detailed data acquisition procedure is described in section 4.4 Data acquisition.

We propose a system where the database can be accessed in two ways, through a website and through an application programming interface (API, a way for a computer program to communicate with another external program). The app we propose to develop, as well as third party apps, can

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[68] https://gdpr-info.eu

only communicate with the central database through this API. The API enforces the data standard, hence all data coming from our or external apps conform to this data standard.

The website has a similar validation protocol, which also enforces the data standard. The website allows users to create a new event and manually enter the details or upload a Comma-Separated Values file (CSV).

The app is the recommended way of submitting monitoring data from transects. The app can store data on the user's device and can therefore function if the user is offline. Data are uploaded once the user reconnects to the internet. The app can be used to record metadata for pan trapping, but as species information will only available after further processing, we recommend either to enter these data directly into the website or upload a CSV file. These CSVs are automatically rigorously validated (1st level validation, see section 4.7.3.1) before being accepted (e.g. by checking if the date is valid and the species occurs in the list of possible species etc.).

Both the app and the website will not accept data without detailed metadata on event (timestamp, location, weather, collection protocol etc.) and recorder (recorder IDs). Data such as timestamp or location can be automatically recorded by the app but have to be entered manually when entering or editing data through the website or into CSV files. Data entry will be automatically documented with timestamp at the time of submission. This ensures that all data can be easily tracked and traced throughout the database, providing a complete audit trail of all data submissions. It is imperative to preserve the original raw data to enable tracing back in the event of data loss or misinterpretation. The data submission procedure is illustrated in Figure 4.2. 1.

Requiring data to conform to a standard before it can be entered ensures that all users enter data in a consistent and standardized manner, which helps to ensure data integrity and reliability, as well as facilitate efficient data management and analysis. In both cases, complete and in-depth metadata should be always provided.

4.3.2 Standard metadata

Metadata is absolutely essential in biological monitoring data because it provides critical information about the sampling protocol and deviations from the protocol, sampling sites, sampling event, environmental conditions, sample identification methods, (the number of) data collectors, limitations or biases, description of variables (data type, unit, accuracy), upload/download data format, licence for data publication (national data and EU data might apply different licences), and so on. Schema of the metadata should be standardized based on community-developed standards for biological data such as Darwin Core[69], Dublin Core[70], Humboldt Core[71], or Ecological Metadata Language[72], which facilitate effective search capabilities, ensure compatibility, and enhance the accessibility and reusability of data. If the metadata contains terms from different biodiversity data standards (merge of standards), mapping of metadata to specific data standards e.g. Darwin Core term should be offered.

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[69] https://dwc.tdwg.org

[70] https://www.dublincore.org

[71] https://mol.org/humboldtcore

[72] https://eml.ecoinformatics.org

4.3.3 Standard terms

Establishing Species Taxonomy Nomenclature in a database is essential for accurate and reliable species identification. A standardized system for naming and categorizing species serves to eliminate ambiguity and simplifies the retrieval of information pertaining to specific species or species groups. For instance, the eBMS system relies on an accepted list of scientific names from Fauna Europaea[73] for species identification. Consequently, it becomes crucial to construct a reference table containing the species list against which all other input data must undergo validation. Detailed procedure is described in section 4.7.2 Species referencing table.

T achieve consistency, accuracy, quality, integration and efficiency of data in a database, the following measures need to be employed:

- Consistent terms, preferably Darwin Core terms, should be implemented in both the entities and attributes of the metadata and in the data tables of the database.
- Standard data precision, e.g. coordinate precision, need to be set up before data collection procedure.
- A unified language should be used in Pan-European data. In cases where different languages are applied in the national data, automatic and systematic translation tools such as DeepL[74] should be adapted. National data curators need to perform quality proof of the auto-translated text (see section 4.7.4 Data downscaling, anonymization, and publication).
- A fixed vocabulary, if necessary, should be used to reduce the risk of data inconsistencies or errors such as typos. E.g. at data entry, use multiple choices instead of free text input field.
- In-depth documentation or appropriate training should be provided to ensure proper implementation (details described in section 4.6.2 Components).
- Standard data format for downloading need to be established. Recommended format should be widely accepted and non-proprietary. For instance, the Darwin Core Archive (DwC-A), which encompasses both the data file as CSV file, and the metadata file as XML file. This format offers several advantages, particularly facilitating data sharing and integration with the Global Biodiversity Information Facility (GBIF).

4.3.4 Standard data versioning

Version control ensures the integrity of monitoring data by providing a systematic approach to track and manage changes made to the data. It allows for the identification and documentation of modifications, ensuring transparency and accountability in the data management process. In principle, version control will be employed in each modification step, including a timestamp and a brief description for the update. This allows the data editors to keep track of changes made by other members. Version control will mainly take place during data validation procedure, which is described in section 4.7.3 Data validation workflow.

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[73] https://www.gbif.org/dataset/90d9e8a6-0ce1-472d-b682-3451095dbc5a

[74] www.deepl.com

4.3.5 Standard data publication rules

Open access to both monitoring data and modelled data should be mandated with a minimum CC-BY-4.0 license[75] for pollinator monitoring elements that involve paid contributors. However, volunteer-based components require a flexible approach to data ownership, particularly for existing initiatives (e.g. eBMS[76], UK PoMS[77]) that contribute to the EU PoMS. A data access policy and license established by the existing initiatives could inform the EU PoMS approach, which ensures acknowledgment of national schemes and enables input into appropriate use of the data. Volunteers in monitoring schemes retain ownership of data but grant organizations the right to use the data, while their personal data can be removed upon request, but species data remains. This should be made very clear to volunteers prior to them participating in EU PoMS. Separate arrangements on data ownership are necessary for targeted monitoring. Volunteers' consent should be obtained before publishing or forwarding individual monitoring data, while processed products may be published or forwarded. Third-party involvement necessitates co-ownership of the data. Permanent identifier such as DOI should be used to access and cite the monitoring data. It is worth noticing that CC-BY-4.0 license pertains to the data source. Consequently, should an individual undertake an analysis with the intention of publication, proper acknowledgment should be made to the dataset in its entirety. It is important to note, however, that the CC-BY license does not encompass individual data observations, especially contributions made by individual paid contributors.

4.4 Data acquisition

The Pollinator Monitoring Scheme requires extensive data collection by volunteers or professionals, depending on the location. Both groups would benefit from an app supporting EU PoMS protocol. Such an app streamlines data collection, enhances standardization, simplifies merging and sharing of datasets, and potentially improves data quality through features like image uploads, precise timing, and GPS tracking. In this section, we explore the requirements for developing this valuable app, discussing target audience, userbase building, and app components in detail.

4.4.1 App

EU PoMS requires substantial data collection. This will be done by volunteers or professionals following a strict protocol and repeatedly visiting a specified location. Both volunteers and professionals would benefit from having a mobile-phone app available that can support these data collection efforts. The advantages of such an app are clear: it can streamline the data collection process and will allow for a better standardization because part of the registration burden (e.g. coordinate reference systems) can be automated. It also allows for quick merging and sharing of datasets as the app uploads data as soon as an internet connection becomes available. It will improve data quality, as data are quickly available allowing for quick validation and feedback to participants. Feedback does not solely consist of validation feedback but can also include personal statistics (such as their total number of observations), to improve participant engagement. Finally,

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[75] https://creativecommons.org/licenses/by/4.0

[76] https://butterfly-monitoring.net/

[77] https://ukpoms.org.uk/

it can also improve data quality by the inclusion of supplementary information to support verification (e.g. through photographs), and it can allow for the recording of precise times and GPS-tracks. Potentially the largest benefit is the outreach to citizen scientists, as easy-to-use recording and reporting tools are essential for building a stable, volunteer based, monitoring system.

In this section, we discuss the major considerations when developing an app platform, followed by our recommendations on how developing such an app can best be approached.

Use of a mobile-phone app for data collection, ©UKCEH

4.4.2 Infrastructure

An app generally consists of two components: 1) The software component that is installed on the phone (i.e. the app); and 2) The supporting infrastructure that allows the app to function. The development of the supporting infrastructure should not be underestimated, as it can easily rival the development effort of the app itself. This infrastructure consists of a central database, a web portal for data maintenance (allow users to manage their own data etc.) and an extensive API. Additionally, the web portal must also include a sophisticated administration sector, to help local administrators support users, validate incoming data, provide translations of the different systems, maintain up-to-date species lists and survey locations for each region etc. The infrastructure will not only require attention during development, but both the app and the infrastructure will require constant maintenance.

This infrastructure can be deployed centralized or separately by each country. The European Butterfly Monitoring Scheme showed that when developing a pan European monitoring scheme, the national identity is of great importance to the recorders. It is essential to avoid the feeling of a top-down implemented methodology by 'Europe'. This is an argument to run separate National schemes and combine their data in a central system afterwards. However, this would require each country to set-up and continuously maintain their own system. This will involve considerable development and maintenance costs and this approach would still require a comprehensive central system where the data are collected.

Therefore, the best approach seems to be to develop a comprehensive central system that offers all desired functionality and make accessing and modifying these data possible both directly and through a series of APIs. Countries are encouraged to use the central system directly, but countries with existing schemes or with a strong desire to build their own system, can connect using the API's. To maintain the momentum of the national schemes, national coordinators should have the opportunity to express their own national culture by altering the appearance of their national monitoring scheme sector of the website, to reflect their national identity. Hybrid approaches are also conceivable, for example, a prebuilt web-package can be made available to countries. By deploying this package, they can easily create their own web portal. This will significantly decrease development costs and give the national coordinator complete control of the system. However, changing, updating, and maintaining this system would be expensive, and the responsibility of the individual country.

A full list of desired app components can be found in Annex 4. B and the full list of identified apps can be found in Annex 4. C.

4.4.3 Target audience

The approach towards app development strongly depends on the target audience. A more volunteer-based system will require a more accessible way of data collection but should also provide more feedback and more methodological support. For a European system, an app should cater to both volunteer and professional contributors. As in some regions in the early phase of EU PoMS (mostly western Europe), the monitoring scheme is likely to have a large contribution from volunteers, but in other regions much of the work will have to be done by professionals initially, but with the ambition to shift towards a greater contribution by volunteers in the longer-term.

Therefore, the app will have to be developed with both groups in mind, for example by providing a separate layout for each group or including user settings that allow users to choose their own data collection mode (e.g. show scientific names). Feedback (e.g. 'this species is unlikely to occur in your current region') and methodological support should be provided but it should be possible to disable them.

It should be noted that national differences in local conditions (such as species abundance) will affect how users will want to use an app. This should be incorporated in the design process.

4.4.4 New development or cooperation

There are currently several apps available that allow recording of biodiversity data, some are part of existing monitoring schemes, while others allow users to store opportunistic observations or assist with species identification. Instead of developing a new app, it is also possible to link up with an existing system.

The development of a completely new app has the major advantage that the app can be tailor made to support EU PoMS, whereas with other apps there is always the risk that the added support feels like a post-hoc add-on. A tailor-made solution increases the chances of the app being widely used. Developing a new app also increases the continuation stability, as the app is less likely to require major upgrades in the near future. Although it will require continued maintenance, and major upgrades after several years.

Another advantage of developing a new app is that it provides a good option for countries where app availability is limited (mostly eastern Europe). Although apps designed for other regions of Europe can function here, they often do not offer localized species lists, translations etc. In eastern Europe it might be less beneficial to cooperate with existing apps, as app usage to collect biodiversity data are less prevalent. In this region, a new app would likely have a bigger impact than cooperating with existing apps, and for some regions the only way to provide an app at all. In western Europe a new app would certainly be seen as competition and to gain a large user base a new app would have to convince people who are currently invested in another system to either switch or use two systems simultaneously. Many potential users would likely stick with their existing system.

There are currently no apps that can completely support the EU PoMS network; hence it seems likely that the developers of one or several of these systems would have to be financially stimulated to implement support for the EU PoMS protocols.

This approach would allow potential volunteers to keep using the app they are already used to and avoid a situation where a newly developed app would have to compete with existing apps. By supporting several large existing apps, a potentially very large group of volunteers can be reached with limited effort. For professionals this is less relevant, as they can be required to use a specific system.

Cooperating with existing apps would also reduce the development and maintenance costs, as for most apps there will already be a development and maintenance strategy available. However, this does decrease continuation certainty, as third-party app developers might not view EU PoMS as a priority and hence can terminate support, terminate specific components, or terminate the app entirely. This can be somewhat mitigated by Service Level Agreements (SLA), to ensure long-term support. However, there are many examples where developers create a functional component that fulfils the requirements but that is clearly an add-on to an otherwise well-thought-out system. This is because integration with the look and feel of the rest of the app is difficult to quantify and hence enforce through a contract.

Therefore, we recommend that, although extensive SLA's will be required, parties with a vested interest and similar monitoring systems should be prioritised when selecting third party apps to support.

To get a better understanding of the currently available systems and their suitability for EU PoMS we first made a list of desired components and their relative importance (this list can be found in

Annex 4. B). We then sent out a survey to all relevant STING[78] (Science and Technology for Pollinating Insects) and SPRING[79] (Strengthening Pollinator Recovery through Indicators and Monitoring) project experts asking to list apps that are used in their region. For each reported app, we listed if they implemented the desired components, and hence how suitable the app is for EU PoMS. Building an overview of the available apps is a difficult task, and the resulting list is likely incomplete. Collecting information on the inner workings of these apps was especially difficult. Several apps are still in development while several promising looking apps appear no longer be actively developed.

The results of our inquiry are reported at the end of this section (Annex 4. C), but due to the great difficulty we had collecting this information, they should be primarily used as an indication of the capability of these apps. Based on our current data we can only conclude that putting together a complete overview of relevant apps will be very challenging and time consuming, we therefore propose a grant structure where third party developers can apply for a small grant to implement the EU PoMS API. This makes our system somewhat independent of the current app landscape.

We therefore recommend both developing a new app and cooperating with existing apps, to maximize the impact of EU PoMS. It is important to note that the support structures will have to be newly developed and continuously maintained either way, and either way will have to be designed for both professional and volunteer users. We recommend maintaining this approach for the duration of EU PoMS, as new apps will continuously appear. Each of these can access our system through API and allow volunteers to collect data for EU PoMS.

These support structures should contain an extensive API to allow third party developers easy access to the central EU PoMS system, including accessing translations, species lists etc. This will lighten the workload to implement the EU PoMS protocols significantly, and decrease the investment required to implement the EU PoMS system in a third-party system, which decreases the risk if a third-party app decide to stop development.

Instead of approaching the apps, we have now identified as promising we recommend making funds available and allow third party apps to apply for a grant. Likely, a relatively small grant equivalent to 10-20 days labour should suffice for most apps. Funds should also be made available for maintenance of these third-party systems after the initial investment, depending on the system this will likely be around 5-10 days annually. We expect no more than ten parties to be interested, but as we have only a limited overview of the available apps, there might be more interest.

Prime apps that should be made aware of this option are ButterflyCount (eBMS), iNaturalist, Spipoll and ObsMap. Their applications should still be carefully weighed as several of these are currently focused on collecting opportunistic data, instead of repeated monitoring and not all are not located in the European Union.

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[78] https://knowledge4policy.ec.europa.eu/participatory-democracy/science-technology-pollinating-insects-sting_en

[79] https://pollinator-monitoring.net/

4.4.5 Recommendations

We recommend developing a single central comprehensive European data storage system where the EU PoMS data are stored and can be modified and maintained. This should consist of a database, a website where data can be entered and modified and an extensive API to access and modify data. This environment should provide sufficient flexibility for national schemes to implement their own national character (without affecting functionality). It should be possible for countries with an existing scheme, or a strong desire to develop a custom system, to connect with the central system using an API. However, usage of the central system for both data entry and data management is strongly preferred. This reduces development and maintenance costs and decreases the workload on a national level. The recommended structures, and the access options, are shown in Figure 4.4. 1.

This structure gives national schemes great flexibility: they can either use the central system directly, make their own section within the central system or use their own system entirely and connect to the central system using the API.

Both the central system and the interface system should be developed with volunteers and professionals in mind. These systems will require ongoing support and maintenance.

By developing an extensive API, it becomes relatively simple for third party developers to also connect with this system. This provides additional stability in every changing app landscape, and allow us to reach many volunteers. We therefore recommend that budget be allocated to supporting third party app developers in implementing the EU PoMS protocols and linking their systems with the new APIs. We further recommend a system where third-party app developers can apply for grants, instead of approaching specific app developers. This will ensure that we can also connect with new, or strongly localized, apps. This will also reduce the need for a comprehensive overview of the app landscape.

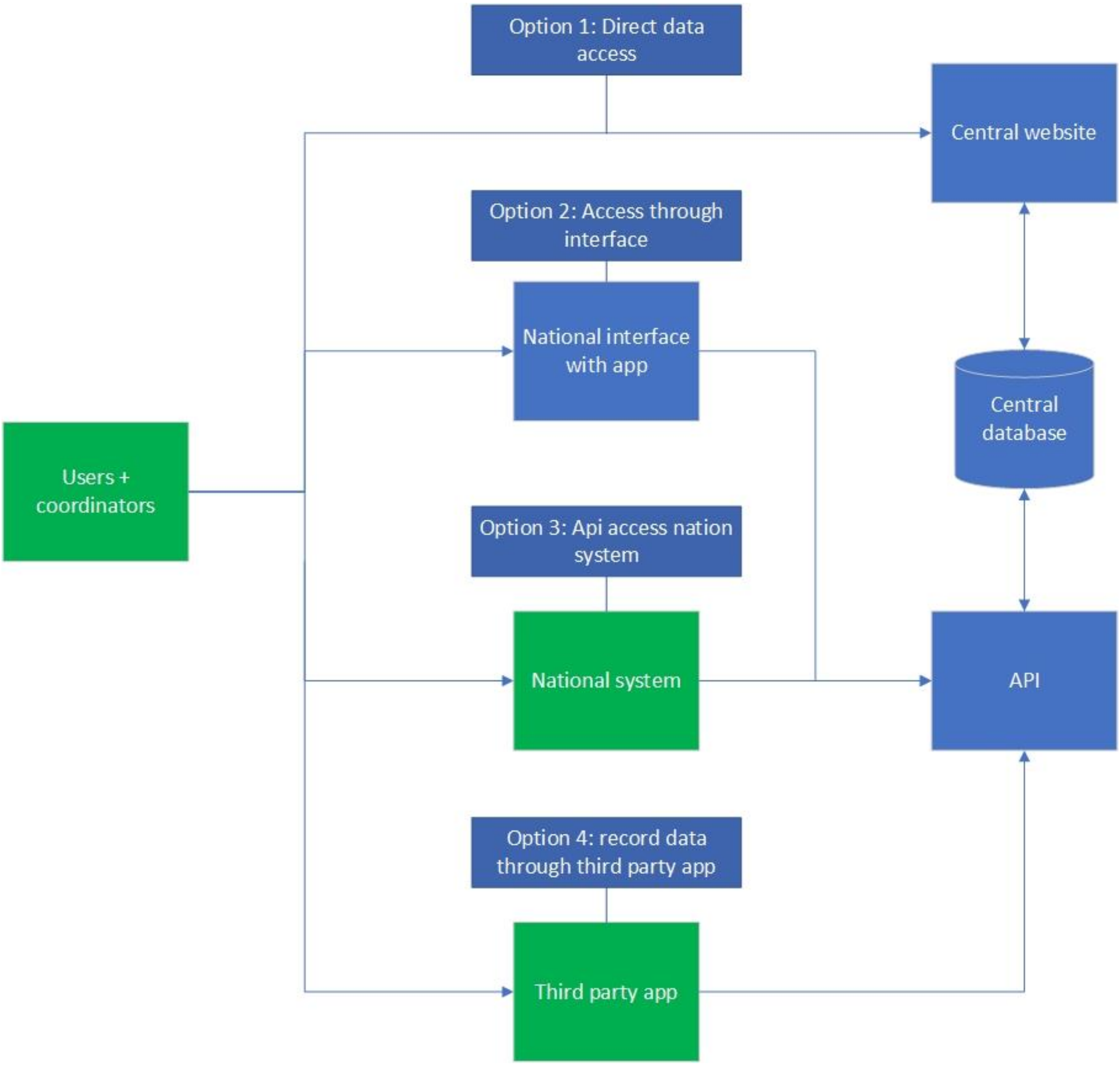
We do caution that a comprehensive description of work will be required, and the overall focus of the app developers is kept in mind. In a system solely focused on the identification of individuals or on the collection of opportunistic observations, a repeated visits based monitoring module can easily look out of place.

In addition to cooperation with third party app developers, we recommend developing a new app, to ensure that in countries where apps are not yet available in abundance, there is also the option to collect data through an app. Because we recommend developing an extensive API, building an app that just implements the EU PoMS systems should be simple and cheap. Although funds have to be allocated for continued maintenance.

The app and surrounding infrastructure are strongly linked to the supporting database (see section 4.5). We recommend to cluster database, app, and infrastructure development to facilitate integration. When development starts, a set of technical requirements should be compiled and a single party should be tasked with implementing all three components. Additionally, we recommend that the development team is supported by an ecologist. There are many small details that are difficult to capture in technical requirement documentation, which an ecologist will be able to clarify. This support could be organised through a group of experienced fieldworkers and data analysts. Input from fieldworkers and data analysist is not strictly necessary but will likely streamline the process and improve the final product. When the app is ready to be tested, experts of different regions need to be involved.

We further recommend that the system be continuously developed. Many wishes and problems will only become apparent after the testing phase. Therefore, several years of continuous development will be required; many existing apps are continuously developed throughout their lifetime. Resources should be allocated to allow for continuous development.

Figure 4.4. 1. Recommendations for data acquisition. Create a central database with an extensive API and central website. National schemes can access this system directly (option 1). A national coordinator can also decide to set up a custom appearance for the central website (option 2), to provide the same functionality with a national character. When a country already has a recording scheme set-up, they can also link in with the central system through the API (option 3). The fourth option is to use a third-party app and send the collected data to the central system using the API. Green items are external, blue items are internal systems that will require maintenance.



Source: Authors' elaboration.

4.4.6 Data sheet

Although we encourage users to directly input data through the app or into the web portal (for users without smartphone), we also offer the possibility to upload CSV data. Mainly to facilitate the processing of pan trapping data in the lab. The use of other systems (e.g. Excel) to store transect data, or metadata should be strongly discouraged. These csv files are according to a predefined structure (a properly formatted empty file should be available on the website). This template includes fixed entities, enforced data types, formats, and a predetermined vocabulary. Before accepting these data into the database, it has to be rigorously (automatically) checked by the API. The website will accept only CSV data, but several tools can be made available for proprietary systems (Excel) to help format data properly. However, all checking must be independently (as well) by the API.


Ochlodes sylvanus, Axel Hochkirch

4.5 Data preservation

The establishment of a centralized online portal for EU PoMS is essential to the monitoring program. This platform would serve as a hub for preserving and validating monitoring data collected across European countries, facilitating the development of novel taxonomic tools, organizing training initiatives, harmonizing, and analysing data, and disseminating research outcomes.

4.5.1 Hardware infrastructure

To optimize pollinator monitoring data management in Europe, the implementation of a unified European cyberinfrastructure is crucial, despite the presence of individual data infrastructures in various European countries. The following technical reasons highlight the significance of this common infrastructure:

- **Centralized data storage and scalability**: the adoption of a common European cyberinfrastructure facilitates centralized data storage, reducing hardware and maintenance costs. This centralized approach promotes scalability by accommodating the increasing data volume. Additionally, it enables the seamless integration of new analytics tools and software updates, ensuring flexibility in implementation. Centralizing infrastructure eliminates the need for individual country-specific setup, which can be challenging due to variations in expertise and capacity among different countries.
- **Efficient data integration and interoperability**: centralizing infrastructure simplifies and expedites the integration of data across different countries (data stores under the same database), promotes interoperability and facilitates comprehensive analysis and modelling.
- **Consistent data governance and security**: by adopting a common data infrastructure, EU agencies can enforce consistent data governance policies, access controls via user management, compliance regulations, and centralized security measures. This ensures data integrity, confidentiality, and compliance with regulatory requirements, fostering trust among stakeholders.
- **Centralized data backup and disaster recovery**: the common database provided by the infrastructure offers centralized data backup and disaster recovery mechanisms. This robust system ensures higher data resiliency, minimizing the risk of data loss and enabling rapid recovery in the event of a disaster.

Recommended hardware infrastructure should incorporate several key components, including a **primary server**, a **mirror server**, a **test server**, and a **backup system**.

Primary server is the central and authoritative server that serves as primary source of data storage and data services. Given the increasing volume of data in the EU PoMS over time, it is strongly advisable to adopt a virtual server as the primary server to facilitate seamless scalability and streamline backup processes. Initially, data storage capacity can begin with a few terabytes and subsequently expand as the data size necessitates larger storage. As hardware costs continue to decrease annually, this approach offers significant cost savings.

Server mirroring aims create a fault tolerant and redundant server-computing infrastructure for performance continuity, disaster recovery and backup. Duplicating the entire contents of a server on another remote server allows data to be restored if the primary server fails. Therefore, the mirror server is required to have identical hardware and software configuration as the primary server, typically set up in a different geographical location or network from the primary server. Mirror servers can be used in load balancing configurations to evenly distribute incoming network traffic among multiple servers, better catering users in different regions. This helps prevent any single server from becoming overwhelmed with requests, improving the overall stability and scalability of the system.

A **test server** is a place where software or system updates, new features, and mechanics are tested before releasing to the primary server. It should have identical software configuration as the primary server but only accessible to developers and testers. It helps to mitigate risks associated with system changes or updates by providing an isolated space for experimentation, troubleshooting, and validation, contributing to the stability, reliability, and security of the overall system.

It is not sufficient to rely on the mirror server for backups, as this server has to be kept continuously up to date any error that is not immediately discovered will also propagate to the mirror server. We therefore recommend a comprehensive **backup system** where periodically (every 1-4 hours) a snapshot of the server is created. These snapshots can be in a rolling rotation (overwritten periodically, commonly used periods are 2-3 months), but should also periodically (e.g. weekly, monthly) be stored in long-term storage.

4.5.2 Software options

When building the data software infrastructure, there's no need to start from scratch, thanks to the existence of established best practices in the field, such as Indicia used by UK PoMS and BExIS used in Safeguard. To lay the foundation for the next phase, it is crucial to thoroughly evaluate and critically assess these existing data solutions (Table 4.5. 1). This evaluation should involve input from various stakeholder groups, incorporating insights gained from real-world implementations. The goal is to customize the data infrastructure to align with specific goals, requirements, and constraints of the EU PoMS.

To find the best option for the EU PoMS database, the following points should be considered:

- Is it an open-source project?
- Is it written in a language/framework that is likely to be supported in the future?
- Is it easily adaptable?
- Are there tutorials, or even better a consultation team, in case of questions during set-up, implementation, and further development?
- What is the deviation of its functionalities compared to the desired functionalities of EU PoMS database?
- Does it have role-based user management system, e.g. national coordinators can edit only data from their countries?
- Does it include metadata documentation?
- Does it support version control?
- Does it have an app for data submission?

— Does it have other modular functions such as online GIS (Geographic Information System), data validation, online data analysis and visualization?

— Does the host of European facility have existing experience with it?

Possible data solutions that meet the requirements of EU PoMS according to the assessment points above are listed below, while technical aspects such as programming language, database software, and so on, are listed in Table 4.5. 1.

Indicia

Indicia[80] is a flexible and cost-effective online recording system for wildlife records that simplifies the construction of websites for biological recording. It allows for easy and rapid data entry and provides support for photo uploads, reporting, mapping, and verification of records. It includes built-in components for data verification, viewing tables, charts, and maps of data, and allows for easy downloading of data in various formats. Indicia also supports multi-lingual websites and can be integrated into existing websites. It is often integrated with Drupal CMS to provide user and role management. It provides a mobile application for collecting data in the field. The Pollinator app iRecord, eBMS, FIT Count is integrated with Indicia. Indicia is an open source and community-owned project that is well-documented (https://indicia-docs.readthedocs.io/en/latest/) and available to download from GitHub. Indicia has been used by the UK Pollinator Monitoring Scheme and the SPRING project moth surveys.

BioCollect

BioCollect[81] is a web-based, feature-rich but simple-to-use tool designed for scientists, ecologists, citizen scientists and natural resource managers to collect and manage their biodiversity, ecological and natural resource management (NRM) data. BioCollect is being developed by the Atlas of Living Australia (ALA) in collaboration with other organizations, including SBDI (Swedish Biodiversity Data Infrastructure). BioCollect provides form-based structured data collection for: 1) Assessment and monitoring activities such as ad-hoc surveys and method-based systematic structured surveys; 2) Activity-based projects such as revegetation, rehabilitation or weed and pest management projects. BioCollect also allows upload of unstructured data in the form of data files, grey literature, images, sound bytes, and video links. BioCollect offers an app (BioCollect app) for data collection and a spatial portal for spatial navigation and searching.

BExIS 2

BEXIS 2[82] is an open-source software (LGPL 3.0) supporting researchers in managing their data throughout the entire data life cycle from data collection, documentation, processing, analysing, to data sharing and publishing. BEXIS 2 is a modular scalable platform suitable for working groups and collaborative project consortia with up to several hundred researchers. It has been designed to

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[80] http://www.indicia.org.uk

[81] https://www.ala.org.au/biocollect

[82] https://bexis2.github.io

meet the requirements of researchers in the field of biodiversity, but it is generic enough to serve other communities as well. BExIS 2 includes features such as data upload from portal as well as API, metadata documentation, user-based data permission management, faceted search, data structure reuse, versioning, data publication with DOIs. It has a professional development team[83] offering personal consultation besides live demo[84] and online tutorials[85]. BExIS 2 is widely used for research projects including EU H2020 project Safeguard and UPSCALE[86], as well as research institutes such as iDiv or University of Hohenheim (Chamanara et al., 2021).

DataVerse

The DataVerse[87] Project is a web application designed for sharing, preserving, citing, exploring, and analysing research data. It enables easy sharing of data with others and simplifies the process of replicating others' work. The platform is suitable for use by researchers, journals, data authors, publishers, data distributors, and affiliated institutions, all of whom can receive academic credit and web visibility. DataVerse supports a variety of data types such as datasets, tables, images, and documents, and offers users the option to share data under various access and reuse licenses. Its features include support for FAIR Data Principles, faceted search, data citation for datasets and files, customization of collections, standardized metadata formats, private URLs for reviewers to view unpublished datasets, APIs for interoperability and custom integrations, integration with DataCite and Single Sign-On (SSO) using institutional credentials, as well as versioning capabilities (Alexander et al., 2020).

FAIRDOM-SEEK

FAIRDOM-SEEK[88] is an open-source platform that enables sharing of diverse scientific research datasets, models, simulations, processes, and outcomes in a web-based catalogue. It maintains relationships among them and provides information on the people and organizations involved. The platform is built on the ISA infrastructure, which is a standard framework for describing experiments and their integration into broader studies and investigations. ISA has been extended within FAIRDOM-SEEK and configured to support non-biological data structures. Detailed and flexible sharing permissions are available to manage catalogued items from initial collaborations within projects to final research results publication, at which point individual items can be assigned a DOI or packaged as Research Objects. FAIRDOM-SEEK uses semantic technology that enables advanced searches and queries of content. Metadata can be collected using standard Excel tools and processes through the use of RightField (Wolstencroft et al., 2017).

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[83] https://bexis2.github.io/about/people

[84] https://demo.bexis2.uni-jena.de

[85] https://bexis2.github.io/resources/manuals

[86] https://upscale-h2020.eu/

[87] https://dataverse.org

[88] https://seek4science.org

ReportNet 3

Reportnet 3[89] is the new e-Reporting platform for reporting environmental and climate data to the European Environment Agency (EEA). The platform embraces the strategic goals of the European Commission's Green Deal and Digital Strategy and hosts reporting tasks on behalf of EEA and the Commission. ReportNet 3 provides a web-based interface for creating and managing reports, as well as for delivering them to end-users. It offers a range of features and capabilities, including Report creation and design, Data connectivity, Report distribution and delivery, and Security and access control. ReportNet 3 uses metadata to define and manage data sources, data models, and report layouts. It supports version control for reports and metadata objects. It has been applied in EEA as the data solutions for WISE (Water Information System for Europe).

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[89] https://reportnet.europa.eu

Table 4.5. 1. Technical entities of Data solutions.

Software	**Indicia**	**BioCollect**	**BExIS 2**	**DataVerse**	**FAIRDOM-SEEK**	**ReportNet 3**
Country	UK	Australia	Germany	US	UK	Europe
Open source	yes	yes	yes	yes	yes	no
Programming language	PHP	Groovy	C#	Java	Ruby on Rails	NA
Database software	PostgreSQL	PostgreSQL	PostgreSQL	PostgreSQL	PostgreSQL	NA
User management	yes, through Drupal CMS	yes	yes	yes	yes	yes
Metadata	yes	yes	yes	yes	yes	yes
Version control	yes	yes	yes	yes	yes	yes
App	yes	yes	no	no	no	no
Map portal	yes	yes	possible	no	no	no
EU experience	no	no	no	no	no	yes
Focus	monitoring data	monitoring data	biodiversity data	Multidisciplinary research data	ecology, genetics, bioinformatics	Environmental reports

Software	Indicia	BioCollect	BExIS 2	DataVerse	FAIRDOM-SEEK	ReportNet 3
Assistance	online tutorial, forum, live chat	Contact person	tutorials, demo, personal consultation from the developers	online tutorial	online tutorial, demo	helpdesk
Instance	eBMS, iRecord, erccis, FIT Count, UK PoMS	SBDI, Atlas of Living Australia	Safeguard, UPSCALE, Biodiversity Exploratories, iDiv, Jena Experiment, KiLi, LandKliF, AquaDiva	Harvard University, Göttingen Research Online	EMBL-EBI, University of Manchester, University of Oxford	WISE
Source code	https://github.com/Indicia-Team	https://github.com/biodiversitydata-se/biocollect	https://bexis2.github.io	https://github.com/IQSS/dataverse	https://github.com/seek4science/seek	NA

Source: Authors' elaboration.

4.6 Web interface

A universal intuitive web interface will be developed and published as the access point of online data portal for EU PoMS. This website should be secure and properly maintained. Within this website, each participating country will have its own subpage, referred to as the national data portal. For small countries that have limited taxonomic expertise or small data sizes, several countries could voluntarily join forces to establish a cluster data portal, e.g. Luxembourg and Belgium can share a common data portal. This collaborative approach allows for the pooling of resources, expertise, and data, enabling more efficient and comprehensive data sharing and utilization within the region. Nevertheless, it is important to acknowledge that cluster portals may encounter challenges related to potentially diminishing the national role and demotivating the commitment of participants.

To enhance user experience and familiarity, the web interface should strive for simplicity and intuitiveness. It is recommended to align the interface design as closely as possible with the INSPIRE[90] knowledge base since it shares a similar architecture. This approach ensures a consistent user experience and leverages the existing familiarity of both the EU Commission and European Member States with the INSPIRE interface. It should further include responsive design, clear navigation, and touch-friendly exercise to ensure a mobile friendly experience.

4.6.1 User management

There are mainly 8 groups of stakeholders who will be actively updating EU PoMS database, their roles and responsibilities related to data management are listed here:

EU data coordinator(s): coordinating overall data management workflow for entire EU PoMS; designing, development, and maintenance of EU PoMS database; helpdesk for national data coordinators; updating species referencing table, approval of national data; data publishing, producing data report; result dissemination to all stakeholders especially to EU policy makers.

EU software developers: designing, development, testing, and maintenance of EU PoMS database; developing new functionalities in response to evolving technology and user requirements; conducting hardware maintenance, expanding storage capacity, and performing disaster recovery as needed.

EU model experts: designing scripts to automate data validation and harmonization; developing models to transform monitoring data into different biodiversity indicators; upload/update modelled data; data visualization and publishing, producing data report, result dissemination especially through scientific publications.

National data coordinators: coordinating overall data management workflow for respective national monitoring scheme; first and second validation of national data, translation into universal language; report to EU data coordinator about challenges and requirements from national data management; result dissemination to all stakeholders especially to national policy makers. The national coordinator provides support to the national experts and volunteers. When a request for

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[90] https://inspire.ec.europa.eu

support cannot be addressed by the national coordinator, the national coordinator can request further assistance from the EU data coordinator.

National taxonomic experts: uploading national monitoring data, second validation of national data, updating species referencing tables.

National data curator(s): first validation of national data, translation into universal language, helpdesk for national volunteers.

National super volunteers: coordinate multiple sampling sites and manage data from several other national volunteers, be able to upload/edit data from these people but not others.

National volunteers: uploading national monitoring data, feedback to national data curators.

The data portal infrastructure should include comprehensive user management according to the roles of the 8 groups of users, incorporating authentication mechanisms. For example, upon successful login, users will be authenticated and seamlessly redirected to their respective national data portal, ensuring a smooth and direct access to the relevant platform tailored to their specific identity.

The national data coordinators, curators, and taxonomic experts will have all data management rights and full access to their national data within their respective national data portal. This ensures that they can carry out the entire national data management workflow seamlessly within their dedicated portals, thereby alleviating the workload at the EU level. However, they will not be granted access rights to other countries' national data. National volunteers will be limited to uploading data solely to their national portal and will have access only to the data they have uploaded themselves.

EU data coordinator(s) and EU software developers will be granted with complete rights and unrestricted access to all national data, allowing for comprehensive data exploration, harmonization, integration, and modelling across multiple countries.

4.6.2 Components

It is essential to seamlessly consolidate all services offered by the EU PoMS into a single portal/website to enhance accessibility and promote efficiency. This unified platform should encompass various essential components, including:

- **Introduction**: an informative sector providing an overview of the EU PoMS, encompassing schemes, methods, and materials utilized, displaying partners involved, acknowledgments, and providing links to related initiatives.
- **Document centre**: a centralized document repository for downloading Standard Operating Procedures (SOPs), metadata schema, data template sheets, and mobile applications (apps).
- **Media and news**: a sector featuring multimedia content and updates related to the EU PoMS, such as news articles, press releases, sampling activities, and relevant media resources.
- **Tutorials and training**: a resourceful area hosting online tutorials, training materials, online training courses.
- **Login page**: an access point for registered users, allowing them to log in securely and access personalized features and functionalities.

- **User-specific information page**: a page where information on the transects/sites linked to a specific user is available (how many years has it been counted, what protocol is in use, where is it located etc.). This will make it easier to introduce a new recorder to a specific data collection location.
- **Data entry**: a page where volunteers can enter new data manually or edit existing data (providing standardized data validation-update mechanisms with version control).
- **File upload page**: a dedicated interface where the upload of CSV file is enabled, and automatic 1st level validation is taking place.
- **Photo overview page**: volunteers have the option to upload photos to enable validation of their observations. The status of these should be made available.
- **Data download page**: this page provides download of yearly EU monitoring data. It also enables users to explore data through online mapping capabilities and faced search to download spatial-specific / taxon-specific / temporal-specific monitoring data. Additionally, it will offer collective, swift download of multi-year, multi-country data (both monitoring data and modelled data). The download button should be readily visible and prominently displayed on the page, ensuring ease of access for users to locate and initiate the download process.
- **Data report page**: a sector offering generated annual data, providing optimally online visualization for indicators to support decision-making processes.

Colletes daviesanus, Axel Hochkirch

4.7 Database structure

The envisioned database is based on the core scheme, and would encompass monitoring data pertaining to bees, butterflies, and hoverflies, including data collected by both taxonomic experts and volunteers. In the future it would further incorporate additional modules for rare and threaten species and moth data. Moreover, the database would feature a dedicated module for harmonized modelling data, ensuring a comprehensive platform for data exploration. Below is an example of a possible database structure, the actual structure will have to be finalized during development, as challenges inevitably arise during development.

4.7.1 Database modules

The proposed database will include 4 schemas: User management (table User, Right, Nation, UsersWithRights), Sampling event (table Recorder, Site, Event), Identification (table Observation, Specimen, Photo), and Reference data (table Species, CommonName, Distribution). The content of each table is listed as follows:

User management:

- **User**: identifier of the registered user, login information for EU PoMS database, contact information of the user. In case it is a shared account, contact information will be from the key contributor.
- **Right**: identifier of the right, role of the user (e.g. National volunteers or EU model experts, see section 4.6.1 User management), nation (linking to table Nation), right (read-only/upload & edit right to this specific nation).
- **Nation**: a specific country or a country cluster (e.g. Luxembourg and Belgium as one country cluster).
- **UsersWithRights**: identifier of the user, identifier of the right.

Sampling event:

- **Recorder**: identifier of the recorder (identical as UserID in table User), number of sampling events he/she has uploaded, recorder accuracy (the proportion of expert-verified records correctly identified by recorders), recorder success (the proportion of recorder-submitted identifications confirmed correct by verifiers) (Falk et al., 2019).
- **Site**: identifier of the sampling site, LUCAS (Land Use/Cover Area frame Survey, (d'Andrimont et al., 2020)) identifier (POINT_ID) if it is based on LUCAS site, nation (linking to table Nation), geometry in graphical and projected coordinate systems, location name for easy navigation, land cover information, soil property.
- **Event**: identifier of sampling event, identifier of the recorder (linking to table Recorder), identifier of the sampling site (linking to table Site), sampling method (including detailed sampling protocol), time stamp when the event is taking place, climate conditions at the sampling event, estimated flower richness at the sampling event, estimated flower cover at the sampling event, upload timestamp.

Identification:

- **Observation**: identifier of the observation (species identification), identifier of sampling event (linking to table Event), identifier of species (linking to table Species), version ID (0 for deleted/obsolete, 1 for raw data, 2 for 1st validation, 3 for 2nd validation, 4 for accepted by EU), abundance of the species (if available), ShouldDownscale (Y/N, if this record need to downscale precision to protect endangered species, e.g. make the geolocation with lower resolution), data entry timestamp, data upload timestamp, data update timestamp (update during data validation), update reason, update person (identifier of user who makes the update).
- **Specimen**: identifier of the specimen identified and preserved in museums, identifier of the observation (linking to table Observation), version ID, name of the museum, specific location of the preserved specimen in museum, preservation timestamp, update timestamp.
- **Photo**: identifier of the photo, identifier of observation (linking to table Observation), version ID, upload timestamp.

Reference data:

- **Species**: identifier of species, version ID, taxon group (bees/butterfly/hoverfly/moth), species name, genus, subfamily, family, upload timestamp, update timestamp (update after taxonomic revisions), update reason, update person (identifier of user who makes the update).
- **CommonName**: identifier of species (linking to table Species), version ID, language, common name, upload time stamp, update timestamp, update reason, update person.
- **Distribution** (spatial table): identifier of species (linking to table Species), version ID, geometry of distribution map, upload timestamp, update timestamp (distribution map update due to climate and land use change, taxonomic revisions), update reason, update person (identifier of user who makes the update).

4.7.2 Species referencing table

It is essential to use constant timeless species name across datasets in EU PoMS but in practice, it is very complex to apply. Species names in taxonomy could change over time due to taxonomic revisions resulting in splitting or merging species, repositioning within the taxonomic hierarchy. Furthermore, there are taxonomic synonyms and discovery of new species, which need to be taken into account. The EU PoMS database should establish a species-referencing table (table Species under schema Reference data in section 4.7.1 Database modules) for standardizing nomenclature to ensure data consistency and accuracy. Information on synonymy and the mapping to common (species) names in different languages should also be provided (table CommonName under schema Reference data in section 4.7.1 Database modules). All other input that includes species information must undergo validation against this referencing table. It is important that this table reflect the most accurate and up-to-date species list, and their taxonomic classification. The species checklist could be built from checklist offered by Catalog of Life[91] (COL), national taxonomic databases e.g. the Dutch Species Register (NSR), national/European red list, checklist

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[91] https://www.catalogueoflife.org

from national monitoring facilities, Global Biodiversity Information Facility[92] (GBIF), as well as newly published data papers and books from EU pollinator research projects such as Safeguard[93], ORBIT[94], TaxoFly[95], STEP[96] and so on. The new annotated checklist of the wild bees of Europe (*Hymenoptera*: *Anthophila*) is published recently (Ghisbain et al., 2023). A European checklist is included in the European Red List of bees (Nieto et al., 2014), with an update published in 2017 (Rasmont et al., 2017). A European Red List of butterflies is published in 2010 (van Swaay et al., 2010). A new manuscript entitled "National records of 3000 European bee and hoverfly species - a contribution to pollinator conservation" includes most updated checklist and distribution maps of European bees and hoverflies (Reverté et al., 2023).

It is noteworthy that the species-referencing table must exhibit flexibility to accommodate cluster species or species complexes (collection of species that may not always be distinguishable in situ yet are known to belong to the same group). For example, *Bombus terrestris*, *lucorum*, *magnus* and *cryptarum*. These groups should be considered and added to the existing lists.

Similarly, a spatial species-referencing table (spatial table Distribution under schema Reference data in section 4.7.1 Database modules) should be established with species distribution map, which would be used to (optimally automatically) validate species identification. The distribution map could be built from literature, newly published data papers or research project deliverables (such as deliverable 1.1 Open database on distributional information on European pollinators of the Safeguard project), as well as spatial information of validated input from the monitoring scheme. Both species referencing tables should be updated continuously, at least annually, by taxonomic experts from each country as well as by the EU data coordinator.

4.7.3 Data validation workflow

A two-step validation system should be implemented to make sure the data are correctly identified, accurate and consistent. Further step of sensitive data downscaling, anonymization and translation would take place after data validation to make sure the corresponding regulations such as GDPR are respected. The entire validation procedure is illustrated in Figure 4.2. 1**.**

4.7.3.1 First data validation

When field data are entered in the national data portal (either via app or website), national data curators will implement the first data validation. This first validation procedure includes the following two steps: (i) identifying and correcting wrong data formats and mismatching attribute types, (ii) identifying and handling outliers, typos, duplications, missing values, inconsistencies. Standardized scripts need to be developed to automate this procedure. Version control will be employed in each step that include a timestamp and a brief description for the update. This allows the national coordinators to keep track of changes made by other members. After successful

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[92] https://www.gbif.org

[93] https://www.safeguard.biozentrum.uni-wuerzburg.de

[94] https://orbit-project.eu

[95] https://www.luomus.fi/en/taxo-fly

[96] http://www.step-project.net

validation, the version ID of table Observation under schema Identification (see section 4.7.1 Database modules) is updated from 1 (raw data) to 2 (1st validation).

4.7.3.2 Second data validation

After the first validation, taxonomic experts from each national portal will perform the second validation whether species are correctly identified. This validation procedure includes:

- Check photographs submitted and verify species identification.
- Check species distribution map and identify obvious outliers.
- Check specimen if sample is available (optional).
- DNA sequencing of specimen (optional).

Clear validation rules would need to be established as SOPs, and each species record could be flagged with a traffic-light system (see Figure 4.2. 1). All records with a red flag would be validated; for records flagged in yellow, a random subset would be validated; records with a green flag are regarded as validated. After validation, recorder accuracy and recorder success will be updated in the recorder table (see table Recorder under schema Sampling event in section 4.7.1 Database modules). Version control will be implemented in the second validation.

These rules should be considered for **assignment of the colour flag**, for example:

1. **Distribution of the taxon**: records from outside the known range of a taxon (e.g. comparing with distribution maps in spatial species referencing table) with significant deviation should automatically be flagged in red, deviation limit is determined considering climate change, land use change, and local rare species. Ideally, standardized script could be developed to automate this procedure.
2. **The commonness of the taxon**: species would be given regional rarity scores and records of very rare species flagged red, rare species yellow, common species green.
3. **Phenology**: records outside the typical season of a species should be flagged in red, at the edge of the season in yellow, with consideration of climate and land use change. Optimally, a standardized script should be created to streamline this process through automation.
4. **The experience and successful rate of the recorder**: every recorder has a profile in the recorder table (see table Recorder under schema Sampling event in section 4.7.1 Database modules), which documents the number of sampling events submitted to EU PoMS, the records accuracy rate and the records success rate (methodology defined in (Falk et al., 2019)). Data from recorders who have little experience (low number of sampling events), or a high error rate would be flagged correspondingly in red or yellow. Standardized scripts will be developed to automate this procedure. In case of red flag and the recorder did not provide any photo for validation, the submitted data could be discarded. If the recorder with high error rate were a trained taxonomic expert, they would be asked to attend the training course again.

After successful validation, the version ID of table Observation under schema Identification (see section 4.7.1 Database modules) is updated from 2 (1st validation) to 3 (2nd validation).

4.7.4 Data downscaling, anonymization, and publication

After second validation, the national data will become validated. At this stage, the national data encompasses the entirety of the collected information. However, a series of procedures need to take place before the data becomes final and openly accessible.

First of all, an automatic standardized procedure would take place to downscale resolution if *ShouldDownscale* field is set to yes in table Observation under schema Identification in section 4.7.1 Database modules. Standard scripts need to be developed together by national data coordinators, national taxonomic experts, and EU model experts, as the downscaling could be species- or location-specific. As EU PoMS will include a rare and threatened species module in the core scheme, this step is critical to protect the geolocation of the rare species, especially when they appear outside of the protected area.

Another automatic procedure is anonymizing personal data of voluntary recorders according to GDPR before data publishing.

If local language is used in the national data, the national data curator will perform the translation of local language into universal language with help of AI-based machine translation service such as DeepL. For fixed vocabulary (see section 4.3.3 Standard terms), the translation should be done and agreed by the national data coordinators prior to the data collection. An automated procedure will be initiated, wherein this pre-established translation is applied.

Finally, the national data will be reviewed and accepted by the EU data coordinator(s) via the European data portal. After acceptance, the version ID of table Observation under schema Identification (see section 4.7.1 Database modules) is updated from 3 (2nd validation) to 4 (accepted by EU).

After data acceptance of all Member States, a complete EU dataset of that year will be generated via data extraction (only when version ID is 4 and sampling event happens that year) and data consolidation of all tables in the 4 schemas (see section 4.7.1 Database modules) by automated standard scripts. This dataset will be exported into CSV format together with metadata and will be published by the EU data coordinator(s). This dataset should be openly accessible with citable (yearly) DOIs under CC-BY-4.0 license. Download of this dataset should be made abundantly available and prominently displayed in the European online data portal.

In addition, multi-year data download and user-specific-generated download should be made available. Specific data extraction, consolidation and export will be executed on the cloud by automated, standard scripts (see Data Download page in section 4.6.2 Components).

Modelled data will be produced based on the observation data and be made available afterwards by the EU model experts. Download and publishing of modelled data should follow the same procedure of the monitoring data (data extraction, data consolidation and publishing).

4.7.5 Next steps

In addition to reinforced transects, the core scheme also includes modules for rare and threatened species (see section 2.8) and moths (see section 2.9). The current data schema design (see section 4.7.1 Database modules) is modular and could be flexibly adapted and extended to store data coming from complementary approaches, e.g. new sampling methods and site information. For instance, sampling sites for RaTS will likely be species specific and so would need to be set up in the schema Sampling event, while schema User management, Identification, and Reference data could directly receive new data without structural changes (see 4.7.1 Database modules).

Additional modules such as pollination services, flower visitors, insect biodiversity could be further incorporated in the future, providing the core scheme of EU PoMS is carried out successfully and continuously. The database would develop new modules to receive and validate these new sets of data.

Genetic information could be further integrated in the schema Reference data (see section 4.7.1 Database modules). For every species in table Species under schema Reference table, it will then contain validated genetic information, taxonomic information, data on geographical distribution, and where available, abundance data and feature images by linking table Observation and Photo in schema Identification. Establishment of a new sequencing facility as well as collaboration with European genomic databases such as Biodiversity Genomics Europe[97] (BGE), European Reference Genome Atlas[98] (ERGA) or BIOSCAN Europe[99] are needed for this enhancement.

In addition to incorporating new data, future implementations in EU PoMS will involve the application of emerging technologies (section 5.2) for both monitoring and data management purposes. Particularly, the integration of AI-based image recognition for species identification is anticipated to significantly enhance efficiency and reduce the personnel costs associated with the second data validation procedure (see section 4.7.3.2 Second data validation). A seamless automatic data flow will be engineered to accommodate these novel technologies. The EU data coordinator(s) and software developers will thoroughly investigate and assess successful existing infrastructures, such as the ARISE project[100], which provides AI-based near-real-time species identification services. These exemplary models will serve as a basis for the implementation of an automatic data flow that integrates these new technologies.

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[97] https://biodiversitygenomics.eu

[98] https://www.erga-biodiversity.eu

[99] https://www.bioscaneurope.org

[100] https://www.arise-biodiversity.nl

Annex 4. A. Glossary

AI: artificial intelligence

ALA: Atlas of Living Australia (ALA) is an online repository of information about Australian plants, animals, and fungi, started in 2006.

API: an Application Programming Interface (API) is a way for multiple computer programs to communicate with each other.

App: a software application specialized programmed for mobile devices.

ARISE: ARISE project is aimed to offer an organized overview of all multicellular life in the Netherlands and the infrastructure to semi-automatically identify all these species.

BIOSCAN Europe: a shared European perspective and framework for effective DNA-based biodiversity monitoring, connecting and enhancing national DNA barcoding infrastructures and initiatives, establishing the European node of iBOL (International Barcode of Life) as a hub for DNA-based biomonitoring.

BGE: Biodiversity Genomics Europe, aims to accelerate the use of genomic science to enhance understanding of biodiversity, monitor biodiversity change, and guide interventions to address its decline.

CC-BY-4.0: Creative Commons Attribution 4.0 International (CC-BY-4.0). Recipients redistributing the work must give credit to the original author of the work (= attribution) and state changes if any, including a URL or link to the original work, this CC-BY licence and a copyright notice. Author can request to remove any attribution given information. Recipients re-distributing the work to third parties may not apply legal terms or technological measures (like Tivoisation) that legally restrict the rights granted by the licence. OKF (Open Knowledge Foundation) recommends this licence. The European Commission has adopted CC-BY-4.0 for sharing documents.

COL: The Catalogue of Life is an online database that provides an index of known species of animals, plants, fungi, and microorganisms. It was created in 2001 as a partnership between the global Species 2000 and the American Integrated Taxonomic Information System.

Creative Commons license: Creative Commons is the nonprofit behind the open licenses and other legal tools that allow creators to share their work. A Creative Commons license is one of several public copyright licenses that enable the free distribution of an otherwise copyrighted "work". A CC license is used when an author wants to give other people the right to share, use, and build upon a work that the author has created.

CSV: A CSV (comma-separated values) file is a text file that has a specific format that allows data to be saved in a table-structured format.

Darwin Core: Darwin Core is an extension of Dublin Core for biodiversity informatics. It is meant to provide a stable standard reference for sharing information on biological diversity.

Darwin Core Archive: Darwin Core Archive is a biodiversity informatics data standard that makes use of the Darwin Core terms to produce a single, self-contained dataset for species occurrence, checklist, sampling event or material sample data.

DataCite: DataCite is an international not-for-profit organization which aims to improve data citation to establish easier access to research data on the Internet, increase acceptance of research data as legitimate and citable contributions to the scholarly record, as well as support data archiving that will permit results to be verified and re-purposed for future study.

DG ENV: The Directorate-General for the Environment (DG ENV) is one of the more than 40 Directorates-General and services that make up the European Commission. Commonly referred to as DG Environment, the objective of the Directorate-General is to protect, preserve and improve the environment for present and future generations.

DMP: Data Management Plan (DMP) describes the data management life cycle for the data to be collected, processed and/or generated by a Horizon 2020 project. A DMP is required for all projects participating in the extended ORD pilot.

DOI: Digital Object Identifier, persistent identifier to uniquely identify various objects, standardized by the International Organization for Standardization (ISO).

Dublin Core: The Dublin Core, also known as the Dublin Core Metadata Element Set, is a set of fifteen main metadata items for describing digital or physical resources.

eBMS: European Butterfly Monitoring Scheme (eBMS) is a joint initiative of Butterfly Conservation Europe and the Centre for Ecology & Hydrology. It is a collation of national Butterfly Monitoring Scheme datasets within Europe, a data system for establishing butterfly monitoring sites in regions currently lacking a national scheme, and the home for the Assessing Butterflies in Europe (ABLE) project.

ECA: European Court of Auditors.

EEA: European Environment Agency.

EML: The Ecological Metadata Language (EML) defines a comprehensive vocabulary and a readable XML markup syntax for documenting research data mostly from earth and environmental science.

ERGA: The European Reference Genome Atlas (ERGA) initiative is a pan-European scientific response to current threats to biodiversity. It aims to sequence reference-quality genomes for all European species.

EU data coordinator: one of 8 stakeholders who actively update EU PoMS database. Its main tasks include coordinating overall data management workflow for entire EU PoMS; designing, development, and maintenance of EU PoMS database; helpdesk for national data coordinators; updating species referencing table, approval of national data; data publishing, producing data report; result dissemination to all stakeholders especially to EU policy makers.

EU model expert: one of 8 stakeholders who actively update EU PoMS database. Its main tasks include designing scripts to automate data validation and harmonization; developing models to transform monitoring data into different biodiversity indicators; upload/update modelled data; data visualization and publishing, producing data report, result dissemination especially through scientific publications.

EU PoMS: EU Pollinator Monitoring Scheme.

EU software developer: one of 8 stakeholders who actively update EU PoMS database. Its main tasks include designing, development, testing, and maintenance of EU PoMS database; developing new functionalities in response to evolving technology and user requirements; conducting hardware maintenance, expanding storage capacity, and performing disaster recovery as needed.

EU: European Union.

FAIR principle: data principles of findability, accessibility, interoperability, and reusability (FAIR).

GBIF: the Global Biodiversity Information Facility (GBIF) is an international organisation that focuses on making scientific data on biodiversity available via the Internet using web services.

GDPR: the General Data Protection Regulation (GDPR) is a European Union regulation on Information privacy in the European Union and the European Economic Area.

GPS: Global Positioning System.

Humboldt Core: Humboldt Core is a community-developed standard for representing critical information about scope, method and completeness of biological inventories.

ID: identifier to uniquely identify one object in the database so you can get to it without scanning the database for the object you need.

iDiv: German Centre for Integrative Biodiversity Research (iDiv), a DFG research centre with staff and members at its main locations in Halle, Jena and Leipzig. It is a central facility of Leipzig University and is run together with the Martin Luther University Halle-Wittenberg and Friedrich Schiller University Jena, as well as in cooperation with the Helmholtz Centre for Environmental Research - UFZ.

ISA framework: built around 'Investigation', 'Study' and 'Assay', the ISA framework helps you to provide rich description of the experimental metadata (i.e. sample characteristics, technology and measurement types, sample-to-data relationships) so that the resulting data and discoveries are reproducible and reusable.

Metadata: a set of data that describes and provides information about other data, but not the content of the data itself.

MVS: the Minimum Viable Scheme (MVS) protocol is part of the Strengthening Pollinator Recovery through INdicators and monitorinG (SPRING) project, funded by the European Commission. It described protocols of pan trapping and transect walks, coupled with simple habitat and flower assessments, and should ideally be conducted on repeated sampling visits to each site each year.

National data coordinator: one of 8 stakeholders who actively update EU PoMS database. Its main tasks include coordinating overall data management workflow for respective national monitoring scheme; first and second validation of national data, translation into universal language; report to EU data coordinator about challenges and requirements from national data management; result dissemination to all stakeholders especially to national policy makers. The national coordinator provides support to the national experts and volunteers. When a support request cannot be addressed by the national coordinator, the national coordinator can request further assistance from the EU data coordinator.

National data curator: one of 8 stakeholders who actively update EU PoMS database. Its main tasks include first validation of national data, translation into universal language, and helpdesk for national volunteers.

National super volunteers: one of 8 stakeholders who actively update EU PoMS database. Its main tasks include coordinating multiple sampling sites and managing data from several other national volunteers, being able to upload/edit data from these people but not others.

National taxonomic expert: one of 8 stakeholders who actively update EU PoMS database. Its main tasks include uploading national monitoring data, second validation of national data, updating species referencing tables.

National volunteers: one of 8 stakeholders who actively update EU PoMS database. Its main tasks include uploading national monitoring data, feedback to national data curators.

NRM: Natural Resource Management.

ORBIT: ORBIT is a three-year project commissioned by the Directorate General for Environment of the European Commission to develop resources for European bee inventory and taxonomy. The aim of ORBIT is to create a centralised taxonomic facility that lays the groundwork for the identification of European wild bees that will support other European projects national action plan for pollinators, and finally the European Red List of Bees.

RaTS: rare and threatened species.

Safeguard: Safeguarding European wild pollinators is an EU funded project aims to reverse wild pollinators decline by identifying emerging threats, developing new approaches that benefit pollinators from field to landscape scales, creating an integrated assessment framework and tools that incorporate evidence to prevent pollinator decline and inform policy makers and the society.

SBDI: Swedish Biodiversity Data Infrastructure.

SLA: a service-level agreement (SLA) is a contract between a service provider and its customers that documents what services the provider will furnish and defines the service standards the provider is obligated to meet.

SOP: a standard operating procedure (SOP) is a step-by-step, repeatable process for any routine task. It is documentation that prevents stress, mistakes, and miscommunication.

SPRING: Strengthening Pollinator Recovery through INdicators and monitorinG (SPRING) project is EU funded project aimed to strengthen taxonomic capacity with regard to pollinating insects, support preparation for the implementation of an EU Pollinator Monitoring Scheme and pilot the scheme in all 27 EU countries.

SSO: Single sign-on (SSO) is an authentication scheme that allows a user to log in with a single ID to any of several related, yet independent, software systems.

STEP: Status and Trends of European Pollinators (STEP) project is funded by EU and aims to document the nature and extent of pollinator declines, examine functional traits associated with particular risk, develop a Red List of important European pollinator groups, in particular bees and lay the groundwork for future pollinator monitoring programmes.

STING: the Science and Technology for PollinatING Insects (STING) project is a collaboration of the Directorate-General for Environment and the Joint Research Centre (JRC).

Taxo-Fly: Taxo-Fly is an EU-funded project gathering taxonomic information for all European hoverfly species. The aim of Taxo-Fly is to create a new taxonomic knowledge base, which lays the ground for the identification of the Hoverflies of Europe, supporting other European Commission funded projects, and European National action plans for pollinators.

UK PoMS: The UK Pollinator Monitoring Scheme (UK PoMS) is a partnership funded jointly by the UK Centre for Ecology & Hydrology (UKCEH) and Joint Nature Conservation Committee (JNCC). UK

PoMS is co-ordinated by UKCEH (UKCEH's contribution is funded by the Natural Environment Research Council award number NE/R016429/1 as part of the UK-SCAPE programme delivering National Capability).

WISE: The Water Information System for Europe (WISE) is a partnership between the European Commission and the European Environment Agency (EEA). WISE was launched in 2007 providing a web-portal entry to water related information ranging from inland waters to marine.

XML: Extensible Markup Language (XML) is a markup language and file format for storing, transmitting, and reconstructing arbitrary data. It defines a set of rules for encoding documents in a format that is both human-readable and machine-readable.

Annex 4. B. List of desired app components

User environment

Name: ***User settings***

Description: A system that stores preferences per user, such as preferred language or preferred species lists as well as the transects and pan trapping locations linked with them.

Importance: High

Approach: There are two possible approaches to this: either a central support system is built and all third-party app developers connect with the central system to load user profiles and the corresponding preferences, or each third party developer uses the settings system already available in their app. It will likely be easier for third party developers to develop an extension to their own system rather than connecting with a new external system. The disadvantage is that, when a user switches to another app (that supports the EU PoMS protocols), they will have to reset their preferences. Alternatively, a hybrid system can be created where third party developers use their own system, but indicate which settings were used when synchronizing with the central database.

The consideration of how much of the support system is implemented by third party developers and how much is centrally implemented is complex but ultimately is not greatly influential; however, we recommend that these data should also be stored in the central database.

Name: ***Translation to local language***

Description: Any app and surrounding support structure has to be translated into the local language.

Importance: High

Approach: Local coordinators will have to be responsible for the translations; a system that allows them to easily translate and maintain the translations has to be available. For this component, we recommend to not focus on cooperation with existing apps but develop a new translation system. These translations have to be made available to third party systems through an API, and third-party developers will to have to implement them.

Name: ***Data access for users***

Description: A portal where users can see their own data, edit entered data and download a copy of their data.

Importance: Mid

Approach: It is important to allow users access to their own data to keep them involved, this is more important for volunteers than for professionals, but both will likely want to be able to see and manage their own data. The app can work without this component but will likely be much less successful. Many existing apps will already have a website to support data access for users where data access to the EU PoMS data could also be added. Any changes would have to be directly communicated with the central database. If a third party does not implement this, users could be referred to the central website, which will have to be developed anyway. Users could change their data there as well, although this might make the organisation structure less clear for users.

Data collection

Name: ***Data collection***

Description: The app has to support data collection using the EU PoMS protocols. This means allowing users to enter species level information, enter both pan trap and transect data as well as floral data. It should also store metadata such as start and end time, the location, and the recorder.

Importance: High

Approach: For the development of a new app and for the negotiations with existing app developers the EUPOMS protocol should be included as a requirement. The exact implementation can differ between systems, but the complete EU PoMS protocol must be supported.

Name: ***Data validation***

Description: The collected data has to be validated, this can be done either by looking at the species, in combination with location and date, and additionally pictures can be collected and validated. To some extent, this can be automated, but this will likely initially involve species experts to manually make decisions in difficult cases. For this, an infrastructure has to be developed that allows (local) experts to view observations, contact recorders and classify datapoints as reliable or questionable.

Importance: Mid

Approach: Some available app systems will have data validation structures in place, if these can be modified to also validate the EU PoMS data, local species experts will not have to switch to an alternate system and will be easier to find. However, it seems unlikely that an app, potentially focused on a different set of species than EU PoMS, will have experts available for all species groups. It might therefore be more efficient to only incorporate this component in the third-party system, if a well-developed system with experts in most species groups is available.

Name: ***Identification support AI***

Description: The identification of species is one of the main limiting factors in the EU PoMS system; if this can be supported by an AI system, the data quality and quantity could potentially be improved.

Importance: Low

Approach: There are already several systems to recognize species from pictures. Several of these are incorporated in apps that allow users to record the result as an observation. This can potentially be a valuable tool to support volunteers. If the developers of these systems do not wish to extend their system to include the EU PoMS pollinator groups across the EU and follow the strict monitoring protocols required for the EU PoMS monitoring system, they can be asked to be part of the general support system. By making their AI system available through an API.

Name: ***Fieldwork protocol help***

Description: Another tool to help volunteers and professionals measure in accordance with the EUPOMS protocol is to provide a summary of the protocol. A quick reference that indicates at what time how many samples should be taken, a list of the required equipment etc. These quick reminders can help make the fieldwork easier but will also help to keep the data collection standardized.

Importance: Low

Approach: As this will likely be static data (it does not change often), it will likely be easily implemented in any new or existing system.

Name: ***Fieldwork forum***

Description: A forum where fieldwork volunteers and professionals from different European regions can discuss their fieldwork process and support each other. It seems likely that practical problems with equipment or the sampling protocol will arise in several regions; having a communication channel with a low threshold, solutions for many of these small practical problems can be shared. Scientists can be involved in the discussions to ensure that practical solutions do not decrease data quality.

Importance: Low

Approach: As this will have to be a pan European system, it should only be implemented at a centralized level, and not by third party developers. There are many ways this system can be implemented, for example as a simple web-forum. The exact implementation is of little consequence, as long as the system is easy to use and the threshold for joining and asking/providing help remains low.

Data processing

Name: ***Data permissions***

Description: It is important that the data storage and processing system conform to the privacy laws in each country. Generally, this means making very clear to the user what is done with the data they enter. Additionally it has to be clear that data cannot be recalled. Although a user has the right to be removed, this is only the case with their personal data, not the biological data they report. This is unlikely to be an issue with professionals, but in a partially volunteer based system this has to be well organised.

Importance: High

Approach: The exact rules regarding privacy depend on the member state. Although the GDPR made significant harmonisations, the implementation by Member States might still differ. Generally, users have the right to know what is being done with their data, who their data are being shared with, and to be removed from the system. Any system, new or based on existing third-party development, has to have a clear structure to deal with this kind of requests.

Name: ***Synchronization with central database***

Description: Quick synchronisation with the central system will allow for a more up to date overview of all the data and allow scientists to more adequately react to developing circumstances. The reality is that some regions might wish to share their data annually, but for the development of this app, we should focus on sharing the data with the central system quickly.

It might not be practical to share the collected data directly, as not every sampling site has internet available, and in the case of pan trapping the data will take months to process. However, the aim should be to upload data to the central system as soon as it is available.

Importance: Mid

Approach: Both new and existing apps will have to have an automated way to send their data to a server, hence synchronizing data with a central server should not be complicated.

A third-party developer will likely send the data to their server and store the records in their system. This is not a problem as long as the data are synchronized quickly with the central server. It is important to make clear that quick synchronization with the central server is a priority.

Name: ***Results feedback to users***

Description: To keep volunteers motivated it is helpful to provide feedback based on the collected data. For example, species x is doing well this year.

Importance: Low

Approach: Providing results to users can only be done once the data has been processed and can be done in many different ways. This can range from yearly emailing a newsletter with highlights to giving live access to current analyses and datasets. Some third-party apps might have systems to accommodate this, but it will strongly depend on the chosen communication method. It seems likely that this will have to be implemented at the central level.

Annex 4. C. Identified apps

Table A.4.C. 1. Overview of identified apps.

Name	Link	Region	By	Species groups	Notes
iNaturalist	https://www.inaturalist.org/	Worldwide	California Academy of Sciences	All	Large community that checks the data
Seek	https://www.inaturalist.org/pages/seek_app	Worldwide	California Academy of Sciences	All	
iRecord	https://irecord.org.uk/		Centre for Ecology and Hydrology	All	
eBMS	https://butterfly-monitoring.net/nl/ebms-data%20access	Europe + some other countries	Centre for Ecology and Hydrology	Butterflies, moths, dragonflies, bumble bees	
Fit count	https://ukpoms.org.uk/index.php/		Centre for Ecology and Hydrology		
NaturaList	https://play.google.com/store/apps/details?id=ch.biolovision.naturalist&hl=de&gl=US	Europe	Biolovision Sàrl		

Name	Link	Region	By	Species groups	Notes
Arise app	https://www.naturalis.nl/wetenschap/arise-nederlandse-soorten-kennen-en-herkennen	NL	Naturalis	All	App is still in testing phase, not yet public. App developed for collection of dead specimens. Location currently only for NL, developed by commercial party commissioned by Naturalis (Arise project)
Avimap	https://sovon.nl/tellen/avimap	Europe	Sovon	Birds, butterflies, mammals, dragonflies, reptiles and amphibians	
ObsIdentify	https://waarneming.nl/apps/obsidentify/	Europe	Stichting Observation International	All	Focused on opportunistic observations
Obsmapp	https://observation.org/apps/obsmapp/	Europe	Stichting Observation International	All	Focused on opportunistic observations
BioMe	https://www.ufz.de/export/data/10/275410_SA_3_Harpke.pdf		UFZ, Helmholtz centre for environmental research	All	

Name	Link	Region	By	Species groups	Notes
Spipoll	https://www.spipoll.org/	France	Office pour les insectes et leur environnement, Museum, Nal Hist Naturelle	All	Developed for doing fit counts, pictures identified by community
Artportalen	https://www.artportalen.se/	Sweden	SLU Artdatabanken	All	Mobile website, not a real app
Naturbasen	https://www.naturbasen.dk/	Denmark	Naturbasen.dk	All	
PlantNet	https://identify.plantnet.org/nl	Worldwide	CIRAD, Inria, INRAE and IRD	Only plants	Only plants, possibly suitable for cooperation, but unlikely to implement EUPOMS protocols
Merlin	https://merlin.allaboutbirds.org/		Cornell Lab of Ornithology	Birds	Only birds, possibly suitable for cooperation, but unlikely to implement EUPOMS protocols
eBird	https://ebird.org/home	USA	Cornell Lab of Ornithology	Birds	Only birds, possibly suitable for cooperation, but unlikely to implement EUPOMS protocols

Name	Link	Region	By	Species groups	Notes
spotteron.app	https://www.spotteron.net/	N.A.	?	Unknown	A platform with different recording apps, spiders, bees and specific birds are available
GBIF app	https://www.gbif.org/tool/81494/anymalsplants-mobile-application	UFZ	Global Biodiversity Information Facility	All	Multiple app system, appears no longer actively maintained
Leps fieldguide	https://leps.fieldguide.ai/figures	Worldwide	Field guide, in Delaware?	All	Appears no longer actively maintained
MapNat	https://www.mapnat.org/		Leibniz University Hannover, UFZ	All	Appears no longer actively maintained

Source: Authors' elaboration.

Table A.4.C. 2. GUI, handling data, and processing properties of identified apps.

Property	iNaturalist	Seek	iRecord	eBMS	Fit count	NaturaList	Arise app	Avimap	Obs identify	Obs map	BioMe
Multiple languages	Y	Y	N	Y	Y	Y	N	Y	Y	Y	?
Species group selection	N	Y	N	Y	N	Y	N	Y	N	Y	?
Download data (can a user download their own data)	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	?
Vegetation data	N, only opportunistic	N, only opportunistic	N, only opportunistic	N	N	N	N	N	N	N	?
Line tracking	N	N	N, but records can be grouped	Y	N	Y	N	Y	N	Y	Y
Transect	N	N	N	Y	N	Y	N	Y	N	N	Y
Pan trap	N	N	N	N	N	?	N	N	N	N	?

Property	**iNaturalist**	**Seek**	**iRecord**	**eBMS**	**Fit count**	**NaturaList**	**Arise app**	**Avimap**	**Obs identify**	**Obs map**	**BioMe**
Record time (effort)	N	N	N	Y	Y	Y	N	Y	N	N	Y
Metadata collection	N	N	N	Y	N	Y	N	Y	N	N	Y
Validation (by picture)	Y	Y	Y	Y	N	N	N	Y	Y	Y	Y
ID assistance	Y, pictures of selected species are shown	Y, pictures of selected species are shown	N	Y, picture guide	Y, detailed explanation of species groups	N	N	N	Y, AI	Y, AI	?
Explanation (protocol)	Y, but no extended protocols supported	Y, but no extended protocols supported	N	Y, short explanation on protocols in app	Y, detailed online explanations available, short summary in app	N	N	N	N	N	?

Property	iNaturalist	Seek	iRecord	eBMS	Fit count	NaturaList	Arise app	Avimap	Obs identify	Obs map	BioMe
Support forum	Y	Y	Y	N, national forums are available (not central)	N	N	N	Y	Y	Y	?
Retract user info	Y	Y	?	N, user name cannot be removed from dataset	N, user name cannot be removed from dataset	Y	N	Y	N	N	?
Auto export data	Y, GBIF	Y, GBIF	Y, at least partially	Y, GBIF?	?	?	N	Y	Y	Y	?

Property	**iNaturalist**	**Seek**	**iRecord**	**eBMS**	**Fit count**	**NaturaList**	**Arise app**	**Avimap**	**Obs identify**	**Obs map**	**BioMe**
Feedback to users	y, challenges	y, challenges	y, dynamic maps, reports and graphs	n, national newsletters are available but no central system	y, dynamic maps and results and scientific research on website (also newsletter)	Y	N	Y	y, badges and challenges	Y, lists	?

Source: Authors' elaboration.

5 Options for future scheme development (complementary modules)

5.1 Options for pan traps

5.1.1 Potential opportunities of using pan traps

While pan traps were excluded from the EU PoMS core scheme (see section 2.2 for rationale), as a survey method they still offer several opportunities for monitoring pollinators. One key benefit is that they can potentially sample different aspects of pollinator community. Moreover, data from the pans can be combined with transect counts to increase the power of an indicator (see chapter 6.12 in Potts et al. (2021), plus section 3.1 here). This approach has also been tested by the UK PoMS (Adjei et al., 2024).

In addition, SPRING pilot data and STING2 expert opinion suggest that pan traps may be more effective at catching bee species, and therefore may be better than transects for estimating bee diversity. As pan traps also capture a wide range of other flying species, this method could be used for the assessment of wider insect biodiversity as part of a monitoring scheme beyond pollinators. A further advantage is that the catch is retained and could potentially be made available for additional studies, such as genomic level monitoring (see section 5.3). Pan traps can also be left out for multiple days, usually this is one or two, thereby allowing a longer window of surveying, compared to transects, and therefore may catch additional species.

Pan traps also offer a good opportunity to engage citizen scientists and volunteers as they can be relatively easily deployed with minimal training and allow users to set up multiple traps in multiple sites in parallel. They are also less affected by the skill level of volunteers and so may have some advantages in terms of standardising methods using volunteers.

5.1.2 Recommendations

The utility of pan traps for assessing wider insect biodiversity should be explored through a pilot programme, which tests its effectiveness as an approach to capture a wider diversity of insect species. The pilot scheme should take into account biogeographic variation, and be benchmarked against standardised reinforced transects. Key aspects that should be assessed should include: (i) the extent to which pan traps provide supplementary information about bees and other pollinators in addition to transects, and (ii), fine tuning of the field methodology to optimise the number, spatial configuration and duration of pan trap exposure. Further bolt on projects could include exploring the feasibility of using pan traps to contribute to genomic level monitoring.

5.2 Emerging technologies and the opportunities for EU PoMS

5.2.1 Summary

This section explores the potential benefits of emerging technologies for EU PoMS. Many exciting advancements are on the horizon, each holding considerable promise for enhancing pollinator monitoring efforts. However, some of these innovations are still in need of further refinement and development. At the forefront of these technologies are image recognition and DNA analyses that, offering rapid identification of pollinators, will probably improve EU PoMS efficiency in the near future.

Insect camera traps designed for diurnal pollinators are currently in the nascent stages of development but show promise in providing valuable phenological data especially if complemented with the more established methods. Also image-based methods for the identification of dead specimens showed promising results for invertebrates, even if comprehensive reference databases tailored specifically for pollinators are still in the works. Furthermore, remote sensing approaches to monitor pollinator habitats, including floral resources, are also emerging. These technologies hold immense potential to provide crucial ecological context data to augment pollinator monitoring efforts in the future.

Moreover, DNA barcoding and metabarcoding techniques hold the potential to reduce costs and expedite specimen identification process. Nevertheless, their usefulness strongly depends on the availability of reference data. Several large ongoing projects are quickly improving both the species coverage and the data quality of reference databases. The costs of specimen identification through these approaches continue to decrease as the use of these techniques becomes routine.

We recommend support for the building of reference databases for both image and DNA-based species identification, and in particular, to collaborate with ongoing EU projects developing DNA barcoding reference data. For building image libraries, Citizen Science coupled with expert entomologist review is a promising approach for building image libraries. While utilising already identified species from other trapping efforts (e.g. pan traps) is an effective method to build up DNA databases from reference samples. This should quickly improve the coverage of reference databases.

Among further emerging technologies potentially useful for EU PoMS are acoustic methods. While they are rapidly evolving, at present they have limited applicability across insect taxa, and is unclear to what extent pollinator species can be identified efficiently and accurately from sounds.

In conclusion, we recommend ongoing horizon scanning of new technologies that are currently not at a level where they can be quickly incorporated in the EU PoMS, but have the potential to provide large benefits later.

5.2.2 Approach to assessing emerging technologies

In this section, we evaluate emerging technologies for insect monitoring by assessing to what extent they can deliver data on pollinator abundance and richness (number of species). Ideally, such technologies should be cost-effective and reduce the lethal capture of pollinators in the long term. As part of the assessment, we have reviewed inputs from several hundred experts and stakeholders provided through a series of webinars organized by EuropaBON[101] during spring 2022 on technology for biodiversity monitoring broadly (Dornelas et al., 2023). In addition, we have compiled recently published papers, websites and services supporting the monitoring of pollinators. The solutions of primary relevance fall into three main categories: (i) techniques to do non-lethal monitoring in the field, (ii) methods to perform taxa identification of specimens in the lab based on imaging, and (iii) DNA methods. We focus on emerging technologies that could mature sufficiently to contribute to European-wide pollinator monitoring within the next five to ten years. We treat them in separate sections following a format of description, potential scope, current status and remaining development time, requirements, estimated costs, advantages, disadvantages and possible future development. The sections are: Citizen Science portals (5.2.3), image-based methods for field-based monitoring (5.2.4), image-based specimen identification (5.2.5), sound recognition (5.2.6), landscape analysis (5.2.7), DNA barcoding (5.2.8), and DNA metabarcoding (5.2.9).

There are additional developing technologies of relevance to pollinator monitoring. These include LiDAR (Rhodes et al., 2022), spectral analysis of thin-film wing interference signals (M. Li et al., 2023), miniature tags (Lee et al., 2021) and moth freezers for conserving specimens after trapping. The further development of these early-stage technologies should be followed closely to assess their potential for implementation in large-scale pollinator monitoring; thee technologies, however, are expected to either be impractical to deploy at continental scale or require several years of further development before being mature enough to be deployed broadly as part of the EU PoMS.


Trachusa byssina, ©NJ Vereecken

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[101] https://europabon.org/

5.2.3 Citizen science portals

A range of online portals for species observations support the reporting of ad hoc or unstructured observations of pollinator species. The rapid uptake of this technology globally results in a large availability of data. These can be used to estimate occurrence and provide an indication of the spatial distribution for species with enough observations. While these data provide important context for pollinator monitoring, most of the benefits to the EU PoMS are indirect. The major problem with these data are their unstructured collection and low repeatability. The effort (how long a recorder spends in an area) is generally not reported, and interesting (often conspicuous or iconic) species and areas are typically overrepresented. This can pose challenges for analysing these data. At the same time, the availability of online portals, particularly with the option to provide (automated) user feedback, has engaged a vast group of people, organisations, and institutions. This can stimulate engagement in more structured monitoring and mobilize taxonomic experts to contribute additional training data for automated monitoring approaches.

Citizen Science portals typically incorporate a community expert review system; it is possible to ensure some level of quality assurance of the taxonomic identity and location of such observations. Increasingly, the portals offer machine learning-based suggestions for species identity when users provide access to images or sounds of the observations and commonly publish these data, including media files, to the Global Biodiversity Information Facility (GBIF). Through these activities, access to image and sound training data for machine learning models is increasing, which is driving advances in image and sound recognition of species in general, but also of pollinators (D. Roy et al., 2024; Spiesman et al., 2021; Stark et al., 2023).

It is important to note that manual in situ imaging tends to produce centred, high-resolution images of individual insects, which are typically different from the images collected by other approaches mentioned below. For this reason, the performance of classification models implemented in portals such as iNaturalist[102], eButterfly[103], Observation.org[104] and others may differ, and sometimes outperform, those implemented in insect camera traps (Spiesman et al., 2021).

Observations based on images acquired by citizen scientists present distinct analytical challenges in the context of monitoring (August et al., 2015). It is difficult to ensure that data from unstructured sampling represents a meaningful statistical population. Without a predefined protocol, recorders might not record all individuals observed, which creates a bias towards easily identified, conspicuous, attractive, or species that are easy to photograph. In addition, busy times, nice weather, and easily accessible locations will be overrepresented. Statistical techniques to cope with these shortcomings are available to an extent (occupancy modelling) (van Strien et al., 2013), but these often require huge amounts of data and do not perform well for all species.

For a subset of pollinators, these methods can potentially quantify large-scale range contractions, expansions, and shifts can be assessed from unstructured data from Citizen Science portals if a species is likely to be seen and reported by the general public. Species range maps for pollinators can support the EU PoMS by providing an estimate of expected local species and by providing

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[102] https://www.inaturalist.org/

[103] https://ebutterfly.com/

[104] https://observation.org/

rulesets to help review data from structured surveys. Cooperating with these portals can potentially also provide a large pool of volunteers. These portals often incorporate a competitive element consisting of a list of species seen (members with a large number of species on their list are held in high regard). Volunteers can potentially be motivated to join a more structured monitoring scheme when there is an option available to export their observations to these portals to expand their list.

In summary, the main benefits of Citizen Science portals are:

- Engagement of diverse audiences in recording pollinating insects, with the potential to support training and development in species identification by connecting citizen scientists to expert verifiers (see Citizen Science section 2.7).
- Building up labelled image datasets to support the development of image classifiers.
- Collecting opportunistic presence-absence data on rare and scarce species that are unlikely to be regularly sampled through EU PoMS (see rare and threatened species section 0).

5.2.4 Insect camera traps for in situ pollinator monitoring

5.2.4.1 Description

Insect camera traps are rapidly maturing as an approach to study and monitor pollinators. They typically employ a time-lapse recording schedule, since the infrared triggers used for motion detection in traditional camera traps for vertebrates are ineffective for small organisms such as pollinating insects (Hobbs and Brehme, 2017). Hence, it is critical to consider where to place and point cameras for monitoring. With a focus on pollinators, it seems obvious to focus on floral resources (Bjerge et al., 2022; Steen, 2017), growing in the wild. To increase trapping chances, floral resources can also be artificially introduced, or even mimicked, to attract and monitor pollinators. The reliability of the data collected attracting insects to a trap, especially when competing with naturally offered resources (mimicking a flower), is a topic of debate. Traps relying on attraction have been reported to perform better in a landscape without many flowers. As with pan traps (see section 5.1), the local floral context greatly influences the trapping efficiency in a non-linear manner. This interaction with the local landscape can affect long-term variation in pollinator detections. This is a problem with several active sampling methods such as pan traps. Like pan traps, attracting insects to the trap makes the data unsuitable for abundance analysis, only the presence-absence of a taxon can be established. It is also possible to point an insect camera trap against an artificial background. These usually comprise a uniform sheet such as a yellow sticky trap (Geissmann et al., 2022), a screen, an illuminated white sheet (Bjerge et al., 2021), or the inside of a plastic pheromone trap (Yalcin, 2015). Attractants and traps can increase insect capture rates, but also disturb and potentially kill the insects (Geissmann et al., 2022). Attractants also differ considerably in their attraction to different insect species or individuals. Even so, artificial backgrounds are useful to improve detection chances and identification of small or cryptic insects when collecting presence-absence data.

The most mature insect camera traps involve recording images against standardized backgrounds (either sticky or non-sticky). A few different solutions are available for monitoring diurnal pollinators against fixed uniform (e.g. yellow) backgrounds by using camera traps; Diopsis[105] (van Klink et al., 2022) and the Insect Detect platform[106] (Sittinger et al., 2024) use a custom-built but fully open access data analysis pipeline. For nocturnal insects, the Diopsis platform turns on UV lights around the camera to shine on the landing platform, whereas the dedicated moth camera traps (AMI traps[107], see section 2.9) use a commercially available UV light attractant, which appears to be more effective on pollinators (D. Roy et al., 2024). The AMI trap is built on open science principles, is commercially available, and has a well-developed data analysis pipeline. There are also systems developed with more high-end camera systems recording images with higher resolution and quality, but these systems have limitations related to durability and automation (Korsch et al., 2023). The estimated TRL for these techniques for pollinator monitoring varies between TRL levels 5 and 7 depending on the individual solutions. The insect camera traps for moths such as the AMI traps (currently at TRL 7) are more mature than insect cameras for monitoring diurnal pollinators (currently at TRL 5 or 6).

5.2.4.2 Potential scope

Unlike destructive sampling, automated imaging should have limited impacts on insect populations and enables observation of elusive insect species, while minimizing labour costs of monitoring (Høye et al., 2021). Above all, automated imaging enables an unprecedentedly high rate and resolution of data collection over long timescales (Alison and Høye, 2024; Edwards et al., 2015). High-frequency imaging can expose diurnal and seasonal patterns in pollinators (Alison et al., 2022; Geissmann et al., 2022), but the increased sampling frequency also increases the chance of repeatedly sampling the same individual. Hence, we can no longer assume data points collected in short succession to be independent.

For all field sensors, an important value in the context of monitoring pollinator species abundance and richness is their ability to provide phenological context for point samples using methods that are more traditional. As such, sensors capturing the phenology of a species in a given season and region will allow for valuable context, when comparing abundance or the occurrence of specific species monitored using other means (e.g. transects, pan or light trapping, or 15-minute counts).

5.2.4.3 Current status and remaining development time

Insect camera traps filming uniform backgrounds, such as the AMI traps and Diopsis cameras, are commercially available and DIY instructions are available for several other insect camera traps. To film natural vegetation any camera can essentially be used, and this is probably why such systems are typically not described as insect cameras. Such systems are less mature, although some success has been achieved on low-stature vegetation or even constructed standardised flowerbeds for pollinator monitoring (Bjerge et al., 2022, 2023). A key missing element with insect camera traps seems to be the on-board processing of acquired data as the systems generate very large volumes of data. Such features are developing slowly since datasets available to train deep learning models to locate and identify pollinators are still small, and cover only a small subset of common species.

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[105] https://diopsis.eu/en/

[106] https://maxsitt.github.io/insect-detect-docs/

[107] https://www.ceh.ac.uk/solutions/equipment/automated-monitoring-insects-trap

5.2.4.4 Requirements

There has been remarkable progress in the development of machine learning models for image classification in recent years, in part enabled by the rapid accumulation of training datasets. Still, insect camera traps will require efficient localisation algorithms as insects will typically be small compared to the image size. Thus, several hundreds of validated images per species are likely needed to allow the recognition of individual species, although this will depend on the recognition difficulty of each species. Development thus far has shown that bees are relatively difficult to identify, and hence they will require a larger training set. It should also be considered that different possible poses could further increase the required size of the training dataset.

Powerful computers or computational clusters are usually required to train the algorithm, however, once trained it no longer requires a large processing capacity to be used, and it can typically be run on a mobile phone. To further mature this technology, it will be important to evaluate how representative the data from insect camera traps are compared to other methods and how the recording schedule affects detections. This involves running insect camera traps in locations where independent data from other trap types are collected simultaneously. For traps with UV light attractant, it will also be important to test the effect of different recording schedules on the data collected. This is because the attractant may prevent the insects from carrying out their normal behaviour and because predation risk may increase with the duration of trapping within and across nights.

5.2.4.5 Estimated costs

The commercially available insect camera traps are typically produced in small quantities and only for monitoring insects. For this reason, they cost €3,000-€5,000 per unit excluding solar panels and batteries. There are low-cost alternatives, which can work well for short-term deployment, but generally, the lifespan of these trap types is not known, and it is possible that a trade-off between price and stability of the systems exist. The installation and maintenance of insect camera traps requires some site visits e.g. once a month. Basic taxonomic expertise is required to properly apply these tools, particularly when training users. The exact costs are difficult to estimate, as it will largely depend upon the data availability, which differs between species groups and countries. If images have to be manually validated, a crude estimate of the time needed is ±30 seconds/image with a very large spread depending on the image quality and candidate species. This equates to €0.05 to €0.49 per image, depending on the country (Breeze et al., 2021). The costs associated with this method mostly involve the collection and preparation of datasets. Training datasets built with images from online portals or from specimens in museum collections may be useful but likely cannot be the sole data source. Once the analysis pipeline is sufficiently developed, the costs of processing image data are reduced to the mere computation costs. Until then, there is still a need to improve training data, models and data management infrastructure. It will also be important to include an estimate of the costs of performing trials with independently collected data to evaluate representativeness and to assess the population effects of drawing moths to UV traps across extended periods.

5.2.4.6 Advantages

The advantage of this approach is firstly that the digital data can be collected automatically and in a standardised way. The implications are that recording can be scheduled according to needs rather than human constraints and that the data collection is cheap. Image-based approaches for some taxa are often simple to validate as experts can immediately check relevant morphological characters from images, if images are of sufficient quality. Furthermore, this technique reduces the expertise required for fieldwork; this can be done by personnel or volunteers with minimal training. Finally, it is important that these methods are non-lethal. Something that is increasingly recognized as important for insect monitoring methods.

5.2.4.7 Disadvantages

With insect camera traps, insects are not captured, therefore it is possible to record a single individual multiple times, and this makes it difficult to establish abundance. Systems focused on detecting insects on colourful backgrounds or flower mimics have the problem that they depend on attracting insects, which causes an interaction with flower abundance in the local landscape. Therefore, data collected with a colourful attractant can only be analysed as presence/absence data. Systems for nocturnal insects (e.g. moths) use a light as the attractant so may be unaffected by bias from focal flower availability although they are potentially biased by changes in light pollution.

Insect camera traps will typically record rather low-resolution images of individual insects as they make up a small proportion of the image and multiple insects may appear in the frame. In such a context, the data generated by insect camera traps can lack the resolution to allow for species identification of bees and hoverflies and complicate validation by an expert. Although the performance of deep learning models is increasing rapidly, they can still struggle with generalisation, which means that when an insect appears in a pose or against a background that the model was not trained on, it may not be able to localise and identify the correct species. Many butterfly species recorded with such traps have folded wings, a behaviour that makes species identification difficult or not possible. On the contrary, most macro moth species will rest in a position that allows for species identification from camera trap images.

Another potential disadvantage is that the involvement of volunteers might decrease when classical diagnostics and species determination are no longer required to recognise different species. Currently, there is a large time investment required to learn to recognise all pollinator species, which ensures volunteers are highly involved.

Finally, depending on the country, theft and vandalism of equipment might be a problem. This may be particularly true when insect camera traps are fitted with solar panels and batteries as this makes them even more conspicuous.

5.2.4.8 Possible future development

For moths, the next step in the development of these systems is extensive testing to assess the hardware stability, the long-term effect of continuous attraction of moths by light, and to evaluate image recognition performance across Europe (section 0). Additionally, the effects of potentially counting repeatedly a single individual on the data quality will have to be assessed. The development of these camera traps would benefit from a pilot in several European countries, preferably linked to an existing monitoring structure (e.g. LED or Malaise traps) to establish how large the effect of repeated counts is on the data quality. This could also rapidly improve image recognition and processing pipelines.

For insect camera traps for diurnal pollinators, the visitation rate and taxonomic biases when recording against an artificial background (e.g. the yellow screen of the Diopsis and Insect Detect) should be compared to encounter/capture rates of other monitoring methods. For insect camera traps recording insects in natural vegetation, the interaction with flower abundance should be quantified. In addition, a strategy for using sentinel plants in a phytometer approach (using the same flowering plants across sampling sites) should be developed. If these issues are addressed, the EU-wide deployment of such systems can likely collect huge datasets in a very economical way.


Halictus scabiosae, Axel Hochkirch

5.2.5 Image-based approaches for identification of dead specimens

5.2.5.1 Description

This method involves collecting specimens in the field, through netting, pan traps or Malaise traps. When such samples are brought back to the lab, image-based (section 5.2.5) and molecular tools (sections 5.2.8 and 5.2.9) can speed up and enhance the data that can be extracted from such samples. As such, unlike with insect camera traps, it necessarily separates image acquisition from the process of insect sampling. Imaging of dead specimens includes systems for bulk photography of specimens in museum collections (Hansen et al., 2020), Petri dishes, or trays (Schneider et al., 2022; Wührl et al., 2022); photography of parts of insects, such as their wings (Salcedo et al., 2019); multi-angle imaging of insects in a liquid medium (Ärje et al., 2020) or 3D imaging (Plum and Labonte, 2021). Specimen imaging can rapidly generate high-resolution images under very controlled conditions, so it produces some of the most promising results for automated insect identification to species-level taxonomic resolution. Among the image-based tools, the BIODISCOVER system (Ärje et al., 2020) allows for detailed close-up images of individual specimens using a robotics-enabled framework, where bulk samples are processed with a collaborative robot individually and imaged. Current work is improving the cycle time and performance of this process and adding functionality to control which specimens are later grouped for storage or potential further molecular identification. In the future, this system could offer an automated solution to estimating the abundance and richness of pollinators. In principle, the DiversityScanner (Wührl et al., 2022) offers the same functionality, but only for specimens smaller than 3 mm in length and thus is not yet relevant for pollinator samples. Recently, the Entomoscope has been presented as a low-cost solution for close-up photography of specimens (Wührl et al., 2024). This system is mainly proposed for species discovery, but could be adapted for imaging of specimens after collection and submitting image data to a central database for subsequent species identification. There are also commercial microscope alternatives, but these are currently prohibitively expensive for most organisations and do not integrate any robotics for the automation of specimens handling.

5.2.5.2 Potential scope

Specimens-based research can potentially process bulk samples collected with traditional means such as pan traps or Malaise traps. Bees and hoverflies are the pollinator taxa which would most likely be collected with such traps and therefore in scope for image-based specimen identification. With automation, it is conceivable that bulk insect samples can be brought to centralized processing labs, where specimens can be identified, counted, and sorted. A possible small fraction of hard-to-identify specimens could then be presented to a group of experts for verification of the identification.

5.2.5.3 Current status and remaining development time

There are two different approaches for specimens-based approaches to species identification from bulk samples. One approach involves imaging multiple specimens at the same time. After imaging, it will be difficult to validate the species identity, as specimens are not kept separately. The other approach involves picking specimens individually and this allows more control over where each specimen is stored and thus opens for validation of species identification. No system has yet been described to fully automate the process of imaging specimens in a way that can be validated. In addition, no system has yet been backed up by the relevant image reference databases, although this work could be underway. It seems that most of the mechanical challenges are available in prototype form but have not been implemented at a large scale.

5.2.5.4 Requirements

There is a need for building a reference collection of all the relevant pollinator species. It is possible, but not certain, that pinned specimens could help in this direction, but efficient tools to identify bulk specimens collected in liquid, should not rely on pinning specimens first. As such, the reference collection should be built from specimens in ethanol.

5.2.5.5 Estimated costs

The primary needs are for imaging devices. None of the devices described in this section are commercially available, but a few price estimates are available. For instance, the standard components in the BIODISCOVER imaging device were estimated at around €5,000 (Ärje et al., 2020). The components for the Entomoscope excluding the lens cost around €1,000 (Wührl et al., 2024). The actual price of producing these pieces of equipment is likely to be more than twice these amounts as labour and other costs are combined. To fully automate these systems, either simpler XYZ robots need to be adapted and tools for manipulating and moving specimens are needed (Wührl et al., 2022) or investments into more sophisticated collaborative robots are needed.

Such systems can easily exceed €20,000. On the other hand, they may save thousands of hours of work for technicians.

5.2.5.6 Advantages

This technique reduces the expertise required to identify specimens, and potentially allows the lab work to be done by personnel or volunteers with minimal training.

5.2.5.7 Disadvantages

Such systems are technically quite sophisticated and require maintenance by people with quite different skills from those traditionally involved with pollinator species identification.

5.2.5.8 Possible future development

Establish a reference collection of up to 50 specimens of all bee and hoverfly species including e.g. those collected in the SPRING project, for high-resolution imaging and completion of DNA barcode libraries. Optimise and run timed trials using lab tools for robot-enabled image-based identification of bulk samples to estimate their cost-efficiency and complementarity to DNA metabarcoding.

Traditional identification can contribute to building reference collections for image- and DNA-based identification. Key projects including the Horizon Europe project MAMBO[108], the Biodiversa+ pilot on automated biodiversity monitoring stations, the COST Action InsectAI[109] and the DNAquaIMG and ANTENNA funded under the Biodiversa+ BioDivMon research call will take steps towards these developments. Additional targeted resources for development and implementation trials would ensure that these technologies could feed into later phases of EU PoMS.

5.2.6 Acoustic approaches

5.2.6.1 Description

Bioacoustic research is a rapidly moving research field. The primary activity is on bird and bat species recognition, but sonification in insects is widespread and studies demonstrating the ability to distinguish insects from their sounds are emerging (Pollack, 2017; van Klink et al., 2024). These have focused on crickets and grasshoppers, but some attempts have also been made to detect honey bees and separate species of bumble bees from their flight buzzing sounds (Gradišek et al., 2017). There is emerging evidence that plants also detect sounds and can change their behaviour accordingly (Gagliano, 2013), by, for example, producing more nectar when pollinators are near (Veits et al., 2019) . Projects such as AudioMoth offer open specialised hardware to record sounds continuously on a large range of frequencies (Hill et al., 2019), making large-scale sound recording an affordable option. As additional passive acoustic recorders enter the market, primarily driven by an interest in monitoring birds and bats, it also becomes clear that equipment cost is often traded against sound quality and the level of background noise. This relates to microphone quality and weather casing. Other considerations are the power and memory constraints on loggers. For pollinators, it remains to be demonstrated that the soundscape can effectively be translated into

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[108] https://www.mambo-project.eu/

[109] https://www.cost.eu/actions/CA22129/

observations of species or even higher taxonomic units (but see Rodriguez et al., 2024). The TRL for this technique for pollinators is estimated at TRL level 3; an experimental proof of concept is available.

5.2.6.2 Potential scope

While passive acoustic monitoring of insects may be the most feasible, they may not collect as many detections as active methods, where an observer is doing active searching. However, as audio recorders can collect data continuously, the challenge probably lies more in storing and processing the large amounts of data acquired. It should be noted though, that for many pollinators sound is a by-product, and as there is much size variation within species (e.g. bumble bee queens vs workers), and since size is one of the most important factors for the production of sound, there is no guarantee that identification to species level will be possible. In this case, the attribution of the organism to a species group may only be possible. It is possible to use sound recorders while doing transect walks to establish an acoustic transect, but it remains to be understood what the constraints and challenges associated with such recording strategies may be.

5.2.6.3 Current status and remaining development time

Passive acoustic recorders are already available and the first algorithms to automatically identify sounds of pollinating insects are starting to emerge (Rodriguez et al., 2024). These algorithms will require substantial further development before they can be widely applied and can distinguish between European pollinator species with sufficient confidence to be used in wide-scale monitoring programs. Even with ongoing developments, it may not be possible to identify every sound at the species level. We expect at least 5-10 years of continuous development before the algorithms support large-scale applications. However, data collection is already possible.

5.2.6.4 Requirements

This method has several requirements; a large network of microphones, algorithms, and computational resources to process sound files. These recorders produce data continuously, requiring a large storage capacity for sound files. Eventually, passive acoustic recorders will likely develop to the point where they can parse sound files themselves and pass on the identified species only. Even under such a scenario, a subset of sound files should be stored to help train and test algorithms.

5.2.6.5 Estimated costs

The costs of a single generic passive acoustic recorder for audible or ultrasound with a weatherproof casing, batteries, and memory cards are estimated at €500 - €1,000 per device from companies such as AudioMoth[110] and Wildlife Acoustics[111]. Other companies (such as AgriSound[112]) have started to offer acoustic sensors specifically for insects (Polly[113]). Microphones provide point observations; therefore, either a large number of microphones would be needed to cover an area

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[110] https://www.openacousticdevices.info/audiomoth

[111] https://www.wildlifeacoustics.com/

[112] https://agrisound.io/

[113] https://agrisound.io/tech/polly/

similar to a typical butterfly or bee transect, or the observer would have to walk with a recorder. Additional costs would include developing a validated reference collection and machine learning time to develop these into usable data.

5.2.6.6 Advantages

This method does not depend on attracting insects. Therefore, it will have no colour or floral context biases. As an automated technique, this can potentially provide a huge high-quality dataset.

5.2.6.7 Disadvantages

Insects are not captured and therefore it is possible to record a single individual multiple times. It might not be possible to identify all species based on their sound. This could potentially be addressed by combining it with other automated methods, such as automated camera traps. It is not clear yet what type of data can be extracted from sound sensors; theoretically, sound sensors indicate insect activity, but it needs to be tested how this relates to insect abundance. It should also be tested how large the effect of potentially counting a single individual repeatedly is and how sensitive the technique is to disturbance (wind, traffic, rain etc.). Depending on the country, theft and vandalism of equipment might be a problem. Recording sounds risks invasion of human privacy, and regulations could forbid placing these recorders in certain locations.

5.2.6.8 Possible future development

In the longer term with considerable investment, this method could automatically and instantaneously identify certain species and pass them on to a central server directly. With a wide network of microphones, it could be possible to track insect occurrence in real-time.

Melitturga syriaca, ©NJ Vereecken

5.2.7 Mapping pollinator habitat extent and quality

5.2.7.1 Description

The habitat of pollinators is important, and aspects such as flower availability, nectar, pollen density, host plant density, and micro-climatic heterogeneity can strongly affect their use in an area and ultimately their survival. However, the collection of these data on the ground can be extremely time-consuming. Therefore, remote sensing techniques are being increasingly used for landscape analyses.

Remote sensing platforms can have two types of sensors, passive or active. Passive sensors record light (visible and non-visible), while active sensors such as LiDAR (Light Detection and Ranging) and SAR (Synthetic Aperture Radar) can measure elevation and structure. From these sensors, a multitude of landscape properties can be derived. There are three main ways to collect remote sensing data of relevance to pollinators: (i) Unmanned Aerial Vehicles (UAV's) also popularly called drones, (ii) Airplanes, and (iii) Satellites.

UAV's - UAV's typically operate 0-200 m above ground level and can offer a sub-millimetre resolution depending on the camera and height. Flying with a basic UAV is relatively easy and requires minimal training; however, more advanced equipment can require intensive training, and in some countries, a licence is needed. It requires some preparation such as permission of the landowner, but as a UAV can be quickly deployed, this technique is relatively flexible. Both the machine and the quality of the resulting data are strongly weather dependent: strong wind and rain make data collection difficult. UAV's mostly collect optical data generally focussed on the visual spectrum, but sensors that collect data in other spectral ranges such as near-infrared or thermal infrared are available as are LiDAR sensors although only larger and more expensive UAVs can carry the larger payloads of these sensors.

Airplanes - These typically operate 1-10 km above ground level. Depending on the camera and flight parameters, this offers a resolution in the centimetre range. An aerial photography flight requires more precise planning, and hence weather is a more important factor for the resulting data. Airplanes can cover large areas, again depending on the camera and flight parameters. This also means that cloud cover is almost inevitable. Although there are commercial services that offer guarantees with regard to cloud coverage. Like UAVs, airplanes can collect LiDAR and optical data; typically, they can carry higher quality equipment than UAVs because they allow for larger payloads. This allows for data collection on a larger scale; however, the higher elevation generally reduces the resolution to less than a UAV might achieve.

Satellites - Most satellites are between 500 and 600 km from earth. Depending on the hardware, most Earth observation satellites offer a resolution of between 0.5-50 m. Although it seems likely that the spatial resolution of satellites will improve further, this is expected to be a relatively slow development. There are statistical techniques to improve data called sub-pixel analysis or spectral unmixing (Somers et al., 2011; Veganzones and Graña, 2008), but these too have limitations and will require further development before they can be deployed at a pan-European scale. Satellites mostly collect optical data, which are sensitive to cloud cover as overpass times are fixed. Some satellites collect LiDAR or radar data, radar satellites are less affected by clouds.

5.2.7.2 Potential scope

The potential scope strongly depends on the data processing; many variables can be derived from remote sensing. However, most studies are strongly area and species dependent, and currently not suitable to be deployed at a pan-European scale without further calibration and validation. However, once properly calibrated, these techniques could offer continuous information on many aspects of small-scale pollinator habitats. In particular, this could include monitoring of vegetation type development, floral cover, and nectar plant availability. In addition, many small-scale habitat structures and other measures could be developed to provide valuable information on pollinator habitat characteristics. There are examples of remote sensing to analyse nesting resources, flower abundance, vegetation structure, plant species composition, elevation, moisture content and landscape composition.

The derivation of these measures from satellite data would be ideal, as it allows for completely automated processing, whereas UAVs and aircraft require a continuous investment. However, satellites are currently limited to a resolution of ±0.3 m; therefore, the desired resolution strongly affects the choice of platform (UAV, airplane or satellite).

The applicability of pollinator habitat analyses using remote sensing strongly depends on the scale and the metrics derived from the raw data. In general, the effectiveness of a metric will strongly depend on its data requirements. It is possible to model the habitat requirements of a single bee species, this will require significant calibration and is therefore unlikely to perform well when analysing other species, or habitats on a pan-European scale. These highly specific models are generally equally sensitive to disturbance and hence are less likely to continuously perform well across Europe. A broader approach seems to perform better, a number of recent studies showed potential for high-resolution remote-sensing technology (using UAVs) to create baseline maps of key pollinator foraging resources across entire farmed landscape (Barnsley et al., 2022; Gonzales et al., 2022). However, the availability of highly detailed habitat information at larger scales (e.g. European) is still a challenge. Cooperation with existing data sources (such as the European Vegetation Archive) would be potentially beneficial.

5.2.7.3 Current status and remaining development time

A wide variety of parameters can already be derived from remote sensing. Using UAVs, vegetation can be mapped (Cruzan et al., 2016); for example, the flower richness in peach-tree orchards (Horton et al., 2017) and cotton flowers have been mapped (Xu et al., 2017). However, in these cotton fields, the flower count was underestimated because many flowers were hidden by leaves (Xu et al., 2017), which is expected to be a problem in many pollinator habitats, especially densely wooded areas with basal flora. A recent study looking at the landscape matrix as a whole using satellite data found a reasonable relationship between spatial statistics representing the landscape structure and in situ collected bee diversity and species richness data (Hofmann et al., 2017). More recently, some studies have shown that multispectral airborne imagery with 3 cm and 7 cm spatial resolutions can be used, for instance, to classify five nectar-rich flowering plant species (Barnsley et al., 2022). A recent JRC technical report has been published describing the quantification of landscape features at the European scale based on the Land use/cover area frame statistical survey (LUCAS[114]) transect data (Czúcz et al., 2022), but spatially explicit information is not provided at this stage. The above-mentioned report, highlights that the monitoring survey European Monitoring of Biodiversity in Agricultural Landscapes (EMBAL[115]) (see section 2.10) is the only EU-

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[114] https://ec.europa.eu/eurostat/statistics-explained/index.php?title=LUCAS_-_Land_use_and_land_cover_survey

[115] https://wikis.ec.europa.eu/pages/viewpage.action?pageId=25560696

level harmonized data collection initiative that will be able to collect information about the quality (condition) of the landscape features, and that will provide Europe-wide ground truth data for remote sensing products, such as Copernicus High Resolution Layers (HRL) and the future LUCAS LF module (see section 2.10).

Across Europe, an increasing number of countries (Denmark, United Kingdom, Netherlands, Finland, Italy) are performing and sharing nation-wide or regional airborne surveys with light detection and ranging (LiDAR) technology, providing meter resolution terrain and habitat/vegetation structure information. Some countries (e.g. Denmark and Netherlands) have already conducted repeated surveys, thus providing multi-temporal LiDAR data for monitoring biodiversity and habitat change (source: MAMBO project).

Currently processing algorithms can derive detailed vegetation properties for small areas or provide coarse information nationwide. To study pollinators at a pan-European scale, highly detailed information on a large scale is required. The algorithms to establish the vegetation properties will have to be developed and tested further before they can be widely deployed. This is independent of the collection platform, and the (floral) differences between countries cannot be addressed by simply increasing the data resolution. We expect this will take between 10 to 15 years, depending on the variable under study. The development of remote sensing tools with sufficient resolution to identify individual flowers at a broad spatial scale for a wide range of plant species is expected to take even longer (maybe 15 to 25 years) although some examples are developing (Mann et al., 2022; Stanski et al., 2021).

5.2.7.4 Requirements

The requirements of these methods strongly depend on the data collection platform. For UAVs, the most important requirements are the device itself, legal permission to fly (applicable legislation will differ between countries), processing software, and computation and storage resources. For airplane and satellite-based remote sensing, only processing software, computation, and storage resources are required. All platforms require the development of new algorithms to process data on a large scale. The complexity of these algorithms depends on the variable(s) to be derived.

5.2.7.5 Estimated costs

The cost of these methods varies greatly and strongly depends on the desired information and therefore the most appropriate platform, spatial and temporal resolution. Currently, a high-resolution (0.5 m) commercial satellite image costs ±€15 per km^2, and a temporal resolution of multiple times a year is required for most variables. Therefore, monitoring a single site would cost about €300 (assuming 5 km^2 per site and four time slices); note that this does not include any processing or analysis. Aerial photography costs about €10 per km^2 and would therefore cost about €200 per year per site. A suitable UAV costs €2,000-€6,000 to buy. Assuming one UAV can be shared between 10 sites, this would cost €300-€600 per site for the first year. Increasingly companies can provide a complete service, which avoids the need to acquire UAVs, and can allow access to the latest technology. It is important to recognise that the UAV will have operating and software costs, which are not currently included here as they are highly variable depending upon type and application, whereas operating costs are already included in the other methods in this section. All methods need additional data processing by a technician with at least graduate level education, and storage facilities.

5.2.7.6 Advantages

Remote sensing is likely to become a relatively cheap and effective way to monitor landscape composition and development on a large scale. With airplanes or satellites, it is not necessary to negotiate access to areas, and a large number of variables can be automatically collected. It is likely that high-resolution landscape data could be useful in various other (not pollinator-related) studies.

5.2.7.7 Disadvantages

The disadvantages are mainly platform-dependent. Although rules are country-dependent, the regulations for UAVs are increasingly strict; in most European countries, rules are already in place (Stöcker et al., 2017). Rules will likely differ between countries, making this method difficult to deploy in a multi-country monitoring scheme. Aerial photography strongly depends upon the availability, pricing, and schedule of specialised companies. Satellites can collect data only at set times and cannot change their trajectory when the weather is unsuitable for data collection (e.g. clouds). The resolution of satellites will have to improve substantially before landscape characteristics, such as flower richness, can be estimated reliably on a large scale. Additionally, for all platforms, only the top ‘layer’ of vegetation is observed, and this can induce errors when estimating specific vegetation properties, such as flower richness (Xu et al., 2017). This could be partially addressed in the processing phase, but a top-down view might not contain all the information (e.g. in forests with closed canopy). Finally, reliable algorithms to identify a broad range of flowers are not yet available, and it remains unclear if the top layer of vegetation will have sufficient information to identify species or establish individual flower counts, especially when floral resources are stratified such as in woodlands with basal floral communities. It is also important to note that although a detailed flower count would be very valuable, it does not necessarily translate directly into nectar or pollen availability or habitat quality (Baude et al., 2016).

5.2.7.8 Possible future development

A high-resolution dataset on numerous landscape properties, such as flower and nectar or pollen availability, vegetation type and vegetation development, could be very valuable, as it can also help identify possible causes behind the decline and hence potential beneficial management. To include these techniques in EU PoMS now requires significant development of techniques and tools to address scaling issues (recognising vegetation on a large scale, with multiple species etc.). Therefore, we recommend remaining informed of projects that can develop these tools. It seems likely these tools will be developed in the near future, at which point they can provide a valuable contribution to pollinator protection and habitat mapping.

5.2.8 DNA barcoding

5.2.8.1 Description

DNA barcoding is a method that leverages the nucleotide variation of short DNA sequences of selected gene regions (DNA barcodes) to identify taxa. To identify an organism, four main steps are performed: (i) DNA is isolated from it; (ii) the DNA barcode region is amplified using Polymerase Chain Reaction (PCR); (iii) the PCR product is sequenced using Sanger technology; and, (iv) the resulting sequence is compared with orthologous sequences present in reference databases and assigned to a taxon based on the similarity with a reference sequence. The primary DNA barcode used for identifying the members of the animal kingdom is a fragment of the cytochrome c oxidase I (COI) gene of about 650 base pairs (Ratnasingham and Hebert, 2013). Universal primers (e.g. Folmer et al., 1994) or clade specific primers are used to amplify the barcode region. An almost complete list of the primer pairs developed for amplifying the COI region used as DNA barcode is available in the Primer Database of the BOLD System. However, not all species can be distinguished using COI marker. Thus, DNA sequences from other markers, such as the ribosomal 16S rRNA or the 12S rRNA, are also used as DNA barcodes for specific clades. Regarding the tools that can be used to perform the taxonomic assignment of the barcode, the most used and promising one is the Identification Engine available on the BOLD Systems[116], which provides the users with the probability of assignment to a specific taxon of the query barcode in addition to the information about the Barcode Index Number (BIN). The interpretation of these results does not require an expert in bioinformatics but simply basic knowledge of taxonomy. At present, the BOLD database includes about 12 million insect COI sequences, corresponding to 253,491 species (retrieved on November 20th, 2023). The TRL is estimated at 7; the technique has been demonstrated in the operational environment. The gaps in the reference sequence databases prevent it from reaching the next level (TLR 8, system complete and qualified), but likely the efforts that are being made for improving the species coverage of these databases (projects founded also by EU Commission, e.g. BIOSCAN) will reduce this gap soon.

5.2.8.2 Potential scope

DNA barcoding can potentially be used to identify taxa from a small fraction of a specimen (e.g. a leg or a wing), preimaginal stages, or even eggs, which are usually not easy to be identified using the morphological approach. The method reduces the dependence on knowledgeable species experts for the identification of species that are difficult to distinguish morphologically. It can also help the discovery of new species (Hebert et al., 2004). However, it is mandatory to maintain expertise in morphology-based taxonomy to complement molecular identification methods such as DNA barcoding or DNA metabarcoding (Piper et al., 2019). A proof of concept using this technique in combination with pan trapping is available (Creedy et al., 2020). There are no complete reference databases for taxa identification using DNA barcodes (and likely they will never include the barcodes of all species described for several reasons), but they mainly lack the barcodes of rare species. At the moment, the most inclusive and accurate database for insects identification is the BOLD system.

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[116] https://v4.boldsystems.org/

5.2.8.3 Current status and remaining development time

The technique is currently used for the identification of different taxa. However, its applicability is related to the completeness of the DNA barcode reference databases. To use this technique on a pan-European scale, the reference barcodes for the majority of the European species have to be stored in curated databases, such as those part of the International Nucleotide Sequence Database Collaboration[117] (INSDC), that are GenBank, the European Nucleotide Archive (ENA), and the DNA Data Bank Japan (DDBJ), and the Barcode of Life Data System[118] (BOLD); in the last two decades, some initiatives have been started to promote DNA barcoding use and develop large numbers of barcode sequences. Among them, the Consortium for the Barcode of Life (CBOL) was initiated by the University of Guelph and launched in 2004, intending to promote DNA barcoding as a new scientific standard (Ratnasingham and Hebert, 2007). Moreover, the International Barcode of Life[119] (iBOL) project began in 2007, which is a research alliance of nations with the aim to "Create a digital identification system for life that is accessible to everyone". The iBOL is now a consortium with 40 member nations and 7 associate member nations. The member nations are represented by networks of researchers or organisations in a country that are engaged in or supporting DNA barcoding as part of iBOL. Among European countries members or associate members are: Austria, Belarus, Bulgaria, Finland, France, Germany, Greece, Italy, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Spain, Switzerland, Turkey and the United Kingdom. In the first programme of iBOL, called BARCODE 500K, 500,000 species were barcoded between 2010 and 2015. The second program is BIOSCAN[120] , which started in 2019 and will end in 2026, with the aim, among others, to barcode another 2 million species. A third program named Planetary Biodiversity Mission will start in 2026 and end in 2045, with the mission of barcoding all multicellular species.

Regarding BOLD, this database includes data that are entered directly into BOLD as well as data gathered from other national databases. Among the species of interest whose barcodes are registered in this database, are bees, butterflies and hoverflies. A relatively high proportion of barcodes of Lepidoptera are registered there, i.e. those of 104,780 lepidopteran species, 80,055 of which are publicly available (information updated in November 2023), representing approximately 64% of the Lepidopteran species described worldwide (until 2019 just the ~ 57% of the lepidopteran species were barcoded). The barcodes of 2,605 species (63,694 specimens) of the family *Syrphidae* (hoverflies) are available (the family currently counts about 6,000 species). In the order *Hymenoptera*, there are over 150,000 described species, and for 49,385 of them the barcodes are available in the BOLD System. For *Apidae*, the largest family of bees consisting of 5,700 described species, there are barcodes for 3,167 (44,746 specimens). It should be noted that uncertainties in the morphological identification of the specimens from which COI sequences were obtained could not be excluded.

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[117] https://www.insdc.org/

[118] http://www.boldsystems.org/

[119] https://ibol.org/

[120] https://www.bioscaneurope.org/

5.2.8.4 Requirements

Specimens have to be collected and stored in absolute ethanol (preferably conserved at -20°C). Minor pre-processing (e.g. specimens sorting) can be conducted at a local institute before sending the samples off to a molecular biology lab where the DNA is extracted and the selected DNA barcode region amplified by PCR. Then, the PCR products are sent to a sequencing service, which returns the electropherograms of the amplified region. After electropherograms checking, the sequences can be compared with those in the reference databases to obtain the identifications. The results can be interpreted by staff trained with basic bioinformatics (about 5 hours of training) and taxonomic skills. Therefore, the requirements are: (i) minimal training of volunteers who collect the specimens; (ii) specialised labs to extract the DNA, perform the PCR and sequence the PCR amplicon; (iii) trained operators to interpret the results.

5.2.8.5 Estimated costs

The costs of molecular identification using DNA barcodes, from DNA extraction to sequencing results, strongly depend on the number of processed samples. Roughly, the out-of-pocket costs are estimated between €5 to €20 per sample and change depending on the price of the DNA extraction kit/protocols, consumables and sequencing service used.

5.2.8.6 Advantages

The collection of the organisms can be done by volunteers. It is possible to identify individuals at any developmental stage using their DNA. Species experts are not needed for species identification to the same extent as morphological species identification. It is possible to obtain the DNA by collecting only a small part of a specimen, so the method is not necessarily destructive. For example, for insects only a small piece of the body (e.g. a leg) can be used in the DNA extraction, thus making it possible to keep the specimen more or less intact for future analysis.

5.2.8.7 Disadvantages

Individuals (or a small part of them) have to be collected to obtain DNA. Specialised molecular biology laboratories are required for DNA extraction and external services are needed for sequencing. To interpret the results, the staff has to be trained. Reference databases do not include all the described species and often miss rare species; moreover, they have to be rigorously curated and maintained.

5.2.8.8 Possible future development

The costs are expected to decrease further, and the entire process will likely become more efficient. DNA barcoding coupled with emergent technologies such as BIODISCOVER[121] or DiversityScanner (Ärje et al., 2020; Bjerge et al., 2022; Wührl et al., 2022), which allow specimen sorting automatisation, can be considered promising to speed up the sorting/identification process. This technique strongly depends on the completeness of the reference databases, whose improvement is ongoing. Therefore, a promising way forward seems to pair DNA barcoding with pan trapping for a limited amount of time. Species that are identified by experts are also barcoded, up to 50

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[121] https://www.researchgate.net/figure/BIODISCOVER-machine-for-imaging-invertebrates_fig1_339164433

individuals per species. This will rapidly improve the databases, both in quantity (number of species) and quality (as this provides data validation).


Andrena cineraria & Apis mellifera, Axel Hochkirch

5.2.9 DNA metabarcoding

5.2.9.1 Description

DNA metabarcoding can be considered as an expansion of DNA barcoding allowing the identification of multiple taxa simultaneously starting from samples containing DNA from more than one organism. The method allows the identification at the species level or above (as in the case of DNA barcoding, the depth of the taxonomic assignment is dependent on the completeness of the reference database used) starting from the specimen whole body, body parts or their DNA molecules dispersed in different matrices (eDNA), e.g. water, air, soil, faeces or pollen, etc. The method combines DNA-based identification and high-throughput Next Generation Sequencing (NGS) technologies. Commonly, universal PCR primers are used to amplify selected DNA regions (barcodes). Nowadays, the available sequencing technologies (e.g. PacBio Sequel) allow the amplification of long DNA barcodes, if the template DNA is not fragmented (eDNA is usually degraded). The TRL of this technique is estimated at level 6, the technology having been demonstrated in relevant environments.

5.2.9.2 Potential scope

DNA-based methods, including DNA metabarcoding, are revolutionizing the field of environmental monitoring. For some environmental compartments and taxonomic groups, the TRL is more advanced (e.g. aquatic biomonitoring; (Pawlowski et al., 2022)). DNA metabarcoding allows the identification of organisms belonging to different species simultaneously starting from bulk or environmental samples, and thus it is very useful in biomonitoring studies, including biodiversity surveys. However, since the taxonomic assignment procedure of DNA metabarcoding reads relies on the available reference databases, the method suffers the same limitations of DNA barcoding (i.e. the taxonomic completeness of the reference databases). Moreover, it is currently not reliable for quantitative diversity assessments. The difficulty in estimating taxa abundances mainly comes from the biases generated by the use of the PCR approach (Krehenwinkel et al., 2017), leading to the lack of an exact correlation between the number of reads generated for a taxon and its abundance in the sample. Even though many studies focused on the establishment of this quantitative correlation, there is still little consensus (van der Loos and Nijland, 2021). The accuracy of qualitative and quantitative estimates can be influenced by both biological and technical biases. For example, organisms with larger biomass could be better represented in environmental samples than those with smaller biomass. Polymerase choice is on the contrary a potential source of technical bias, since this enzyme can preferentially amplify some barcodes instead of others due to their GC contents (Nichols et al., 2018). Moreover, different primer pairs can have different amplification efficiency on the target taxa, due to mismatches with the template DNA at the 3’ site of the primer. To overcome some of these issues, other innovative and promising approaches such as PCR-free approaches (Linard et al., 2015) that can be used (Gauthier et al., 2020; Linard et al., 2016). However, when adopting them, increased costs to generate the barcodes and greater bioinformatics effort for their analysis have to be addressed. Importantly, the classical DNA metabarcoding approach can be used in biomonitoring programs when only qualitative information (presence and absence of taxa) is required. There are several advantages in its implementation within insect monitoring schemes: (i) it may be a means to scale up insect surveillance by increasing the number of samples that can be processed within a certain time, and to reduce the time needed for sorting and identify specimens collected with Malaise or pan traps for instance; (ii) it allows the identification of degraded/partially preserved organisms that cannot be identified by morphological examination or from the DNA they released in the living environment (eDNA); (iii) it can be adopted for the development of more efficient invasive alien insect surveillance programs. Even the collection fluid from pan traps can be processed rather than the bulk of organisms themselves, since it contains the eDNA of the target organisms, in the same way it has been done for the ethanol in which the organisms were stored (Hajibabaei et al., 2012).

DNA metabarcoding can be also used to study plant-pollinator networks by identifying pollen samples collected from different insect species. This approach has been tested in several studies and in different landscape contexts giving highly promising results for the reconstruction of plant-pollinator interactions (e.g. Baksay et al., 2022; Bell et al., 2017; Galliot et al., 2017; Lucas et al., 2018). Pollen can also be collected from specimens preserved in old collections of insects, such as museums, to determine historical plant-pollinator networks (Gous et al., 2019). Like for insects, the successful characterization of the plant species through DNA based identification depends on the availability of comprehensive barcode reference databases. The information on plant-pollinator networks obtained through DNA analyses of pollen samples may have implications for the design of agri-environment schemes (Gresty et al., 2018). DNA metabarcoding has also been used for the determination of the main pollinators of certain plant species, using ‘sticky flowers’ placed near the plants (Tiusanen et al., 2016).

When working with metabarcoding it is important to keep research setup and corresponding biases in mind. Several studies have pointed out that these biases can lead to erroneous conclusions (Abarenkov et al., 2010; Zinger et al., 2019).

5.2.9.3 Current status and remaining development time

The method has to be seriously considered for large-scale monitoring programs aiming to recover the presence/absence of taxa, even the rare ones since the reference databases species completeness is rapidly improving. BIOSCAN[122] Europe initiative is currently performing the gap analyses on reference DNA barcoding marker databases for European species, which will lead to understand of which European species reference barcodes need to be developed. Their development will further increase DNA metabarcoding accuracy in terms of species determination in the near future.

5.2.9.4 Requirements

Similar to DNA barcoding, collection and pre-processing can be conducted by minimally trained volunteers. Samples have to be processed in molecular biology labs, while the analysis of NGS data requires experts in bioinformatics but the obtained results require minimal effort for their interpretation. Likely, bioinformatics expertise will soon no longer be required since apps are being developed to directly process the outputs of the NGS sequencing platform and provide the final table with the detected taxa list. Since high numbers of data are produced for each sample processed, large technical infrastructure and storage capacity are required, especially in the case of application of this methodology in long-term monitoring programs.

For using the method in large scale monitoring programs, samples collection and processing procedures have to be standardized (e.g. samples collection, DNA extraction procedures, PCR primers, bioinformatics pipelines) to obtain repeatable and comparable results (e.g. Bruce et al., 2021; Dickie et al., 2018).

5.2.10 Estimated costs

The costs for processing a bulk insect sample for DNA metabarcoding analyses are rapidly decreasing, mainly due to the rapid decrease of NGS costs. On average, the cost of processing one bulk sample and obtaining DNA reads of one DNA marker using the NGS platform spans from €25 to €60 (DNA extraction, library preparation and NGS sequencing), depending on the required sequencing depth and the number of processed samples.

5.2.10.1 Advantages

Similar to DNA barcoding, the collection of samples suitable for DNA metabarcoding can be done by volunteers with some training or through expert networks as standardisation of the trapping is critical. The interpretation of the DNA metabarcoding results, in terms of organism identification, does not require specific expertise, just basic knowledge that can be achieved in a one- or two-day workshop. The technology allows the processing of high numbers of samples in a relatively short time, which might be particularly useful if large numbers of specimens are collected from transects

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[122] https://ibol.org/bioscan/

and/or pan traps as part of EU PoMS. Additionally, this technique could potentially give insight into plant-pollinator relations when pollen DNA is extracted.

5.2.10.2 Disadvantages

As for DNA barcoding, the taxonomic completeness of the reference sequence databases represents an important aspect to be considered. However, the increasing effort of the past years in improving barcode reference databases will contribute to reducing the gap soon. For several reasons, reference databases are unlikely to include all the described species, and in particular those that are particularly rare and/or threatened. However, this aspect does not prevent the effective application of the DNA metabarcoding approach in biomonitoring the presence/absence of taxa mostly because the species lacking from reference databases are mainly the rare ones. Another disadvantage regards the lack of universality of the primers and the biases that can derive from their use, e.g. missing information on the presence of certain taxa. Currently, DNA metabarcoding for metazoans does not allow quantitative diversity assessments in terms of number of individuals; however, a correlation between the number of reads generated for a taxon and its biomass in the sample is present (Bista et al., 2018).

The raw sequence data provided by the NGS sequencing service have to be analysed through dedicated pipelines in order to obtain the taxonomic assignment of the organisms. This procedure requires the appropriate bioinformatics expertise and computational resources. Online tools allowing the proper analysis of raw DNA metabarcoding data with limited bioinformatics expertise (achievable in a two/three-day workshop) have been recently published (e.g. mBRAVE[123]). In the future, it is likely that even more user-friendly applications will be developed.

5.2.10.3 Possible future development

The metabarcoding technique is in rapid development. However, the results strongly depend on the availability of reference data. Reference databases are rapidly being developed too in the context of projects such as BIOSCAN and ARISE[124]. To support the development of reference databases, species identified by experts (the current processing method of pan trap samples) can be added to these databases. Therefore, similar to DNA barcoding, a promising way forward seems to pair these two methods for a few years, possibly adding an imaging step to enhance this cheaper and more scalable method as well. Species that are identified by experts should also be barcoded and imaged, up to 50 specimens per species. This will rapidly improve the databases, both in quantity (number of species) and quality (as this provides data validation).

5.2.11 Conclusions and recommendations

Emerging technologies are rapidly developing and can potentially have a large effect on future pollinator monitoring schemes. A summary of the leading emerging technologies is provided in Table 5.2. 1, which gives the estimated Technology Readiness Level, advantages, disadvantages estimated costs and future development requirements for each technology separately.

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[123] https://www.mbrave.net/

[124] https://www.arise-biodiversity.nl/

Overall, image recognition and DNA based techniques show great promise. The image recognition-based camera trap has been developed to the point where it can be broadly tested in several European countries. Ideally, these traps should be paired with another monitoring system (e.g. LED traps, section 0, or Malaise traps, section 5.4). This will help establish how strong the effect of repeatedly counting an individual is on abundance estimates. If these traps can provide reliable abundance data, they can contribute significantly to the pollinator dataset going forward. Other image-based monitoring tools are also highly interesting but are less mature. The *in-situ* insect cameras for diurnal pollinators such as bees, butterflies and hoverflies will also need further study into the visitation rates at the traps and additional study into the effects of temporally dynamic floral resources as their attractive nature causes them to compete with local floral resources. The lab-based specimen identification based on image recognition can become highly beneficial in the near future. If this is developed to the point where it can reliably be deployed, it could drastically decrease the costs of pan trap bulk sample processing. However, further development and testing and improved training datasets will be required before it can be widely deployed.

Acoustic technologies also show great promise, as they can potentially provide unique data that can be collected on a large scale without landscape-dependent biases. However, at this point, it is unclear which species can be monitored with acoustic sensors and how well these species can be distinguished based on their sound, especially on a European scale. This technique will likely require significant continued development before it can be useful within the context of the EU PoMS.

Habitat mapping using UAVs or satellites is already available to an extent; however, to apply it on a large enough scale to be useful in European context will require additional development. This technique does not produce data on pollinators directly but focuses on their habitat. Therefore, it could be used to assess the impact of management on the landscape, which could be very valuable when assessing if subsidies or regulations have the desired effect. We recommend letting this technique develop further and reassess the potential benefits and required effort again in a few years.

DNA barcoding and metabarcoding can potentially decrease dramatically the costs of pan trap processing and speed up this process. The pan traps would still produce presence-absence level data. However, their usefulness strongly depends on the availability of reference databases. These are rapidly being developed but are currently not complete. There are several ongoing large projects to improve this, and both the coverage and the data quality of these databases are improving quickly. These analyses are currently fairly expensive, but costs are expected to drop as the use of these techniques becomes more common.

We strongly recommend supporting image-based moth monitoring by starting a large-scale pilot to further test and refine the insect camera traps. We further recommend supporting the development of an image library of pollinator species to support the specimens-based identification of pollinators from bulk samples in the lab and to contribute to the completion of DNA reference databases for pollinators. This can be done by offering the already identified species from sweep netting and pan trapping efforts as reference samples, which should quickly improve the coverage of these databases.

Finally, we recommend monitoring the development of the other methods, as these are currently not at a level where they can be quickly incorporated in the EU PoMS, but can provide large benefits later.

Table 5.2. 1. Overview of the leading emerging technologies.

Name	**Technology Readiness Level (TRL)**	**Advantages**	**Disadvantages**	**Costs**	**Future development**
Citizen Science portals	9	Motivating citizen scientists Knowledge sharing Large amount of data	Data not representative Data quality unknown Data processing difficult	-	Important knowledge sharing tool, stay informed.
Moth monitoring image recognition	8	Non-lethal sampling Easy to deploy Requires no expertise Proven to be effective (large statistical power) Validation is possible (images stored) Low costs	Limited to moths Does not capture all moths (but most) Cannot be used near other light sources Has to be emptied in the morning (for non-lethal sampling)	€100 per trap, €75 per visit by expert	Ready for deployment, investment in network and coordination required
In situ insect camera	5	Non-lethal sampling Large amount of data collected Validation is possible, images stored Requires no expertise	Only presence absence data or low detection chance Poor image resolution per insect Theft potential	€3,000-€6,000 per camera	Study on attraction dependence required

Name	Technology Readiness Level (TRL)	Advantages	Disadvantages	Costs	Future development
Dead specimen image recognition	5	Reduces lab work expertise and costs	Technically sophisticated, maintenance requires skill	€5,000-€20,000 per machine	Large potential, further testing and development required. Next step is a broader test on existing material.
Acoustic approaches	3	Large dataset No environmental bias	Possible repeated 'captures' Identification to species level impossible? Relation of sound and abundance unclear Technique sensitivity unclear	€500-€1000 per device	Large potential, further testing and development required. Next step is a pilot study.
Habitat mapping	6	Relatively cheap Large study area Useful in many other contexts (e.g. management/subsidy effect studies)	No direct information on pollinators Rules and regulations differ per country Information depends on habitat type (grass or forest)	€15-€200 per site	Requires further development and scaling. Stay informed.

Name	Technology Readiness Level (TRL)	Advantages	Disadvantages	Costs	Future development
DNA barcoding	8	Collection requires no expertise Only a small part of specimen required (rest can be stored)	Collection required Expertise may sometimes be required to interpret results Strongly dependent on reference databases	€5-€20 per sample	Reference databases are the bottleneck, these are improving. Potentially pair with expert identification to expand databases and verify quality.
DNA metabarcoding	6	Collection requires no expertise Samples can be processed quickly Pollen DNA can also be extracted	Strongly depends on reference databases, which are incomplete PCR Primers cause bias Data interpretation requires expertise	€25-€60	Reference databases are the bottleneck, these are improving. Potentially pair with expert identification to expand databases and verify quality.

Source: Authors' elaboration.

5.3 Options to include genomic-level monitoring

5.3.1 Summary

Genetic diversity within populations plays a pivotal role in ensuring the survival of species, especially under current rapid environmental change driven by human-induced climate shifts and habitat fragmentation. Populations with high genetic diversity exhibit heightened adaptive capabilities, long-term survival, and increased resilience. Therefore, it is crucial to systematically monitor the genetic diversity of wild populations to implement the most effective conservation strategies that maintain their well-being. Various genomic approaches can be applied for monitoring population genetic diversity (e.g. whole genome sequencing, reduced representation sequencing), with each having specific advantages and limitations, and these have been assessed here. Given the high importance of pollination as an ecosystem service, we propose a four-step genetic monitoring program for pollinator species:

1. Conduct an initial pilot study for monitoring the genetic diversity of four selected species representing the main target pollinator groups of the core scheme (i.e. wild bees, hoverflies, and butterflies).
2. Assess and refine parameters of the selected genetic monitoring approach, considering also the potential development of expedited monitoring methodologies such as Single Nucleotide Polymorphisms (SNP) chips.
3. Evaluate and adjust the pilot study program for optimizing results (e.g. specimen sampling strategies optimization, need for extended geographic or temporal coverage, need for extended focus on specific regions).
4. Design DNA-based monitoring programs for additional pollinating species in the EU based on insights gained from steps 1-3. Use Essential Biodiversity Variables (EBVs) and indicators based on EBVs (similar to the Swedish and Swiss national programs) for monitoring genetic diversity with DNA-based methods. In parallel, evaluate the potential for using proxy-based indicators that do not require DNA-data but focus on population census size and population maintenance, which have been suggested and adopted in the context of the Convention on Biological Diversity (CBD).

Indicators to detect main threats to genetic diversity have recently been designed and implemented. Both DNA-based indicators and proxy-based ones exist, and their use is initiated in pilot work. Genetic diversity occurs within and between populations of the species. Thus, main losses in genetic diversity occur when single populations are too small to secure adaptive capacity (their effective population size, Ne, is below 500) and when genetically distinct populations are lost. Ideally, these trends are monitored with DNA-based measurements that allow: (i) identification of genetically distinct populations within species; (ii) monitoring of the degree of genetic exchange between populations over time; (iii) assessing of the effective population size of individual populations; and (iv) other types of genetic diversity estimates (such as heterozygosity, allelic richness nucleotide diversity, inbreeding levels, etc.). Two countries that have developed and started to apply DNA-based indicators are Sweden and Switzerland, and a few pollinators are included in their programs.

Pragmatic proxy-based indicators for genetic diversity have been developed as a complement to DNA-based monitoring. Since DNA-techniques can be adopted only by relatively rich countries and for a limited set of species, proxy indicators are helpful for rapid, cost-effective assessments of species for which information on population existence and approximate census size are available. Frequently, such data have already been developed and are accessible in Red List databases, species Action Plans, Citizen Science data, scientific publications, reports and from expert consultation. The proxy-based indicators have recently been assessed for over 900 species, including several pollinators, in nine countries. Both DNA-based and proxy-based lines of monitoring genetic diversity are suggested to be initiated within the EU Pollinator Monitoring Scheme. However, DNA-based monitoring is the most relevant and important approach to be adopted since population structure and census sizes are often not available for pollinator insects.

5.3.2 Introduction

Genetic diversity is variation within species that occurs at the DNA level. Specific parts of DNA such as those providing the code for a specific protein product (a coding region = a gene) can occur in different DNA sequence variants – so-called alleles (Allendorf et al., 2022). Genetic diversity occurs within species as variation in allele occurrence within populations and between populations. Between-population genetic diversity can reflect genetic adaptations to local environmental conditions (Hoban, Paz-Vinas, et al., 2021). Decades of population and conservation genetic research have demonstrated that populations with high genetic diversity are typically characterized by higher adaptive capacity, good potential for long-term survival, and high resilience. Thus, within population genetic diversity helps populations adapt to environmental change.

5.3.2.1 The importance of genetic diversity for adaptive potential

To assure the best possible opportunities for species to survive in the current times of very rapid environmental perturbations due to human induced climate change, habitat decline and fragmentation, it is crucial to maintain as high level of genetic diversity within and between populations as possible (Hoban, Paz-Vinas, et al., 2021). This conclusion is recognized by the scientific community (e.g. Allendorf et al., 2022; Frankham et al., 2010) as well as by global biodiversity policy agreements; the UN Convention of Biological Diversity[125] (CBD) entered into force in 1993 and stipulates that biodiversity at the levels of ecosystems, species and genetic diversity should be mapped, monitored, conserved and used sustainably. An updated global biodiversity framework was negotiated by CBDs 15th Conference of the Parties (COP15) in Montreal in December 2022. This Kunming-Montreal Global Biodiversity Framework (KMGBF) is very clear in its Goals for genetic diversity of all wild (and domestic) species. Its Goal A states that the following should be reached to 2050 (Convention on Biological Diversity, 2022a): “The genetic diversity within populations of wild and domesticated species is maintained, safeguarding their adaptive potential.”

The KMGBF Target 4 to be reached by 2030 says parties need to (Convention on Biological Diversity, 2022a): “Ensure urgent management actions to … maintain and restore the genetic diversity within and between populations of native, wild and domesticated species to maintain their adaptive potential, including through in situ and ex situ conservation and sustainable management practices”.

The fact that the importance of genetic diversity to assure adaptive potential of wild populations is recognized is a strong step forward that has been preceded by very active work by the scientific community (Díaz et al., 2020; Hoban et al., 2020, 2022, 2023; Hoban, Bruford, et al., 2021; Hoban, Paz-Vinas, et al., 2021; Laikre et al., 2020, 2021). This work involved the network of scientists of the EU Cost Action project G-BiKE[126] (Genomic Biodiversity Knowledge for Resilient Ecosystems) who together with three additional conservation genetics expert groups (the IUCN Conservation Genetics Working Group, the Society for Conservation Genetics Working Group and the GEO BON Genetic Composition Working Group)

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[125] www.cbd.int

[126] www.gbikegenetics.eu

formed the Coalition for Conservation Genetics[127]. The work of these initiatives has included proposing pragmatic indicators to monitor trends in genetic diversity (Kershaw et al., 2022). Two of the proposed indicators can be assessed with proxies in the absence of DNA-based information; however, their estimates based on DNA information are more accurate.

5.3.2.2 Pragmatic proxy-based indicators to monitor trends in genetic diversity

Trends in genetic diversity have not been monitored systematically to date, largely due to a long period of poor implementation of the CBD with respect to genetic variation (Bruford et al., 2017; Laikre, 2010; Laikre et al., 2010, 2016). A couple of recent studies, however, indicated current substantial loss of genetic diversity within populations of vertebrates and plant species (Exposito-Alonso et al., 2022; Leigh et al., 2019).

Pragmatic indicators for genetic diversity designed for the CBD context have been proposed by researchers forming the Coalition for Conservation Genetics and associated groups (first introduced by Laikre et al. (2020) and further developed by Hoban et al. (Hoban et al., 2020, 2023; Hoban, Bruford, et al., 2021; Hoban, Paz-Vinas, et al., 2021; Laikre et al., 2021). These three indicators are: (i) the proportion of populations within species with effective population size (N_e) above 500 (called N_e500 indicator); (ii) the proportion of distinct populations maintained within species (the PM indicator); and (iii) the number of species and populations in which genetic diversity is being monitored using DNA-based methods (the DNA-based indicator).

Ideally, the indicator (iii) is used to assess (i) and (ii), but for most countries assessing large numbers of species for their genetic diversity is not possible and thus, indicators (i) and (ii) can also be assessed using census size and population occurrence as proxies (Hoban et al., 2020), and e.g. Red List data provides opportunities for estimating such proxies (Thurfjell et al., 2022). To use census size as proxy, we use the commonly observed relationship between N_e and N_c of 0.1 – i.e., N_e is typically 10 percent of the census size (see (Hoban et al., 2020, 2023) for more details). A detailed review of available information on N_e/N_c relationship in pollinators remains to be carried out.

Indicator (i) has been adopted as a so-called ‘Headline Indicator’ in the monitoring framework of the Kunming-Montreal Global Biodiversity Framework (Convention on Biological Diversity, 2022b), implying that all parties need to report on it. Work is currently ongoing to apply these indicators in several countries (Hoban et al., 2023) and results from over 900 species (> 5,000 populations) in nine countries were recently presented (Mastretta-Yanes et al., 2024). Although pollinating species are not reported separately in this work, several pollinators were included in the assessments. For instance, in one of this nine countries (i.e. Sweden) 10 pollinator species were assessed. The N_e500 indicator value for these pollinators was 0.03 (i.e. only on average 3% of species populations have an effective size above 500), while the PM indicator value was 0.57, i.e. on average 57% of populations are maintained over time (L. Laikre, personal communication, 2024). There are several challenges with assessing the proxy indicators for pollinators and other insects but clearly this is work is important to pursue in parallel to genomic monitoring efforts. Genomics can also be used to verify the proxy indicators and improve them.

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[127] www.coalitionforconservationgenetics.org

5.3.2.3 Genetic/genomic indicators including Essential Biodiversity Variables (EBVs) for genetic diversity

In parallel to the pragmatic CBD indicators, monitoring programs of genetic diversity using various types of DNA-based methods have been initiated in several countries (Hvilsom et al., 2022; O'Brien et al., 2022). The genetic variables monitored in these programs relate to EBVs for genetic diversity, and include measures of genetic diversity within and between populations (Hoban et al., 2022). For instance, Sweden has a national program for environmental monitoring of genetic diversity which includes three EBV based indicators: (i) ΔH indicator, which is focussed on quantifying trends in genetic diversity within populations and measures trends in EBVs heterozygosity, allelic richness, Watterson´s theta, nucleotide diversity, inbreeding (FROH), and other relevant variables depending on the DNA-techniques used; (ii) N_e indicator that measures the effective population size of individual genetic groups and metapopulations; and (iii) ΔFST indicator that monitors the retention of genetically distinct populations over time, the genetic differentiation between genetically distinct populations and estimates degree of genetic exchange between populations (Andersson et al., 2022; Johannesson and Laikre, 2020, 2022, 2023). These indicators have so far been applied only to a few species, including the Atlantic salmon using SNP arrays (Johannesson and Laikre, 2023; L. Laikre, personal communication, 2024), the brown trout using both SNP arrays (Andersson et al., 2022) and whole genome sequencing (WGS) (Kurland et al., 2024), moose using WGS (Dussex et al., 2023) and Arctic char using WGS (Saha et al., 2024). Several pollinator species are also included in the genetic monitoring programme (see Posledovich et al., 2021) with N_e being assessed as well as EBVs, but not yet trends in EBVs over time (M. Webster and Liu, 2022).

5.3.2.4 Monitoring of genomic diversity of pollinators

Several initiatives for monitoring genetic diversity include pollinating insects (a non-exhaustive and illustrative list of ongoing national programs of genomic monitoring of pollinator species based on internet searches is reported in Table A.5.3. 2 in Annex 5.3. A). In Switzerland, a pilot program of nation-wide genomic monitoring[128] is ongoing using five diverse species including one insect, the false heath fritillary (*Melitaea diamina*). In 2019, the Earlham Institute started a program[129] that uses bumble bee genomics to better understand current threats to United Kingdom pollinator populations. However, it is important to highlight that insects differ in many aspects from vertebrates, which have so far been the main focus of research and management efforts to monitor genetic diversity. Therefore, increased focus on insects is highly warranted (M. T. Webster et al., 2023).

A systematic European assessment of regional or national initiatives monitoring the genetic diversity of pollinators is desirable; this activity can be the basis of an open and centralized platform hosting relevant information of pollinator genomic monitoring programs.

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[128] https://gendiv.ethz.ch/en/pilot-study-for-monitoring-genetic-diversity-in-switzerland/

[129] https://www.earlham.ac.uk/research-project/population-genomics-pollinating-insects

5.3.2.5 Requirements for genomic level monitoring

Several attention points need to be considered when initiating genomic level monitoring with DNA-based techniques:

1. Sampling needs to be standardized and include collection of individuals of focal species that are properly preserved to allow successful DNA extraction (e.g. by rapid freezing or preservation in ethanol). Together with each individual, metadata has to be appropriately collected.
2. Tissue samples of the same organism from which the DNA was extracted and used to generate genomic data need to be stored safely in centralised tissue banks (e.g. LIB biobank at Museum Koenig Bonn[130], Germany) with the aim of long-term storage (for a detailed description of biodiversity biobanking see Corrales and Astrin (2023)). The appropriate preservation of tissues will allow repetition and verification of analyses, and future monitoring with improved techniques.
3. DNA of high quality and concentration needs to be extracted and used for sequencing. It is advisable to store the DNA extracts for future use (although if tissue is stored additional DNA extractions can be performed).
4. The sequencing/genotyping methodology used should be standardized for the geographic area under study allowing the consistent estimation of relevant genetic diversity measures and indicators.

5.3.2.6 Criteria to select target species for genomic level monitoring

A range of criteria should be used to select appropriate target species for EU population genomic monitoring activities. The following main aspects should be considered: (i) the species distribution (focussing on the biogeographic regions of Europe; European overseas territories should be considered also); (ii) the conservation status of the species (relying on the IUCN Red List of Threatened Species); (iii) the rarity of the species (rare vs abundant species); and (iv) the species biology (e.g. social vs non-social, feeding biology of the larvae and other biological traits like number of generations per year, non-migratory vs migratory).

Population genomic monitoring programs can be costly and knowledge, time and funding for them can be limited, therefore they should be focused on adequately selected taxa identified by taxonomic experts. If applicable, umbrella species (Lambeck, 1997), which are defined as species whose conservation is expected to confer protection also to many other naturally co-occurring taxa, should be chosen for genomic monitoring. Species that are readily identifiable using available identification keys should be preferred over hard to distinguish cryptic species pairs or species complexes. For species that are easy to identify, Citizen Science approaches for material sampling may be applied. However, the latter approach must be carefully considered due to the technical requirements of the sampled material (e.g. appropriate preservative solution and storing conditions of the samples to successfully obtain high-quality and high molecular weight DNA), and would require adequate training and support for volunteers, and a logistic protocol for sending samples.

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[130] https://bonn.leibniz-lib.de/en/biobank

5.3.3 Prioritization criteria

The prioritization criteria are here intended as a set of factors that should be considered in selecting the species for a genomic level monitoring program(s). Species prioritisation for genomic level monitoring should be done at the European level, in collaboration with Member States. The process could be guided by an expert working group representing the EC, the Member States and relevant European stakeholders.

In selecting the species for genomic level monitoring programs, it is important to consider both relevant species of interest for a wide number of Member States (e.g. species with a wide range of distribution) as well as species of interest for a more restricted number of Member States (e.g. in case of species with a narrow range). Collaboration with non-EU Countries should also be considered whenever the species range exceeds the EU area. These reported criteria were applied in the open consultation with STING2 expert pool to provide a tentative list of possible and appropriate species for demonstrative pilot studies (Table A.5.3. 1 in Annex 5.3. A).

1. **Species distribution pattern**. Regarding different species distribution patterns, the choice can be made between geographically localized species, which are often endemic, and species with a wider distribution, including those with a distribution across the entire Palaearctic region and beyond. The obvious advantages for using common and widespread species for genomic level monitoring are ease of material collecting, and opportunity to gather a higher number of specimens from denser sampling points and typically across larger geographic areas and over multiple years. Highest weight should be given to species endemic to the EU, as for these the EU has the full monitoring responsibility. An important aspect is the fact that distribution information is often incomplete or outdated for rare insect species. A higher investment in resources, including detailed expert planning to identify correct localities, repeated site visits including taxonomic expert fieldwork time and travel costs over several years, is needed to obtain specimens of rare species.

2. **Conservation status**. Regarding the conservation status of species, the IUCN Red List assessments, where available, can be used as a reference to address prioritisation criteria, even if for some taxa the available information is still limited. Rare and threatened species often represent national and European endemics for which the European Union has a high conservation responsibility to reach internationally agreed targets. The proposal for a rare and threatened species module (RaTS, see section 2.8) estimated ~40% of all insect species are too rare to be covered by a standardised monitoring scheme and that tailored monitoring schemes are needed for these taxa. RaTS proposes a formula to prioritise species for monitoring schemes. A prioritisation mechanism to select species for genomic level monitoring should essentially be the converse of that for RaTS, with the highest score assigned to Least Concern species, with the lowest extinction risk, and with the highest data availability (lowest numbers of years since last record or last survey). The rationale for including Least Concern species in genomic-level monitoring is twofold: (i) to gather information on the genetic population status of these species, which can be representative of other species and help identify general threats, and (ii) to ensure the feasibility of longitudinal studies, enabling the monitoring of changes over time. Non-threatened species, according to Red List criteria, may still exhibit low genetic indicator values, as recently demonstrated by genetic indicator assessments in nine countries (Mastretta-Yanes et al., 2024). Information available in Annex II, IV and V of the Council Directive 92/43/EEC of 21 May 1992 on the conservation of natural habitats and of wild fauna and flora should be considered. However, an important limitation of 92/43/EEC Annexes II, IV and V relies on the fact that among the pollinator taxa only Lepidoptera species are currently considered.

3. **Rarity**. Rare species are, by definition, species characterised by low numbers of individuals but rarity as such is not related to species distribution. The investment in resources for specimen sampling for rare species is higher than for common and/or widespread species. The uncertainty of field sampling success can compromise a planned genomic monitoring scheme for rare species. Thus, rarity as prioritization mechanism should have low priority in genomic level monitoring.
4. **Species Biology**. The feeding biology of the larvae, and other biological traits, can be used to classify pollinators into different functional groups. The different functional groups should be represented in the pool of species target of genomic level monitoring (unless strong a priori reasons to focus on one of them are present). The proposed strategy, i.e. include in the species pool one or more species as representative of each/main functional group, allows for the inclusion of a functional diversity aspect as indicator. For instance, the larvae of some pollinator species are monophagous or oligophagous on specific host plant species or groups of related plant species (e.g. butterflies, hoverflies). Further aspects of the insect biology that could be considered refers to sociality of some pollinator groups (bees and bumble bees; social vs solitary species) and the migratory behaviour of some species. Migratory species should not be included in monitoring programs, at least not in the initial phase of the monitoring scheme.

Additionally, when selecting the appropriate species for genomic-level monitoring the species identification difficulty (e.g. expert taxonomists needed vs species identification possible even in the absence of strong morphological expertise) should be considered (at least in the short-term) as prioritisation mechanism. So far, DNA barcoding has become a valuable tool for species identification, enabling the identification of morphologically challenging species as well. Reference databases for this purpose are steadily growing. However, for some taxa, the identification power of DNA barcoding is limited, and additional work is needed to ensure accurate species identification. The size of the specimens might be considered in the short-term planning, as indeed, some current methodologies require a minimum amount of DNA from each single specimen. Technical requirements intrinsic to the methodologies adopted to generate the DNA data are discussed below.

5.3.3.1 Applying criteria and experts' consultation to select target species for the pilot studies

To provide a tentative list of possible and appropriate species of hoverflies, bees, bumble bees and/or butterflies to prioritise in pilot studies to demonstrate the use of genomic-level monitoring of pollinators, an open consultation was performed within the STING2 expert pool. In accordance with the prioritization criteria mentioned above, the experts were asked to suggest their candidate species by considering the following aspects: (i) the species has Palaearctic, Western Palearctic or even a narrower distribution (e.g. Mediterranean, Continental, Boreal); (ii) the species has to be collected in different localities of its distributional range (e.g. 20-40 localities; exceptions could be done for the rare species), and for each locality 10-15 individuals (exceptions could be done for the rare species) have to be collected and stored in absolute ethanol, DNA stable, or similar preservative solutions; (iii) ideally the species has to be easily identifiable, even in the field; and (iv), the species should be non-migratory.

The results of the consultation led to the identification of 15 potential pollinator species (four hoverflies, four gossamer-winged butterflies, two bumble bees and five solitary bees) as possible candidates for a pilot study. Detailed information on the proposed species is provided in Table A.5.3. 1 of Annex 5.3. A. A future larger scale and more systematic approach to select the target species should be conducted at the European level, in coordination with Member States. One possible strategy to achieve the goal is the establishment of a commission of experts in taxonomy and genomics, including representatives of EU Member States and stakeholders from neighbouring Countries, which periodically evaluate and prioritise the species that have to be prioritized for genomic level monitoring programs.

5.3.4 Sampling protocols and guidelines for proper storage of the collected organisms for genomic studies

5.3.4.1 Permits

Sample collecting permits and other documentation must be obtained prior to sampling campaigns. The types of permits needed depend on the country and its legislation/policies, and on the areas chosen for samples (national/regional natural parks, other protected areas, private land), and if the purpose of the sampling is genetic work. If specimens are to be exported for genetic analyses, all national and international permits stating the purpose of transaction have to be obtained in advance of shipping. The specimen sampling for genomic monitoring must address the “Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization” of the UN Convention on Biological Diversity (CBD), primarily aiming at sharing the benefits arising from the utilisation of genetic resources in a fair and equitable way (entered into force on 12 October 2014)[131].

5.3.4.2 Collection and storage

Specimens can be collected individually by a handheld insect net or by using different types of traps. The method of choice will depend on the biology and habitat of the species and on the purpose of the collection. Most of the methodologies here proposed to obtain DNA data for genomic level monitoring require high molecular weight genomic DNA (HMW-gDNA; out-of-pocket costs, not staff, for obtaining HMW-gDNA using commercial kit or standard protocols span from €5 to €20 per sample). Even if the selected methodology does not strictly require this standard, it usually benefit from HMW-gDNA (e.g. Corrales and Astrin, 2023)). The sensitivity of the different approaches to DNA integrity and quantity is discussed below. Thus, it is crucial to consider the sample preservation methods that best fit the requirements of the adopted downstream methodology as well as the logistics of the sampling campaign. The DNA integrity of an organism is be affected by the initial preservation procedure of the specimen (starting at the organism’s death) and, consequently, samples previously collected from on-going monitoring initiatives can be used in genomic monitoring programs only if appropriately preserved. Flash-freezing live individuals in a –80 °C deep freezer (propylene glycol can be used as a cryoprotectant, Whitman et al. (2019) or in liquid nitrogen will ensure the highest DNA integrity and allows us to obtain long-reads required to produce reference genomes or to adopt a whole genome resequencing approach. For techniques that do not require long reads (such as RAD or MLST), the specimens can be preserved in different preservative solutions such as absolute ethanol, RNAlater®, DNAgard® Tissue, or DNA/RNA Shield (costs ranging from €2 to €5 per specimen). These are non-hazardous commercial stabilisation solutions that can be used as preservation solutions for several months at room temperature (Zimkus et al., 2018). In comparison with absolute ethanol, the above-mentioned solutions are more expensive.

The most common preservation method is 95–99% or absolute ethanol molecular biology grade (€0.1 to €0.3 per specimen), which can preserve DNA for long periods at room temperature and above (Zimkus et al., 2018), although such temperatures prevent to obtain HMW-gDNA. During field collections, single specimens are put into vials with chosen preservative solution. During field activities, the collected specimens is ideally kept refrigerated in dark condition at temperatures not higher than 4 to 8°C (e.g. temporarily stored in a cool box); then the vials with the collected specimens have to be transferred as soon as possible to freezing temperature of –20/–30°C and protected from sunlight (Krogmann and Holstein, 2010). Dry specimens stored in museum collections could be used as starting material for DNA

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[131] https://www.cbd.int/abs/text/

extraction, however, their DNA may be (too) degraded (low quantity and fragmented) and might be exploited for genomic monitoring purposes having the species reference genome and adopting NGS technology to generate the DNA data (for details see section 5.3.6 SWOT analysis).

During fieldwork activities, it is recommended to use tubes with pre-printed external thermal-labels with a linear or 2D barcode, or vials with laser-etched barcodes. This is preferred over manual vial labelling to avoid issues such as misspellings, illegible handwriting, or smearing, which can lead to sample mix-up.

It is recommended that both tissue and DNA of individuals collected are stored also after the DNA extraction. This is to allow applying new techniques for monitoring as they arise. The field of genomics develops very rapidly and many analyses that are too expensive or complex today will be readily available in a near future.

Individual (or population) metadata documentation should follow model documents already established by the European Reference Genome Archive (ERGA) and Biodiversity Genomics Europe (BGE). Comprehensive metadata include at least habitat description, species abundance, accurate locality information including georeferencing (GPS reading with uncertainty), date and collector should be collected. Photos of the habitat(s) in which the organisms are collected will assist in defining habitat structure. Metadata should comply with, e.g. the Global Genome Biodiversity Network (GGBN) Data Standard - TDWG (Droege et al., 2016) to make data management consistent. A possible tool facilitating organism metadata acquisition and integration is represented by the platform PlutoF (Abarenkov et al., 2010). Metadata should be linked to voucher specimens, DNA extracts and genomic data via Globally Unique Identifiers (GUIDs).

5.3.4.3 Specimen vouchers

The species identification of the collected specimens should be performed in the field, whenever possible. However, for some species, this operation requires a detailed observation of the specimens under a binocular microscope (preferably reducing the exposure to air, light, and heat produced by microscope lights). Taxonomic experts must validate the identification of collected specimens in order to guarantee the specimen's correct identity and the validity of the name (experts are updated on nomenclatural changes of their focus group) before genomic analysis. If needed, in most cases the collected specimens can also be identified using DNA-barcoding.

Specimen vouchers and associated DNA extracts should be accessed into open access Natural History Museums or recognized University collections and biodiversity biobanks, respectively. Formal agreements must be established between EU or the representative of the genomic monitoring program and the relevant national institution (centralise the samples in one Institution for each country is the preferred solution) in order to deposit the voucher specimens in the institution of the country where these have been collected. Specimen vouchers in dry collections should be registered in a collections database system using a Globally Unique Identifier (GUID), which is essential to assess the identification of the original specimen and its metadata. Tissues and DNA samples should be registered in a biobank using a unique identifier, with linking to the voucher specimen. Genomic sequencing results should be cross-linked to both specimen vouchers and genomic samples (Corrales et al., 2023).

5.3.5 Stocktake of potential methodologies useful to develop a program of DNA-based genetic diversity monitoring

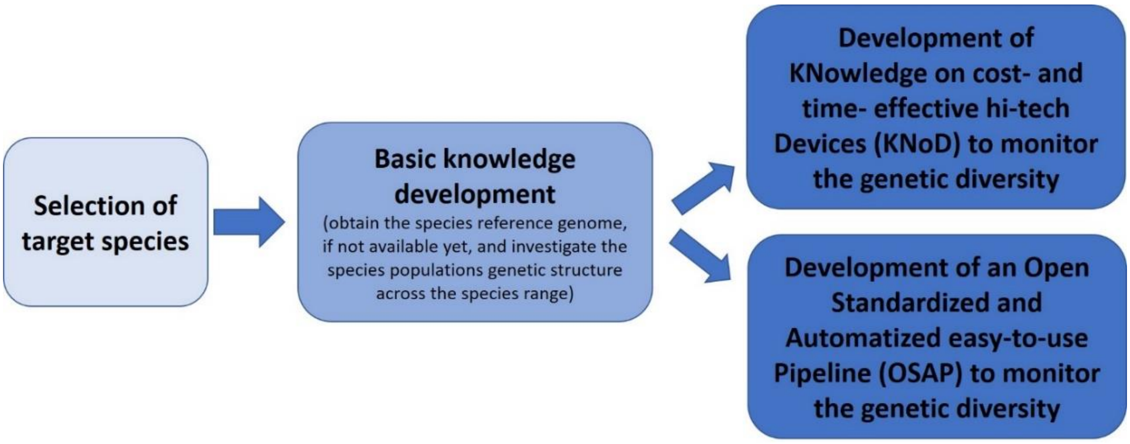
Genomic sequencing produces deep knowledge of the genetic features of populations and species. This information will detect differences in levels of genetic diversity in populations and species and will help to understand adaptive differences. Present-day genomic technologies provide unique tools for describing genomic diversity and could provide data for well-informed decisions in species conservation.

International initiatives such as the Earth BioGenome Project and European Reference Genome Archive[132] (ERGA) project aim at providing reference-quality genomes of European species by using the most advanced technologies (Blaxter et al., 2022; Formenti et al., 2022). Species reference genomes are needed to understand and protect biodiversity. Within the ERGA initiative, the number of pollinator species for which reference genomes are available is increasing.

Two strategies could be developed for a scalable, repeatable, broad-scale genomic level monitoring scheme to estimate relevant genetic diversity indicators for the target pollinator species (Figure 5.3. 1):

1. Develop the knowledge on the population genetic structure of the target species and then transfer this KNowledge On cost- and time- effective hi-tech Devices (KnoD, as an example, see Andersson et al. (2022).
2. Define an Open framework where laboratory protocols, NGS sequencing platform and bioinformatics analyses of the generated data are Standardized and Automatized into an easy-to-use Pipeline (OSAP) and a relative web-based interface.

Figure 5.3. 1. Strategies envisioned to developed, scalable over space and repeatable over time, for a wide-scale DNA-based genetic diversity monitoring scheme to estimate relevant genetic diversity indicators for the target pollinator species.



Source: Authors' elaboration.

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[132] https://www.erga-biodiversity.eu/

The first step of the KNoD strategy is the generation of deep knowledge of the population genetic structure of the target species (see Criteria to select target species for genomic level monitoring) over the geographic range of interest. This knowledge allows the selection of the most informative genetic target regions (e.g. a matrix of Single Nucleotide Polymorphisms, SNPs) that have to be targeted by cost- and time- effective hi-tech devices and used in genomic monitoring programs (i.e., estimate indicators of genetic diversity). For this aim, previously published studies and results obtained by ongoing initiatives (Annex 5B) such as databases and reports have to be exploited. The generation of this knowledge requires appropriate resources in terms of funds to support both material costs (e.g. consumables, DNA extraction kits, library preparation and sequencing) and personnel costs (e.g. field staff involved in sampling activities, molecular biologists, bioinformaticians) including travel expenses. The cost to generate the knowledge depends strongly on the strategy used to generate genomic-level data (see estimated costs reported for each technology), the efficiency and automatisation level of the laboratory processing the sample, and the already available genomic resources for the target species (e.g. high-quality reference genomes already available and accessible in public repositories). Once the knowledge on the population genetic structure for the target species is generated (e.g. the informative SNPs matrix), it must be transferred to hi-tech commercial devices that will be easily adopted to characterize and monitor the population genetic structure of the target species across its range (e.g. EP1 96.96 Dynamic array IFC as in Andersson et al. (2022).

In the case of the OSAP strategy, one of the methodologies reported below must be selected to generate the genetic data (genomic level data are obviously more informative and, when possible, they have to be preferred). Then, these data must be analysed with appropriate bioinformatics pipelines to obtain the selected genetic diversity indicators. Once the strategy to generate the data are selected and the pipeline of analyses defined and optimized, the procedure can be repeated on newly collected organisms. A crucial aspect of the OSAP strategy is the adoption of standardized sample processing protocols by the different stakeholders (e.g. DNA extraction, library preparation and sequencing) and the development of a web-based and user-friendly application allowing us to perform the appropriate analyses to obtain genetic diversity indicators.

The main advantage of OSAP on KNoD relies upon the fact that it allows a continuous improvement of the characterization of the population genetic structure of the target species as the amount of data increases and, additionally, the genomic data generated can be exploited even for purposes other than population genomic monitoring. Conversely, OSAP requires continuous investments of funds in maintaining storage and computational resources required to analyse the data by the web-based application.

Technology Readiness Level[133] (TRL) of these envisioned strategies must be differentiated from those of sequencing strategies and available tools for DNA-sequences data analyses. The next generation sequencing technologies (NGS) have a high TRL level as they are in the market with commercial sequencing services available (TRL = 9) (e.g. Macrogen[134], Novogene[135], BGI[136]) and their performance is increasing continuously both in terms of the quality and quantity of the data, and the costs to generate this data are decreasing. Similarly, dedicated open-source tools for DNA-sequence data analyses are already available (TRL = 8/9). Thus, the TRL of the whole workflow of the strategy (Figure 5.3. 1) is approximately 3 or 4. With the pilot studies (estimated 3 to 4 years in order to be concluded) it can be

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[133] https://ec.europa.eu/research/participants/data/ref/h2020/wp/2014_2015/annexes/h2020-wp1415-annex-g-trl_en.pdf

[134] https://macrogen-europe.com/

[135] https://macrogen-europe.com/

[136] www.bgi.com

increased to TRL = 6 or 7. The last increase of TRL for the whole workflow will be established once the generated knowledge will be transferred to commercial devices (e.g. Dynamic Array IFC) or the whole OSAP architecture will be developed allowing to genotype populations of the selected pollinator species across the EU.

The technologies that can be used to generate the genetic data on which both strategies rely can be divided into two, partially overlapping, categories: technologies not requiring or technologies requiring the availability of a reference genome for the target species. The discussed approaches have pros and cons, which are detailed and discussed in the SWOT (strengths, weaknesses, opportunities and threats) analyses reported in section 5.3.6.

5.3.5.1 Techniques that do not require a reference genome of the target species

Reduced-representation sequencing methods, Restriction site-associated DNA sequencing (RAD-seq) approaches (e.g. original RADseq, 2bRAD, ddRAD-Seq, GBS, DArT) – reduced-representation techniques are a family of methods to sequence genomic DNA next to restriction sites generated by the digestion of genomic DNA with one or two restriction enzymes (see Annex 5C for more details on the available approaches). Currently, the sequencing costs to generate an appropriate number of reads adopting reduced representation sequencing methods varies between €50 to €70 per sample (the costs might vary depending on the number of required loci as well as on the organism genome size). Useful tools to retrieve genomic information on the possible target species are Animal Genome Size[137] and Genomes on a Tree – GoaT[138]. Several companies provide full-service analyses, including the whole process of DNA extraction, library preparation and sequencing (e.g. https://www.floragenex.com/). Out-of-pocket costs to generate RAD data starting from DNA extraction to next generation sequencing range from €200 to €300 per sample (depending on the coverage and estimated loci). Several companies provide the service (e.g. CD Genomics Agri-genome; Floragenex).

Genome skimming – this method consists of a low-coverage whole genome sequencing (up to ~5%) and provides an extensive dataset consisting of DNA fragments (skims) of high-copy fractions of total genomic DNA (e.g. organellar genomes, nuclear ribosomal DNA, multi-copy elements) (Coissac et al., 2016; Dodsworth, 2015). Genome skimming allows also obtaining shallow coverage of single copy nuclear genes. This fraction can be improved by adopting a sufficiently high sequencing effort. The genome skimming approach is more appropriate for phylogenetic/phylogeographic studies since the retrieved genetic information content is limited even if it is still much more informative than a Multi Locus Sequence Typing (MLST) approach. The genome skimming approach, in terms of DNA sequence generation, costs about €50-100 per sample. It also offers the possibility to obtain shallow coverage of single copy nuclear DNA, and thousands of low-depth nuclear markers can be obtained by adopting a sufficiently high sequencing effort. Out-of-pocket costs to generate skim data starting from DNA extraction ranges from €200 to €300 per sample (depending on the adopted sequencing depth).

Multilocus sequence typing (MLST) – MLST was originally developed to characterize the allelic profile of bacterial strains. A small number of genetic loci (usually 5-10), selected to represent the diversity of a species, are amplified through PCR, and then sequenced using a Sanger sequencing platform. Each unique sequence at each locus represents an allele (usually identified with a number), so the combination of alleles (allelic profile) allows assigning an individual to a specific strain. In the case of eukaryotes, this

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[137] https://www.genomesize.com/

[138] https://goat.genomehubs.org/

approach is mainly used for taxonomic assignment at the species level, but it is rarely used in population genetic studies since the provided information is usually limited. Out-of-pocket costs, except the lab technician costs, to generate MLST data starting from DNA extraction spans from €10 to €20 per locus per sample (the costs can be reduced if high level of automatization is present in the lab). MinION (Oxford Nanopore Technologies) represents a promising expeditious approach to reduce the costs to generate MLST markers for a batch of samples.

5.3.5.2 Techniques requiring reference genome of the target species

A gap analysis on the publicly accessible high-quality genomes of European pollinators species, as well as of ongoing initiatives that will produce such type of data (i.e. reference genomes), must be conducted mandatorily before starting any population genomic monitoring programs relying on techniques that require a reference genome. Information on the availability of high-quality genome for the candidate target species can be mined online from general tools such as Genomes on a Tree – GoaT[139] or NCBI[140]. More dedicated tools are: (i) Hymenoptera Genome Database[141], which represents a useful and updated genome informatics resource for Hymenoptera; and (ii) Lepbase: the Lepidopteran genome database[142], which provides a set of resources for moth and butterfly genome research. Species included in the ERGA pilot projects, and for which high-quality genomes are available or will be available in the near future, are: Lepidoptera (*Vanessa atalanta, Pararge aegeria, Parnassius mnemosyne, Zygaena transalpina*), hoverflies (*Eristalis tenax, Syritta pipiens*), bumble bees (*Bombus terrestris, Bombus pascuorum, Bombus monticola, Bombus lapponicus*) and other bees (*Xylocopa violacea, Andrena humilis, Osmia cornuta*); updates on the status of the ERGA project[143]. From the Darwin Tree of Life[144] several high-quality genomes of pollinator species have been released as well (e.g. 53 genomes of *Syrphidae*, 14 genomes of *Apidae* and 8 of *Andrenidae*, 12 genomes of *Lycaenidae*), and many more are in process of annotation.

Target enrichment approaches – Target enrichment approaches belong to a family of methods, within the so-called reduced-representation methods (RADseq family approaches belong to this category too), targeting specific regions of the genome of interest. The genomic regions of interest (and their corresponding probes) can be selected starting from the reference genomes of the target species. A brief description of the different approaches (Amplicon-based sequencing, Target Capture Sequencing, RAD capture) with their main features is reported in Annex 5.3. B.

Whole-Genome resequencing (WGS) – Whole-genome resequencing consists of sequencing the genomes of multiple individuals of a species; the obtained reads are then mapped to the reference genome of the species. This approach allows for the detection and comparison of variable sites between individuals or populations. WGS consists of different methods (high-coverage sequencing of individuals hcWGS, low-coverage sequencing of individuals lcWGS, pool-seq), mainly differing by the sequencing coverage. The sequencing coverage has a strong impact on the possibility of accurately identifying variable sites. hcWGS is considered optimal for DNA re-sequencing because it should include all variant types (Sims et al., 2014), while lcWGS is useful when research questions are targeted at the population-level (Lou et al., 2021). However, WGS is still difficult in its application in conservation biology and wildlife

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[139] https://goat.genomehubs.org/

[140] https://www.ncbi.nlm.nih.gov/

[141] https://hymenoptera.elsiklab.missouri.edu/

[142] http://lepbase.org/

[143] https://sites.google.com/mail.dcu.ie/ergapilotproject/pilot-resources?authuser=0

[144] https://www.darwintreeoflife.org/

populations monitoring (Fuentes-Pardo and Ruzzante, 2017). Out-of-pocket costs for whole genome resequencing starting from extracted DNA span from €400 to €1,000 per sample (depending on the genome size of the target species).

The costs referring to all the technologies adopted to generate the DNA data will be consistently reduced if a high number of samples is processed.

5.3.6 SWOT analysis of the proposed strategies and methodologies to generate genomic level data

An overview of the SWOT analysis for leading emerging genomic technologies is given in Table 5.3. 1 and covers the strengths, weaknesses, opportunities and threats for each technology separately.

Bombus jonellus, Axel Hochkirch

Table 5.3. 1. Overview of the SWOT analysis for difference technologies.

Technologies	**Strengths**	**Weaknesses**	**Opportunities**	**Threats**
Reduced-representation sequencing method (Tech 1)	Cost-effective compared to WGS, limited need for prior genomic knowledge, a subset of the genomic information is recovered	Quite sensitive to the quality and quantity of DNA input, substantial computational resources and specific expertise are needed.	Provides population genomic level information at a cheaper price than WGS, it can be easily applied on large spatial and temporal scales, it allows the possibility to identify genetic markers to be used in subsequent monitoring activities by adopting, for example, Tech 3 and 4.	Optimization and standardization of the method is needed to obtain comparable results across time and space, to obtain the required DNA quality and quantity ad-hoc sampling is needed.
Genome skimming (Tech 2)	Cost-effective compared to WGS, limited need for prior genomic knowledge, no amplification biases, not very sensitive to the quality of DNA input, a small subset of the genomic information is recovered.	It may provide inaccurate representation due to biases towards certain genomic regions (high copy fraction of the genome); substantial computational resources and specific expertise are needed.	Provide information almost at the population genomic level at a cheaper price than other techniques, it can be applied to already collected samples.	Optimization and standardization of the method is needed to obtain comparable results across time and space, may fail to identify rare genetic variants, genomic regions of interest need to be carefully chosen to avoid biases (less seriously than Tech 3).
Multi-locus sequence typing (MLST) (Tech 3)	Inexpensive, not very sensitive to the quality and quantity of DNA input, limited need for prior genomic knowledge; computational resources and specific expertise are not needed.	A very small subset of the genomic information is recovered (few loci) and may provide inaccurate representation due to a priori selected and PCR amplified genomic regions.	Due to its inexpensiveness and easily standardisable protocols, it can be easily applied on large spatial and temporal scales (the molecular biology lab work can be performed even in basic molecular biology laboratories); it can be applied to already collected samples and museum specimens.	May fail to identify rare genetic variants (highly probable), genomic regions of interest need to be carefully chosen to avoid biases.

Technologies	Strengths	Weaknesses	Opportunities	Threats
Target enrichment approaches (Tech 4)	Cost-effective compared to WGS, not very sensitive to the quality of the input DNA, no amplification biases; a subset of the genomic information is recovered.	Sensitive to the quantity of DNA input, prior genomic knowledge is needed (reference genome advisable but the info can be obtained also from tech 1), substantial computational resources and specific expertise are needed.	Being highly parallelizable, it can be easily applied on large spatial and temporal scales; it can be applied to already collected samples.	May fail to identify rare genetic variants (less seriously than Tech 3), genomic regions of interest need to be carefully chosen to avoid biases.

Source: Authors' elaboration.

5.3.7 Estimated costs for a genomic level monitoring scheme

We estimate the costs of including population genomic analysis of 10 species every reporting cycle (6 years) on a 10-year basis, assuming that each Member State sends in 30 individual specimens (possibly from two to five populations) of each of the 10 focal species. Each group of 30 is henceforth referred to as a “sample”. These costs are divided into establishment costs, those that are paid up front and do not often reoccur and annual costs, which represent the costs of maintaining the work. We also split these costs into material costs and staff costs, estimating material costs based on commercial costs of different consumable and non-consumable materials and staff costs based on the number of hours worked doing each activity, multiplied by and appropriate salary rate in each country (drawn from the main STING cost exercise, section 2.5). As it is not practical for all countries to undertake the genetic analysis independently, one country is designated as the co-ordinator, which undertakes the genetic analysis.

1. **Establishment materials**. All countries will need a -20°C/-30°C Freezer (~€6,000), a cool bag (€5) and a cool pack (€15) for proper storage of the specimens. The coordinator will need an Ultra Low Temperature Freezer in order to store extracted DNA (€15,000). In total, these costs range from €10-13,000 for each Member State but an additional €21,000 for the co-ordinator. These do not include the costs of large lab equipment, maintenance of equipment and replacement costs.
2. **Annual materials**. In all countries, in order to preserve each specimen, 5 ml of DNA shield solution will need to be applied to the preserved specimens (€100/100ml). The co-ordinator will also need a DNA extraction kit (€5), additional consumables (€2) and a storage vial (€0.5) for each specimen to extract the DNA. For each sample of 30, they will also require PCR for MLST (€2/locus/sample), multi-locus sequencing (€10/locus), and a DNA quality check and quantitation kit (€2) for each sample. The DNA will be sent to a suitable sequencing laboratory in appropriate shipping containers (€300) and sequences for €400/Sample. Analysing the samples can be resource intensive. The data will need approximately 25,000 hours of computing time (at €2.37/VCPU hour, based on an average across Microsoft Amazon and Google) and around 2TB of temporary storage (at €0.045/GB, based on an industry average). Collectively, these lab and digital resources will result in a cost of ~€65,000 for the co-ordinator.
3. **Annual staff.** Preparing the sample will take ~3hrs of an experienced researcher and ~4.6hrs of technical time. Once sequenced, the obtained data will need to be integrated and modelled. These are highly specialised activities and will take a specialist researcher around 64 working days (~3 months) per species, with support from a senior researcher (~18 working days per species). Specialists will also be required to support the Member States, based on ~60 working days per year (based on the time required for user help in the Copernicus programme, B. Smets, personal communication, 2024) and a further 60 days will be required to update and maintain the workflow (based on the time required to maintain Citizen Science workflows, B. Oteman, personal communication, 2024). Collectively these factors increase staff costs by €134,824 in the co-ordinating country.

5.3.8 Recommendations and future directions

To initiate a monitoring program of pollinator genetic diversity within the EU, we propose the following four steps to start the work:

Step 1. A pilot project focussing on a few species to initiate monitoring of genetic diversity in pollinating species in Europe. This part is suggested to include at least one species for each of the pollinator groups hoverflies, bumble bees, solitary bees and butterflies (Table 5.3. 2 and Table A.5.3. 1 in Annex 5.3. A; *Syritta pipiens*, *Bombus lapidarius*, *Anthophora plumipes*, *Phengaris teleius/Cyaniris semiargus*). For each species, sampling should be carried out to reflect as many of the biogeographic regions and habitats of occurrence as possible. Depending on species distribution, we propose to sample approximately 10-20 individuals per population (or occurrence area within which extensive genetic exchange is regarded to occur) with 20-30 independent collecting sites in total. All samples should be stored individually by adopting appropriate preservative solutions (for details see section 5.3.4 on collection and storage). For DNA extraction, only sufficient amount of tissue should be used, while the rest of the specimens should be stored for potential further use together with sampled individuals that are not being analysed immediately. We envision that at least 400-900 individuals will be sequenced per species and sampling point in time. Sampling at the same localities should be repeated after 3-6 years in the pilot to generate data on temporal stability. We propose to use whole genome sequencing (WGS) for best possible genome assessment and to assess all relevant parameters including genome-wide nucleotide diversity, heterozygosity, inbreeding from runs of homozygosity (FROH), various types of genetic load, as well as to address indications of selection over space and time, and to identify the genes involved in such dynamics. Additionally, already proposed indicators for genetic diversity should be assessed (see Dussex et al., 2023).

Table 5.3. 2. Target species for pilot studies as resulted by experts' consultation (Table A.5.3. 1 in Annex 5.3. A).

Hoverflies	**Bumble bees**	**Solitary bees**	**Butterflies**
Syritta pipiens	*Bombus lapidarius*	*Anthophora plumipes*	*Phengaris teleius*
Volucella pellucens	*Bombus pascuorum*	*Dasypoda hirtipes*	*Cyaniris semiargus*
Cheilosia scutellata		*Andrena flavipes*	*Phengaris nausithous*
Cheilosia derasa		*Osmia bicornis*	*Lycaena dispar*
		Lasioglossum villosulum	

Source: Authors' elaboration.

The pilot project should also include analyses of existing sample collections from these four species, when individual tissue samples that can be used for DNA extraction to assess temporal trends over longer time scales are available. It is important that if such historic samples are available, information on the exact locality of collection of the individuals is also available so that the genomic composition of these historical samples can be compared with that of present-day ones.

From the review carried out within this project, we ranked the species suggestions within each of these groups as follows (with 1 indicating the highest priority for inclusion in a pilot project). Ranking criteria included good possibility of sampling, generally widespread species, Red List criteria (highest score given to the Least Concern species with the lowest extinction risk), species ecological role (both umbrella species and non-umbrella species among the four proposed pilot species), and availability of a reference genome.

Step 2. As data begin to accumulate from Step 1, it is important to evaluate and further refine the monitoring approaches and methods. This includes research to elaborate sample sizes in terms of individuals and sequencing coverage (including potential to use SNP chips) needed to detect changes of various magnitude that appears feasible based on initial data. This will link to evaluating parameter and indicator assessments, including recommendations for threshold values (e.g. Andersson et al., 2022; Dussex et al., 2023).

Step 3. Evaluate and modify the monitoring programs for the four pilot species in terms of sampling strategies, geographic coverage, temporal scale of continued monitoring, need for extended focus on specific regions, need for extending the geographic scale of monitoring. Safeguard continue monitoring of these species according to the elaborated strategies.

Step 4. Based on findings and learnings from Step 1-3 design monitoring programs for additional pollinating species in EU.

Clearly, funding is needed to carry out these tasks. We propose that a Horizon Europe (type) project be devoted at least to the initial parts of this work to test, refine and upscale approaches and technologies. Furthermore, collaborations between science and policy makers are needed to ensure that genetic diversity monitoring requirements are included in relevant policies and reported on (e.g. to the Convention on Biological Diversity), and that findings are made available for practical management initiatives over Europe. Collaborations between science and industry will facilitate the development of cost-effective tools (DNA-extractions, sequencing, bioinformatics pipelines, parameter and indicator assessment pipelines, and tools for reporting and making results widely available).

Annex 5.3. A. Species for pilot studies and ongoing initiatives.

Table A.5.3. 1. Results of the experts' consultation to select target species for pilot studies.

Priority	Order	Family	Target species	Species distribution	IUCN Red list status (Europe)	Easily collectible?	Sampling method	Easily ID in the field	Collection within ongoing initiatives?	Material already available	Reference genome available	Ongoing monitoring programs
1	Hymenoptera	Apidae	*Anthophora plumipes*	Widespread at West-Palearctic level and Southeast Asia	Least concern (LC)	Sometimes. In higher numbers in suitable habitats and main flight period.	Nets on suitable flowers, transects	Yes	Yes, transect walks	Yes	Yes. PRJEB62774	Not known
1	Hymenoptera	Apidae	*Bombus lapidarius*	Throughout Europe, incl. Britain and Ireland	Least concern (LC)	Yes	Transects, nets, pan traps	Yes	Wild bee monitoring program in Germany	Possibly	Yes. PRJEB51891	Yes. Germany, pilot phase: https://wildbienen.thuenen.de/
1	Lepidoptera	Lycaenidae	*Cyaniris semiargus*	Widespread	Least concern (LC)	Yes	Insect nets	Yes	Yes, eBMS	Not known	Yes	Yes. Included in the European Grassland Butterfly indicator

Priority	Order	Family	Target species	Species distribution	IUCN Red list status (Europe)	Easily collectible?	Sampling method	Easily ID in the field	Collection within ongoing initiatives?	Material already available	Reference genome available	Ongoing monitoring programs
1	Lepidoptera	Lycaenidae	*Phengaris teleius*	Throughout Central and Eastern Europe	Vulnerable (VU, A2c) / Habitats Directive	Yes	Transects, nets, larvae/egg samples	Yes	Yes, eBMS	Yes	Not known	Yes. SW-Germany long-term study since 1989
1	Diptera	Syrphidae	*Syritta pipiens*	Most of the Palaearctic region and throughout Europe	Least concern (LC)	Yes. In habitats in high numbers on flowers.	Insect net, Malaise traps.	Yes (with hand lens)	Yes, Malaise trapping.	Yes	Yes. INSDC ID PRJEB42079.	No
2	Hymenoptera	Apidae	*Bombus pascuorum*	Widespread at EU level	Least concern (LC)	Yes (transects, pantraps not so effective)	Netting on transects or focal plots	Yes (after some training)	Yes, EU-PoMS + Wild bee monitoring program in Germany	Possibly	Yes. PRJEB43540	Yes. BeeWalk in UK (https://beewalk.org.uk/node/13). Germany pilot: https://wildbienen.thuenen.de/
2	Hymenoptera	Melittidae	*Dasypoda hirtipes*	Throughout Europe, incl. Britain	Least concern (LC)	Yes	Transects, nets, pan traps	Yes	Wild bee monitoring program in Germany	Possibly	In progress (Darwin Tree of Life Project)	Yes. Germany, pilot phase: https://wildbienen.thuenen.de/

Priority	Order	Family	Target species	Species distribution	IUCN Red list status (Europe)	Easily collectible?	Sampling method	Easily ID in the field	Collection within ongoing initiatives?	Material already available	Reference genome available	Ongoing monitoring programs
2	Lepidoptera	Lycaenidae	*Phengaris nausithous*	Throughout Central and Eastern Europe	Near Threatened (NT) / Habitats Dir.	Yes	Transects, nets, larvae/egg samples	Yes	Yes, eBMS	Yes	Not known	Yes. SW-Germany long-term study since 1989
2	Diptera	Syrphidae	*Volucella pellucens*	Throughout Europe except the southernmost areas.	Least concern (LC)	Yes. Not high numbers, planning and efforts needed.	Insect net, Malaise traps.	Yes	Yes, Malaise trapping.	Possibly	No (in preparation)	No
3	Hymenoptera	Andrenidae	*Andrena flavipes*	Widespread at EU level	Least concern (LC)	Yes	Insect nets	Yes (after some training)	Yes, EU-PoMS	Possibly	No	No
3	Lepidoptera	Lycaenidae	*Lycaena dispar*	Throughout Central and Eastern Europe	Least concern (LC) / Habitats Directive	Yes	Transects, nets, larvae/egg samples	Yes	Yes, eBMS	Yes	Not known	Yes. SW-Germany long-term study since 1989

Priority	Order	Family	Target species	Species distribution	IUCN Red list status (Europe)	Easily collectible?	Sampling method	Easily ID in the field	Collection within ongoing initiatives?	Material already available	Reference genome available	Ongoing monitoring programs
3	Diptera	Syrphidae	*Cheilosia scutellata*	Almost throughout Europe.	Least concern (LC)	Sometimes. In higher numbers in suitable habitats and main flight period.	Insect net, Malaise traps.	Yes (with hand lens)	Yes, Malaise trapping in forested areas.	No	No (in preparation). INSDC ID PRJEB62180	No
4	Hymenoptera	Apidae	*Osmia bicornis*	Widespread at west-Palearctic level	Least concern (LC)	Yes	Transects, pan traps, nest-trapping	Yes	Bred for pollination, easily nests in bug hotels	Yes	Yes. PRJEB44455	Not known
4	Diptera	Syrphidae	*Cheilosia derasa*	Widespread in central and southern Europe, but highly fragmented	Least concern (LC)	No. Not high numbers, planning and efforts needed.	Insect net	No	No. Needs dedicated collecting campaign.	No	No	No

Priority	Order	Family	Target species	Species distribution	IUCN Red list status (Europe)	Easily collectible?	Sampling method	Easily ID in the field	Collection within ongoing initiatives?	Material already available	Reference genome available	Ongoing monitoring programs
5	Hymenoptera	Halictidae	*Lasioglossum villosulum*	Widely distributed throughout Europe	Least concern (LC)	Yes	Insect nets, pan traps	Yes (after some training)	In NL collected for genetic analyses within Safeguard project	Possibly	Not known	No

Source: Authors' elaboration.

Table A.5.3. 2. Ongoing initiatives of pollinators genetic diversity monitoring.

Project's name	Aims	Target taxa	Method	Countries	Website
Pilot study for monitoring genetic diversity in Switzerland	Testing the feasibility of a future monitoring of the genetic diversity of species in Switzerland	False heath fritillary (*Melitaea diamina*)	WGS	CH	www.gendiv.ethz.ch
Swedish National Genetic Diversity Monitoring Program	Monitoring of genetic diversity	*Bombus balteatus*, green-veined white butterfly, apollo butterfly, clouded apollo	WGS	SE	https://www.naturvardsverket.se
Population Genomics of Pollinating Insects	Using bumble bee genomics to better understand current threats to UK pollinator populations	Bumble bee (*Bombus muscorum, Bombus distinguendus, Bombus vestalis*)	WGS (?)	UK	https://www.earlham.ac.uk/research-project/population-genomics-pollinating-insects
Serbian Pollinator Advice Strategy (SPAS)	Development of new genomic toolkit for genetic diversity monitoring	hoverflies, genus *Merodon*	ddRADseq	RS	https://spas.pmf.uns.ac.rs/en/about-project/
Butterfly GEnetics Monitoring Scheme (BGEMS): 2020 Pilot study	To develop the world's first spatially replicated, long-term genetic monitoring scheme linked with population abundance data	*Maniola jurtina* (L.)	RADseq, microsatellite	UK	https://butterfly-monitoring.net/project/bgems

Project's name	Aims	Target taxa	Method	Countries	Website
Using museum collections to detect and quantify introgression into wild bumble bees	Generate and compare genomic data from several hundred bumble bees collected during past 150 years from different regions of Sweden and Europe and commercial hives.	*Bombus terrestris*	WGS	SE + others EU countries	

Source: Authors' elaboration.

Annex 5.3. B. Technical details on some of the potential methodologies useful to develop a program of genomic-level monitoring

RAD-seq

RAD-seq provides sequence data from loci spread across the genome as determined by the molecular protocol, such as the choice of restriction enzymes (Andrews et al., 2016).

original RADseq - In the *original RADseq* protocol (Baird et al., 2008; Miller et al., 2007), genomic High Molecular Weight (HMW)-DNA is digested with one restriction enzyme and then the obtained DNA fragments are reduced to the appropriate length for sequencing by mechanical shearing (fragment sizes varies at each locus).

2bRAD - The *2bRAD* method uses type IIB restriction enzymes; the enzyme cleaves DNA upstream and downstream of the recognition site and thus the obtained fragments possess a uniform length (33–36 bp) (Wang et al., 2012).

ddRAD-Seq - In *ddRAD-Seq* (double digest RAD Sequencing) two restriction enzymes are used to digest the genomic DNA and the fragments obtained are using NGS technologies (Peterson et al., 2012). As in the others RAD-seq approaches, hundreds to tens of thousands of loci can be obtained and analysed allowing genome wide SNP discovery.

Genotyping by sequencing (GBS) - GBS allows the identification of genetic variants and quickly genotype samples. The complexity of the genome is reduced by a common-cutter enzyme, the obtained fragments are PCR amplified (short fragments are preferentially amplified) and then fragments ends are sequenced on short-read sequencing platforms (e.g. Elshire et al., 2011). The main difference compared to the original RADseq consists in the lack of the size selection step; it also requires lower amount of DNA. GBS is cost-effective, but it produces extensive missing data and requires complex bioinformatics analysis. GBS is most used on crop plant genomes. An extensive review on RADseq-family methods (original RAD, 2bRAD, GBS, ddRAD and ezRAD) is provided by Andrews et al. (2016).

Diversity array technology (DArT) - DArT is an approach, similar to RADseq, allowing the discovery and genotyping of thousands of SNPs in hundreds of individuals (Elbasyoni et al., 2018).

Target enrichment approaches

Amplicon-based sequencing – This method consists of highly multiplexed PCRs, targeting genome regions of interest, followed by high-throughput sequencing (NGS) with the goal of genotyping hundreds of markers for thousands of individuals in a single sequencing lane (Aykanat et al., 2016; Campbell et al., 2015). The genome regions amplified by PCR have to be known a priori and correspond to genomic loci of interest, obtained by the genome of the target species. A pair of PCR primers have to be developed for each of the selected genome regions. This technology is best suited for projects aiming to genotype <500 loci of many individuals (>1500) or for species where continued monitoring is anticipated (Meek and Larson, 2019).

Target Capture Sequencing (TCS) - TCS coupled with NGS allows the investigation of selected genomic region(s) of the target species. This approach allows the enrichment of specific regions of a genome using DNA baits to select the fragments of interest, thus removing the problem of amplification biases. The baits, oligonucleotides ad hoc synthetized, are designed corresponding to genomic loci of interest starting from the analyses of the whole genome of the target species (e.g. Gnirke et al., 2009; Hodges et al., 2007) or using information provided by reduced-representation approaches, such as RAD-seq (in this case a reference genome for the target species is not required). TCS constitutes an efficient approach to explore the genetic diversity over many genomic regions and individuals of the target species. The fact that this technique allows multiplexing several samples, thereby reducing the cost of large-scale applications, makes it highly interesting for population genetics studies. Sequence capture technique requires access to a reference genome for baits development. TCS appears to have a high intra- and interspecific reproducibility (in terms of SNPs and markers), a prerequisite for comparative studies across populations, even if sampling and molecular analysis are performed at different times. TCS possesses a greater transferability across species (George et al., 2011) than other methodologies (e.g. RADseq family) (Harvey et al., 2016).

RAD capture (Rapture). - In Rapture, baits isolation and sequencing library preparation are divided into two different steps. This protocol uses an in-solution capture of chosen baits to target sequencing reads to specific genomic loci (Ali et al., 2016; Hoffberg et al., 2016). In this last case, a reference genome of the target species is not required. Rapture approach combines the benefits of RAD-seq and TCS approaches, it is best suited for projects including <1500 individuals or where >500 loci are required (Meek and Larson, 2019).

5.4 Options for Malaise traps

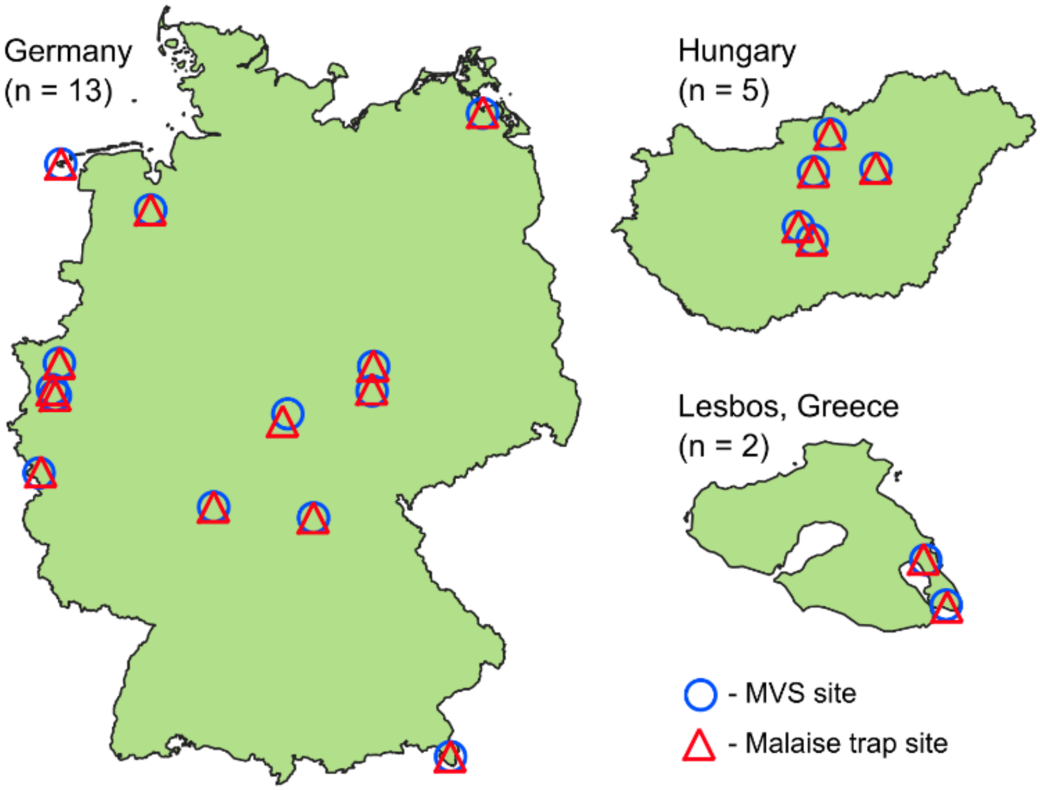
5.4.1 Background

The proposed core scheme focuses on using standardised reinforced transects to survey bees, hoverflies and butterflies, light traps to survey moths, and bespoke methods to monitor rare and threatened species. However, the pollinating insect community of the EU includes many other taxonomic groups, such as ants, beetles, wasps, and non-hoverfly flies. Given ongoing losses of insect biodiversity (Cardoso et al., 2020; Outhwaite et al., 2022; Raven and Wagner, 2021) it is important to understand which insects are in decline and how they are continuing to change through time, which in turn requires broad insect sampling and monitoring programs.

The SPRING project provided a pilot of Malaise traps as a possible option to complement the core scheme proposed by STING2 (see section 2.3 and 2.4), noting that in 2022-2023 the SPRING project tested both transects and pan traps (as proposed by STING1 Minimum Viable Scheme (MVS), Potts et al. (2021)) as well as a small pilot for Malaise traps. Malaise traps are small netted tents that can trap any passing flying insect, and also a number of wingless and non-flying insects out of almost all insects orders (Skvarla et al., 2021); they are a passive sampling method, so the only time investment is their initial construction at the start of the year and then sample bottles can be collected, reset, and sent for analysis once every two weeks. Passive in this respect means that insects are not attracted by colours like in pan traps. These traps capture passing flying insect, however, some insect taxa are more likely to escape the trap than others and an effect of Malaise trap design has been shown (Uhler et al., 2022). A variety of protocols already exist for genetically identifying insects from Malaise trap samples (e.g. via DNA metabarcoding, hereafter 'metabarcoding'; see section 5.3; (Uhler et al., 2021; Watts et al., 2019)), both of which provide a broader perspective of the insect community at each site (Kirse et al., 2021; X. Li and Wiens, 2023). Lastly, recent advances in insect metabarcoding have improved its time and cost efficiency, making it viable for use in broad-scale insect monitoring programs (Buchner et al., 2023).

To determine what unique information might be gained by including Malaise traps in the SPRING pilot of the MVS, the project compared insect richness at each co-located site where insects were observed and determined via SPRING MVS methods (transects and pan traps) and collected by Malaise traps with follow-up identification of insect species via metabarcoding. SPRING piloted work in 13 sites in Germany and 5 sites in Hungary sampled during 2022, and 2 sites in Greece sampled during 2023 (Figure 5.4. 1). The approach compared: (i) the total number of insect taxa found using both methods, and (ii) the total number of insect pollinators (specifically bees, butterflies, and hoverflies).

Figure 5.4. 1. Minimum Viable Scheme (MVS used in SPRING based on Potts et al. (2021)) and matching Malaise trap locations in Germany (2022), Hungary (2022), and Greece (2023).



Source: SPRING project.

5.4.2 Methods

For reasons of standardisation, the SPRING protocol for Malaise trapping was based on the LIFEPLAN protocol[145], which in turn is based on the Global Malaise Program protocol. Some modifications were applied for implementation as part of SPRING. We used three Townes-type Malaise traps differing in the colour of the roof (black or white) and in the size of the capture area (the vertical wall of netting). Except for four sites in Germany with traps with white roof and a capture area of 1.75 m^2 (Hallmann et al., 2017) the trap type of the German Malaise trap program coordinated by the German LTER network (Welti et al., 2022) with black roof and a capture area of 1.2 m^2 was used in Germany and Greece. In Hungary the “ez-Malaise Trap II” (MegaView Science Co., Bugdorm, Taiwan) with a white roof and a capture area of 1.8 m^2 was employed. For comparison of different Townes-type Malaise traps and comparability of results see Uhler et al. (2022)

Malaise traps were set up in a site proximate to each SPRING MVS site, typically a few hundred meters away. Traps were generally exposed for 14 days, emptied, and then reset, although shorter and longer exposure periods (ranging from 11–35 days) were occasionally necessary owing to logistical constraints. Traps were primarily placed in open areas (typically agricultural fields or

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[145] https://www.helsinki.fi/en/projects/lifeplan/instructions

grasslands), adjacent to forest edges or hedgerows, or within forest clearings. It is recognised that single Malaise may be highly biased in community sampled based on location, for instance forest edge vs open field. Further, forest edges and hedgerows can highly modify the catch of Malaise traps, and so it can be assumed that trap catches cannot be readily compared among each other, and that a 'regular' Malaise traps within the open habitat type would have caught fewer insects; this also applies for forest openings which attract insects from surrounding forest areas. All captured insects were preserved in 80% denatured ethanol (1% methyl ethyl ketone) and transported to the lab to determine wet biomass (following methods in Welti et al. (2022). Afterwards samples were size fractioned by sorting them into larger (>4 mm) versus smaller (<4 mm) fractions. These fractions were recombined in a 1:4 ratio to increase the concentration and thus representation of small species, and later on species identity via metabarcoding (following methods in Buchner et al. (2023). Insect DNA sequences of mitochondrial cytochrome oxidase I were assigned to Operational Taxonomic Units (OTUs) based on a 97% similarity threshold.

To compare methods, we quantified the total number of unique insect taxa identified at each site by pan traps, transect walks, and Malaise traps. For pan traps and transect walks, we counted all unique pollinator taxa collected at each site and sampling date, including each bee, butterfly, and hoverfly morphological group (e.g. a *Bombus* species and a 'ginger bumble bee' were considered separate taxa). At the time that this experiment was run (2022-2023), the field protocols for SPRING specified that pollinators on transects and pan traps were to be recorded to group level (not species level as required by reinforced transects proposed by STING2). A later development of the SPRING pan trap and transect protocols shifted to species level identification (post-2023). For Malaise traps, we considered only taxa caught during the two-week period that overlapped the period when the pan trap and transect walk data was collected. Thus, we do not present any of the additional of data generated throughout the Malaise trap sampling season. Not all insect OTUs captured during these periods could be assigned to species names because of incomplete reference data or conflicting matches in the databases. Therefore, species richness was estimated using two different taxa lists. The first list included only OTUs that could be unambiguously matched to a barcode with a species name. We refer to richness quantified using this list as 'species-level' richness. The second taxa list included all species-level identifications, and OTUs that could only be resolved to genus or family level. Despite their coarser resolution, these identifications can still be used to estimate the likely species richness of each insect family (detailed further in Buchner et al. (2023)), which we refer to as 'OTU-based' richness.

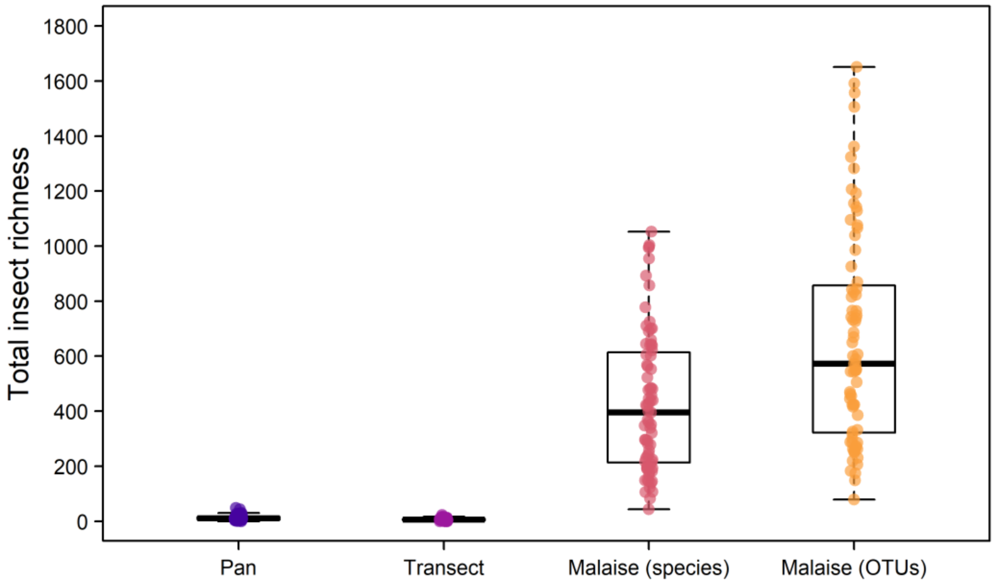
In addition to total richness, we also compared pollinator richness (i.e. bees, butterflies, and hoverflies only) for each site and sampling date determined using each method, given that the pan traps and transect walks are designed to target the pollinator community whereas Malaise traps are more general. For this comparison, we combined the data from the pan traps and transect walks into a single taxa list to produce a full SPRING MVS perspective of pollinator richness, which we then compared to the Malaise trap data. We also determined which species names were unique to Malaise traps, which are those that are not also present in the SPRING MVS taxa list from the same sites and sampling periods. We did this to ascertain whether Malaise traps, which are not targeted towards pollinators, were providing any unique information about the pollinator community not provided by the SPRING MVS methods.

5.4.3 Results

5.4.3.1 Total insect richness

Across the 20 co-located sites, which encompassed 75 sampling dates, total insect richness was around an order of magnitude lower in the SPRING MVS methods compared to Malaise traps (Figure 5.4. 2), though only bees, hoverflies and butterflies were included for the SPRING MVS methods, whereas Malaise traps included all flying insects, whether they were pollinators or not. Specifically, pan traps captured an average of 12.3 ± 9.2 total insect taxa (mean ± SD), and transect walks captured 6.4 ± 4.2 taxa. In contrast, the average species-level richness for Malaise traps was 428.6 ± 255.9 and OTU-based richness was 664.3 ± 390.6.

Figure 5.4. 2. Total insect richness for bees, hoverflies and butterflies in pan traps (dark purple), transect walks (light purple), species-level insect identifications from Malaise traps (pink), and OTU-based richness (orange).

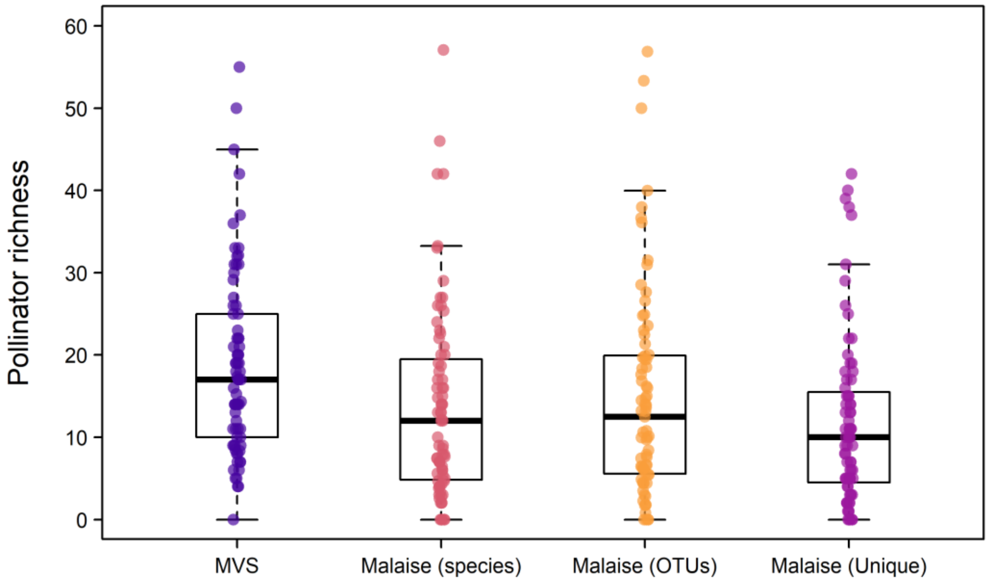


Source: SPRING project.

5.4.3.2 Pollinator richness

Pollinator richness was similar among methods but tended to be higher in the SPRING MVS scheme (Figure 5.4. 3). SPRING MVS methods together captured an average of 18.7 ± 11.2 different pollinator species, whereas Malaise traps captured an average of 13.7 ± 11.7 different species-level pollinators and 14.9 ± 12.7 different OTU-based pollinators. However, on average 11.7 ± 10.3 species-level identifications were unique to Malaise traps, meaning that about 85% of these taxa were either not present in the SPRING MVS taxa list or were identified to a higher taxonomic level.

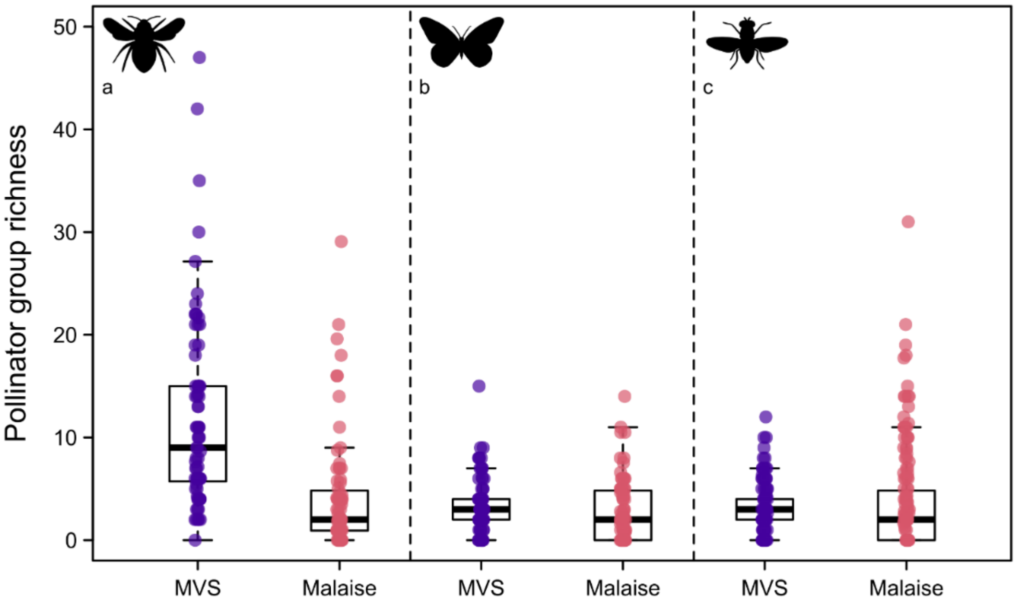
Figure 5.4. 3. Pollinator richness from pan traps and transect walks combined (SPRING MVS), from Malaise trap species-level identifications (species), from Malaise trap OTUs (OTUs), and the number of species-level identifications that were unique to Malaise traps (Unique).



Source: SPRING project.

Regarding specific pollinator groups, the higher number of pollinators caught by SPRING MVS methods was primarily driven by the higher number of bees (Figure 5.4.4a), with an average of 11.8 ± 9.2 bee taxa in SPRING MVS versus 4.2 ± 5.6 bees identified to species-level in Malaise traps. In contrast, the number of butterflies and hoverflies was similar among methods, with Malaise traps sometimes capturing more hoverflies (Figure 5.4.4b, Figure 5.4. 4c).

Figure 5.4. 4. Richness of (a) bees, (b) butterflies, and (c) hoverflies captured by a combination of pan traps and transect walks (SPRING MVS; purple) versus species-level identifications in Malaise traps ('species'; pink).



Source: SPRING project.

The number of unique species caught by each method can be estimated by comparing the overlap between the total pan trap, transect walk, and Malaise trap taxa lists across countries. This is only a rough approximation as no corrections were made for the morpho-groups and higher-level identifications. The estimated total numbers of unique pollinator species for each method were: pan traps, 156; transect walks, 63, and Malaise traps, 160.

5.4.4 Discussion

A comparative list of characteristics of SPRING MVS methods (pan traps, transect walks) and Malaise traps is compiled in Table 5.4. 1. The SPRING results demonstrate the specific benefits of Malaise traps for capturing a large number of insects that are otherwise not observed by using the SPRING MVS methods. This finding makes sense given that pan traps and transect walks target bees, butterflies, and hoverflies, which comprise only 14 insect families out of hundreds that can be found in Malaise traps (Buchner et al., 2023; Chimeno et al., 2023). Genetic methods can also identify a variety of taxa that are difficult to distinguish morphologically, or are unknown to science (Buchner et al., 2023; X. Li and Wiens, 2023), further augmenting the number of identified insects. A similar approach could also be applied to identifying pan trap specimens. Incorporating Malaise traps and metabarcoding into SPRING MVS protocols could therefore have substantially expanded the scope of monitoring to a much broader proportion of the insect community, though this would require additional investment of both time and cost.

While SPRING MVS methods outperformed Malaise traps in sampling the target pollinator community, particularly bees, our results show that Malaise traps can still provide some unique information about pollinators. Specifically, a high proportion of species of bees, butterflies, and hoverflies from Malaise traps were not present in the associated pan trap or transect walk taxa lists. This difference may be due to differences in levels of identification, such as the broad group identified in a transect walk for this specific pilot (noting that the proposed core scheme reinforced transect will identify all specimens to species, section 2.4), whereas Malaise samples were identified to the species-level via genetic methods. The difference is expected to be even higher in the Mediterranean, as wild bee diversity is much higher there and thus more difficult to be recorded by traditional methods. Furthermore, Malaise traps are passive samplers that are continually sampling, whereas pan traps and transect walk samples are only collected on a single day (see Table 5.4.1), meaning that certain pollinators may potentially be missed by the core scheme methods but caught in Malaise traps. This could indicate a role for Malaise traps in surveying rare and threatened species (see section 2.8) Consequently, although Malaise traps collect fewer pollinators, the information they do provide is often unique and potentially otherwise unavailable, or difficult to obtain, from core scheme methods combined with morphological identification.

However, while Malaise traps may offer a promising perspective of a broader proportion of the insect community sampled, they are not without their limitations. Currently, Malaise trap community information is limited to presence/absence because genetic methods cannot provide accurate information on relative abundance, although research to address this issue is ongoing (e.g. Sickel et al., 2023). Consequently, species losses will only be registered in Malaise trap data when the species is extirpated. Given that the EU PoMS specifically requires species abundance data, it means that currently Malaise traps are not able to provide this for the EU PoMS core scheme.

Additionally, metabarcoding processing requires the destruction of the sample, thus while DNA can be stored for future research the specimens cannot be re-examined nor vouchered. These limitations mean that, although Malaise traps can collect a wide variety of insects, they are best used in combination with other methods (e.g. pan traps and transect walks) that provide relative abundance information and that preserve specimens for future use. See section 0 for further discussion of opportunities to use emerging technologies to support pollinator monitoring, such as the integration of image-based and molecular approaches (abundance derived from imaging and species identity derived from molecular methods).

Table 5.4. 1. Comparison of methods and protocols for Malaise traps, pan traps and transect walks applied within the SPRING project. This table assumes that bulk samples from pan traps are processed by morphological identification while bulk samples of Malaise trap samples are processed by DNA metabarcoding.

Feature	Malaise traps	Pan traps	Transect (SPRING MVS)
Target group	All flying insects (bulk samples)	Pollinators (plus other non-pollinating insects)	Pollinators
Species abundance	Not yet possible	Not yet possible	yes
Influence of local floral context (few m^2) on abundance	Unknown	Non-linear, complex and unimodal response (see section 2.2)	Positive relationship (except at very high flower densities, see section 2.2)
Exposure time (hrs, for SPRING pilot)	DE: Apri-Oct ~5,000 hrs	DE: monthly (Apr-Sept), 6 x 6 h = 36 hrs	DE: monthly (Apr-Sept) 6 x (10 x 50 m) = ~12 hrs

Feature	**Malaise traps**	**Pan traps**	**Transect (SPRING MVS)**
Human taxonomic skill requirements	Currently high (low once DNA libraries complete)	Currently high (though potential to be low with DNA methods)	Currently high (though potential to be low with DNA methods)
Data quality	High (in case of available reference library entries)	High (species level identification)	High (species identification), but depending on strong taxonomic skills
Biases & limitations	Trap location No abundance data Storage of bulk materials	Floral context No abundance data	High level of training needed: incorrect determination cannot be checked without reference specimen
Sample	Specimens homogenized	Specimens preserved	Most specimens alive, small number captured
Upscaling (increasing sites and coverage)	Feasible	Feasible with taxonomist support	Feasible with trained experts and taxonomic support

Source: Authors' elaboration.

6 Conclusions

The revised EU Pollinators Initiative (A New Deal for Pollinators) and more recently the Regulation on Nature Restoration provided a new impetus to the setting up of an EU Pollinator Monitoring Scheme (EU PoMS). To meet this renewed ambition, the JRC has been entrusted the task to mobilize high-level experts covering different aspects of the monitoring scheme to be set in place. This scheme will be for its scope and scale the first ever scheme worldwide to help addressing pollinators decline.

In this report, these experts provide updated recommendations for the design of an EU PoMS, resulting from the work carried out during the second part of the STING project (Science and Technology for Pollinating Insects) under Simon Potts' chair. The proposed framework comprises two main components: the core scheme, which includes those taxa that are essential to monitor as part of EU PoMS (i.e. wild bees, butterflies, hoverflies, moths, as well as rare and threatened species of pollinators), and complementary modules that still need further assessment (i.e. Malaise trapping, genomic level monitoring and pan trapping). This report also provides refined proposals for pollinator indicators, as well as options for data management and further developments of the scheme.

The options presented in this report are better fine-tuned and targeted with respect to those presented in the first STING expert proposal (Potts et al., 2021), following substantial advances in data, evidence and knowledge of pollinator monitoring. This work offers additional and better-tailored support to the revised EU Pollinators Initiative, particularly for priority I of the initiative, which aims at improving knowledge of pollinator decline, its causes and consequences, and entails the development of a comprehensive European pollinator monitoring system and indicators.

Several components of the work presented here, including methodological details for the sampling protocol, allocation strategy for sampling sites and pollinator indicator options, will need to be refined and finalized during the upcoming next phase of the STING project, as acknowledged throughout the text.

In the new project, called STING+, the JRC will engage with a pool of experts to enhance the methodological foundations of the EU PoMS, which will integrate the provisions of the Nature Restoration Regulation (Article 10). The new expert pool under STING+ will also provide technical and scientific guidance for the use of Member State authorities involved in the preparation and deployment of national pollinator monitoring schemes.

References

Abarenkov, K., Tedersoo, L., Nilsson, R. H., Vellak, K., Saar, I., Veldre, V., Parmasto, E., Prous, M., Aan, A., Ots, M., Kurina, O., Ostonen, I., Jõgeva, J., Halapuu, S., Põldmaa, K., Toots, M., Truu, J., Larsson, K. H., and Kõljalg, U. (2010). Plutof-a web based workbench for ecological and taxonomic research, with an online implementation for fungal its sequences. *Evolutionary Bioinformatics*, *2010*(6), 189–196. https://doi.org/10.4137/EBO.S6271

Adjei, K. P., Carvell, C., Isaac, N. J. B., Mancini, F., and O'Hara, R. B. (2024). Integrating data from different taxonomic resolutions to better estimate community alpha diversity. *Ecography*, *2024*(5), e07182. https://doi.org/https://doi.org/10.1111/ecog.07182

Akçakaya, H. R., Bennett, E. L., Brooks, T. M., Grace, M. K., Heath, A., Hedges, S., Hilton-Taylor, C., Hoffmann, M., Keith, D. A., Long, B., Mallon, D. P., Meijaard, E., Milner-Gulland, E. J., Rodrigues, A. S. L., Rodriguez, J. P., Stephenson, P. J., Stuart, S. N., and Young, R. P. (2018). Quantifying species recovery and conservation success to develop an IUCN Green List of Species. *Conservation Biology*, *32*(5), 1128–1138. https://doi.org/https://doi.org/10.1111/cobi.13112

Albertazzi, S., Monterastelli, E., Giovanetti, M., Flaminio, S., Zenga, E. L., Bortolotti, L., and Quaranta, M. (2021). An Analysis of Ecological Indicators Applied to Agricultural Ecosystems: What to Retain to Shape a Future Indicator for Pollinators. *The 1st International Electronic Conference on Biological Diversity, Ecology and Evolution*, 31. https://doi.org/10.3390/BDEE2021-09476

Alexander, S. M., Jones, K., Bennett, N. J., Budden, A., Cox, M., Crosas, M., Game, E. T., Geary, J., Hardy, R. D., Johnson, J. T., Karcher, S., Motzer, N., Pittman, J., Randell, H., Silva, J. A., da Silva, P. P., Strasser, C., Strawhacker, C., Stuhl, A., and Weber, N. (2020). Qualitative data sharing and synthesis for sustainability science. *Nature Sustainability*, *3*(2), 81–88. https://doi.org/10.1038/s41893-019-0434-8

Ali, O. A., O'Rourke, S. M., Amish, S. J., Meek, M. H., Luikart, G., Jeffres, C., and Miller, M. R. (2016). RAD Capture (Rapture): Flexible and Efficient Sequence-Based Genotyping. *Genetics*, *202*(2), 389–400. https://doi.org/10.1534/genetics.115.183665

Alison, J., Alexander, J. M., Zeugin, N. D., Dupont, Y. L., Iseli, E., Mann, H. M. R., and Høye, T. T. (2022). Moths complement bumblebee pollination of red clover: a case for day-and-night insect surveillance. *Biology Letters*, *18*(7). https://doi.org/ARTN 2022018710.1098/rsbl.2022.0187

Alison, J., and Høye, T. T. (2024). Automated visual systems for insect monitoring and conservation. In J. Pryke, M. Samways, T. New, P. Cardoso, & R. Gaigher (Eds.), *Routledge Handbook of Insect Conservation* (pp. 475–486). Routledge.

Allendorf, F. W., Funk, W. C., Aitken, S. N., Byrne, M., and Luikart, G. (2022). *Conservation and the Genomics of Populations* (Third Edit). Oxford University Press.

Ammann, L., Bosem-Baillod, A., Herzog, F., Frey, D., Entling, M. H., and Albrecht, M. (2024). Spatio-temporal complementarity of floral resources sustains wild bee pollinators in agricultural landscapes. *Agriculture, Ecosystems and Environment*, *359*(September 2023), 108754. https://doi.org/10.1016/j.agee.2023.108754

Anderson, M., Rotheray, E. L., and Mathews, F. (2023). Marvellous moths! pollen deposition rate of bramble (Rubus futicosus L. agg.) is greater at night than day. *Plos One*, *18*(3), ARTN e0281810. https://doi.org/10.1371/journal.pone.0281810

Andersson, A., Karlsson, S., Ryman, N., and Laikre, L. (2022). Monitoring genetic diversity with new indicators applied to an alpine freshwater top predator. *Molecular Ecology*, *31*(24), 6422–6439. https://doi.org/10.1111/mec.16710

Andrews, K. R., Good, J. M., Miller, M. R., Luikart, G., and Hohenlohe, P. A. (2016). Harnessing the power of RADseq for ecological and evolutionary genomics. *Nature Reviews. Genetics*, *17*(2), 81–92. https://doi.org/10.1038/nrg.2015.28

Arce, A. N., Rodrigues, A. R., Yu, J., Colgan, T. J., Wurm, Y., and Gill, R. J. (2018). Foraging bumblebees acquire a preference for neonicotinoid-treated food with prolonged exposure. *Proceedings of the Royal Society B: Biological Sciences*, *285*(1885), 8–11. https://doi.org/10.1098/rspb.2018.0655

Ärje, J., Melvad, C., Jeppesen, M. R., Madsen, S. A., Raitoharju, J., Rasmussen, M. S., Iosifidis, A., Tirronen, V., Gabbouj, M., Meissner, K., and Høye, T. T. (2020). Automatic image-based identification and biomass estimation of invertebrates. *Methods in Ecology and Evolution*, *11*(8), 922–931. https://doi.org/https://doi.org/10.1111/2041-210X.13428

August, T., Harvey, M., Lightfoot, P., Kilbey, D., Papadopoulos, T., and Jepson, P. (2015). Emerging technologies for biological recording. *Biological Journal of the Linnean Society*, *115*(3), 731–749. https://doi.org/10.1111/bij.12534

Aykanat, T., Lindqvist, M., Pritchard, V. L., and Primmer, C. R. (2016). From population genomics to conservation and management: a workflow for targeted analysis of markers identified using genome-wide approaches in Atlantic salmon Salmo salar. *Journal of Fish Biology*, *89*(6), 2658–2679. https://doi.org/10.1111/jfb.13149

Bailey, D., Herzog, F., Bogers, M., Lüscher, G., and Fjellstad, W. (2012). Habitat indicators. In F. Herzog, K. Balázs, P. Dennis, J. Friedel, I. Geijzendorffer, P. Jeanneret, M. Kainz, & P. Pointereau (Eds.), *Biodiversity Indicators for European Farming Systems. A Guidebook* (Vol. 17, pp. 1–101). Forschungsanstalt Agroscope Reckenholz-Tänikon ART.

Baird, N. A., Etter, P. D., Atwood, T. S., Currey, M. C., Shiver, A. L., Lewis, Z. A., Selker, E. U., Cresko, W. A., and Johnson, E. A. (2008). Rapid SNP Discovery and Genetic Mapping Using Sequenced RAD Markers. *PLOS ONE*, *3*(10), e3376.

Baksay, S., Andalo, C., Galop, D., Burrus, M., Escaravage, N., and Pornon, A. (2022). Using Metabarcoding to Investigate the Strength of Plant-Pollinator Interactions From Surveys of Visits to DNA Sequences. *Frontiers in Ecology and Evolution*, *10*. https://doi.org/ARTN 73558810.3389/fevo.2022.735588

Barnsley, S. L., Lovett, A. A., and Dicks, L. V. (2022). Mapping nectar-rich pollinator floral resources using airborne multispectral imagery. *Journal of Environmental Management*, *313*. https://doi.org/ARTN 11494210.1016/j.jenvman.2022.114942

Baude, M., Kunin, W. E., Boatman, N. D., Conyers, S., Davies, N., Gillespie, M. A. K., Morton, R. D., Smart, S. M., and Memmott, J. (2016). Historical nectar assessment reveals the fall and rise of floral resources in Britain. *Nature*, *530*(7588), 85–88. https://doi.org/10.1038/nature16532

Bell, K. L., Fowler, J., Burgess, K. S., Dobbs, E. K., Gruenewald, D., Lawley, B., Morozumi, C., and Brosi, B. J. (2017). Applying Pollen DNA Metabarcoding to the Study of Plant-Pollinator Interactions. *Applications in Plant Sciences*, *5*(6). https://doi.org/ARTN 160012410.3732/apps.1600124

Billaud, O., Vermeersch, R., and Porcher, E. (2021). Citizen science involving farmers as a means to document temporal trends in farmland biodiversity and relate them to agricultural practices. *Journal of Applied Ecology*, *58*(2), 261–273.

Birkin, L., and Goulson, D. (2015). Using citizen science to monitor pollination services. *Ecological Entomology*, *40*, 3–11.

Bishop, G. A., Fijen, T. P. M., Raemakers, I., van Kats, R. J. M., and Kleijn, D. (2024). Bees go up, flowers go down: Increased resource limitation from late spring to summer in agricultural landscapes. *Journal of Applied Ecology*, *61*(3), 431–441. https://doi.org/10.1111/1365-2664.14576

Bista, I., Carvalho, G. R., Tang, M., Walsh, K., Zhou, X., Hajibabaei, M., Shokralla, S., Seymour, M., Bradley, D., Liu, S. L., Christmas, M., and Creer, S. (2018). Performance of amplicon and shotgun sequencing for accurate biomass estimation in invertebrate community samples. *Molecular Ecology Resources*, *18*(5), 1020–1034. https://doi.org/10.1111/1755-0998.12888

Bjerge, K., Alison, J., Dyrmann, M., Frigaard, C. E., Mann, H. M. R., and Høye, T. T. (2023). Accurate detection and identification of insects from camera trap images with deep learning. *PLOS Sustainability and Transformation*, *2*(3), e0000051. https://doi.org/10.1371/journal.pstr.0000051

Bjerge, K., Mann, H. M. R., and Høye, T. T. (2022). Real-time insect tracking and monitoring with computer vision and deep learning. *Remote Sensing in Ecology and Conservation*, *8*(3), 315–327. https://doi.org/https://doi.org/10.1002/rse2.245

Bjerge, K., Nielsen, J. B., Sepstrup, M. V., Helsing-Nielsen, F., and Høye, T. T. (2021). An automated light trap to monitor moths (Lepidoptera) using computer vision-based tracking and deep learning. *Sensors*, *21*(2), 343.

Blaxter, M., Archibald, J. M., Childers, A. K., Coddington, J. A., Crandall, K. A., Di Palma, F., Durbin, R., Edwards, S. V., Graves, J. A. M., Hackett, K. J., Hall, N., Jarvis, E. D., Johnson, R. N., Karlsson, E. K., Kress, W. J., Kuraku, S., Lawniczak, M. K. N., Lindblad-Toh, K., Lopez, J. V., … Lewin, H. A. (2022). Why sequence all eukaryotes? *Proceedings of the National Academy of Sciences of the United States of America*, *119*(4). https://doi.org/10.1073/pnas.2115636118

Bloom, E. H., and Crowder, D. W. (2020). Promoting data collection in pollinator citizen science projects. *Citizen Science: Theory and Practice*, *5*(1).

Bonney, R., and Dickinson, J. L. (2012). Overview of citizen science. *Citizen Science: Public Participation in Environmental Research*, 19–26.

Borgelt, J., Dorber, M., Høiberg, M. A., and Verones, F. (2022). More than half of data deficient species predicted to be threatened by extinction. *Communications Biology*, *5*(1), 679. https://doi.org/10.1038/s42003-022-03638-9

Boyd, R. J., August, T. A. T., Cooke, R., Logie, M., Mancini, F., Powney, G. D., Roy, D. B., Turvey, K., and Isaac, N. J. B. (2023). An operational workflow for producing periodic estimates of species occupancy at national scales. *Biological Reviews*, *98*(5), 1492–1508. https://doi.org/https://doi.org/10.1111/brv.12961

Breeuwer, A., Berendse, F., Willems, F., Foppen, R., Teunissen, W., Schekkerman, H., and Goedhart, P. (2009). Do meadow birds profit from agri-environment schemes in Dutch agricultural landscapes? *Biological Conservation*, *142*(12), 2949–2953. https://doi.org/https://doi.org/10.1016/j.biocon.2009.07.020

Breeze, T., Bailey, A. P., Balcombe, K. G., Brereton, T., Comont, R., Edwards, M., Garratt, M. P., Harvey, M., Hawes, C., Isaac, N., Jitlal, M., Jones, C. M., Kunin, W. E., Lee, P., Morris, R. K. A., Musgrove, A., O'Connor, R. S., Peyton, J., Potts, S. G., … Carvell, C. (2021). Pollinator monitoring more than pays for itself. *Journal of Applied Ecology*, *58*(1), 44–57. https://doi.org/https://doi.org/10.1111/1365-2664.13755

Breeze, T., Fernandez, M., McCallum, I., Morán-Ordóñez, A., Pereira, H., and Junker, J. (2023). D3.4 Cost-effectiveness analysis of monitoring schemes. *ARPHA Preprints*, *4*, ARPHA Prepr.

Bretagnolle, V., and Gaba, S. (2015). Weeds for bees? A review. *Agronomy for Sustainable Development*, *35*(3), 891–909. https://doi.org/10.1007/s13593-015-0302-5

Brlík, V., Šilarová, E., Škorpilová, J., Alonso, H., Anton, M., Aunins, A., Benkö, Z., Biver, G., Busch, M., Chodkiewicz, T., Chylarecki, P., Coombes, D., de Carli, E., del Moral, J. C., Derouaux, A., Escandell, V., Eskildsen, D. P., Fontaine, B., Foppen, R. P. B. B., … Klvaňová, A. (2021). Long-term and large-scale multispecies dataset tracking population changes of common European breeding birds. *Scientific Data*, *8*(1), 21. https://doi.org/10.1038/s41597-021-00804-2

Bruce, K., Blackman, R., Bourlat, S. J., Hellström, A. M., Bakker, J., Bista, I., Bohmann, K., Bouchez, A., Brys, R., Clark, K., Elbrecht, V., Fazi, S., Fonseca, V., Hänfling, B., Leese, F., Mächler, E., Mahon, A. R., Meissner, K., Panksep, K., … Deiner, K. (2021). A practical guide to DNA-based methods for biodiversity assessment. *Advanced Books*, *1*. https://doi.org/10.3897/ab.e68634

Bruford, M. W., Davies, N., Dulloo, M. E., Faith, D. P., and Walters, M. (2017). *Monitoring Changes in Genetic Diversity BT - The GEO Handbook on Biodiversity Observation Networks* (M. Walters & R. J. Scholes (eds.); pp. 107–128). Springer International Publishing. https://doi.org/10.1007/978-3-319-27288-7_5

Bryn, A., Van der Wal, R., Norton, L., and Hofmeester, T. (2023). Citizen science: data collection by volunteers. In *Monitoring Biodiversity* (pp. 108–121). Routledge.

Buchner, D., Beermann, A., Hörren, T., Enss, J., Frenzel, M., Li, Y., Müller, J., Pauls, S. U., Sorg, M., Haase, P., and Leese, F. (2023). German-wide Malaise trap metabarcoding estimates over 33,000 insect species. *BioRxiv*, 2023.05.04.539402. https://doi.org/10.1101/2023.05.04.539402

Buckland, S. ., Magurran, A. ., Green, R. ., and Fewster, R. . (2005). Monitoring change in biodiversity through composite indices. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *360*(1454), 243–254. https://doi.org/10.1098/rstb.2004.1589

Buckland, S. T., Studeny, A. C., Magurran, A. E., Illian, J. B., and Newson, S. E. (2011). The geometric mean of relative abundance indices: a biodiversity measure with a difference. *Ecosphere*, *2*(9), art100. https://doi.org/10.1890/ES11-00186.1

Butchart, S. H. M., Resit Akçakaya, H., Chanson, J., Baillie, J. E. M., Collen, B., Quader, S., Turner, W. R., Amin, R., Stuart, S. N., and Hilton-Taylor, C. (2007). Improvements to the Red List Index. *PLOS ONE*, *2*(1), e140.

Cagliero, R., Licciardo, F., and Legnini, M. (2021). The Evaluation Framework in the New CAP 2023–2027: A Reflection in the Light of Lessons Learned from Rural Development. *Sustainability*, *13*(10), 5528. https://doi.org/10.3390/su13105528

Campbell, N. R., Harmon, S. A., and Narum, S. R. (2015). Genotyping-in-Thousands by sequencing (GT-seq): A cost effective SNP genotyping method based on custom amplicon sequencing. *Molecular Ecology Resources*, *15*(4), 855–867. https://doi.org/10.1111/1755-0998.12357

Cardoso, P., Barton, P. S., Birkhofer, K., Chichorro, F., Deacon, C., Fartmann, T., Fukushima, C. S., Gaigher, R., Habel, J. C., Hallmann, C. A., Hill, M. J., Hochkirch, A., Kwak, M. L., Mammola, S., Ari Noriega, J., Orfinger, A. B., Pedraza, F., Pryke, J. S., Roque, F. O., … Samways, M. J. (2020). Scientists' warning to humanity on insect extinctions. *Biological Conservation*, *242*, 108426. https://doi.org/10.1016/j.biocon.2020.108426

Chamanara, J., Gaikwad, J., Gerlach, R., Algergawy, A., Ostrowski, A., and König-Ries, B. (2021). BEXIS2: A FAIR-aligned data management system for biodiversity, ecology and environmental data. *Biodiversity Data Journal*, *9*. https://doi.org/10.3897/BDJ.9.E72901

Chandler, M., See, L., Copas, K., Bonde, A. M. Z., López, B. C., Danielsen, F., Legind, J. K., Masinde, S., Miller-Rushing, A. J., and Newman, G. (2017). Contribution of citizen science towards international biodiversity monitoring. *Biological Conservation*, *213*, 280–294.

Charvolin, F. (2022). Faune France: Amateur Naturalists' Attachment and Indebtedness in a Citizen Science Biodiversity Database. *Science as Culture*, 1–21.

Chen, I.-C., Hill, J. K., Ohlemüller, R., Roy, D. B., and Thomas, C. D. (2011). Rapid Range Shifts of Species Associated with High Levels of Climate Warming. *Science*, *333*(6045), 1024–1026. https://doi.org/10.1126/science.1206432

Chimeno, C., Schmidt, S., Cancian de Araujo, B., Perez, K., von Rintelen, T., Schmidt, O., Hamid, H., Pramesa Narakusumo, R., and Balke, M. (2023). Abundant, diverse, unknown: Extreme species richness and turnover despite drastic undersampling in two closely placed tropical Malaise traps. *PLOS ONE*, *18*(8), e0290173.

Chmiel, J. A., Daisley, B. A., Pitek, A. P., Thompson, G. J., and Reid, G. (2020). Understanding the Effects of Sublethal Pesticide Exposure on Honey Bees: A Role for Probiotics as Mediators of Environmental Stress. *Frontiers in Ecology and Evolution*, *8*(February), 1–19. https://doi.org/10.3389/fevo.2020.00022

Coissac, E., Hollingsworth, P. M., Lavergne, S., and Taberlet, P. (2016). From barcodes to genomes: extending the concept of DNA barcoding. *Molecular Ecology*, *25*(7), 1423–1428. https://doi.org/10.1111/mec.13549

Convention on Biological Diversity. (2022a). *DECISION ADOPTED BY THE CONFERENCE OF THE PARTIES TO THE CONVENTION ON BIOLOGICAL DIVERSITY 15/4. Kunming-Montreal Global Biodiversity Framework*.

Convention on Biological Diversity. (2022b). *DECISION ADOPTED BY THE CONFERENCE OF THE PARTIES TO THE CONVENTION ON BIOLOGICAL DIVERSITY 15/5. Monitoring framework for the Kunming-Montreal Global Biodiversity Framework*.

Corrales, C., and Astrin, J. J. (2023). Biodiversity Biobanking – a Handbook on Protocols and Practices. In *Advanced Books* (Vol. 1). Pensoft Publishers.

Corrales, C., Luciano, S., and Astrin, J. J. (2023). Biodiversity biobanks: a landscape analysis. *ARPHA Preprints*, *4*(e103105). https://doi.org/10.3897/arphapreprints.e103105

Creedy, T. J., Norman, H., Tang, C. Q., Chin, K. Q., Andujar, C., Arribas, P., O'Connor, R. S., Carvell, C., Notton, D. G., and Vogler, A. P. (2020). A validated workflow for rapid taxonomic assignment and monitoring of a national fauna of bees (Apiformes) using high throughput DNA barcoding. *Molecular Ecology Resources*, *20*(1), 40–53. https://doi.org/10.1111/1755-0998.13056

Cruzan, M. B., Weinstein, B. G., Grasty, M. R., Kohrn, B. F., Hendrickson, E. C., Arredondo, T. M., and Thompson, P. G. (2016). Small Unmanned Aerial Vehicles (Micro-Uavs, Drones) in Plant Ecology. *Applications in Plant Sciences*, *4*(9). https://doi.org/ARTN 160004110.3732/apps.1600041

Czúcz, B., Baruth, B., Terres, J. M., Gallego Pinilla, F., Hagyo, A., Angileri, V., Nocita, M., Perez-Soba Aguilar, M., Koeble, R., and Paracchini, M. L. (2022). *Classification and quantification of Landscape Features across the EU: A brief review of existing definitions, typologies, and data sources for quantification of landscape features in agricultural land across the EU* (Issue ISBN: 978-92-76-47818-8). https://doi.org/10.2760/59418

d'Andrimont, R., Yordanov, M., Martinez-Sanchez, L., Eiselt, B., Palmieri, A., Dominici, P., Gallego, J., Reuter, H. I., Joebges, C., Lemoine, G., and van der Velde, M. (2020). Harmonised LUCAS in-situ land cover and use database for field surveys from 2006 to 2018 in the European Union. *Scientific Data*, *7*(1). https://doi.org/10.1038/s41597-020-00675-z

de Jong, Y., Verbeek, M., Michelsen, V., Bjørn, P. de P., Los, W., Steeman, F., Bailly, N., Basire, C., Chylarecki, P., Stloukal, E., Hagedorn, G., Wetzel, F., Glöckler, F., Kroupa, A., Korb, G., Hoffmann, A., Häuser, C., Kohlbecker, A., Müller, A., … Penev, L. (2014). Fauna Europaea – all European animal species on the web. *Biodiversity Data Journal*, *2*, e4034. https://doi.org/10.3897/BDJ.2.e4034

De Rijck, K., Schade, S., Rubio, J.-M., and Van Meerloo, M. (2020). *Best Practices in Citizen Science for Environmental Monitoring: Commission Staff Working Document.* https://doi.org/http://dx.doi.org/10.25607/OBP-1779

Dennis, E. B., Morgan, B. J. T., Freeman, S. N., Roy, D. B., and Brereton, T. (2016). Dynamic Models for Longitudinal Butterfly Data. *Journal of Agricultural, Biological, and Environmental Statistics*, *21*(1), 1–21. https://doi.org/10.1007/s13253-015-0216-3

Díaz, S., Zafra-Calvo, N., Purvis, A., Verburg, P. H., Obura, D., Leadley, P., Chaplin-Kramer, R., De Meester, L., Dulloo, E., Martín-López, B., Shaw, M. R., Visconti, P., Broadgate, W., Bruford, M. W., Burgess, N. D., Cavender- Bares, J., DeClerck, F., Fernández-Palacios, J. M., Garibaldi, L. A., … Zanne, A. E. (2020). Set ambitious goals for biodiversity and sustainability. *Science*, *370*(6515), 411–413. https://doi.org/10.1126/science.abe1530

Dickie, I. A., Boyer, S., Buckley, H. L., Duncan, R. P., Gardner, P. P., Hogg, I. D., Holdaway, R. J., Lear, G., Makiola, A., Morales, S. E., Powell, J. R., and Weaver, L. (2018). Towards robust and repeatable sampling methods in eDNA-based studies. *Molecular Ecology Resources*, *18*(5), 940–952. https://doi.org/10.1111/1755-0998.12907

Dobson, A. D. M., Milner-Gulland, E. J., Aebischer, N. J., Beale, C. M., Brozovic, R., Coals, P., Critchlow, R., Dancer, A., Greve, M., Hinsley, A., Ibbett, H., Johnston, A., Kuiper, T., Le Comber, S., Mahood, S. P., Moore, J. F., Nilsen, E. B., Pocock, M. J. O., Quinn, A., … Keane, A. (2020). Making Messy Data Work for Conservation. *One Earth*, *2*(5), 455–465. https://doi.org/https://doi.org/10.1016/j.oneear.2020.04.012

Dodsworth, S. (2015). Genome skimming for next-generation biodiversity analysis. In *Trends in plant science* (Vol. 20, Issue 9, pp. 525–527). https://doi.org/10.1016/j.tplants.2015.06.012

Domínguez-Garcia, V., Molina, F. P., Godoy, O., and Bartomeus, I. (2024). Interaction network structure explains species' temporal persistence in empirical plant–pollinator communities. *Nature Ecology & Evolution*, *8*(3), 423–429. https://doi.org/10.1038/s41559-023-02314-3

Dornelas, M., Chow, C., Patchett, R., Breeze, T., Brotons, L., Beja, P., Carvalho, L., Jandt, U., Junker, J., Kissling, W. D., Kühn, I., Lumbierres, M., Lyche Solheim, A., Mjelde, M., Moreira, F., Musche, M., Pereira, H., Sandin, L., and van Grunsven, R. (2023). Deliverable 4.2 Novel technologies for biodiversity monitoring - Final Report. *ARPHA Preprints*, *4*, e105600. https://doi.org/10.3897/ARPHAPREPRINTS.E105600

Droege, G., Barker, K., Seberg, O., Coddington, J., Benson, E., Berendsohn, W. G., Bunk, B., Butler, C., Cawsey, E. M., Deck, J., Döring, M., Flemons, P., Gemeinholzer, B., Güntsch, A., Hollowell, T., Kelbert, P., Kostadinov, I., Kottmann, R., Lawlor, R. T., … Zhou, X. (2016). The global genome biodiversity network (GGBN) data standard specification. *Database*, *2016*, 1–11. https://doi.org/10.1093/database/baw125

Dussex, N., Kurland, S., Olsen, R. A., Spong, G., Ericsson, G., Ekblom, R., Ryman, N., Dalén, L., and Laikre, L. (2023). Range-wide and temporal genomic analyses reveal the consequences of near-extinction in Swedish moose. *Communications Biology*, *6*(1). https://doi.org/10.1038/s42003-023-05385-x

Ebitu, L., Avery, H., Mourad, K. A., and Enyetu, J. (2021). Citizen science for sustainable agriculture–A systematic literature review. *Land Use Policy*, *103*, 105326.

ECORYS, and IfLS. (2018). Synthesis of Rural Development Programmes (RDPs) ex-post evaluations of period 2007-2013 : evaluation study. *EC- Directorate-General for Agriculture and Rural Development*, 534.

Edwards, J., Smith, G. P., and McEntee, M. H. F. (2015). Long-term time-lapse video provides near complete records of floral visitation. *Journal of Pollination Ecology*, *16*(0), 91–100. https://doi.org/10.26786/1920-7603(2015)16

Eitzel, M., Cappadonna, J., Santos-Lang, C., Duerr, R., West, S. E., Virapongse, A., Kyba, C., Bowser, A., Cooper, C., and Sforzi, A. (2017). Citizen science terminology matters: Exploring key terms. *Citizen Science: Theory and Practice*, 1–20.

Elbasyoni, I. S., Lorenz, A. J., Guttieri, M., Frels, K., Baenziger, P. S., Poland, J., and Akhunov, E. (2018). A comparison between genotyping-by-sequencing and array-based scoring of SNPs for genomic prediction accuracy in winter wheat. *Plant Science : An International Journal of Experimental Plant Biology*, *270*, 123–130. https://doi.org/10.1016/j.plantsci.2018.02.019

Ellis, R. (2011). Jizz and the joy of pattern recognition: Virtuosity, discipline and the agency of insight in UK naturalists' arts of seeing. *Social Studies of Science*, *41*(6), 769–790.

Elshire, R. J., Glaubitz, J. C., Sun, Q., Poland, J. A., Kawamoto, K., Buckler, E. S., and Mitchell, S. E. (2011). A Robust, Simple Genotyping-by-Sequencing (GBS) Approach for High Diversity Species. *PLOS ONE*, *6*(5), e19379.

Engel, M. S., Ceríaco, L. M. P., Daniel, G. M., Dellapé, P. M., Löbl, I., Marinov, M., Reis, R. E., Young, M. T., Dubois, A., Agarwal, I., Lehmann A., P., Alvarado, M., Alvarez, N., Andreone, F., Araujo-Vieira, K., Ascher, J. S., Baêta, D., Baldo, D., Bandeira, S. A., … Zacharie, C. K. (2021). The taxonomic impediment: a shortage of taxonomists, not the lack of technical approaches. *Zoological Journal of the Linnean Society*, *193*(2), 381–387. https://doi.org/10.1093/zoolinnean/zlab072

European Central Bank. (2023). *Exchange Rates*. https://data.ecb.europa.eu/search-results?searchTerm=Exchange rates

European Commission. (2000). *Communication from the Commission to the Council and the European Parliament - Indicators for the integration of environmental concerns into the common agricultural policy, COM(2000) 20 final*.

European Commission. (2020). *Communication from the Commission to the European Parliament, the Council, the European Economic and Social Committee and the Committee of the Regions. EU Biodiversity Strategy for 2030. COM(2020) 380 final.*

European Commission. (2021a). *Better Regulation Guidelines, Commission Staff Working Document SWD(2021) 305 final*.

European Commission. (2021b). *Better Regulation Toolbox, Commission Staff Working Document SWD(2021) 305 final.*

European Commission. (2023). *Communication from the Commission to the European Parliament, the Council, the European Economic and Social Committee and the Committee of the Regions. Revision of the EU Pollinators Initiative. A new deal for pollinators. COM/2023/35 final*.

European Commission. (2024). *Price Comparison Tool for Parcel Delivery in the EU*. https://single-market-economy.ec.europa.eu/sectors/postal-services/parcel-delivery-eu/find-best-price-your-eu-parcel-delivery_en

European Commission Directorate-General for Agriculture and Rural Development. (2015). *The monitoring and evaluation framework for the common agricultural policy 2014-2020*. Publications Office of the European Union. https://doi.org/10.2762/311150

European Commission Directorate-General for Agriculture and Rural Development. (2017). *Technical handbook on the monitoring and evaluation framework of the Common Agricultural Policy 2014 – 2020*.

European Commission Eurostat. (2022). *Farms and farmland in the European Union - statistics*. https://ec.europa.eu/eurostat/statistics-explained/index.php?title=Farms_and_farmland_in_the_European_Union_-_statistics#:~:text=Farms in the EU managed,for agriculture (2.2 %25)

European Court of Auditors. (2020). *Special Report 15/2020: Protection of wild pollinators in the EU — Commission initiatives have not borne fruit.* https://doi.org/10.2865/962753

Everett, G., and Geoghegan, H. (2016). Initiating and continuing participation in citizen science for natural history. *BMC Ecology*, *16*, 15–22.

Exposito-Alonso, M., Booker, T. R., Czech, L., Gillespie, L., Hateley, S., Kyriazis, C. C., Lang, P. L. M., Leventhal, L., Nogues-Bravo, D., Pagowski, V., Ruffley, M., Spence, J. P., Toro Arana, S. E., Weiß, C. L., and Zess, E. (2022). *Genetic diversity loss in the Anthropocene*.

Falk, S., Foster, G., Comont, R., Conroy, J., Bostock, H., Salisbury, A., Kilbey, D., Bennett, J., and Smith, B. (2019). Evaluating the ability of citizen scientists to identify bumblebee (Bombus) species. *PLoS ONE*, *14*(6), e0218614. https://doi.org/10.1371/journal.pone.0218614

Fijen, T. P. M., Read, S. F. J., Walker, M. K., Gee, M., Nelson, W. R., and Howlett, B. G. (2022). Different landscape features within a simplified agroecosystem support diverse pollinators and their service to crop plants. *Landscape Ecology*, *37*(7), 1787–1799. https://doi.org/10.1007/s10980-022-01423-x

Fijen, T. P. M., Roovers, A., van Deijk, J., and van Grunsven, R. H. A. (2023). Nocturnal pollination is equally important as, and complementary to, diurnal pollination for strawberry fruit production. *Agriculture Ecosystems & Environment*, *350*. https://doi.org/ARTN 10847510.1016/j.agee.2023.108475

Firbank, L. G., Petit, S., Smart, S., Blain, A., and Fuller, R. J. (2007). Assessing the impacts of agricultural intensification on biodiversity: a British perspective. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *363*(1492), 777–787. https://doi.org/10.1098/rstb.2007.2183

Fjellstad, W. J., Dramstad, W. E., Strand, G. H., and Fry, G. L. A. (2001). Heterogeneity as a measure of spatial pattern for monitoringagricultural landscapes. *Norsk Geografisk Tidsskrift*, *55*(2), 71–76. https://doi.org/10.1080/00291950119811

Folmer, O., Blacket, M. J., Hoeh, W., Lutz, R., and Vrijenhoek, R. (1994). DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Mol Mar Biol Biotechnol*, *3*(5), 294–299.

Formenti, G., Theissinger, K., Fernandes, C., Bista, I., Bombarely, A., Bleidorn, C., Ciofi, C., Crottini, A., Godoy, J. A., Höglund, J., Malukiewicz, J., Mouton, A., Oomen, R. A., Paez, S., Palsbøll, P. J., Pampoulie, C., Ruiz-López, M. J., Svardal, H., Theofanopoulou, C., … Zammit, G. (2022). The era of reference genomes in conservation genomics. *Trends in Ecology & Evolution*, *37*(3), 197–202. https://doi.org/10.1016/j.tree.2021.11.008

Frankham, R., Ballou, J. D., and Briscoe, D. A. (2010). *Introduction to Conservation Genetics* (2nd ed.). Cambridge University Press. https://doi.org/DOI: 10.1017/CBO9780511809002

Freeman, S. N., Isaac, N. J. B., Besbeas, P., Dennis, E. B., and Morgan, B. J. T. (2021). A Generic Method for Estimating and Smoothing Multispecies Biodiversity Indicators Using Intermittent Data. *Journal of Agricultural, Biological and Environmental Statistics*, *26*(1), 71–89. https://doi.org/10.1007/s13253-020-00410-6

Frenzel, M., Preiser, C., Dussl, F., Höhne, R., Nickels, V., and Creutzburg, F. (2016). TERENO (Terrestrial Environmental Observatories) wild bee monitoring in six agriculturally dominated landscapes of Saxony-Anhalt (Germany). In *Helmholtz Centre for Environmental Research - UFZ*. PANGAEA. https://doi.org/10.1594/PANGAEA.864908

Fuentes-Pardo, A. P., and Ruzzante, D. E. (2017). Whole-genome sequencing approaches for conservation biology: Advantages, limitations and practical recommendations. *Molecular Ecology*, *26*(20), 5369–5406. https://doi.org/10.1111/mec.14264

Gabrielsen, P., and Bosch, P. (2003). *Environmental Indicators: Typology and Use in Reporting*.

Gagliano, M. (2013). The flowering of plant bioacoustics: how and why. *Behavioral Ecology*, *24*(4), 800–801. https://doi.org/10.1093/beheco/art021

Galliot, J. N., Brunel, D., Bérard, A., Chauveau, A., Blanchetête, A., Lanore, L., and Farruggia, A. (2017). Investigating a flower-insect forager network in a mountain grassland community using pollen DNA barcoding. *Journal of Insect Conservation*, *21*(5–6), 827–837. https://doi.org/10.1007/s10841-017-0022-z

Garratt, M. P. D., Potts, S. G., Banks, G., Hawes, C., Breeze, T., O'Connor, R. S., and Carvell, C. (2019). Capacity and willingness of farmers and citizen scientists to monitor crop pollinators and pollination services. *Global Ecology and Conservation*, *20*, e00781.

Garratt, M. P. D., Senapathi, D., Coston, D. J., Mortimer, S. R., and Potts, S. G. (2017). The benefits of hedgerows for pollinators and natural enemies depends on hedge quality and landscape context. *Agriculture, Ecosystems & Environment*, *247*, 363–370. https://doi.org/10.1016/j.agee.2017.06.048

Gauthier, M., Konecny-Dupré, L., Nguyen, A., Elbrecht, V., Datry, T., Douady, C., and Lefébure, T. (2020). Enhancing DNA metabarcoding performance and applicability with bait capture enrichment and DNA from conservative ethanol. *Molecular Ecology Resources*, *20*(1), 79–96. https://doi.org/10.1111/1755-0998.13088

Geissmann, Q., Abram, P. K., Wu, D., Haney, C. H., and Carrillo, J. (2022). Sticky Pi is a high-frequency smart trap that enables the study of insect circadian activity under natural conditions. *Plos Biology*, *20*(7). https://doi.org/ARTN e300168910.1371/journal.pbio.3001689

George, R. D., McVicker, G., Diederich, R., Ng, S. B., MacKenzie, A. P., Swanson, W. J., Shendure, J., and Thomas, J. H. (2011). Trans genomic capture and sequencing of primate exomes reveals new targets of positive selection. *Genome Research*, *21*(10), 1686–1694. https://doi.org/10.1101/gr.121327.111

Ghisbain, G., Rosa, P., Bogusch, P., Flaminio, S., Le Divelec, R., Dorchin, A., Kasparek, M., Kuhlmann, M., Litman, J., Mignot, M., Müller, A., Praz, C., Radchenko, V. G., Rasmont, P., Risch, S., Roberts, S., Smit, J., Wood, T. J., Michez, D., and Reverté, S. (2023). The new annotated checklist of the wild bees of Europe (Hymenoptera: Anthophila). *Zootaxa*, *5327*(1), 1–147. https://doi.org/10.11646/zootaxa.5327.1.1

Gnirke, A., Melnikov, A., Maguire, J., Rogov, P., LeProust, E. M., Brockman, W., Fennell, T., Giannoukos, G., Fisher, S., Russ, C., Gabriel, S., Jaffe, D. B., Lander, E. S., and Nusbaum, C. (2009). Solution hybrid selection with ultra-long oligonucleotides for massively parallel targeted sequencing. *Nature Biotechnology*, *27*(2), 182–189. https://doi.org/10.1038/nbt.1523

Gonzales, D., de Ibarra, N. H., and Anderson, K. (2022). Remote Sensing of Floral Resources for Pollinators - New Horizons From Satellites to Drones. *Frontiers in Ecology and Evolution*, *10*. https://doi.org/ARTN 86975110.3389/fevo.2022.869751

Goulson, D., Nicholls, E., Botías, C., and Rotheray, E. L. (2015). Bee declines driven by combined Stress from parasites, pesticides, and lack of flowers. *Science*, *347*(6229). https://doi.org/10.1126/science.1255957

Gous, A., Swanevelder, D. Z. H., Eardley, C. D., and Willows-Munro, S. (2019). Plant-pollinator interactions over time: Pollen metabarcoding from bees in a historic collection. *Evolutionary Applications*, *12*(2), 187–197. https://doi.org/10.1111/eva.12707

Gradišek, A., Slapnicar, G., Sorn, J., Lustrek, M., Gams, M., and Grad, J. (2017). Predicting species identity of bumblebees through analysis of flight buzzing sounds. *Bioacoustics-the International Journal of Animal Sound and Its Recording*, *26*(1), 63–76. https://doi.org/10.1080/09524622.2016.1190946

Gregory, R. D., van Strien, A. J., Vorisek, P., Gmelig Meyling, A. W., Noble, D. G., Foppen, R. P. ., and Gibbons, D. W. (2005). Developing indicators for European birds. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *360*(1454), 269–288. https://doi.org/10.1098/rstb.2004.1602

Gresty, C. E. A., Clare, E., Devey, D. S., Cowan, R. S., Csiba, L., Malakasi, P., Lewis, O. T., and Willis, K. J. (2018). Flower preferences and pollen transport networks for cavity-nesting solitary bees: Implications for the design of agri-environment schemes. *Ecology and Evolution*, *8*(15), 7574–7587. https://doi.org/10.1002/ece3.4234

Grobe, P., Gleisberg, M., Klasen, B., Monje, J., Penzlin, A., Weibulat, T., and Triebel, D. (2019). Long-Term Reusability of Biodiversity and Collection Data using a National Federated Data Infrastructure. *Biodiversity Information Science and Standards*, *3*. https://doi.org/10.3897/biss.3.37414

Hajibabaei, M., Spall, J. L., Shokralla, S., and van Konynenburg, S. (2012). Assessing biodiversity of a freshwater benthic macroinvertebrate community through non-destructive environmental barcoding of DNA from preservative ethanol. *Bmc Ecology*, *12*. https://doi.org/Artn 2810.1186/1472-6785-12-28

Hallmann, C. A., Sorg, M., Jongejans, E., Siepel, H., Hofland, N., Schwan, H., Stenmans, W., Müller, A., Sumser, H., Hörren, T., Goulson, D., and de Kroon, H. (2017). More than 75 percent decline over 27 years in total flying insect biomass in protected areas. *PLOS ONE*, *12*(10), e0185809. https://doi.org/10.1371/journal.pone.0185809

Hansen, O. L. P., Svenning, J.-C., Olsen, K., Dupont, S., Garner, B. H., Iosifidis, A., Price, B. W., and Høye, T. T. (2020). Species-level image classification with convolutional neural network enables insect identification from habitus images. *Ecology and Evolution*, *10*(2), 737–747. https://doi.org/https://doi.org/10.1002/ece3.5921

Harjes, J., Link, A., Weibulat, T., Triebel, D., and Rambold, G. (2020). FAIR digital objects in environmental and life sciences should comprise workflow operation design data and method information for repeatability of study setups and reproducibility of results. *Database*, *2020*. https://doi.org/10.1093/database/baaa059

Harvey, M. G., Smith, B. T., Glenn, T. C., Faircloth, B. C., and Brumfield, R. T. (2016). Sequence Capture versus Restriction Site Associated DNA Sequencing for Shallow Systematics. *Systematic Biology*, *65*(5), 910–924. https://doi.org/10.1093/sysbio/syw036

Hebert, P. D. N., Penton, E. H., Burns, J. M., Janzen, D. H., and Hallwachs, W. (2004). Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly Astraptes fulgerator. *Proceedings of the National Academy of Sciences of the United States of America*, *101*(41), 14812–14817. https://doi.org/10.1073/pnas.0406166101

Hellwig, N., Sommerlandt, F. M. J., Grabener, S., Lindermann, L., Sickel, W., Krüger, L., and Dieker, P. (2024). Six Steps towards a Spatial Design for Large-Scale Pollinator Surveillance Monitoring. *Insects*, *15*(4), 229. https://doi.org/10.3390/insects15040229

Hill, A. P., Prince, P., Snaddon, J. L., Doncaster, C. P., and Rogers, A. (2019). AudioMoth: A low-cost acoustic device for monitoring biodiversity and the environment. *Hardwarex*, *6*. https://doi.org/ARTN e0007310.1016/j.ohx.2019.e00073

Hoban, S., Archer, F. I., Bertola, L. D., Bragg, J. G., Breed, M., Bruford, M. W., Coleman, M. A., Ekblom, R., Funk, W. C., Grueber, C. E., Hand, B. K., Jaffé, R., Jensen, E., Johnson, J. S., Kershaw, F., Liggins, L., MacDonald, A. J., Mergeay, J., Miller, J. M., … Hunter, M. E. (2022). Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. *Biological Reviews*, *97*(4), 1511–1538. https://doi.org/10.1111/brv.12852

Hoban, S., Bruford, M. W., D'Urban Jackson, J., Lopes-Fernandes, M., Heuertz, M., Hohenlohe, P. A., Paz-Vinas, I., Sjögren-Gulve, P., Segelbacher, G., Vernesi, C., Aitken, S., Bertola, L. D., Bloomer, P., Breed, M., Rodríguez-Correa, H., Funk, W. C., Grueber, C. E., Hunter, M. E., Jaffe, R., ... Laikre, L. (2020). Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. *Biological Conservation*, *248*. https://doi.org/10.1016/j.biocon.2020.108654

Hoban, S., Bruford, M. W., Funk, W. C., Galbusera, P., Griffith, M. P., Grueber, C. E., Heuertz, M., Hunter, M. E., Hvilsom, C., Stroil, B. K., Kershaw, F., Khoury, C. K., Laikre, L., Lopes-Fernandes, M., MacDonald, A. J., Mergeay, J., Meek, M., Mittan, C., Mukassabi, T. A., ... Vernesi, C. (2021). Global commitments to conserving and monitoring genetic diversity are now necessary and feasible. *BioScience*, *71*(9), 964–976. https://doi.org/10.1093/biosci/biab054

Hoban, S., da Silva, J. M., Mastretta-Yanes, A., Grueber, C. E., Heuertz, M., Hunter, M. E., Mergeay, J., Paz-Vinas, I., Fukaya, K., Ishihama, F., Jordan, R., Köppä, V., Latorre-Cárdenas, M. C., MacDonald, A. J., Rincon-Parra, V., Sjögren-Gulve, P., Tani, N., Thurfjell, H., and Laikre, L. (2023). Monitoring status and trends in genetic diversity for the Convention on Biological Diversity: An ongoing assessment of genetic indicators in nine countries. *Conservation Letters*, *16*(3). https://doi.org/10.1111/conl.12953

Hoban, S., Paz-Vinas, I., Aitken, S., Bertola, L. D., Breed, M., Bruford, M. W., Funk, W. C., Grueber, C. E., Heuertz, M., Hohenlohe, P., Hunter, M. E., Jaffé, R., Fernandes, M. L., Mergeay, J., Moharrek, F., O'Brien, D., Segelbacher, G., Vernesi, C., Waits, L., and Laikre, L. (2021). Effective population size remains a suitable, pragmatic indicator of genetic diversity for all species, including forest trees. *Biological Conservation*, *253*. https://doi.org/10.1016/j.biocon.2020.108906

Hobbs, M. T., and Brehme, C. S. (2017). An improved camera trap for amphibians, reptiles, small mammals, and large invertebrates. *Plos One*, *12*(10), e0185026. https://doi.org/10.1371/journal.pone.0185026

Hochachka, W. M., Fink, D., Hutchinson, R. A., Sheldon, D., Wong, W.-K., and Kelling, S. (2012). Data-intensive science applied to broad-scale citizen science. *Trends in Ecology & Evolution*, *27*(2), 130–137.

Hochkirch, A., Casino, A., Penev, L., Allen, D., Tilley, L., Georgiev, T., Gospodinov, K., and Barov, B. (2022). *European Red List of insect taxonomists*. Publications Office of the European Union. https://doi.org/10.2779/364246

Hochkirch, A., Samways, M. J., Gerlach, J., Böhm, M., Williams, P., Cardoso, P., Cumberlidge, N., Stephenson, P. J., Seddon, M. B., Clausnitzer, V., Borges, P. A. V, Mueller, G. M., Pearce-Kelly, P., Raimondo, D. C., Danielczak, A., and Dijkstra, K.-D. B. (2021). A strategy for the next decade to address data deficiency in neglected biodiversity. *Conservation Biology*, *35*(2), 502–509. https://doi.org/10.1111/cobi.13589

Hodges, E., Xuan, Z., Balija, V., Kramer, M., Molla, M. N., Smith, S. W., Middle, C. M., Rodesch, M. J., Albert, T. J., Hannon, G. J., and McCombie, W. R. (2007). Genome-wide in situ exon capture for selective resequencing. *Nature Genetics*, *39*(12), 1522–1527. https://doi.org/10.1038/ng.2007.42

Hoffberg, S. L., Kieran, T. J., Catchen, J. M., Devault, A., Faircloth, B. C., Mauricio, R., and Glenn, T. C. (2016). RADcap: sequence capture of dual-digest RADseq libraries with identifiable duplicates and reduced missing data. *Molecular Ecology Resources*, *16*(5), 1264–1278. https://doi.org/10.1111/1755-0998.12566

Hofmann, S., Everaars, J., Schweiger, O., Frenzel, M., Bannehr, L., and Cord, A. F. (2017). Modelling patterns of pollinator species richness and diversity using satellite image texture. *Plos One*, *12*(10). https://doi.org/ARTN e018559110.1371/journal.pone.0185591

Hopkins, G. W., and Freckleton, R. P. (2002). Declines in the numbers of amateur and professional taxonomists: implications for conservation. *Animal Conservation*, *5*(3), 245–249. https://doi.org/10.1017/S1367943002002299

Horton, R., Cano, E., Bulanon, D., and Fallahi, E. (2017). Peach Flower Monitoring Using Aerial Multispectral Imaging. *Journal of Imaging*, *3*(1), 2.

Høye, T. T., Ärje, J., Bjerge, K., Hansen, O. L. P., Iosifidis, A., Leese, F., Mann, H. M. R., Meissner, K., Melvad, C., and Raitoharju, J. (2021). Deep learning and computer vision will transform entomology. *Proceedings of the National Academy of Sciences of the United States of America*, *118*(2), e2002545117. https://doi.org/10.1073/pnas.2002545117

Hvilsom, C., Segelbacher, G., Ekblom, R., Fischer, M. C., Laikre, L., Leus, K., O'Brien, D., Shaw, R., and Sork, V. (2022). Selecting species and populations for monitoring of genetic diversity. In *Selecting species and populations for monitoring of genetic diversity*. IUCN, International Union for Conservation of Nature. https://doi.org/10.2305/iucn.ch.2022.07.en

Image, M., Gardner, E., Clough, Y., Smith, H. G., Baldock, K. C. R., Campbell, A., Garratt, M., Gillespie, M. A. K., Kunin, W. E., McKerchar, M., Memmott, J., Potts, S. G., Senapathi, D., Stone, G. N., Wackers, F., Westbury, D. B., Wilby, A., Oliver, T. H., and Breeze, T. D. (2022). Does agri-environment scheme participation in England increase pollinator populations and crop pollination services? *Agriculture, Ecosystems and Environment*, *325*(May 2021), 107755. https://doi.org/10.1016/j.agee.2021.107755

IPBES. (2016). *The assessment report of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services on pollinators, pollination and food production* (S.G. Potts, V. L. Imperatriz-Fonseca, & H. T. Ngo (eds.)). Secretariat of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services, Bonn, Germany. https://doi.org/https://doi.org/10.5281/zenodo.3402856

IUCN Species Survival Commission. (2001). *IUCN Red List categories and criteria, version 3.1*. IUCN.

IUCN Standards and Petitions Committee. (2024). *Guidelines for Using the IUCN Red List Categories and Criteria. Version 16. Downloadable from https://www.iucnredlist.org/documents/RedListGuidelines.pdf* (pp. 1–122).

Johannesson, K., and Laikre, L. (2020). *Monitoring of genetic diversity in environmental monitoring (in Swedish). Report to the Swedish Agency for Marine and Water Management (dnr. HaV 3642-2018, 3643-2018).*

Johannesson, K., and Laikre, L. (2022). *Pilot monitoring, environmental monitoring of genetic diversity. Report on several species in aquatic environments (in Swedish). Report to the Swedish Agency for Marine and Water Management dnr. HaV 02213-2020, 02212-2020.*

Johannesson, K., and Laikre, L. (2023). *Environmental monitoring of genetic diversity. Report on progress for several species (in Swedish). Report to the Swedish Agency for Marine and Water Management dnr. HaV 1716-22, 2007-21, 1717-2022.*

Johnston, A., Matechou, E., and Dennis, E. B. (2023). Outstanding challenges and future directions for biodiversity monitoring using citizen science data. *Methods in Ecology and Evolution*, *14*(1), 103–116.

Kasiske, T., Dauber, J., Harpke, A., Klimek, S., Kühn, E., Settele, J., and Musche, M. (2023). Livestock density affects species richness and community composition of butterflies: A nationwide study. *Ecological Indicators*, *146*, 109866. https://doi.org/10.1016/j.ecolind.2023.109866

Kershaw, F., Bruford, M. W., Funk, W. C., Grueber, C. E., Hoban, S., Hunter, M. E., Laikre, L., MacDonald, A. J., Meek, M. H., Mittan, C., O'Brien, D., Ogden, R., Shaw, R. E., Vernesi, C., and Segelbacher, G. (2022). The Coalition for Conservation Genetics: Working across organizations to build capacity and achieve change in policy and practice. *Conservation Science and Practice*, *4*(4). https://doi.org/10.1111/csp2.12635

Kirse, A., Bourlat, S. J., Langen, K., and Fonseca, V. G. (2021). Metabarcoding Malaise traps and soil eDNA reveals seasonal and local arthropod diversity shifts. *Scientific Reports*, *11*(1), 10498. https://doi.org/10.1038/s41598-021-89950-6

Kissling, W. D., Ahumada, J. A., Bowser, A., Fernandez, M., Fernández, N., García, E. A., Guralnick, R. P., Isaac, N. J. B., Kelling, S., Los, W., McRae, L., Mihoub, J., Obst, M., Santamaria, M., Skidmore, A. K., Williams, K. J., Agosti, D., Amariles, D., Arvanitidis, C., … Hardisty, A. R. (2018). Building essential biodiversity variables (<scp>EBV</scp> s) of species distribution and abundance at a global scale. *Biological Reviews*, *93*(1), 600–625. https://doi.org/10.1111/brv.12359

Kleijn, D., Kohler, F., Báldi, A., Batáry, P., Concepción, E. D., Clough, Y., Díaz, M., Gabriel, D., Holzschuh, A., Knop, E., Kovács, A., Marshall, E. J. P., Tscharntke, T., and Verhulst, J. (2009). On the relationship between farmland biodiversity and land-use intensity in Europe. *Proceedings of the Royal Society B: Biological Sciences*, *276*(1658), 903–909. https://doi.org/10.1098/rspb.2008.1509

Kleijn, D., and van Zuijlen, G. J. C. (2004). The conservation effects of meadow bird agreements on farmland in Zeeland, The Netherlands, in the period 1989–1995. *Biological Conservation*, *117*(4), 443–451. https://doi.org/https://doi.org/10.1016/j.biocon.2003.08.012

Klein, K., Ogan, S., Rottstock, T., Tönnshof, C., Ackermann, A., Alkassab, A., Balzar, L., Beer, H., Beyer, Böhner, H., Briem, F., Dauber, J., Dieker, P., Erasmi, S., Finn, D., Früchtenicht, E., Gerighausen, H., Gocht, A., Göderz, H., … Yang, J. (2024). *MonViA Indikatorenbericht 2024 : Bundesweites Monitoring der biologischen Vielfalt in Agrarlandschaften*. Verbundprojekt MonViA.

Korsch, D., Bodesheim, P., Brehm, G., and Denzler, J. (2023). Automated Visual Monitoring of Nocturnal Insects with Light-based Camera Traps. *ArXiv*, *abs/2307.15433*.

Krehenwinkel, H., Wolf, M., Lim, J. Y., Rominger, A. J., Simison, W. B., and Gillespie, R. G. (2017). Estimating and mitigating amplification bias in qualitative and quantitative arthropod metabarcoding. *Scientific Reports*, *7*. https://doi.org/ARTN 1766810.1038/s41598-017-17333-x

Kreitmair, K. V, and Magnus, D. C. (2019). Citizen science and gamification. *Hastings Center Report*, *49*(2), 40–46.

Krogmann, L., and Holstein, J. (2010). Chapter 18. Preserving and Specimen Handling: Insects and other Invertebrates. In *Manual on field recording techniques and protocols for all taxa biodiversity inventories* (pp. 463–481). ABC TAXA.

Kuhn, E., Musche, M., Harpke, A., Feldmann, R., Wiemers, M., and Settele, J. (2022). Tagfalter-Monitoring Deutschland: Jahresauswertung 2021. *Oedippus*, *40*, 6–35.

Kurland, S., Saha, A., Keehnen, N., de la Paz Celorio-Mancera, M., Díez-del-Molino, D., Ryman, N., and Laikre, L. (2024). New indicators for monitoring genetic diversity applied to alpine brown trout populations using whole genome sequence data. *Molecular Ecology*, *33*(2). https://doi.org/10.1111/mec.17213

Kurze, S., Heinken, T., and Fartmann, T. (2018). Nitrogen enrichment in host plants increases the mortality of common Lepidoptera species. *Oecologia*, *188*(4), 1227–1237. https://doi.org/10.1007/s00442-018-4266-4

Laikre, L. (2010). Genetic diversity is overlooked in international conservation policy implementation. *Conservation Genetics*, *11*(2), 349–354. https://doi.org/10.1007/s10592-009-0037-4

Laikre, L., Allendorf, F. W., Aroner, L. C., Baker, C. S., Gregovich, D. P., Hansen, M. M., Jackson, J. A., Kendall, K. C., McKelvey, K., Neel, M. C., Olivieri, I., Ryman, N., Schwartz, M. K., Bull, R. S., Stetz, J. B., Tallmon, D. A., Taylor, B. L., Vojta, C. D., Waller, D. M., and Waples, R. S. (2010). Neglect of genetic diversity in implementation of the convention on biological diversity: Conservation in practice and policy. *Conservation Biology*, *24*(1), 86–88. https://doi.org/10.1111/j.1523-1739.2009.01425.x

Laikre, L., Hoban, S., Bruford, M., Segelbacher, G., Allendorf, F., Gajardo, G., González Rodríguez, A Hedrick, P., Heuertz, M., Hohenlohe, P., Jaffé, R., Johannesson, K., Liggins, L., MacDonald, A., Orozco-terWengel, P., Reusch, T., Rodríguez-Correa, H., Russo, I.-R., Ryman, N., and Vernesi, C. (2020). Post-2020 goals overlook genetic diversity. *Science*, *367*(6482), 1083–1085. https://doi.org/10.1126/science.abb2748

Laikre, L., Hohenlohe, P. A., Allendorf, F. W., Bertola, L. D., Breed, M., Bruford, M. W., Funk, W. C., Gajardo, G., González-Rodríguez, A., Grueber, C. E., Hedrick, P. W., Heuertz, M., Hunter, M. E., Johannesson, K., Liggins, L., MacDonald, A. J., Mergeay, J., Moharrek, F., O'Brien, D., … Hoban, S. (2021). Authors' Reply to Letter to the Editor: Continued improvement to genetic diversity indicator for CBD. *Conservation Genetics*, *22*(4), 533–536. https://doi.org/10.1007/s10592-021-01359-w

Laikre, L., Lundmark, C., Jansson, E., Wennerström, L., Edman, M., and Sandström, A. (2016). Lack of recognition of genetic biodiversity: International policy and its implementation in Baltic Sea marine protected areas. *Ambio*, *45*(6), 661–680. https://doi.org/10.1007/s13280-016-0776-7

Lambeck, R. J. (1997). Focal species: A multi-species umbrella for nature conservation. In *Conservation Biology* (Vol. 11, Issue 4, pp. 849–856). https://doi.org/10.1046/j.1523-1739.1997.96319.x

Land-Zandstra, A., Agnello, G., and Gültekin, Y. S. (2021). Participants in citizen science. *The Science of Citizen Science*, *243*, 259.

Lee, I., Hsiao, R., Carichner, G., Hsu, C.-W., Yang, M., Shoouri, S., Ernst, K., Carichner, T., Li, Y., Lim, J., Julick, C. R., Moon, E., Sun, Y., Phillips, J., Montooth, K. L., Green, D. A., Kim, H.-S., and Blaauw, D. (2021). mSAIL: milligram-scale multi-modal sensor platform for monarch butterfly migration tracking. In *Proceedings of the 27th Annual International Conference on Mobile Computing and Networking* (pp. 517–530). Association for Computing Machinery. https://doi.org/10.1145/3447993.3483263

Leigh, D. M., Hendry, A. P., Vázquez-Domínguez, E., and Friesen, V. L. (2019). Estimated six per cent loss of genetic variation in wild populations since the industrial revolution. In *Evolutionary Applications* (Vol. 12, Issue 8, pp. 1505–1512). Wiley-Blackwell. https://doi.org/10.1111/eva.12810

Leung, B., and Gonzalez, A. (2024). Global monitoring for biodiversity: Uncertainty, risk, and power analyses to support trend change detection. *Science Advances*, *10*(7). https://doi.org/10.1126/sciadv.adj1448

Li, M., Runemark, A., Hernandez, J., Rota, J., Bygebjerg, R., and Brydegaard, M. (2023). Discrimination of Hover Fly Species and Sexes by Wing Interference Signals. *Advanced Science*. https://doi.org/10.1002/advs.202304657

Li, X., and Wiens, J. J. (2023). Estimating Global Biodiversity: The Role of Cryptic Insect Species. *Systematic Biology*, *72*(2), 391–403. https://doi.org/10.1093/sysbio/syac069

Linard, B., Arribas, P., Andújar, C., Crampton-Platt, A., and Vogler, A. P. (2016). Lessons from genome skimming of arthropod-preserving ethanol. *Molecular Ecology Resources*, *16*(6), 1365–1377. https://doi.org/10.1111/1755-0998.12539

Linard, B., Crampton-Platt, A., Gillett, C. P. D. T., Timmermans, M. J. T. N., and Vogler, A. P. (2015). Metagenome Skimming of Insect Specimen Pools: Potential for Comparative Genomics. *Genome Biology and Evolution*, *7*(6), 1474–1489. https://doi.org/10.1093/gbe/evv086

Liquete, C., Bormpoudakis, D., Maes, J., McCallum, I., Kissling, W. D., Brotons, L., Breeze, T., Moran, A., Lumbierres, M., Friedrich, L., Herrando, S., Lyche Solheim, A., Fernandez, M., Fernández, N., Hirsch, T., Carvalho, L., Vihervaara, P., Junker, J., Georgieva, I., … Pereira, H. M. (2024). D2.3 EuropaBON Proposal for an EU Biodiversity Observation Coordination Centre (EBOCC). *ARPHA Preprints*, *5*, ARPHA Prepr.

Liu, J., Slik, F., Zheng, S., and Lindenmayer, D. B. (2022). Undescribed species have higher extinction risk than known species. *Conservation Letters*, *15*(3), e12876. https://doi.org/https://doi.org/10.1111/conl.12876

Lou, R. N., Jacobs, A., Wilder, A. P., and Therkildsen, N. O. (2021). A beginner's guide to low-coverage whole genome sequencing for population genomics. *Molecular Ecology*, *30*(23), 5966–5993. https://doi.org/10.1111/mec.16077

Lucas, A., Bodger, O., Brosi, B. J., Ford, C. R., Forman, D. W., Greig, C., Hegarty, M., Neyland, P. J., and de Vere, N. (2018). Generalisation and specialisation in hoverfly (Syrphidae) grassland pollen transport networks revealed by DNA metabarcoding. *Journal of Animal Ecology*, *87*(4), 1008–1021. https://doi.org/10.1111/1365-2656.12828

MacKenzie, D. I., Nichols, J. D., Royle, J. A., Pollock, K. H., Bailey, L. L., and Hines, J. E. (2006). *Occupancy Estimation and Modeling : Inferring Patterns and Dynamics of Species Occurrence*. Elsevier/Academic Press.

Maes, D., Verovnik, R., Wiemers, M., Brosens, D., Beshkov, S., Bonelli, S., Buszko, J., Cantú-Salazar, L., Cassar, L.-F., Collins, S., Dincă, V., Djuric, M., Dušej, G., Elven, H., Franeta, F., Garcia-Pereira, P., Geryak, Y., Goffart, P., Gór, Á., … Warren, M. S. (2019). Integrating national Red Lists for prioritising conservation actions for European butterflies. *Journal of Insect Conservation*, *23*(2), 301–330. https://doi.org/10.1007/s10841-019-00127-z

Mann, H. M. R., Iosifidis, A., Jepsen, J. U., Welker, J. M., Loonen, M. J. J. E., and Høye, T. T. (2022). Automatic flower detection and phenology monitoring using time-lapse cameras and deep learning. *Remote Sensing in Ecology and Conservation*, *8*(6), 765–777. https://doi.org/https://doi.org/10.1002/rse2.275

Mastretta-Yanes, A., da Silva, J. M., Grueber, C. E., Castillo-Reina, L., Köppä, V., Forester, B. R., Funk, W. C., Heuertz, M., Ishihama, F., Jordan, R., Mergeay, J., Paz-Vinas, I., Rincon-Parra, V. J., Rodriguez-Morales, M. A., Arredondo-Amezcua, L., Brahy, G., DeSaix, M., Durkee, L., Hamilton, A., … Hoban, S. (2024). Multinational evaluation of genetic diversity indicators for the Kunming-Montreal Global Biodiversity Framework. *Ecology Letters*, *27*(7). https://doi.org/10.1111/ele.14461

McKinley, D. C., Miller-Rushing, A. J., Ballard, H. L., Bonney, R., Brown, H., Cook-Patton, S. C., Evans, D. M., French, R. A., Parrish, J. K., and Phillips, T. B. (2017). Citizen science can improve conservation science, natural resource management, and environmental protection. *Biological Conservation*, *208*, 15–28.

Meek, M. H., and Larson, W. A. (2019). The future is now: Amplicon sequencing and sequence capture usher in the conservation genomics era. *Molecular Ecology Resources*, *19*(4), 795–803. https://doi.org/https://doi.org/10.1111/1755-0998.12998

Meier, E., Lüscher, G., Buholzer, S., Herzog, F., Indermaur, A., Riedel, S., Winizki, J., Hofer, G., and Knop, E. (2021). State of biodiversity in the Swiss agricultural landscape. *Status Report ALL-EMA 2015-2019, Agroscope Science*, *111*, 113.

Merenlender, A. M., Crall, A. W., Drill, S., Prysby, M., and Ballard, H. L. (2016). Evaluating environmental education, citizen science, and stewardship through naturalist programs. *Conservation Biology*, *30*(6), 1255–1265.

Michener, W., Vieglais, D., Vision, T., Kunze, J., Cruse, P., and Janée, G. (2011). DataONE: Data Observation Network for Earth — Preserving Data and Enabling Innovation in the Biological and Environmental Sciences. *D-Lib Magazine*, *17*(1/2). https://doi.org/10.1045/january2011-michener

Miller, M. R., Dunham, J. P., Amores, A., Cresko, W. A., and Johnson, E. A. (2007). Rapid and cost-effective polymorphism identification and genotyping using restriction site associated DNA (RAD) markers. *Genome Research*, *17*(2), 240–248. https://doi.org/10.1101/gr.5681207

Morkvenas, Ž., and Schwarz, G. (2012). Indicator and Monitoring Frameworks for the Assessment of the Effectiveness of Agri- Environmental Measures: Key Issues for a Practical Application in Lithuania. *Baltic Compass*, 1–43.

Mortimer, S., Mauchline, A., Park, J., Finn, J., Edwards, D., and Morris, J. (2010). Evaluation of Agri-Environment and Forestry Schemes with Multiple Objectives. *EuroChoices*, *9*(1), 48–54. https://doi.org/https://doi.org/10.1111/j.1746-692X.2010.00149.x

Murguía-Romero, M., Serrano-Estrada, B., Ortiz, E., and Villaseñor, J. L. (2021). Taxonomic identification keys on the web: tools for better knowledge of biodiversity. *Revista Mexicana de Biodiversidad*, *92*(0), 923592. https://doi.org/10.22201/ib.20078706e.2021.92.3592

Nichols, R. V, Vollmers, C., Newsom, L. A., Wang, Y., Heintzman, P. D., Leighton, M., Green, R. E., and Shapiro, B. (2018). Minimizing polymerase biases in metabarcoding. *Molecular Ecology Resources*, *18*(5), 927–939. https://doi.org/10.1111/1755-0998.12895

Nieto, A., Roberts, S., Kemp, J., Rasmont, P., Kuhlmann, M., García Criado, M., Biesmeijer, K., Bogusch, P., Dathe, H. H., De la Rúa, P., De Meulemeester, T., Dehon, M., Dewulf, A., Ortiz-Sánchez, F. J., Lhomme, P., Pauly, A., Potts, S. G., Praz, C., Quaranta, M., … Michez, D. (2014). *European Red List of Bees*. Luxembourg: Publications Office of the European Union. https://doi.org/10.2779/77003

O'Brien, D., Laikre, L., Hoban, S., Bruford, M. W., Ekblom, R., Fischer, M. C., Hall, J., Hvilsom, C., Hollingsworth, P. M., Kershaw, F., Mittan, C. S., Mukassabi, T. A., Ogden, R., Segelbacher, G., Shaw, R. E., Vernesi, C., and MacDonald, A. J. (2022). Bringing together approaches to reporting on within species genetic diversity. *Journal of Applied Ecology*, *59*(9), 2227–2233. https://doi.org/10.1111/1365-2664.14225

Ockermüller, E., Kratschmer, S., Hainz-Renetzeder, C., Sauberer, N., Meimberg, H., Frank, T., Pascher, K., and Pachinger, B. (2023). Agricultural land-use and landscape composition: Response of wild bee species in relation to their characteristic traits. *Agriculture, Ecosystems and Environment*, *353*(August 2022). https://doi.org/10.1016/j.agee.2023.108540

OECD. (2021). *Applying Evaluation Criteria Thoughtfully*. https://doi.org/https://doi.org/https://doi.org/10.1787/543e84ed-en

Oppermann, R., Schraml, A., Sutciliffe, L., Lüdemann, J., Bugter, R., van Doorn, A., van der Sluis, T., Fuchs, D., Jongman, R., and Domingo, J. (2017). *European Monitoring of Biodiversity in Agricultural Landscapes (EMBAL). Final Report*.

Oswald, E. C. (2020). Getting to know other ways of knowing: Boundary experiences in citizen science. *Citizen Science: Theory and Practice*, *5*(1).

Outhwaite, C. L., McCann, P., and Newbold, T. (2022). Agriculture and climate change are reshaping insect biodiversity worldwide. *Nature*, *605*(7908), 97–102. https://doi.org/10.1038/s41586-022-04644-x

Pawlowski, J., Bruce, K., Panksep, K., Aguirre, F. I., Amalfitano, S., Apothéloz-Perret-Gentil, L., Baussant, T., Bouchez, A., Carugati, L., Cermakova, K., Cordier, T., Corinaldesi, C., Costa, F. O., Danovaro, R., Dell'Anno, A., Duarte, S., Eisendle, U., Ferrari, B. J. D., Frontalini, F., … Fazi, S. (2022).

Environmental DNA metabarcoding for benthic monitoring: A review of sediment sampling and DNA extraction methods. *Science of the Total Environment*, *818*. https://doi.org/ARTN 15178310.1016/j.scitotenv.2021.151783

Peterson, B. K., Weber, J. N., Kay, E. H., Fisher, H. S., and Hoekstra, H. E. (2012). Double digest RADseq: An inexpensive method for de novo SNP discovery and genotyping in model and non-model species. *PLoS ONE*, *7*(5). https://doi.org/10.1371/journal.pone.0037135

Piper, A. M., Batovska, J., Cogan, N. O., Weiss, J., Cunningham, J. P., Rodoni, B. C., and Blacket, M. J. (2019). Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance. *Gigascience*, *8*(8). https://doi.org/ARTN giz09210.1093/gigascience/giz092

Plum, F., and Labonte, D. (2021). scAnt—an open-source platform for the creation of 3D models of arthropods (and other small objects). *PeerJ*, *9*, e11155. https://doi.org/10.7717/peerj.11155

Pocock, M. J. O., Roy, H. E., Preston, C. D., and Roy, D. (2015). The Biological Records Centre: a pioneer of citizen science. *Biological Journal of the Linnean Society*, *115*(3), 475–493.

Pocock, M. J. O., Tweddle, J. C., Savage, J., Robinson, L. D., and Roy, H. E. (2017). The diversity and evolution of ecological and environmental citizen science. *PloS One*, *12*(4), e0172579.

Pollack, G. S. (2017). Insect bioacoustics. *Acoustics Today*, *13*, 26–34.

Ponti, M., Hillman, T., Kullenberg, C., and Kasperowski, D. (2018). Getting it right or being top rank: Games in citizen science. *Citizen Science: Theory and Practice*, *3*(1), 1.

Posledovich, D., Ekblom, R., and Laikre, L. (2021). *Mapping and monitoring genetic diversity in Sweden. A proposal for species, methods and costs* (pp. 4–75). Report to the Swedish Environmental Protection Agency, Report nr. 6959.

Potts, S. G., Biesmeijer, J. C., Kremen, C., Neumann, P., Schweiger, O., and Kunin, W. E. (2010). Global pollinator declines: trends, impacts and drivers. *Trends in Ecology & Evolution*, *25*(6), 345–353. https://doi.org/10.1016/j.tree.2010.01.007

Potts, S. G., Dauber, J., Hochkirch, A., Oteman, B., Roy, D. B., Ahnre, K., Biesmeijer, K., Breeze, T., Carvell, C., Ferreira, C., Fitzpatrick, U., Isaac, N. J. B., Kuussaari, M., Ljubomirov, T., Maes, J., Ngo, H., Pardo, A., Polce, C., Quaranta, M., … Vujic, A. (2021). *Proposal for an EU Pollinator Monitoring Scheme* (Vol. JRC122225, Issue KJ-NA-30416-EN-N (online)). Publications Office of the European Union. https://doi.org/10.2760/881843 (online)

Powney, G. D., Carvell, C., Edwards, M., Morris, R. K. A., Roy, H. E., Woodcock, B. A., and Isaac, N. J. B. (2019). Widespread losses of pollinating insects in Britain. *Nature Communications*, *10*(1), 1018. https://doi.org/10.1038/s41467-019-08974-9

Purvis, A. (2020). A single apex target for biodiversity would be bad news for both nature and people. *Nature Ecology & Evolution*, *4*(6), 768–769. https://doi.org/10.1038/s41559-020-1181-y

Rasmont, P., Devalez, J., Pauly, A., Michez, D., and Radchenko, V. G. (2017). Addition to the checklist of IUCN European wild bees (Hymenoptera: Apoidea). *Annales de La Société Entomologique de France (N.S.)*, *53*(1), 17–32. https://doi.org/10.1080/00379271.2017.1307696

Ratnasingham, S., and Hebert, P. D. N. (2007). BOLD: the barcode of life data system (www.barcodinglife.org). *Molecular Ecology Notes*, *7*(3), 355–364. https://doi.org/10.1111/j.1471-8286.2007.01678.x

Ratnasingham, S., and Hebert, P. D. N. (2013). A DNA-based registry for all animal species: the barcode index number (BIN) system. *Plos One*, *8*(7), e66213. https://doi.org/10.1371/journal.pone.0066213

Raven, P. H., and Wagner, D. L. (2021). Agricultural intensification and climate change are rapidly decreasing insect biodiversity. *Proceedings of the National Academy of Sciences*, *118*(2). https://doi.org/10.1073/pnas.2002548117

Requier, F., Andersson, G. K. S., Oddi, F. J., and Garibaldi, L. A. (2020). Citizen science in developing countries: how to improve volunteer participation. *Frontiers in Ecology and the Environment*, *18*(2), 101–108.

Reverté, S., Miličić, M., Ačanski, J., Andrić, A., Aracil, A., Aubert, M., Balzan, M. V., Bartomeus, I., Bogusch, P., Bosch, J., Budrys, E., Cantú-Salazar, L., Castro, S., Cornalba, M., Demeter, I., Devalez, J., Dorchin, A., Dufrêne, E., Đorđević, A., … Vujić, A. (2023). National records of 3000 European bee and hoverfly species: A contribution to pollinator conservation. *Insect Conservation and Diversity*, *16*(6), 758–775. https://doi.org/https://doi.org/10.1111/icad.12680

Reynolds, J. H., Knutson, M. G., Newman, K. B., Silverman, E. D., and Thompson, W. L. (2016). A road map for designing and implementing a biological monitoring program. *Environmental Monitoring and Assessment*, *188*(7). https://doi.org/10.1007/s10661-016-5397-x

Rhodes, M. W., Bennie, J. J., Spalding, A., Ffrench-Constant, R. H., and Maclean, I. M. D. (2022). Recent advances in the remote sensing of insects. *Biological Reviews*, *97*(1), 343–360. https://doi.org/10.1111/brv.12802

Richter, A., Comay, O., Svenningsen, C. S., Larsen, J. C., Hecker, S., Tøttrup, A. P., Pe'er, G., Dunn, R. R., Bonn, A., and Marselle, M. (2021). Motivation and support services in citizen science insect monitoring: A cross-country study. *Biological Conservation*, *263*, 109325.

Rodriguez, A., Desjonquères, C., Hevia, V., Llorente, M., Ulloa, J., and Llusia, D. (2024). Towards acoustic monitoring of bees: wingbeat sounds are related to species and individual traits. *Philosophical Transactions of the Royal Society B*, *379*(1904). https://doi.org/10.1098/rstb.2023.0111

Roy, D., Alison, J., August, T., Bélisle, M., Bjerge, K., Bowden, J. J., Bunsen, M. J., Cunha, F., Geissmann, Q., Goldmann, K., Gomez-Segura, A., Jain, A., Huijbers, C., Larrivée, M., Lawson, J., Mann, H., Mazerolle, M., McFarland, K., Pasi, L., … Høye, T. T. (2024). Towards a standardized framework for AI-assisted, image-based monitoring of nocturnal insects. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *379*(1904). https://doi.org/10.1098/rstb.2023.0108

Roy, D., Bourn, N., Collins, S., Dennis, E., Schmucki, R., Settele, J., Sevilleja, C., van Swaay, C. A. M., and Wynhoff, I. (2020). *Assessing Butterflies in Europe: Executive Summary*.

Roy, H. E., Baxter, E., Saunders, A., and Pocock, M. J. O. (2016). Focal plant observations as a standardised method for pollinator monitoring: Opportunities and limitations for mass participation citizen science. *PloS One*, *11*(3), e0150794.

Ruck, A., van der Wal, R., SC Hood, A., L. Mauchline, A., G. Potts, S., F. WallisDeVries, M., and Öckinger, E. (2023). Farmland biodiversity monitoring through citizen science: A review of existing approaches and future opportunities. *Ambio*, 1–19.

Saha, A., Kurland, S., Kutschera, V. E., Díez-del-Molino, D., Ekman, D., Ryman, N., and Laikre, L. (2024). Monitoring genome-wide diversity over contemporary time with new indicators applied to Arctic charr populations. *Conservation Genetics*, *25*(2), 513–531. https://doi.org/10.1007/s10592-023-01586-3

Salcedo, M. K., Hoffmann, J., Donoughe, S., and Mahadevan, L. (2019). Computational analysis of size, shape and structure of insect wings. *Biology Open*, *8*(10). https://doi.org/10.1242/bio.040774

Sbrocchi, C., Pecl, G., van Putten, I., and Roetman, P. (2022). A citizen science community of practice: relational patterns contributing to shared practice. *Citizen Science: Theory and Practice*.

Schneider, S., Taylor, G. W., Kremer, S. C., Burgess, P., McGroarty, J., Mitsui, K., Zhuang, A., deWaard, J. R., and Fryxell, J. M. (2022). Bulk arthropod abundance, biomass and diversity estimation using deep learning for computer vision. *Methods in Ecology and Evolution*, *13*(2), 346–357. https://doi.org/10.1111/2041-210X.13769

Sharma, N., Greaves, S., Siddharthan, A., Anderson, H. B., Robinson, A.-M., Colucci-Gray, L., Wibowo, A. T., Bostock, H., Salisbury, A., and Roberts, S. (2019). From citizen science to citizen action: analysing the potential for a digital platform to cultivate attachments to nature. *Journal of Science Communication*.

Sickel, W., Zizka, V., Scherges, A., Bourlat, S. J., and Dieker, P. (2023). Abundance estimation with DNA metabarcoding – recent advancements for terrestrial arthropods. *Metabarcoding and Metagenomics*, *7*. https://doi.org/10.3897/mbmg.7.112290

Silvertown, J. (2009). A new dawn for citizen science. *Trends in Ecology & Evolution*, *24*(9), 467–471. https://doi.org/10.1016/J.TREE.2009.03.017

Sims, D., Sudbery, I., Ilott, N. E., Heger, A., and Ponting, C. P. (2014). Sequencing depth and coverage: key considerations in genomic analyses. *Nature Reviews. Genetics*, *15*(2), 121–132. https://doi.org/10.1038/nrg3642

Sittinger, M., Uhler, J., Pink, M., and Herz, A. (2024). *Insect detect: An open-source DIY camera trap for automated insect monitoring*. *19*(4), e0295474. https://doi.org/10.1371/journal.pone.0295474

Skvarla, M. J., Larson, J. L., Fisher, J. R., and Dowling, A. P. G. (2021). A Review of Terrestrial and Canopy Malaise Traps. *Annals of the Entomological Society of America*, *114*(1), 27–47. https://doi.org/10.1093/aesa/saaa044

Somers, B., Asner, G. P., Tits, L., and Coppin, P. (2011). Endmember variability in Spectral Mixture Analysis: A review. *Remote Sensing of Environment*, *115*(7), 1603–1616. https://doi.org/10.1016/j.rse.2011.03.003

Spiesman, B. J., Gratton, C., Hatfield, R. G., Hsu, W. H., Jepsen, S., McCornack, B., Patel, K., and Wang, G. H. (2021). Assessing the potential for deep learning and computer vision to identify bumble bee species from images. *Scientific Reports*, *11*(1). https://doi.org/ARTN 758010.1038/s41598-021-87210-1

Stanski, K., Myers-Smith, I. H., and Lucas, C. G. (2021). Flower Detection Using Object Analysis: New Ways to Quantify Plant Phenology in a Warming Tundra Biome. *IEEE Journal of Selected Topics in Applied Earth Observations and Remote Sensing*, *14*, 9287–9296. https://doi.org/10.1109/JSTARS.2021.3110365

Stark, T., Stefan, V., Wurm, M., Spanier, R., Taubenböck, H., and Knight, T. M. (2023). YOLO object detection models can locate and classify broad groups of flower-visiting arthropods in images. *Scientific Reports*, *13*(1). https://doi.org/ARTN 1636410.1038/s41598-023-43482-3

Steen, R. (2017). Diel activity, frequency and visit duration of pollinators in focal plants: in situ automatic camera monitoring and data processing. *Methods in Ecology and Evolution*, *8*(2), 203–213. https://doi.org/10.1111/2041-210x.12654

Stoate, C., Boatman, N. D., Borralho, R. J., Carvalho, C. R., De Snoo, G. R., and Eden, P. (2001). Ecological impacts of arable intensification in Europe. *Journal of Environmental Management*, *63*(4), 337–365. https://doi.org/10.1006/jema.2001.0473

Stöcker, C., Bennett, R., Nex, F., Gerke, M., and Zevenbergen, J. (2017). Review of the Current State of UAV Regulations. *Remote Sensing*, *9*(5). https://doi.org/ARTN 45910.3390/rs9050459

Stuart, S. N., Wilson, E. O., McNeely, J. A., Mittermeier, R. A., and Rodríguez, J. P. (2010). The Barometer of Life. *Science*, *328*(5975), 177. https://doi.org/10.1126/science.1188606

Sutcliffe, L. M. E., Schraml, A., Eiselt, B., and Oppermann, R. (2019). The LUCAS Grassland Module Pilot – qualitative monitoring of grassland in Europe. *Palaearctic Grasslands - Journal of the Eurasian Dry Grassland Group*, *40*, 27–31. https://doi.org/10.21570/EDGG.PG.40.27-31

Thompson, C. J., Koshkina, V., Burgman, M. A., Butchart, S. H. M., and Stone, L. (2017). Inferring extinctions II: A practical, iterative model based on records and surveys. *Biological Conservation*, *214*, 328–335. https://doi.org/https://doi.org/10.1016/j.biocon.2017.07.029

Thurfjell, H., Laikre, L., Ekblom, R., Hoban, S., and Sjögren-Gulve, P. (2022). Practical application of indicators for genetic diversity in CBD post-2020 global biodiversity framework implementation. *Ecological Indicators*, *142*. https://doi.org/10.1016/j.ecolind.2022.109167

Tiusanen, M., Hebert, P. D. N., Schmidt, N. M., and Roslin, T. (2016). One fly to rule them all-muscid flies are the key pollinators in the Arctic. *Proceedings of the Royal Society B-Biological Sciences*, *283*(1839). https://doi.org/10.1098/rspb.2016.1271

Tosi, S., and Nieh, J. C. (2019). Lethal and sublethal synergistic effects of a new systemic pesticide, flupyradifurone (Sivantow), on honeybees. *Proceedings of the Royal Society B: Biological Sciences*, *286*(1900). https://doi.org/10.1098/rspb.2019.0433

Tosi, S., Sfeir, C., Carnesecchi, E., vanEngelsdorp, D., and Chauzat, M. P. (2022). Lethal, sublethal, and combined effects of pesticides on bees: A meta-analysis and new risk assessment tools. *Science of the Total Environment*, *844*(January), 156857. https://doi.org/10.1016/j.scitotenv.2022.156857

Trulong, M. X. ., and Van der Wal, R. Exploring the landscape of Automated Species Identification apps: development, promise and user appraisal. *BioScience*.

Tscharntke, T., Steffan-Dewenter, I., Kruess, A., and Thies, C. (2002). Characteristics of insect populations on habitat fragments: A mini review. *Ecological Research*, *17*(2), 229–239. https://doi.org/10.1046/j.1440-1703.2002.00482.x

Tulloch, A. I. T., Possingham, H. P., Joseph, L. N., Szabo, J., and Martin, T. G. (2013). Realising the full potential of citizen science monitoring programs. *Biological Conservation*, *165*, 128–138.

Uhler, J., Haase, P., Hoffmann, L., Hothorn, T., Schmidl, J., Stoll, S., Welti, E. A. R., Buse, J., and Müller, J. (2022). A comparison of different Malaise trap types. *Insect Conservation and Diversity*, *15*(6), 666–672. https://doi.org/10.1111/icad.12604

Uhler, J., Redlich, S., Zhang, J., Hothorn, T., Tobisch, C., Ewald, J., Thorn, S., Seibold, S., Mitesser, O., Morinière, J., Bozicevic, V., Benjamin, C. S., Englmeier, J., Fricke, U., Ganuza, C., Haensel, M., Riebl, R., Rojas-Botero, S., Rummler, T., … Müller, J. (2021). Relationship of insect biomass and richness with land use along a climate gradient. *Nature Communications*, *12*(1), 5946. https://doi.org/10.1038/s41467-021-26181-3

Van De Gevel, J., van Etten, J., and Deterding, S. (2020). Citizen science breathes new life into participatory agricultural research. A review. *Agronomy for Sustainable Development*, *40*, 1–17.

van der Loos, L. M., and Nijland, R. (2021). Biases in bulk: DNA metabarcoding of marine communities and the methodology involved. *Molecular Ecology*, *30*(13), 3270–3288. https://doi.org/10.1111/mec.15592

van Klink, R., August, T., Bas, Y., Bodesheim, P., Bonn, A., Fossøy, F., Høye, T. T., Jongejans, E., Menz, M. H. M., Miraldo, A., Roslin, T., Roy, H. E., Ruczyński, I., Schigel, D., Schäffler, L., Sheard, J. K., Svenningsen, C., Tschan, G. F., Wäldchen, J., … Bowler, D. E. (2022). Emerging technologies revolutionise insect ecology and monitoring. *Trends in Ecology & Evolution*, *37*(10), 872–885. https://doi.org/https://doi.org/10.1016/j.tree.2022.06.001

van Klink, R., Sheard, J. K., Høye, T. T., Roslin, T., Do Nascimento, L. A., and Bauer, S. (2024). Towards a toolkit for global insect biodiversity monitoring. *Philosophical Transactions B*, *379*(1904), in press. https://doi.org/10.1098/rstb.2023.0101

van Strien, A. J., van Swaay, C. A. M., and Termaat, T. (2013). Opportunistic citizen science data of animal species produce reliable estimates of distribution trends if analysed with occupancy models. *Journal of Applied Ecology*, *50*(6), 1450–1458. https://doi.org/10.1111/1365-2664.12158

van Swaay, C. A. M., Cuttelod, A., Collins, S., Maes, D., Munguira, M. L., Šašić, M., Settele, J., Verovnik, R., Verstrael, T., Warren, M., Wiemers, M., and Wynhoff, I. (2010). *European Red List of Butterflies*. https://doi.org/10.2779/83897

van Swaay, C. A. M., Dennis, E. B., Schmucki, R., Sevilleja, C. G., Aghababyan, K., Åström, S., Balalaikins, M., Bonelli, S., Botham, M., Bourn, N., Brereton, T., Cancela, J. P., Carlisle, B., Collins, S., Dopagne, C., Dziekanska, I., Escobés, R., Faltynek Fric, Z., Feldmann, R., … Roy, D. B. (2020). *Assessing butterflies in Europe - Butterfly indicators 1990-2018 Technical report*.

van Swaay, C. A. M., Dennis, E. B., Schmucki, R., Sevilleja, C. G., Astrom, S., Balalaikins, M., Barea-Azcon, J. M., Bonelli, S., Botham, M., Cancela, J. P., Collins, S., De Flores, M., Dapporto, L., Dopagne, C., Dziekanska, I., Escobes, R., Faltynek Fric, Z., Fernandez-Garcia, J. M., Fontaine, B., … Roy, D. (2022). *European Grassland Butterfly Indicator 1990-2020: Technical report*.

van Swaay, C. A. M., Nowicki, P., Settele, J., and van Strien, A. J. (2008). Butterfly monitoring in Europe: methods, applications and perspectives. *Biodiversity and Conservation*, *17*(14), 3455–3469. https://doi.org/10.1007/s10531-008-9491-4

Veganzones, M. A., and Graña, M. (2008). Endmember extraction methods:: A short review. *Knowledge-Based Intelligent Information and Engineering Systems, Pt 3, Proceedings*, *5179*, 400–407.

Veits, M., Khait, I., Obolski, U., Zinger, E., Boonman, A., Goldshtein, A., Saban, K., Seltzer, R., Ben-Dor, U., Estlein, P., Kabat, A., Peretz, D., Ratzersdorfer, I., Krylov, S., Chamovitz, D., Sapir, Y., Yovel, Y., and Hadany, L. (2019). Flowers respond to pollinator sound within minutes by increasing nectar sugar concentration. *Ecology Letters*, *22*(9), 1483–1492. https://doi.org/10.1111/ele.13331

Vorisek, P., Klvanova, A., Wotton, S., and Gregory, R. D. (2008). *A Best Practice Guide for Wild Bird Monitoring Schemes* (P. Vorisek, A. Klvanova, S. Wotton, & R. D. Gregory (eds.); First). JAVA.

WallisDeVries, M. F., and van Swaay, C. A. M. (2017). A nitrogen index to track changes in butterfly species assemblages under nitrogen deposition. *Biological Conservation*, *212*, 448–453. https://doi.org/10.1016/j.biocon.2016.11.029

Walton, R. E., Sayer, C. D., Bennion, H., and Axmacher, J. C. (2020). Nocturnal pollinators strongly contribute to pollen transport of wild flowers in an agricultural landscape. *Biology Letters*, *16*(5). https://doi.org/10.1098/rsbl.2019.0877

Wang, S., Meyer, E., McKay, J. K., and Matz, M. V. (2012). 2b-RAD: a simple and flexible method for genome-wide genotyping. *Nature Methods*, *9*(8), 808–810. https://doi.org/10.1038/nmeth.2023

Watts, C., Dopheide, A., Holdaway, R., Davis, C., Wood, J., Thornburrow, D., and Dickie, I. A. (2019). DNA metabarcoding as a tool for invertebrate community monitoring: a case study comparison with conventional techniques. *Austral Entomology*, *58*(3), 675–686. https://doi.org/10.1111/aen.12384

Webster, M., and Liu, Y. (2022). *Genetic Variation in Mountain Bumblebees; Final Report to Swedish Environmental Protection Agency (Naturvårdsverket), case number NV-04697-21*.

Webster, M. T., Beaurepaire, A., Neumann, P., and Stolle, E. (2023). Population Genomics for Insect Conservation. In *Annual Review of Animal Biosciences* (Vol. 11, pp. 115–140). https://doi.org/10.1146/annurev-animal-122221-075025

Welti, E. A. R., Zajicek, P., Frenzel, M., Ayasse, M., Bornholdt, T., Buse, J., Classen, A., Dziock, F., Engelmann, R. A., Englmeier, J., Fellendorf, M., Förschler, M. I., Fricke, U., Ganuza, C., Hippke, M., Hoenselaar, G., Kaus-Thiel, A., Kerner, J., Kilian, D., … Haase, P. (2022). Temperature drives variation in flying insect biomass across a German malaise trap network. *Insect Conservation and Diversity*, *15*(2), 168–180. https://doi.org/10.1111/icad.12555

White, E. R. (2019). Minimum Time Required to Detect Population Trends: The Need for Long-Term Monitoring Programs. *BioScience*, *69*(1), 40–46. https://doi.org/10.1093/biosci/biy144

Whitman, J. D., Yanega, D., Watson, C. B., and Strode, V. W. (2019). Collection and preservation of terrestrial arthropods. In W. Yong (Ed.), *Biobanking: Methods in Molecular Biology, vol. 1897* (pp. 163–189). Humana Press, New York, NY. https://doi.org/https://doi.org/10.1007/978-1-4939-8935-5_17

Wiemers, M., Balletto, E., Dincă, V., Fric, Z. F., Lamas, G., Lukhtanov, V., Munguira, M. L., van Swaay, C. A. M., Vila, R., Vliegenthart, A., Wahlberg, N., and Verovnik, R. (2018). An updated checklist of the European Butterflies (Lepidoptera, Papilionoidea). *ZooKeys*, *811*, 9–45. https://doi.org/10.3897/zookeys.811.28712

Wilkinson, M. D., Dumontier, M., Aalbersberg, Ij. J., Appleton, G., Axton, M., Baak, A., Blomberg, N., Boiten, J. W., da Silva Santos, L. B., Bourne, P. E., Bouwman, J., Brookes, A. J., Clark, T., Crosas, M., Dillo, I., Dumon, O., Edmunds, S., Evelo, C. T., Finkers, R., … Mons, B. (2016). Comment: The FAIR Guiding Principles for scientific data management and stewardship. *Scientific Data*, *3*. https://doi.org/10.1038/sdata.2016.18

Wolstencroft, K., Krebs, O., Snoep, J. L., Stanford, N. J., Bacall, F., Golebiewski, M., Kuzyakiv, R., Nguyen, Q., Owen, S., Soiland-Reyes, S., Straszewski, J., Van Niekerk, D. D., Williams, A. R., Malmström, L., Rinn, B., Müller, W., and Goble, C. (2017). FAIRDOMHub: A repository and collaboration environment for sharing systems biology research. *Nucleic Acids Research*, *45*(D1), D404–D407. https://doi.org/10.1093/nar/gkw1032

Woodcock, B. A., Isaac, N. J. B., Bullock, J. M., Roy, D. B., Garthwaite, D. G., Crowe, A., and Pywell, R. F. (2016). Impacts of neonicotinoid use on long-term population changes in wild bees in England. *Nature Communications*, *7*. https://doi.org/10.1038/ncomms12459

Woodcock, B. A., Oliver, A. E., Newbold, L. K., Soon Gweon, H., Read, D. S., Sayed, U., Savage, J., Bacon, J., Upcott, E., and Howell, K. (2022). Citizen science monitoring reveals links between honeybee health, pesticide exposure and seasonal availability of floral resources. *Scientific Reports*, *12*(1), 14331.

Wührl, L., Pylatiuk, C., Giersch, M., Lapp, F., von Rintelen, T., Balke, M., Schmidt, S., Cerretti, P., and Meier, R. (2022). DiversityScanner: Robotic handling of small invertebrates with machine learning methods. *Molecular Ecology Resources*, *22*(4), 1626–1638. https://doi.org/https://doi.org/10.1111/1755-0998.13567

Wührl, L., Rettenberger, L., Meier, R., Hartop, E., Graf, J., and Pylatiuk, C. (2024). Entomoscope: An Open-Source Photomicroscope for Biodiversity Discovery. *Ieee Access*, *12*, 11785–11794. https://doi.org/10.1109/Access.2024.3355272

Xu, R., Paterson, A., and Li, C. (2017). Cotton flower detection using aerial color images. In *2017 ASABE Annual International Meeting* (p. 1). ASABE. https://doi.org/https://doi.org/10.13031/aim.201701080

Yalcin, H. (2015). Vision based automatic inspection of insects in pheromone traps. *2015 Fourth International Conference on Agro-Geoinformatics (Agro-Geoinformatics)*, 333–338. https://doi.org/10.1109/Agro-Geoinformatics.2015.7248113

Zacharias, S., Anttila, S., Back, J., Bottcher, K., Mallast, U., Mirtl, M., Schaub, M., and Trotsiuk, V. (2021). *Discussion paper on eLTER Standard Observations (eLTER SOs). Deliverable D3.1 EU Horizon 2020 eLTER PLUS Project, Grant agreement No. 871128*.

Zimkus, B. M., Hassapakis, C. L., and Houck, M. L. (2018). Integrating current methods for the preservation of amphibian genetic resources and viable tissues to achieve best practices for species conservation. *Amphibian and Reptile Conservation*, *12*(2), 1-27 (e165).

Zinger, L., Bonin, A., Alsos, I. G., Balint, M., Bik, H., Boyer, F., Chariton, A. A., Creer, S., Coissac, E., Deagle, B. E., Barba, M., Dickie, I. A., Dumbrell, A. J., Ficetola, G. F., Fierer, N., Fumagalli, L., Gilbert, M. T. P., Jarman, S., Jumpponen, A., … Taberlet, P. (2019). DNA metabarcoding-Need for robust experimental designs to draw sound ecological conclusions. *Molecular Ecology*, *28*(8), 1857–1862. https://doi.org/10.1111/mec.15060

List of abbreviations and definitions

ABLE: Assessing Butterflies in Europe project which aims to collate butterfly monitoring data across Europe, to facilitate the start of new schemes in the EU, and to develop indicators to help policy design and evaluation.

Abundance: the sum of individuals from a given species within a given area.

Alpha taxonomist: experts specialized in taxonomy, the discipline of identifying, describing, and naming species, as responsible for the discovery and formal classification of species based on morphological (physical appearance), but also other characteristics (such as genetics).

CAP: EU's Common Agricultural Policy.

CAP Indicators: the performance of the CAP can be measured at different levels using three types of indicators: Output indicators give the direct 'product' of the measure; Result indicators give the direct, immediate effect of the measure/programme; and Impact indicators go beyond the direct, immediate effect but look at the longer term (e.g. rural unemployment rate).

Citizen science: any activity that involves the public in scientific research and thus has the potential to bring together science, policy makers, and society as a whole in an impactful way.

Complementary modules: part of EU PoMS which still requires further refinement, and could provide important measures of: bee diversity (using pan traps), wider flying insect biodiversity (using Malaise traps), and genetic diversity of wild pollinator populations. However, these three complementary modules variously require further methodological testing, piloting and refining before they could become part of a core scheme.

Core scheme: Part of EU PoMS which includes methods which are ready to be used to monitor wild bees, hoverflies, butterflies (using reinforced transects), moths (using light traps) and rare and threatened species (using species-specific methods).

Diversity: is a quantitative measure that reflects the number of different species and how evenly the individuals are distributed among those species.

eBMS: European Butterfly Monitoring Scheme.

eLTER-RI: Integrated European Long-Term Ecosystem, critical zone and socio-ecological Research Infrastructure

EMBAL: European Monitoring of Biodiversity in Agricultural Landscapes.

EU PI: EU Pollinators Initiative is the EU framework to tackle the decline of wild pollinators. The revised EU Pollinators Initiative sets objectives for 2030 and actions under three priorities. The key priority is improving pollinator conservation and tackling the causes of their decline.

EU PoMS: EU Pollinator Monitoring Scheme is a proposal for an integrated framework for monitoring pollinators across the EU.

EuropaBON: Europa Biodiversity Observation Network: integrating data streams to support policy project

Farmland Pollinator Indicator: a generic term for an indicator (or combination of indicators) designed to describe the status and trends of pollinators in agricultural landscapes.

FSDN: EU Farm Sustainability Data Network.

General Pollinator Indicator: a statistic representing the aggregate levels of biodiversity in pollinating insects, and how it changes over time.

INSIGNIA: Monitoring of Environmental Pollution using Honey Bees.

Light traps: a key method of the EU PoMS core scheme for surveying nocturnal moths. It is a non-lethal trap using a LED light source to attract night active moths, to temporarily trap them in bucket for identification and later release.

LUCAS: Europe’s Land Use-Land Cover Area Frame Survey.

Malaise traps: a tent-like structure, where insects fly into the screen and migrate to the highest point where a collection container is situated.

Metric: a measurement or calculation of one aspect of biodiversity, such as species richness or abundance.

Monitoring under adaptive management: a framework that enables (pollinator) monitoring to evolve iteratively in the face of uncertainty with regard how farmland pollinators will respond to measures, such as CAP interventions, or interactions of CAP interventions and environmental factors.

Multispecies models: a statistical model in which data from multiple species are modelled together, typically involving the sharing of information between species. Multispecies models are preferred in situations where there is insufficient data to estimate all parameters for every species.

MVS: minimum viable scheme of the 2021 STING1 proposal of EU PoMS, which had two modules: standardised transects and pan traps. The MVS was tested by the SPRING project, but it is not part of the STING2 recommendations.

ORBIT: Taxonomic resources for European bees project, creating a centralised taxonomic facility that lays the groundwork for the identification of European wild bees that will support other European initiatives such as EU PoMS.

Pan traps: brightly coloured bowls (often yellow, white or blue), filled with water and a drop of detergent, which attract flying insects and trap them in the water.

Para taxonomist: a wide range of professionals, volunteers and interested citizens with different levels of taxonomic expertise, from basic familiarity with species collection and identification to highly experienced volunteers.

Professional recorders: someone who undertakes biological recording as part of their job for which they are paid (noting that the line between professional recorder and volunteer recorder is often permeable).

Rare and threatened species: any pollinator species that is rare, geographically localised or ecologically highly specialised. This is a key method of the EU PoMS core scheme for surveying rare and threatened species using species-specific methods.

Reinforced transects: a key method of the EU PoMS core scheme for surveying wild bees, hoverflies and butterflies. The reinforced transect comprises a fixed 500m transect that is first walked to record butterflies, and then the same 500m transect is then walked to record wild bees plus hoverflies. This process is then repeated with a second butterfly, and second bee plus hoverflies walk. Overall the fixed 500m transect is walked on four occasions during a single day, taking a fixed amount of observation time per walk, with 8 rounds of sampling per season.

Species richness: the count, or total number, of all species within a given biological community, ecosystem, biome, or other defined area.

SPRING: Strengthening Pollinator Recovery through Indicators and Monitoring project is EC funded project aimed to strengthen taxonomic capacity with regard to pollinating insects, support preparation for the implementation of an EU PoMS.

STING1: Science and Technology for Pollinating Insects 1 (2019-2021) was a technical expert group, comprising 21 international experts from 10 countries. The remit of STING1 was to develop an initial proposal for a European pollinator monitoring scheme as part of Action 1 of the EU Pollinators Initiative.

STING2: Science and Technology for Pollinating Insects 2 (2022-2024) is a technical expert group, comprising 26 international experts from 12 countries, with members being representatives of universities, research institutes and NGO's. The remit of STING2 is to: provide technical assistance in implementing and fine-tuning the EU pollinator monitoring scheme (EU PoMS); test, refine and validate proposals for pollinator indicators; and develop options for data management/storage/access and models to process and harmonise pollinator data.

Surveillance monitoring (sometimes called trend monitoring)**:** describes monitoring of the status and trends of pollinators in agricultural landscapes, independent of any management actions or scientific or political question.

Taxo-Fly: Taxonomic Information for European Hoverfly Species project, developing resources for European hoverfly inventory and taxonomy. The project will make taxonomic information on hoverflies easily available and accessible and the information will be usable by researchers as well as Citizen Scientists. The overall objective is to create a new taxonomic knowledge base, which lays the ground for the identification of the hoverflies of Europe.

TETTRIS: Transforming European Taxonomy through Training, Research and Innovations. A contribution of the taxonomic community gathered around CETAF, the Consortium of European taxonomic facilities, to provide knowledge, systems and services to tackle biodiversity loss.

TRL: Technology Readiness Levels. Technology readiness levels (TRLs) are a method for estimating the maturity of technologies during the acquisition phase of a program. TRL is determined during a technology readiness assessment (TRA) that examines program concepts, technology requirements, and demonstrated technology capabilities. TRLs are based on a scale from 1 to 9 with 9 being the most mature technology.

Volunteer recorders: someone who is willing to help and undertake biological recording without being paid though expenses may be (partially) covered (noting that the line between being a volunteer recorder and a professional is often permeable).

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