J R C T E C H N I C A L R E P O R T S

Water Framework Directive Intercalibration Technical Report

Northern Lake Phytoplankton ecological assessment methods

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Introduction

The European Water Framework Directive (WFD) requires the national classifications of good ecological status to be harmonised through an intercalibration exercise. In this exercise, significant differences in status classification among Member States are harmonized by comparing and, if necessary, adjusting the good status boundaries of the national assessment methods.

Intercalibration is performed for rivers, lakes, coastal and transitional waters, focusing on selected types of water bodies (intercalibration types), anthropogenic pressures and Biological Quality Elements. Intercalibration exercises were carried out in Geographical Intercalibration Groups - larger geographical units including Member States with similar water body types - and followed the procedure described in the WFD Common Implementation Strategy Guidance document on the intercalibration process (European Commission, 2011).

In a first phase, the intercalibration exercise started in 2003 and extended until 2008. The results from this exercise were agreed on by Member States and then published in a Commission Decision, consequently becoming legally binding (EC, 2008). A second intercalibration phase extended from 2009 to 2012, and the results from this exercise were agreed on by Member States and laid down in a new Commission Decision (EC, 2013) repealing the previous decision. Member States should apply the results of the intercalibration exercise to their national classification systems in order to set the boundaries between high and good status and between good and moderate status for all their national types.

Annex 1 to this Decision sets out the results of the intercalibration exercise for which intercalibration is successfully achieved, within the limits of what is technically feasible at this point in time. The Technical report on the Water Framework Directive intercalibration describes in detail how the intercalibration exercise has been carried out for the water categories and biological quality elements included in that Annex.

The Technical report is organized in volumes according to the water category (rivers, lakes, coastal and transitional waters), Biological Quality Element and Geographical Intercalibration group. This volume addresses the intercalibration of the Lake Northern Phytoplankton ecological assessment methods.

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1. Introduction

In the Northern Lake Phytoplankton GIG:

- Five Member States (Finland, Ireland, Norway, Sweden and UK) compared and harmonised their national lake phytoplankton assessment systems;
- All methods address eutrophication pressure and follow a similar assessment principle (including biomass metrics and composition metrics);
- Intercalibration "Option 3" was used - direct comparison of assessment methods supported by common metrics (standardized using "continuous benchmarking");
- After several iterations of boundary adjustments all boundaries are in agreement to comparability criteria defined in the IC Guidance, so no further boundary adjustment is needed;
- The final results include EQRs of Finnish, Irish Norwegian, Swedish and UK lake phytoplankton assessment systems for 7 common intercalibration lake types.

2. Description of national assessment methods

In the Northern Phytoplankton GIG, five countries participated in the intercalibration with finalised phytoplankton assessment methods (Table 2.1, detailed descriptions Annex A).

Table 2.1 Overview of the national phytoplankton assessment methods.

MS	Method/metrics	Status
FI	Lake ecological status assessment: phytoplankton	Finalized agreed
	1. Chlorophyll a 2. Total biovolume 3. Trophic index, TPI (SE, but with additional FI indicator values) 4. Bloom intensity: % Cyanobacteria (impact taxa)	
IE	Lake Phytoplankton assessment method	Finalized agreed
	1. Chlorophyll a 2. Irish Phytoplankton composition abundance Index (IPI)	
NO	Lake phytoplankton ecological status classification method	Finalized agreed*
	1. Chlorophyll a 2. Total biovolume 3. Trophic index: PTINO (Ptacnik 2009) 4. Cyanobacteria biomass (max. July-Sept.)	
SE	Ecological assessment methods for lakes, quality factor phytoplankton	Finalized agreed
	1. Chlorophyll a (only used if biovolume is not available) 2. Total biovolume 3. Trophic index: TPI 4. Bloom intensity: % cyanobacteria (all taxa)	
UK	Lake Phytoplankton assessment method	Finalized agreed
	1. Chlorophyll a 2. Taxonomic Composition PTIuk 3. Cyanobacteria biomass (mean. July-Sept.)	

2.1. Methods and required BQE parameters

The WFD normative definitions require that assessment is made of taxonomic composition and abundance, biomass and the frequency and intensity of planktonic blooms.

In summary, all Northern GIG countries cover the parameters needed to be indicative of the BQE as a whole. Further detail is given below concerning each metric type (biomass, composition and blooms).

1. **Biomass - all countries meet this requirement:**
   All countries assessment systems include parameters which are indicative of phytoplankton biomass. This is generally assessed using chlorophyll a, which is a valid and accepted surrogate of biomass. Some countries as FI, NO and SE also include total biovolume as a direct measure of biomass derived from cell volume and counts. SE only uses chl-a for biomass assessment if biovolume data is missing.
2. **Taxonomic composition – all countries meet this requirement:**
   All countries currently have a metric which includes an assessment of taxonomic composition and relative abundance. FI, IE, and SE include metrics which relate to selected indicator taxa. FI, SE also include % Cyanobacteria as a taxonomic composition metric. UK and NO include weighted average metrics which take information from species or genera covering the full phytoplankton community.
3. **Intensity and frequency of blooms - not all countries meet this requirement:**
   UK and NO have now included a separate bloom intensity metric using Cyanobacteria biovolume as a proxy for bloom intensity. Bloom frequency is considered too variable by all the NGIG countries to measure with current monitoring methods, but may be included in future assessment systems whenever Cyano pigment sensors become more commonly used. FI measure bloom intensity and frequency using a public weekly observation network, but the data are not yet possible to use in the national assessment system for intercalibration purposes.

Following problems related to the bloom metrics have been discussed in the GIG:

- Definition of a "bloom": There is no clear agreement regarding the definition of a bloom, either within the GIG or as a result of work carried out by WISER and this should be regarded as a significant short-coming of the directive. Proposed definitions regard a bloom as either an "abnormal" biomass of cyanobacteria or other "nuisance" phytoplankton taxa. The taxa most often associated with blooms are the cyanobacteria, although other taxa can be involved, e.g. chlorophytes or dinophytes. Due the potential for toxin production the cyanobacteria are potentially the more important as they clearly produce "undesirable impacts" which are one of the key indicators of a failure to be at Good status;
- Detection of "blooms": WISER proposes two potential bloom metrics for NGIG: Cyanobacteria biovolume and Evenness (see WISER D3.1.2 report). Cyano biovolume can be justified as a bloom metric because the intensity of such blooms are clearly related with pressure (see WISER D3.1.2) they are associated with undesirable impacts (Annex V, WFD) and health threats (WHO), and can be

easily monitored with pigment sensors (if properly calibrated). The Evenness metric has been used neither by any NGIG country nor for the common NGIG metric. Analysis has been carried out by IE, FI and SE to demonstrate that the final EQR of their assessment methods are significantly related to cyanobacteria biomass. See Annex A.

Combination rules of metrics

All NGIG countries have decided to use average or median of the normalised EQRs for the single metrics as combination rules.

FI: Metrics used include chlorophyll-a, biovolume, Swedish TPI taxonomic composition metric using Finnish indicator scores and also % Cyanobacteria. Median metric score is used to combine single metrics into BQE assessment.

IE: Two metrics indicative of phytoplankton biomass (Chlorophyll a) and composition and abundance (IPI) are normalized and averaged to give status of the QE. The abundance of bloom forming cyanobacteria are assessed twice per year (n = 6 per reporting period). Their abundance forms part of the score of the composition metric.

Two Bloom metrics (Cyano biomass and Evenness) were not significant in explaining additional variation with TP in a stepwise multiple regression that included biomass (chlorophyll a) and composition (WISER PTI). Therefore the bloom metrics as currently represented will not increase confidence in assessment. Guidance indicates that including metrics should increase confidence:

Guidance document 13, p11: "Where several parameters responsive to the same pressure are identified, these may be grouped and the results for individual parameters in the group combined in order to increase confidence in the assessment of the impact of that pressure on the quality element."

Although it is tempting to include a redundant metric to satisfy the word of the directive there may not be a case for this statistically or through the requirement to increase confidence stipulated by the guidance document. Ongoing research and particularity advances in remote sensing may address this issue with time.

NO: The EQRs for Chlorophyll, biovolume, PTI taxonomic composition metric (modified from Ptacnik 2009) and maximal Cyano biovolume as bloom metric are normalized, then the EQRs for chl-a and for biovolume is averaged before averaging the combined biomass metric with the tax. comp. metric and the bloom metric to give the final BQE level EQR. Bloom metric is not used if the normalized EQR is higher than the average of the other metrics. See Annex on national methods for further details.

A bloom metric is included in spite of the arguments provided by IE to justify why a bloom metric may not be needed. The arguments to include Cyano biovolume is that such blooms are clearly associated with undesirable impacts and health threats, and can be easily monitored with pigment sensors (if properly calibrated).

SE: Chlorophyll, biovolume, % Cyano and Swedish Trophic index taxonomic metric are used as a national metric. Average metric score is used to combine single metrics into BQE assessment.

UK: Chlorophyll, UK PTI metric, and median Cyano biovolume (bloom metric) combined using normalized average metric scores. Bloom metric is not used if the normalized EQR is higher than the average of the other metrics.

2.2. Sampling and data processing

There are variations in sampling procedures which will contribute to differences between methods. Different definitions of growing season make it difficult to apply all MS methods to all data. For example countries which assess taxonomic composition over full growing season, cannot be applied to those that only assess status in late summer. Benchmark standardization may compensate for these effects but because sampling methods are not always sufficiently comparable option 2 is used for comparison.

In space: phytoplankton in pelagial of lakes in epilimnion or euphotic zone at deepest point or mid-point (NO, SE). FI: 0-2 m integrated, IE: sub-surface dip samples, UK: shore side or outlet sampling. More sampling points in large lakes at least for biomass (FI, NO, SE, IE, UK?). UK method of shore/outlet sampling may not be representative for the pelagic phytoplankton.

In time (period and frequency is critical because of seasonal plankton succession): summer all countries, monthly in vegetation season.

FI: May-Sept for chl-a, June-Aug for other metrics (1-12x every 1-3 or 6 years; more than three samples used for assessment);

IE: 2x taxa (June-early September annually), 4-12x for chl_a (annually), 3 years data then used for assessment;

NO: May-October, 6-12x;

SE: July-August (1-2x but 3 years data used for assessment);

UK: Jan-Dec:12x for chl-a; July-Sept. 3x for taxonomic composition (3 years data normally used for assessment, but a one year minimum in any classification period).

Low sampling frequencies for taxonomic samples in FI and SE may not be sufficient to provide representative information, but the assessments are normally done by using data from 3 years of monitoring, thus increasing the number of samples used for assessment. Different definitions of growing season need to be resolved to facilitate comparison. Countries which assess taxonomic composition over full growing season may not be able to be compared with those that only assess status based on late summer samples only.

2.3. National reference conditions

RC setting is considered WFD compliant for all MS national methods:

- For chlorophyll biomass metrics as an IC result;
- For all other metrics in most cases the near-natural reference conditions were defined by pressure criteria combined with in-lake TP;

- For IE also paleolimnological studies were checked for national reference lakes.

2.4. National boundary setting

All NGIG countries have set boundaries or EQRs for chlorophyll that are the same or only slightly different to the values agreed during phase 1 IC. All other metrics in all national methods now seem compliant with the WFD normative definitions.

Table 2.2 Overview of the methodologies used to derive the class boundaries for the national phytoplankton assessment methods

MS	Evaluation of WFD compliance	Approach to derive class boundaries
IE	Compliant	Boundaries based on %iles of reference sites and demonstrated to be ecologically relevant (see Appendix A)
FI	Compliant, boundaries for biovolume have been adjusted.	Chlorophyll boundary EQR values taken from values agreed for phase 1 intercalibration. Boundary for TPI metric and the % Cyano metric derived from discontinuity in relationship between pressure and biological response. Biovolume GM, MP and PB boundaries were found to be too high for humic lowland types, but Finland has adjusted these now to be more in line with chla boundaries. New comparability calculations demonstrates that Finland is now within the bias band for all lake types.
NO	Compliant for all NGIG lake types,	Chlorophyll boundary EQR values taken from values agreed for phase 1 intercalibration. H/G boundaries for the other metrics are based on % iles of reference sites, but also checking that the proportions of sensitive and tolerant taxa at the boundary are in line with the normative definitions, while G/M boundary is derived from discontinuities in relationships with sensitive and tolerant taxa and with Cyano biovolume. GM boundary for bloom metric (max Cyano biomass) also match the WHO low risk threshold (1 mg/l)
SE	Compliant, boundaries for biovolume have been adjusted.	HG boundaries for the SE typologies are based on 75%iles of reference sites. The lower classes were divided equidistantly from that. The obtained values were examined and weighed based on expert knowledge of phytoplankton behaviour along nutrient gradients. See national guidance on classification for Sweden.
UK	Compliant	Chlorophyll boundary EQR values taken from values agreed for phase 1 intercalibration. Boundaries for PTI metric based on changes in the proportion of sensitive and tolerant taxa combined with expert judgement. Boundaries for cyanobacteria biomass metric based on risk that WHO bloom risk threshold is exceeded.

3. Results of WFD compliance checking

The table below lists the WFD compliance criteria and describes the WFD compliance checking process and results.

Table 3.1 List of the WFD compliance criteria and the WFD compliance checking process and results

Compliance criteria	Compliance checking conclusions
1. Ecological status is classified by one of **five classes** (high, good, moderate, poor and bad)	Yes for all countries
2. High, good and moderate ecological status are set in line with the WFD's **normative definitions (Boundary setting procedure)**	All NGIG countries have set boundaries or EQRs for chlorophyll that are the same or only slightly different to the values agreed during phase 1 IC. All other metrics in all national methods now seem compliant with the WFD normative definitions See the table above
3. **All relevant parameters** indicative of the biological quality element are covered. A **combination rule** to combine parameter assessment into BQE assessment has to be defined	Yes, see table and text above
4. Assessment is adapted to **intercalibration common types** that are defined in line with the typological requirements of the WFD Annex II and approved by WG ECOSTAT	Yes, see details at Feasibility check – Typology
5. The water body is assessed against type-specific near-natural reference conditions	Yes, see text above
6. Assessment results are expressed as **EQRs**	Yes, all countries express their results as EQRs.
7. Sampling procedure allows for **representative** information about water body quality/ ecological status **in space and time**	There are variations in sampling procedures which will contribute to differences between methods. Details see above
8. All data relevant for assessing the biological **parameters** specified in the WFD's normative definitions are covered by the **sampling procedure**	Yes, for biomass and taxonomic composition, but not for blooms: The current sampling procedures are not sufficient to estimate bloom frequency and duration, perhaps except for lakes that are sampled 12 times per growing season (weekly-forthnightly) (done only for a few lakes in NO and FI). There is a risk that also bloom intensity may not be reliably measured with the few samples (1-2) taken during the growing season in SE and FI. The Finnish visual observation network is used to assess the intensity and frequency of blooms (as supporting expert judgement), but so far, the data are still under analyses to find its applicability for the bloom metric, so no conclusion can be made at this point.
9. Selected taxonomic level achieves adequate **confidence and precision** in classification	Yes, for the purpose of intercalibration, the taxonomic level is sufficiently comparable among countries. Most MS use species level for most taxa and genus level or higher for a few taxa that are hard to determine to species level. MSs consider their methods to have adequate confidence and precision. Taxa names were harmonized before comparisons were done. This increases the confidence and precision and reduces the variability between the countries' methods. WISER common metric operates on genus level, while some MSs require

Compliance criteria	Compliance checking conclusions
	the species level. Use of genus level in the common metric reduces the country effect that would be present at the species level resolution. IE – confidence estimates have recently been produced. For the normalized EQR for the BQE as a whole (averaged metrics) the average standard deviation was 0.023. This is very good compared to published figure for biological metrics.

Conclusions of the compliance checking:

The GIG lead considers all methods cover the parameters needed to be indicative of the BQE as a whole and are WFD compliant.

However, there are still some sources of variability that is explained in the following:

- Sampling methods differ slightly among the MSs: potential comparability problems may arise from shoreline/outlet sampling in UK, as well as from low frequency sampling in SE, FI and IE;
- All MSs have both biomass and composition metrics, nevertheless, detection of blooms is approached in different ways:
  - NO and UK use a bloom intensity metric (abundance of Cyanobacteria) as a part of the national method,
  - SE and FI consider % Cyano combined with total biovolume as an indirect bloom metric;
  - IE argue that a bloom metric is not needed as it does not increase confidence in assessment.
- The SE method has low correlation with pressure for one lake type (LN2a) (r^2 = 0.20), which may in part be caused by a poor correlation of the % Cyanobacteria with pressure (see SE method in Annex A) or truncation of EQRs at 1.0;
- The boundary setting for the FI national methods using statistical distributions and percentiles (equal distances) is now well documented to be ecologically relevant in relation to the normative definitions. Similar documentation has also been provided for SE.

4. Results IC Feasibility checking

4.1. Typology

Seven common intercalibration types were defined in the Northern Phytoplankton GIG (Table 4.1).

Additional information:

- Finland - Lakes in Northern Finland have been agreed to match better with the mid-altitude NGIG common types: LN5 for low alkalinity, clear water lakes and LN6 for low alkalinity, meso-humic lakes than with the equivalent lowland common types (LN2 and LN3). However, some of the national types do not directly correspond to the common types, since one national type can represent several common types, and vice versa. The assessment for those types will be

adapted to the IC results for the common types. For specific national types that cannot be intercalibrated, FI will apply EQR boundaries that are at least as strict as those intercalibrated

- Ireland: Because of climate, the altitude criterion is applied in IE. All NGIG upland types are considered to not exist in IE.
- Norway: Lakes in Northern Norway have been agreed to match better with the mid-altitude NGIG common types: LN5 for low alkalinity, clear water lakes and LN6 for low alkalinity, meso-humic lakes than with the equivalent lowland common types (LN2 and LN3). Most of the Norwegian national lake types are basically the same as the GIG types, although there are some national types that do not match the GIG types, e.g. very, large, very deep lakes (for which site-specific reference conditions are needed) and mountain lakes. For specific national types that cannot be intercalibrated, Norway will apply EQR boundaries that are at least as strict as those intercalibrated.
- Sweden: lakes in Northern Sweden have been agreed to match better with the mid-altitude NGIG common types: LN5 for low alkalinity, clearwater lakes and LN6 for low alkalinity, meso-humic lakes than with the equivalent lowland common types (LN2 and LN3). However, some of the national types do not directly correspond to the common types, since one national type can represent several common types, and vice versa. The assessment for those types will be adapted to the IC results for the common types, as specified by SE for each lake in the NGIG dataset. In this specification each lake has been typified both with the SE types and with the NGIG common types. For specific national types that cannot be intercalibrated, SE will apply EQR boundaries that are at least as strict as those intercalibrated;
- UK lake types are the same as the GIG types, except that because of climate the altitude criterion is be applied in UK. All NGIG upland types are considered to not exist in UK.

Table 4.1 Common Intercalibration water body types and list of the MS sharing each type

Common IC type	Type characteristics	MS sharing IC common type
LN1	Lowland, shallow, moderate alkalinity, clear	FI, IE, NO, SE, UK
LN2a	Lowland, shallow, low alkalinity, clear	All countries in NGIG
LN2b	Lowland, deep, low alkalinity, clear	NO, UK, FI (only few lakes), SE (type exists, but no data provided)
LN3a	Lowland, shallow, low alk., humic,	FI, SE, NO, UK (only 1 lake with data), IE
LN5	Mid-altitude, low alk., shallow, clear	FI, SE, NO
LN6a	Mid-altitude, shallow, low alk., humic,	FI, SE, NO
LN8a	Lowland, shallow, mod alk, humic	FI, SE, NO, UK (only 1 lake with data), IE (only 1 lake with data)

Table 4.2 Correspondence between national types and Common types in the Northern GIG

IC type	IE	FI	NO	SE	UK	
					England, Wales, Scotland	Northern Ireland
L-N1	Type 8 Lowland, moderateeerate alkalinity, deep, large	Vh, SVh	Type 3 Lowland, small, moderate alkalinity, clear	South, clear	Type MAS Moderate alkalinity shallow clear	Type NI7+8 Moderate alkalinity deep small+large
L-N2a	Type 4 Lowland, low alkalinity, deep, large	Vh, SVh	Type 6 Lowland, large, low alkalinity, clear	South, clear	Type LAS Low alkalinity shallow clear	Type NI3+4 low alkalinity deep small +large
L-N2b	-	-			Type LAD Low alkalinity deep clear	-
L-N3a	Type 4 Lowland, low alkalinity, deep, large	Ph, Kh, SKh,	Type 2 Lowland, small, low alkalinity, humic	South, humic	Type LAS (subtype) Low alkalinity shallow humic lowland	-
L-N5a	-	-	Type 12+17 boreal, small+large, low alkalinity, clear	North, clear	Type LAS Low alkalinity shallow clear Mid-high altitude	-
L-N6a	-	-	Type 13 boreal, small, low alkalinity, humic	North, humic	Type LAS (subtype) Low alkalinity shallow humic Mid-high altitude	-
L-N8a	Type 8 Lowland, moderate alkalinity, deep, large	Ph, Kh, SKh,	Type 4+9 lowland, small+large, moderate alkalinity, clear	South, humic	Type MAS (subtype) Moderate alkalinity shallow humic lowland	-

Conclusions:

- IC is feasible for all types listed as common IC types (same as those used in IC phase 1), as at least three countries in the GIG share each of the common IC types;
- Due to a warmer climate in UK and IE the Northern mid-altitude types (LN5 and LN6a) are not considered applicable in those countries.

4.2. Pressures addressed

The GIG dataset has been used to provide an independent test of the relationship between the final EQR and eutrophication pressure, using mean growing season total phosphorus. Details of the resulting regression parameters are shown in the table below. Scatter plots are shown in Annex G. All countries have significant relationships.

Table 4.3 Regression parameters for relationship between final EQRs (standardised to remove country effects) and total P for each NGIG type.

LN1 (TP range 5-50 µg/l)

	Intercept	slope	adj r^2	p
SE	1.517	-0.685	0.522	<0.001
FI	1.871	-0.954	0.635	<0.001
NO	1.723	-0.918	0.711	<0.001
UK	1.610	-0.777	0.758	<0.001
IE	1.506	-0.683	0.750	<0.001

LN2a (TP range 2-50 µg/l)

	Intercept	slope	adj r^2	p
SE	1.086	-0.231	0.192	<0.001
FI	1.917	-1.073	0.407	<0.001
IE	1.097	-0.308	0.330	<0.001
NO	1.387	-0.623	0.477	<0.001
UK	1.267	-0.467	0.456	<0.001

LN2b (TP range 3-20 µg/l)

	Intercept	slope	adj r^2	p
FI	1.613	-0.856	0.498	<0.001
NO	1.401	-0.714	0.498	<0.001
UK	1.344	-0.606	0.459	<0.001

LN3a (TP range 2-90 µg/l)

	Intercept	slope	adj r^2	p
SE	1.311	-0.468	0.509	<0.001
FI	2.242	-1.158	0.579	<0.001
IE	1.204	-0.414	0.614	<0.001
NO	1.568	-0.674	0.589	<0.001
UK	1.395	-0.532	0.630	<0.001

LN5 (TP range 1-55 µg/l)

	Intercept	slope	adj r^2	p
SE	1.302	-0.508	0.410	<0.001
FI	1.818	-1.018	0.438	<0.001
NO	1.499	-0.827	0.588	<0.001

LN6a (TP range 2-70 µg/l)

	Intercept	slope	adj r^2	p
SE	1.300	-0.446	0.405	<0.001
FI	2.231	-1.065	0.408	<0.001
NO	1.301	-0.477	0.416	<0.001

LN8a (TP range 3-170 µg/l)

	Intercept	slope	adj r^2	p
SE	1.347	-0.496	0.631	<0.001
FI	1.936	-0.852	0.680	<0.001
IE	1.406	-0.592	0.860	<0.001
NO	1.564	-0.685	0.722	<0.001
UK	1.503	-0.617	0.757	<0.001

The pressure-response relationship for the common metric against TP has an R^2 = 0.52 ($p<0.001$). Final EQRs relationships with pressure (TP) for all types combined are significant ($p<0.001$): adjusted R^2 for NO - 0.47, UK - 0.50, FI - 0.42, SE - 0.18 and IE - 0.42 (see Figure 4.1).

Conclusions

- the Intercalibration is feasible in terms of pressures addressed because all method assess eutrophication pressure;
- All countries had significant relationships with eutrophication but the SE method is poorly correlated with pressure for LN2a (r^2 = 0.20, see table above).

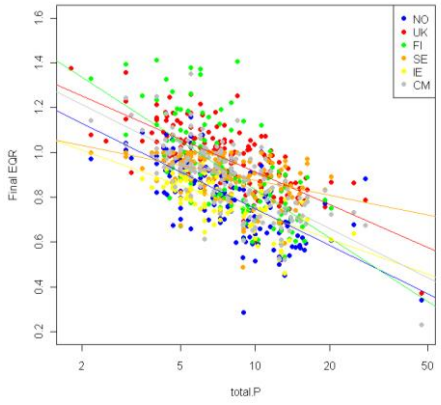

Figure 4.1 Relationship between final EQR for each NGIG country and total phosphorus, methods applied to all NGIG data (CM = Common metric)

4.3. Assessment concept

The assessment concepts of phytoplankton assessment methods are quite similar:

- All MSs include chlorophyll a in their methods, but with varying definitions of the growing season. This was discussed and accepted during phase 1 as representing different climatic conditions, and has been overcome by applying a range of reference values (but using the same EQRs);
- Taxonomic composition is represented either through indicator taxa or through weighted average scores;
- Only NO has phytoplankton taxonomic data for spring/early summer (these samples will be excluded from the assessment in the IC exercise);
- The littoral/outlet sampling used by UK may partly explain why UK is usually on the negative side of the mean in the bias band for most types, as this sampling regime implies increased likelihood of presence of benthic/littoral taxa with higher trophic scores than the pelagic taxa for lakes at the same TP level;

Conclusion: Intercalibration is feasible in terms of **assessment concepts.**

Table 4.4 Evaluation if IC feasibility regarding assessment concept

Method	Assessment concept
FI	Structural community characteristics are used, including two biomass metrics and one composition metrics (SE trophic index* based on selected indicator taxa) and one bloom metric % Cyano (impact taxa only). Pelagic zone
IE	Structural community characteristics are used, including one biomass metric and one composition metrics (trophic index based on 9 indicator taxa). Pelagic zone
NO	Structural community characteristics are used, including two biomass metrics, one composition metric (trophic index based on all taxa scores) and one bloom metric (max. Cyano biovolume). Pelagic zone
SE	Structural community characteristics are used, including two biomass metrics and two composition metrics (% Cyano and a trophic index based on selected indicator taxa). Pelagic zone
UK	Structural community characteristics are used, including one biomass metric, one composition metric (trophic index based on all taxa scores) and one bloom intensity metric (mean Cyano biomass). Littoral zone/outlet sampling

*The SE composition metric has been modified using additional Finnish taxa indicator scores.

5. Collection of IC dataset

Data were compiled by WISER WP3.1. Data providers were SYKE in FI, SLU in SE, NIVA in NO, EPA in IE and Environment Agency in UK (primarily England and Wales, but also including data from SEPA in Scotland and EANI in Northern Ireland). Taxa names were harmonised. The table below show the number of lake-years available from each country and type (biological data, chl-a and TP). Some countries, especially FI, has submitted many more lake-years with only chl-a and TP, but with no taxonomic or biovolume data.

Table 5.1 Overview of the data acceptance criteria used for the data quality control

Data acceptance criteria	Data acceptance checking		
The sampling and analytical methodology All MS counting methods are similar (Utermöhl technique), 2 broad sampling methods used: Integrated samples or sub-surface samples.	SE	Epilimnion or euphotic zone integrated samples	
	FI	0-2 m integrated sample.	
	NO	Epilimnion or euphotic zone integrated samples	
	IE	Sub-surface sample	
	UK	Sub-surface sample, shore or outlet samples	
Level of taxonomic precision required and taxa lists with codes Taxa list in Annex F	SE	477 taxa	Total of 1131 taxa in database, 40% found in at least 3 countries, 23% in at least 4 countries. Only 8% found in all countries. All countries record data to at least genus or species level. Data is considered sufficiently good to do comparisons. Biovolume based data are provided by all countries to the common dataset.
	FI	744 taxa	
	NO	702 taxa	
	IE	112 taxa	
	UK	547 taxa	
The minimum number of sites / samples per intercalibration type	There are sufficient lake years (probably need at least 15 lake years per country) to enable country comparisons for all NGIG types. The number of lake-years varied between 131 and 333 between the common IC types. IE has only 6 lake-years in NGIG (across all NGIG types). This issue was raised as a problem at the validation workshop. The justification to include Ireland in the NGIG intercalibration is that data from UK includes NGIG lakes from Northern Ireland, which should not have climatic nor biogeographical differences relative to Irish lakes of the same type. Each country's methods are applied to the whole NGIG dataset within each type, so the Irish method is tested on all NGIG data.		
Sufficient covering of all relevant quality classes per type	Relatively few poor and bad status sites, especially for low alkalinity lakes (LN2, LN5, LN6). Gradient was extended by combination of some types with CBGIG-data (LCB3) to provide a better basis for boundary setting (to get more sites in poor and bad status included).		

Table 5.2 Overview of the Northern GIG phytoplankton IC dataset Number of lake (water body) years per type /MS

Type /MS	FI	IE	NO	SE	UK	Total
LN1	66	1	87	0	14	168
LN2a	64	2	77	51	31	225
LN2b	8	0	108	0	30	**146**
LN3a	130	2	38	139	24	333
LN5	18	0	63	50	0	131
LN6a	32	0	28	165	0	**225**
LN8a	65	1	43	32	23	164
	383	6	444	437	122	1392

6. Common benchmarking

Common approach for setting reference conditions was developed:

- Both true and partial reference sites are used,
- Common pressure criteria and lake TP + chl-a are used.

Reference criteria for screening of sites in near-natural conditions:

- <10% intensive agriculture, <1% artificial land use, >80% natural areas in catchment;
- < 10 persons/km^2;
- No major point sources;
- <10 µg TP/l for clear water lakes and < 20 µg TP/l for humic lakes;
- Chlorophyll < type-specific H/G boundary from IC phase 1 (i.e. max. 10 µg/l);
- Additional pressures (hydromorphological modifications, acidification, contamination, and alien species) were not screened as considered to be of minor importance to phytoplankton in Northern lakes.

The latter two criteria were included, as there are some lakes with low intensity agriculture close to lake margins causing eutrophication impact. Such lakes have been removed from the list of reference lakes by applying these two criteria.

Reference sites

The number of ref sites is sufficient to make a statistically reliable estimate. The table below shows the number of reference lakes per type and country, and is based on the validated NGIG reference lakes after the final checking in September 2011:

- NGIG has compiled 183 true reference lakes.
- Most NGIG types have sufficient (>10) number of reference lakes to allow calculation of reference value (median);
- For LN8a there are only 4 true reference lakes, but these have data for 9 lake years from 3 countries - these limited data were used to check the reference values for chl-a from IC phase 1, and found them to be consistent;

Table 6.1 Overview of the NGIG reference lakes for each type and country

Type	FI	IE	NO	SE	UK	Total
LN1a	3	0	8	0	0	11
LN2a	13	1	17	1	3	35
LN2b	1	0	41	0	5	47
LN5	2	n.a.	28	5	n.a.	35
LN3a	15	0	8	1	11	35
LN6a	7	n.a.	1	8	n.a.	16
LN8a	2	0	1	1	0	4
Total	43	1	104	16	19	183

See Annex B for reference values for each metric and Annex C for list of reference lakes.

Description of setting reference conditions:

- NGIG use the median of the validated reference sites (for each type) as the reference values for each national and common metric;
- A range of reference values was agreed for chl-a in phase 1 to account for NGIG natural gradients of climate, alkalinity and colour. Each country has decided where in this range their reference value should be for each type;
- UK uses a site-specific model to estimate the reference value for each lake within the range given for each type from phase 1;
- The reference values for each national metric and type is given in Annex B;
- The reference values for chl-a and for the common metric is given in the table below. These values are from IC phase 1 (as given on p. 63 in Poikane 2009), but has been checked with the data from validated reference lakes in IC phase 2 and found to be consistent (see Table 6.2a)
- The reference value of the common metric PTI was calculated from the relationship between PTI and total P and produced country specific values for low and moderate alkalinity lakes (see Table 6.2b)

Table 6.2 a and b. Overview of the chl-a and PTI reference values for each type and country

a.

Type	Chl-a
LN1a	3.0
LN2a	2.0
LN2b	2.0
LN5	3.0
LN3a	1.5
LN6a	2.5
LN8a	4.0
Total	43

b.

MS	Ref PTI: Low alk	Ref PTI: Mod alk
FI	-0.432	-0.347
IE	-0.380	-0.360
NO	-0.871	-0.492
SE	-0.307	-0.190
UK	-0.680	No lakes

6.1. Benchmark standardisation

Standardisation, to remove bio-geographic differences is an important step in the intercalibration process. Two, slightly different, approaches were used to standardise the common metric and the national metrics. Both approaches are based on continuous benchmarking which uses the full pressure gradient to identify country specific differences and both quantify country differences using mixed linear models:

- For the common metric, standardisation was initially carried out at the metric level;
- for the national methods standardisation could only be achieved using the final EQR;
- As only one of the two metrics used for the common metric was standardised (PTI), the final common multi-metric EQR was subsequently checked to determine if any country specific differences remained and if necessary standardised in exactly the same way as the national multi-metric EQRs.

Common Metric Standardisation – PTI metric only

The NGIG common metric is the average of normalised Chlorophyll a EQRs and the standardised WISER phytoplankton trophic index (PTI) EQR:

- The chlorophyll EQRs were those agreed in phase 1 intercalibration, they are normalised to standard values of 0.8, 0.6, 0.4 and 0.2 using piecewise linear transformation before averaging;
- The PTI metric was standardised by converting it to an EQRs using country specific PTI metric reference values. The different country reference values thus reflect variation in the phytoplankton community that is not removed by the common typology, such as climate and the resulting EQR will be standardized;
- For NGIG benchmark standardisation used the "division" method, as described in the IC guidance, but rather than relying on the distribution of the PTI metric in benchmark or reference sites for each country it is based on continuous benchmark standardisation which uses the entire environmental gradient;
- Division was used as there was clear evidence that for low and moderate alkalinity lakes PTI metric values for different countries converged with increasing pressure;
- Mixed linear models, with both slope and intercept allowed to vary by country, were fitted to the GIG data set to determine the relationship between PTI and mean total phosphorus concentration, for each country. Country specific reference WISER PTI values were determined from the linear model using a standard TP concentration and then used to calculate EQRs. This approach is significantly more robust than taking the median value of the metric from each countries reference sites as it is independent of national views of reference. Details of the method used are given in Annex F which describes the common metric.

No attempt was made to standardise the Chlorophyll-a metric as it was assumed that the metric would not have any significant country effects and that the final combined common metric EQR would not require further standardisation. This assumption was challenged at the validation workshop and as a result the final common metric EQR (the combination of Chlorophyll a and PTI EQRs) was also checked to determine if it needed to be standardised. Thus the common metric EQR was standardised in the same way as each of the national method EQRs.

Standardisation of National Methods and combined Common Metric EQRs

Details of the approach used to standardise both the national EQRs and the common metric EQR are given in Annex E. In summary, a continuous benchmarking approach was used, where mixed linear models were used to determine the relationship between the national metric and common metric EQRs. As for the PTI metric (used in the common metric) the models provide country specific offset values that represent differences between the EQR values generated by each (national) method when it is applied to the other countries in the GIG. However, unlike the PTI metric there was no evidence that these country differences converged with increasing pressure and thus standardisation

of the EQRs (national and final common metric) were made by subtracting the country offset value.

Benchmark standardization in summary

Both common metrics and national metrics were benchmark standardized using "continuous benchmarking" approach (see table below)

Table 6.3 Description of benchmark standardization approach in the Northern Phytoplankton GIG.

	Normalisation	Benchmark standardization (BS): calculation of offsets	Application of offsets
Common metrics Components			
PTI metric	Standardised by converting it to EQRs using country specific PTI metric reference values.	Mixed linear models, fitted to the GIG data set to determine the relationship between PTI and mean TP concentration, for each country	Division - as there was clear evidence that for low and moderate alkalinity lakes PTI metric values for different countries converged with increasing pressure
Chl-a metrics	Normalised to standard values of 0.8, 0.6, 0.4 and 0.2 using piecewise linear transformation before averaging	No BS, assumed that the metric would not have any significant country effect	
Final Common metrics			
PTI+chla	Not normalised	Mixed linear models: The relationship between the common metric EQR and log of TP was determined and a linear mixed model with Country as a random factor was fitted within the linear range.	Where the resulting random factors were **significantly different**, the Common Metric EQR was adjusted by subtracting the random factor (the relative country off-set). Subtraction was used as there was no evidence, based on the scatter plots, that relationships converged.
National EQRs			
National EQRs	Normalised using piecewise linear transformation	Mixed linear models By fitting a series of linear relationships which take the gradient between the National EQR and TP from all countries, but calculates the intercept (offset) of the national normalised EQRs for each country	This offset is then subtracted from the national normalised EQR values before the comparison with the other countries' methods was done.

7. Comparison of methods and boundaries

7.1. IC Option and Common Metrics

We used **option 3a supported by the use of a common metric**. We used this approach rather than a simple option 2 approach because some countries either have too little data or too short gradient on their own for some types to get significant relationships with the common metric.

By combining the dataset we were able to plot regressions for each national method against the common metric, as a basis for the bias calculations.

The NGIG common metric is the average of normalised Chlorophyll a EQRs and the standardised WISER phytoplankton trophic index (PTI) EQR. The chlorophyll EQRs were those agreed in phase 1 intercalibration, they are normalised to standard values of 0.8, 0.6, 0.4 and 0.2 using piecewise linear transformation of the boundary EQRs before averaging. The WISER PTI metric is standardised to remove significant country differences using linear regressions derived from linear mixed models with country as a random factor. The median value of this standardised PTI from all reference lake years is used together with a fixed upper anchor to convert the PTI to an EQR which is independent of country.

No attempt was made to determine a priori boundary values for the PTI EQRs and these EQR values are averaged with the transformed chlorophyll EQR. A priori boundary values for the PTIEQRs are not needed in option 3a.

It should be noted that when using an independent biological common metric it is possible that non-linear relationships will occur when making comparisons with the national metric EQRs. This will occur where a MS has nonlinear class intervals and as a result these relationships were examined for linearity. Consideration was also give to using other metrics, including total biomass and biomass of cyanobacteria, but these were rejected as they did not improve the performance of the common metric when judged by linear regression with Total P, a surrogate of pressure.

Further details of the development of the IC common metric are provided in Annex E. The standardisation of the common metric is also summarised in section 6.3 above.

7.2. Results of the regression comparison

Results of regression comparison show that all methods reasonably related to the common metrics, except:

- SE for LN2a ($R^2 = 0.32 < ½ \text{ max } R^2$) and
- FI regression slope for LN3a and 6a (in segmented regression for LN3a and LN6a this concerns the HG slope, but not the GM slope, which is >0.5).

The GIG still considers the SE and FI methods also for these types to be reasonably related to the common metric.

Regression parameters for relationship between national and common metric for each NGIG common type are shown in the tables below. Plots showing the national regressions and EQR boundaries on national and common scale are shown in Annex G.

Table 7.1 Regression parameters for relationship between national and common metric for LN1 type

	UK	NO	IE	SE	FI (Global)	FI EQR <0.55	FI EQR >0.55
Intercept	0.04	0.170	-0.08	0.02	0.22	-0.05	0.33
Slope	1.06	0.943	1.25	1.12	0.72	1.28	0.61
Pearson's r	0.94	0.94	0.90	0.86	0.94	0.89	0.91
R^2	0.89	0.878	0.816	0.736	0.875	0.794	0.837

For Finland segmented regression demonstrated different linear relationships above and below a break point of FI EQR = 0.55. The regression parameters for the upper segment (EQR> 0.55) have been used to determine the FI HG boundary on the common metric scale and the lower segment (EQR<0.55) for the GM boundary.

Table 7.2 Regression parameters for relationship between national and common metric for LN2a type

	UK	NO	IE	SE	FI
Intercept	0.081	0.216	-0.070	0.142	0.320
slope	0.940	0.800	1.154	0.876	0.622
Pearson's r	0.849	0.859	0.671	0.572	0.688
R^2	0.721	0.737	0.455	0.328*	0.474

WARNING! Min R^2< 1/2 * Max R^2

All countries have a significant relationship with pressure and achieve required relationship with common metric, but R^2 for SE is < half the maximum R^2. Despite this, boundaries for SE have been used to set the harmonisation band.

Table 7.3 Regression parameters for relationship between national and common metric for type LN2b.

	UK	NO	FI
Intercept	0.028	0.097	0.198
slope	1.108	1.059	0.835
Pearson's r	0.84	0.87	0.86
R^2	0.70	0.75	0.75

Table 7.4 Regression parameters for relationship between national and common metric for type LN3a.

	UK	NO	IE	SE	FI (Global)	FI EQR <0.715	FI EQR >0.715
Intercept	-0.006	0.243	-0.129	0.086	0.412	0.253	0.504
slope	1.059	0.760	1.338	0.957	0.460	0.717	0.382
Pearson's r	0.844	0.913	0.870	0.756	0.889	0.813	0.832
R^2	0.713	0.749	0.757	0.572	0.790	0.661	0.693

For Finland segmented regression demonstrated different linear relationships above and below a break point of FI EQR = 0.715. The regression parameter for the upper segment have been used to determine the FI HG boundary on the common metric scale and the lower segment has been used for the GM boundary.

Table 7.5 Regression parameters for relationship between national and common metric for type LN5.

	NO	SE	FI
Intercept	0.19	0.02	0.33
slope	0.96	1.13	0.65
Pearson's r	0.96	0.81	0.94
R^2	0.928	0.658	0.892

Table 7.6 Regression parameters for relationship between national and common metric for type LN6a.

	NO	SE	FI (Global)	FI EQR <0.72	FI EQR >0.72
Intercept	0.075	0.112	0.495	0.252	0.537
slope	0.998	0.906	0.338	0.710	0.309
Pearson's r	0.86	0.61	0.80	0.87	0.75
R^2	0.74	0.38	0.69	0.76	0.557

For Finland segmented regression demonstrated different linear relationships above and below a break point of FI EQR = 0.72. The regression parameter for the upper segment have been used to determine the FI HG boundary on the common metric scale and the lower segment has been used for the GM boundary.

Table 7.7 Regression parameters for relationship between national and common metric for type LN8a.

	UK	NO	IE	SE	FI	FI EQR <0.75	FI EQR >0.75
Intercept	0.124	0.189	0.028	0.020	0.238	0.045	0.520
slope	0.928	0.895	1.164	1.071	0.651	1.026	0.391
Pearson's r	0.868	0.928	0.929	0.886	0.892	0.855	0.734
R^2	0.754	0.861	0.863	0.786	0.795	0.731	0.539

Segmented regression shows split for FI at FI EQR>0.75, value above are for regression where FI EQR <0.75 and >0.75. Parameters for segmented regression used for both HG and GM boundaries. (Parameters for FI global regression shown for information).

Conclusions:

- All methods passed the minimum criteria for such relationships: r > 0.5 and slope >0.5 < 1.5, r^2 min > 0.5 r^2 max,
- Exceptions are: R^2 for SE is < half the maximum R^2 and the slope for FI is < 0.5 for LN3a and LN6a.

7.3. Evaluation of comparability criteria

For each NGIG common type the national boundaries were compared using the comparability criteria in Annex V of the IC guidance:

- Option 3a was used for all countries and methods were applied to all appropriate countries' data;
- Member state final EQRs were related to the biological common metric by linear regression;
- After several iterations of boundary adjustments all HG and GM boundaries above the lower limit of the bias band;
- Finally a class comparison was made by comparing the status class when each national method was applied to lakes from as many countries as possible. The absolute average class difference for 3 classes (H, G and M) was calculated for each type. In all cases the methods achieved the comparability criteria of <1.0 absolute average class difference.

Boundaries comparisons and harmonisation

The results are shown in the graphs below for each NGIG type intercalibrated. The details of results are given in Annex G for each lake type showing reference conditions, relationships between national method and pressure, relationships between national method and common metric, and box plots for biomass and bloom metrics in each status class.

In summary:

- All methods comply with the IC comparability criteria (after adjustment of class boundaries for certain metrics in NO, SE, UK and FI, and adjusting the combination rule for NO and UK);
- For Finland a segmented regression was used to fit the national EQRs to the common metric because the regression was clearly not linear over the whole gradient. As the segmented regression splits at national EQR of 0.55-0.75 depending on type, either the upper or the lower regression could be used for the GM prediction, but for HG, the upper segment should be used. The lower segment was used for the final GM bias calculations.

- Some weaknesses still remain in the Swedish method: No use of chl-a, constraining the EQR to max 1.0 for all sites (lake years), applying % of all Cyanobacteria instead of only impact Cyanobacteria

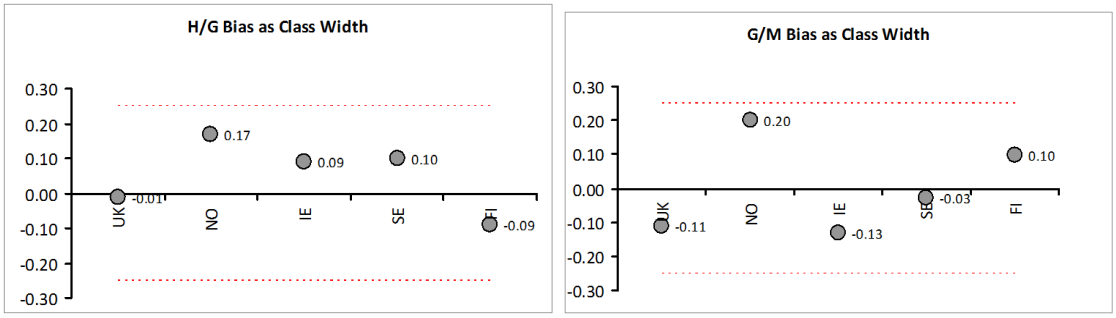

Figure 7.1 Comparison of Northern GIG phytoplankton methods for LN1 type: High-Good (H/G) and Good-Moderate (G/M) class boundary biases.

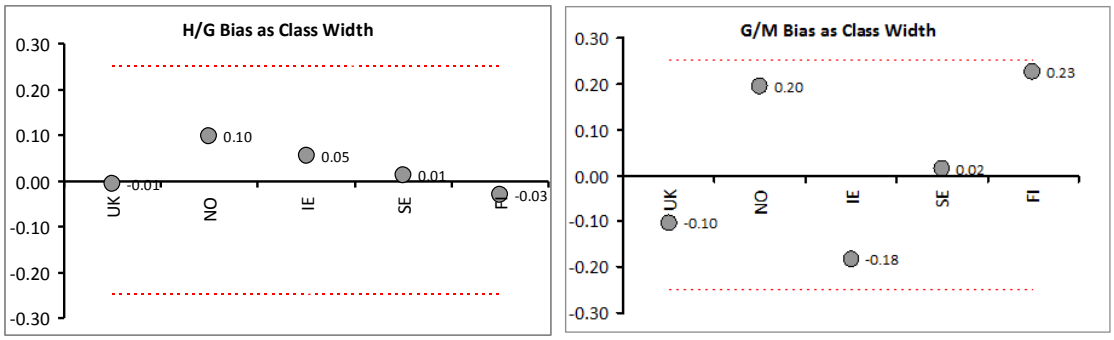

Figure 7.2 Comparison of Northern GIG phytoplankton methods for LN2a type: High-Good (H/G) and Good-Moderate (G/M) class boundary biases LN2a

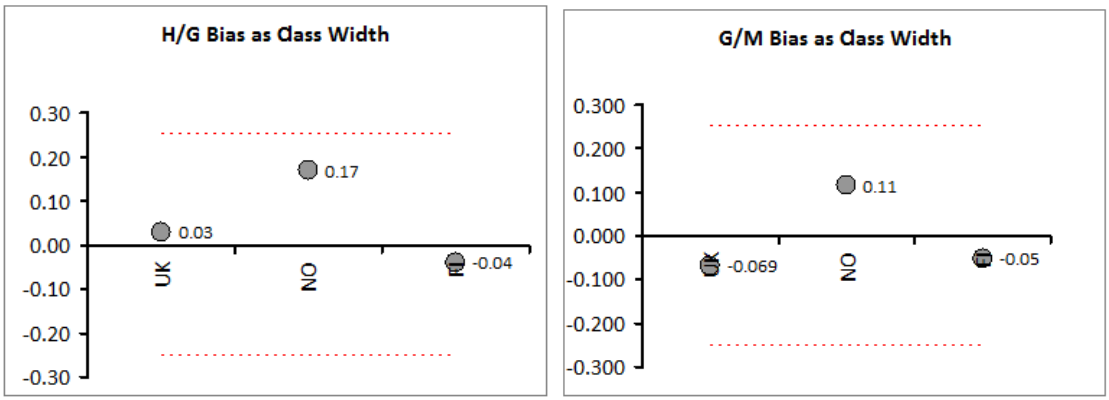

Figure 7.3 Comparison of Northern GIG phytoplankton methods for LN2b type: High-Good (H/G) and Good-Moderate (G/M) class boundary biases LN2b

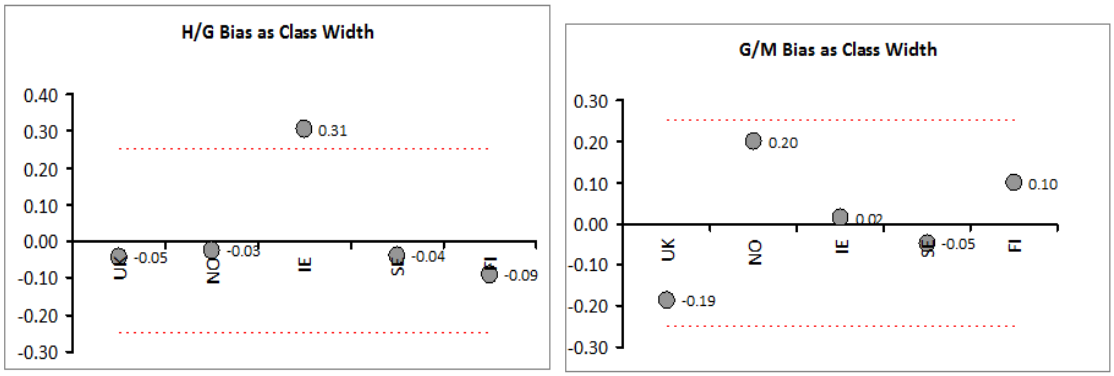

Figure 7.4 Comparison of Northern GIG phytoplankton methods for LN2a type: High-Good (H/G) and Good-Moderate (G/M) class boundary biases LN3a

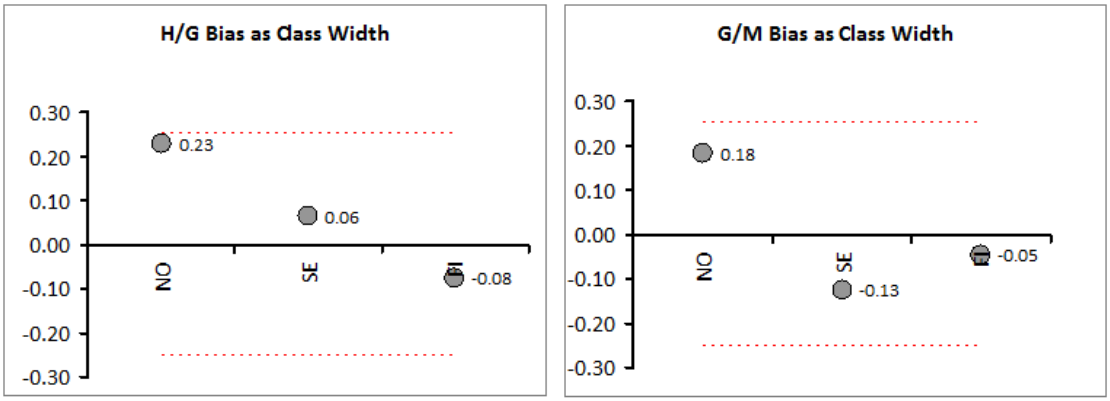

Figure 7.5 Comparison of Northern GIG phytoplankton methods for LN2a type: High-Good (H/G) and Good-Moderate (G/M) class boundary biases LN5

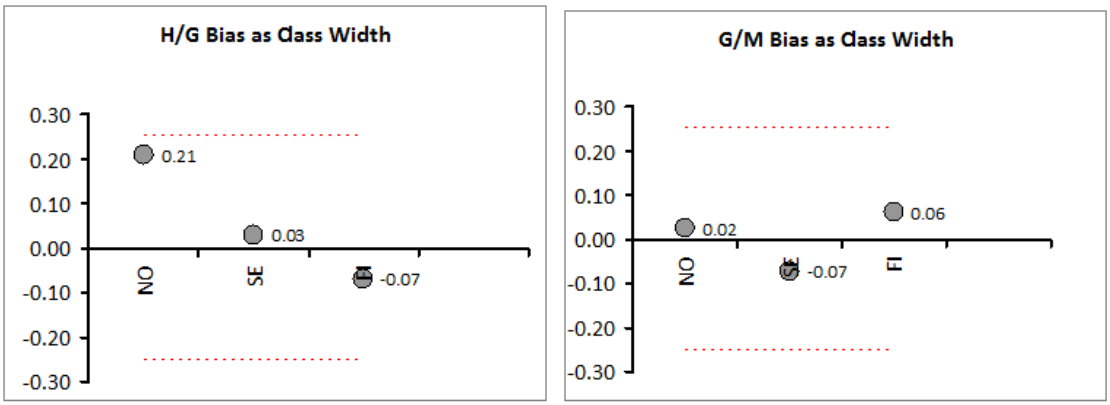

Figure 7.6 Comparison of Northern GIG phytoplankton methods for LN2a type: High-Good (H/G) and Good-Moderate (G/M) class boundary biases LN6a

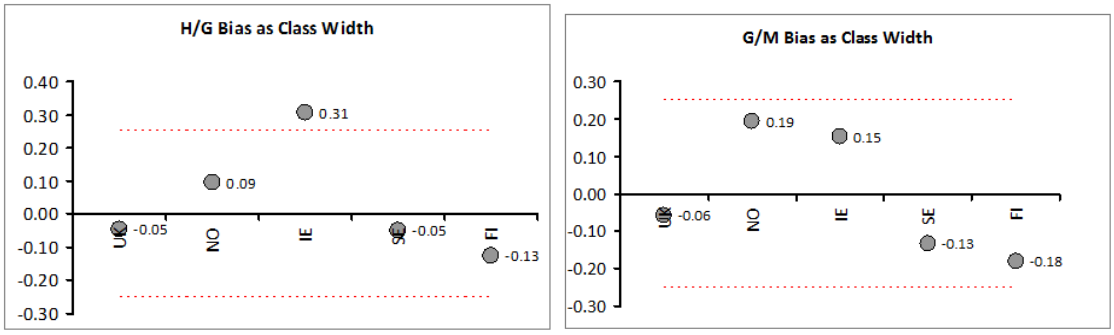

Figure 7.7 Comparison of Northern GIG phytoplankton methods for LN2a type: High-Good (H/G) and Good-Moderate (G/M) class boundary biases LN8a

Table 7.8 The absolute average class difference for 3 classes (H, G and M) for each type

Type /MS	UK	NO	IE	SE	FI
LN1	0.26	0.25	0.26	0.25	0.24
LN2a	0.25	0.29	0.27	0.26	0.23
LN2b	0.18	0.14			0.15
LN3a	0.29	0.30	0.31	0.29	0.28
LN5		0.17		0.17	0.13
LN6a		0.16		0.12	0.12
LN8a	0.27	0.26	0.35	0.26	0.26

IC results

H/G and G/M boundary EQR values for the national methods for each type is shown in the table below.

As each national method use a combination of two or more single metrics, the class boundaries had to be normalised for each method. The class boundaries for the intercalibrated single metrics are given in the Annex A on national methods for each NGIG type separately. The combined normalised boundaries are by default 0.8 and 0.6 for the HG and GM boundaries, respectively.

Table 7.9 Overview of the IC results:

Member State	Classification	Ecological Quality Ratios, all NGIG types	
	Method	High-good boundary	Good-moderate boundary
FI	EQRnorm: = median of EQR norm for the single metrics: chlorophyll, biovolume, TPIfi and % Cyano (impact taxa)	0,8 All types	0,6 All types
IE	EQRnorm: = average of EQR norm for the single metrics: chlorophyll, IPI tax. comp. metric	0,8 All types	0,6 All types

NO*	EQRnorm: = average of EQR norm for the single metrics: chlorophyll, biovolume, PTIno and max cyano biomass *	0,8 All types	0,6 All types
SE	EQRnorm: = average of EQR norm for the single metrics: biovolume, TPIse and % Cyano (all taxa)	0,8 All types	0,6 All types
UK*	EQRnorm: = average of EQR norm for the single metrics: chlorophyll, PTIuk and median cyano biomass *	0,8 All types	0,6 All types

*see Annex A for info on combination rules for single metrics in NO & UK national methods

7.4. Correspondence between common intercalibration types and national typologies/assessment systems

The EQR boundaries agreed for the common types (see Annex A and B on National methods with boundaries specified for each metric in each country) will be used for the national types corresponding to the common types according to the types.

For national types not included in the common types all countries will use at least as stringent EQRs for each metric as for the common types most closely resembling those national types.

7.5. Gaps of the current intercalibration

Intercalibration is completed for NGIG phytoplankton for the common IC types used in phase 1 (see types table above).

The GIG considers that in the future it would be useful to determine common total phosphorus boundary values for all common types (nutrient standards). These could be developed using the existing common data set, making use of the classifications of the common metric following harmonisation.

The comparison exercise has demonstrated the comparability of the existing national metrics, but the GIG considers that in the future it would be possible to combine the best metrics from each of the national and common metric to provide a single assessment system that could work across the whole of the GIG.

For other common types, e.g. mountain lakes, very large, very deep lakes, small polyhumic lakes (colour > 90 mg Pt/l), very shallow and also deep moderate alkalinity lakes, high alkalinity lakes, there are not yet enough data, nor national assessment systems to intercalibrate national methods. Depending on funding and data acquisition, the GIG will consider to continue the intercalibration of those types in the coming years.

8. Description of IC type-specific biological communities

8.1. Biological communities at reference sites

Indicator species analysis was done for LN2a (as representative of Northern clear-water lakes) and LN3a (as representative of Northern humic lakes) to provide an objective description of the taxa composition at reference conditions (see Annex D and G, including a list of the actual taxa that are commonly found in reference lakes). Biological community at reference sites was also described in Phase 1 technical report annex separately for clear-water lakes and for humic lakes.

Clearwater lakes (L-N1, L-N2a, b, L-N5):

Taxonomic composition: Proportion of reference taxa exceeds the proportion of impact taxa. Dominance of reference taxa, such as chrysophytes, whereas impact taxa, such as harmful Cyanobacteria, are in very low abundance. Typical taxa found in the LN2a lake type at reference conditions are: *Kephyrion, Chroomonas, Chrysolykos, Pseudokephyrion, Uroglena, Stichogloea, Merismopedia*.

Biomass: Concentration of chlorophyll and biovolume is low. Typical chl-a reference value is 2,0 ±0,5 µg/l and a biovolume of ca. 0,2 mg/l. (Annex D and G).

Blooms: Nuisance blooms never or rarely reported. If present, only short lived (only seen on calm days) and minor in extent. Biovolume of Cyanobacteria are rarely exceeding 0.05 mg/l (90^{th} %ile).

Humic lakes (L-N3a, L-N6a, L-N8a)

Taxonomic composition: There are very minor effects of human impact on phytoplankton diversity, reference taxa vs. impact taxa, their abundance and biomass. Dominance of reference taxa, whereas impact taxa are in very low abundance. Typical taxa found in the LN3a lake type at reference conditions are: *Botryococcus, Bitrichia, Chroococcus, Staurastrum, Merismopedia, Cyclotella, Rhabdogloea, Kephyrion, Radiocystis*.

Biomass: Biomass and concentration of chlorophyll is low, corresponding to typespecific reference conditions. Typical chl-a reference value is 3.0 ±0.5 µg/l and a biovolume of ca. 0.3 mg/l.

However, the biomass is usually higher than in high status clear water lakes. Oxygen-depletion in the bottom water may occur, but then as a natural condition (due to the humic substances).

Blooms: Nuisance blooms never or rarely reported by public. If present, short lived (seen on calm days) and minor in extent. Biovolume of Cyanobacteria are rarely exceeding 0.1 mg/l (90^{th} %ile).

8.2. Description of biological communities representing the "borderline" conditions between good and moderate ecological status

A list of the indicator values used for the actual taxa in the taxonomic composition common metric is given in Annex D, as distinguished into three indicator groups:

reference taxa, taxa typical at the HG boundary and taxa typical at the GM boundary. The indicator taxa representing the GM boundary are given below, along with box plots of chl-a and TP at Reference, HG, GM, MP and PB boundaries for two lake types representing the NGIG Clearwater lakes (LN2a) and the NGIG humic lakes (LN3a).

8.3. Description of LN2a phytoplankton community and supporting parameters

The boundaries for the common metric (see Table 2.1 and also section 8.3 and 9 below) were used to select lakes at occurring within ±0.25 (a quarter of a class) of proposed common metric boundaries.

Table 8.1 Boundaries on the common metric scale for LN2a

Class Boundary	LN2a Common Metric boundaries
H/G	0.828
G/M	0.640
M/P	0.451
P/B	0.226*

* set at ½ M/P.

A description of the environmental conditions associated with GM boundary as required by by the guidance, is given as boxplots of TP and chlorophyll a *and associated statistics for LN2a in Figure 8.1,*

Table 8.2 and Table 8.3. Box plots for the same parameters at the reference conditions and at the HG boundary are shown for comparison. There were not sufficient LN2a lakes in the poor and bad status classes to show the box-plots for the same parameters at the lower class boundaries.

The phytoplankton community close to the GM boundary is highly diverse, representing the highly dynamic nature of such communities. Many taxa from many different algae classes are typical, some representing the sensitive taxa dominating in reference lakes and others representing early warning indicators of eutrophication, e.g. pennate diatoms. The following taxa are typical for the phytoplankton community close to the GM boundary: chrysophytes (e.g. *Dinobryon, Mallomonas, Spiniferomonas, Ochromonas*), chlorophytes incl. desmids (e.g. *Dictyosphaerium, Elakatothrix, Monomastix, Monoraphidium, Quadrigula, Synura, Staurodesmus*), cryptophytes (e.g. *Cryptomonas, Plagioselmis*), dinophytes (e.g. *Gymnodinium*), pennate diatoms (e.g. *Aulacoseira, Fragilaria, Tabellaria*), cyanobacteria (e.g. *Snowella*), as well as *Chrysochromulina* and *Gonyostomum semen.*

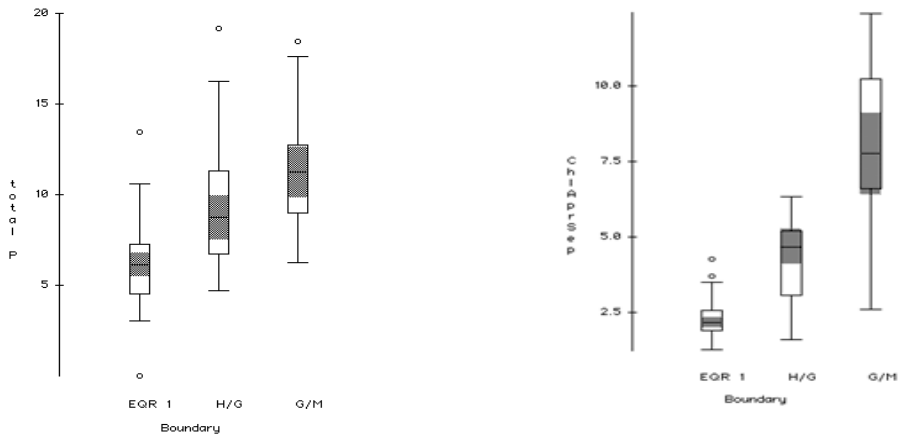

Figure 8.1 Box plot of (a) TP µg l^{-1} and (b) Chlorophyll a µg l-1 (April-September) for LN2a lakes occurring within ±0.25 of proposed common metric class boundaries. Shaded areas are 95% C.I. for comparing medians.

Table 8.2 Summary statistics of Chlorophyll a µg l^{-1} for LN2a boundary groups (boundary ±0.25 class).

Group	Count	Mean	Median	StdDev	Lower 25%tile	Upper 75%tile
EQR1	44	2.25	2.14	0.61	1.89	2.55
High/Good	34	4.28	4.70	1.27	3.07	5.22
Good/Moderate	18	7.94	7.78	2.62	6.63	10.25
Moderate/Poor	0					
Poor/Bad	0					

Table 8.3 Summary statistics of TP µg l^{-1} for LN2a boundary groups (boundary ±0.25 class).

Group	Count	Mean	Median	StdDev	Lower 25%tile	Upper 75%tile
EQR1	44	6.2	6.2	2.2	4.6	7.3
High/Good	34	9.2	8.8	3.5	6.8	11.3
Good/Moderate	18	11.5	11.3	3.5	9.0	12.8
Moderate/Poor	0					
Poor/Bad	0					

Further description of the characteristics of the phytoplankton community at reference conditions and in the various status classes are given in the table below (taken from the phase 1 IC M6 report). The box-plot distribution of the supporting parameters and all metric values in the different classes are shown in the Annex G for each lake type.

Table 8.4 Degradation of NGIG clear water lakes (LN1, LN2a, LN2b, LN5) upon eutrophication

Indicator	Classification				
	High	Good	Moderate	Poor	Bad
Taxonomic Composition Phytoplankton	Proportion of reference taxa exceeds the proportion of impact taxa. Dominance of reference taxa, such as chrysophytes, Impacted taxa, such as Cyanobacteria, are in low abundance	Significant decrease in relative biomass of sensitive taxa, but they are still present in higher abundance than impact taxa. Early warning indicators, such as pennate diatoms, become apparent in the phytoplankton community	Large changes occurring in the phytoplankton community: The sensitive taxa are still present, but in low abundance, the early warning indicators are often dominant, whereas the impact indicators increase to relatively high abundance	Very low proportion of sensitive phytoplankton species. Early warning taxa are replaced by impact taxa, which now dominates the phytoplankton community	Phytoplankton totally dominated by harmful algal blooms or impact taxa. Sensitive species less than 1 percent of total biomass.
Biomass Phytoplankton	Concentration of chlorophyll is low.	Increase is not sufficient to cause more than slight changes in depth distribution of reference taxa of submerged macrophyte (most sensitive for type). No increase in oxygen depletion.	Sufficient to restrict depth distribution of submerged macrophytes Sufficient biomass to reduce oxygen during periods of stratification. Could have implications for most sensitive fish species.	Phytoplankton biomass sufficient to inhibit growth of sensitive submerged macrophytes (isoetids). Phytoplankton biomass is high enough to cause oxygen depletion in surface sediments and bottom waters, and sufficient to cause detrimental impacts on fish.	Macrophytes disappear due to light inhibition. Oxygen depletion common in bottom waters Fish kills may occur
Incidence of Algal Blooms (meaning obvious aggregations of phytoplankton, typically cyanobacteria)	Nuisance blooms never or rarely reported. If present, only short lived (only seen on calm days) and minor in extent.	Nuisance blooms may be present but only minor in extent and if present it does not normally interfere with use. Absence of continuous blooms of filamentous cyanobacteria.	Persistent blooms may occur during suitable conditions. Blooms may last for more than a week and up to 1-2 months, and often interfere with human use.	Persistent blooms of harmful algae for several months during summer. Down wind shore likely to have marked aggregation of scums	Harmful algal blooms extensive, reports of death of other animals attributed to algal toxins.

8.4. Description of LN3a phytoplankton community and supporting parameters, representing NGIG humic (meso-humic) lakes.

The boundaries for the common metric (see Table 8.5) were used to select lakes at occurring within ±0.25 (a quarter of a class) of proposed common metric boundaries.

Table 8.5. Boundaries on the common metric scale for LN3a. * set at ½ M/P.

Boundary	LN2a common metric boundaries
H/G	0.832
G/M	0.618
M/P	0.400
P/B	0.200*

The phytoplankton community close to the GM boundary is highly diverse, representing the highly dynamic nature of such communities. Many taxa from many different algae classes are typical, some representing the sensitive taxa dominating in reference lakes and others representing early warning indicators of eutrophication, e.g. pennate diatoms. The following taxa are typical for the phytoplankton community close to the GM boundary: chrysophytes (e.g. *Monochrysis*), chlorophytes incl. desmids (e.g. *Ankyra, Chlamydomonas, Cosmarium, Elakatothrix, Koliella, Micractinium, Pseudosphaerocystis, Schroederia , Tribonema, Ulothrix*), pennate diatoms (e.g. *Asterionella, Melosira, Tabellaria*), cyanobacteria (e.g. *Pseudanabaena*), and *Gonyostomum semen*.

Taxa characteristic of other boundaries in Annex D.

A description of the environmental conditions associated with GM boundary as required by the guidance, is given as boxplots of TP and chlorophyll a and associated summary statistics for LN3a in Figure 8.2, Table 8.6 and Table 8.7 Box plots for the same parameters at the reference conditions and at the other boundaries are shown for comparison.

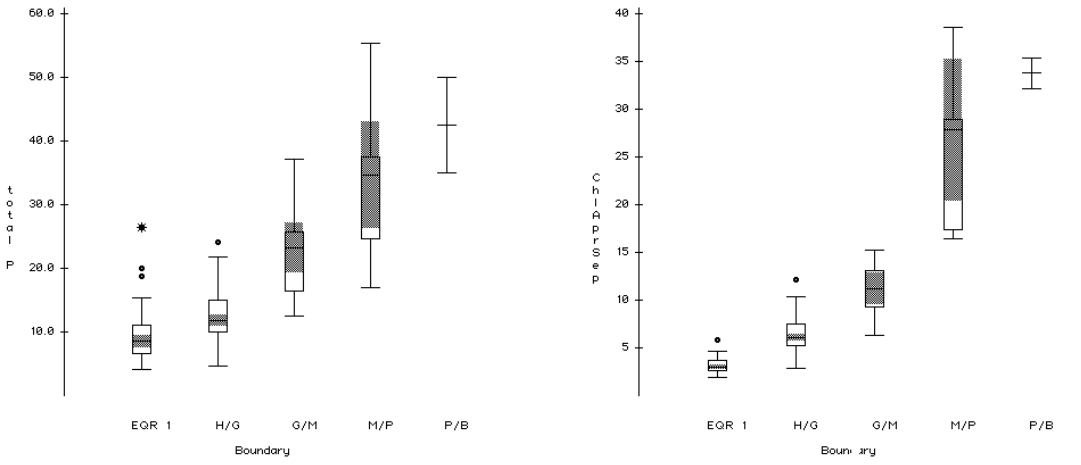

Figure 8.2Box plot of TP µg l^{-1} ***Chlorophyll a µg l^{-1} (April-September)*** *for LN3a lakes occurring within ±0.25 of proposed common metric class boundaries. Shaded areas are 95% C.I. for comparing medians.*

Table 8.6 Summary statistics of Chlorophyll-a µg l^{-1} for LN3a boundaries (boundary ±0.25 class).

Group	Count	Mean	Median	StdDev	Lower 25%tile	Upper 75%tile
EQR1	52	3.13	2.94	0.77	2.52	3.58
High/Good	72	6.38	6.13	1.75	5.36	7.53
Good/Moderate	14	11.10	11.25	2.51	9.31	13.16
Moderate/Poor	6	26.23	27.90	8.22	17.48	29.00
Poor/Bad	2	33.83	33.83	2.23	32.25	35.40

Table 8.7 Summary statistics of Total Phosphorus (TP) µg l^{-1} for LN3a boundaries (boundary ±0.25 class).

Group	Count	Mean	Median	StdDev	Lower 25%tile	Upper 75%tile
EQR1	52	9.4	8.4	4.2	6.5	11.0
High/Good	72	12.6	11.9	4.0	10.0	14.9
Good/Moderate	14	22.9	23.3	6.9	16.5	25.9
Moderate/Poor	6	34.1	34.7	13.2	24.7	37.7
Poor/Bad	2	42.5	42.5	10.6	35.0	50.0

Further description of the characteristics of the phytoplankton community at reference conditions and in the various status classes is given in the table below (taken from the phase 1 IC M6 report). The box-plot distribution of the supporting parameters and all metric values in the different classes are shown in the Annex G for each lake type.

Table 8.8 Degradation of NGIG humic lakes (ln3a, 6a, 8a) upon eutrophication. Note: Impact taxa are a mixture of cyanobacteria diatoms, green algae, and euglenoids

Indicator	Classification				
	High	Good	Moderate	Poor	Bad
Taxonomic Composition Phytoplankton	There are very minor effects of human impact on phytoplankton diversity, reference taxa vs. impact taxa, their abundance and biomass. Dominance of reference taxa. Impact taxa in low abundance.	A significant decrease in relative biomass of reference taxa, but they are still prominent compared to impact taxa*.	Relative proportion of impact taxa* prominent. REF taxa relatively low in abundance, but still occur.	Proportion of impact taxa very prominent and low abundance of REF phytoplankton taxa.	Phytoplankton totally dominated by impact taxa. REF species in very low percentages of biomass. No desmids.
Biomass Phytoplankton	Biomass and concentration of chlorophyll is low, corresponding to type-specific reference conditions. However, the biomass is usually higher than in high status clear-water lakes. Oxygen-depletion in the bottom water may occur, but then as a natural condition (due to the humic substances)	Increase in biomass is noticeable, but does not cause significant aggravation of the type-specific oxygen depletion in the bottom water , nor to cause other negative impacts on other biota.	Biomass is sufficient to cause some impacts on other biota (e.g. on depth distribution of submerged macrophytes), and significantly aggravates the oxygen depletion, having negative impact on bottom fauna and fish	Phytoplankton biomass is high enough to cause non-type-specific severe anoxia in profundal sediments and bottom waters and cause enhanced internal P-loading. Sufficient to largely inhibit growth of submerged macrophytes. and to cause detrimental impacts on fish.	Phytoplankton biomass is so high that macrophytes disappear due to light inhibition and widespread non-type-specific anoxia of the deeper water layers.
Incidence of Algal Blooms (meaning obvious aggregations of phytoplankton, typically cyanobacteria)	Nuisance blooms never or rarely reported by public. If present, short lived (seen on calm days) and minor in extent.	Blooms may be present but mostly only minor in extent compared to reference conditions.	Persistent blooms may occur given suitable conditions. Blooms may last for more than one week (duration may be weeks).	Persistent blooms of harmful algae for > 1 month during summer. Downwind shore likely to have marked aggregation of scums.	Harmful algal blooms extensive, reports of death of other animals attributed to algal toxins.

Annexes

A. Description of Member states assessment methods

A.1 Finland: Finnish classification method for phytoplankton in lakes

Summary

This document outlines how status was assigned for the biological quality element lake phytoplankton and how boundaries were assigned in Finland. The metrics included in the intercalibrated Finnish lake phytoplankton assessment method are the biomass metrics chlorophyll *a* and total biomass (total biovolume), and the taxonomic composition metrics TPI and the percentage of harmful cyanobacteria. The percentage of harmful cyanobacteria also acts as the bloom intensity index of the Finnish phytoplankton method. The reference value and HG boundary for each phytoplankton metric and lake type were set from the median and the 75th %ile of the reference lake distribution for each lake type, as based on the statistical analysis of reference lakes of the type. The GM, MP and PB boundaries were also set using statistical distributions of reference lakes, and were checked against the response plots of indicator taxa (cyanobacterial biomass and tolerant to sensitive phytoplankton species) with respect to normative definitions of the WPD at points of ecological change. The Finnish classification method for phytoplankton in lakes is used to assess eutrophication pressure.

Introduction

In Finland, the ecological status for the biological quality element (BQE) lake phytoplankton is assessed using four parameters: the biomass metrics chlorophyll *a* and total biomass (total biovolume), and the taxonomic composition metrics TPI and the percentage on harmful cyanobacteria. The EQR's for these parameters are normalized so that their boundaries and class widths are on the same scale and then combined by taking the median of the metrics (Figure A.1). The Finnish lake phytoplankton method assesses eutrophication pressure. In the Finnish phytoplankton method intensity of cyanobacterial blooms is taking into account in the metric the percentage of harmful cyanobacteria, as well as in the cyanobacterial bloom taxa with high trophic scores, of the TPI composition metric.

This document summarizes the lake phytoplankton metrics and the process of boundary setting giving examples for the NGIG lake type LN2a. The summary is based on NGIG intercalibration phase 2 work, and the chapters and appendices on lake phytoplankton in the Finnish guidance on ecological classification by Vuori et al. (2010), which is at present under update:

Vuori K.-M., Mitikka S. & Vuoristo H. (eds.) 2010. Guidance on ecological classification of surface waters in Finland. Part I: Reference conditions and classification criteria, Part II: Environmental impact assessment. Environmental Administration Guidelines 3/2009. 120 pp. (in Finnish with English abstract).

http://www.ymparisto.fi/download.asp?contentid=116967&lan=fi

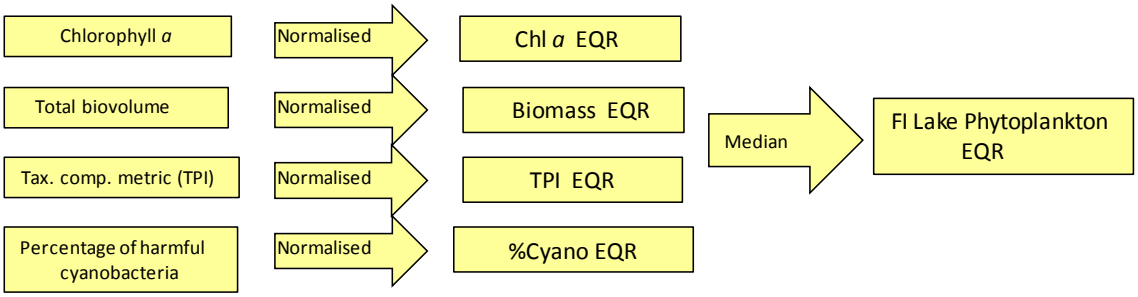

Figure A.1 Phytoplankton metrics are normalized in the intercalibrated Finnish method to provide the median EQR value for the biological quality element lake phytoplankton.

Table A.1 NGIG lake types intercalibrated by Finland

Lake Characterisation	National FI lake type	Altitude (m)	Mean depth (m)	Alkalinity (meq l^{-1})	Colour (mg l^{-1} PtCo)
Lowland, shallow, moderate alkalinity, clear	(Vh, SVh)	<200	3 - 15	0.2 - 1	< 30
Lowland, shallow, low alkalinity, clear	Vh, SVh	<200	3 - 15	< 0.2	< 30
Lowland, deep, low alkalinity, clear	only 6 lakes in Finland	<200	3 - 15	< 0.2	< 30
Lowland, shallow, low alkalinity, meso-humic	Ph, Kh, Sh	<200	3 - 15	< 0.2	30 - 90
Lowland, shallow, moderate alkalinity, meso-humic	´(Ph, Kh, Sh)	<200	3 - 15	0.2 - 1	30 - 90
Mid-altitude, shallow, low alkalinity, clear	(PoLa)	200-800	3 - 15	< 0.2	< 30
Mid-altitude, shallow, moderate alkalinity, meso-humic	(PoLa)	200-800	3 - 15	< 0.2	30 - 90

Metric description

Chlorophyll *a* (µg/l)

Integrated samples from the depth of 0-2 m are taken from mid-lake stations (typically located at the deepest part of the lake). Chlorophyll *a* is determined following extraction using spectrophotometric analysis. Sampling frequency for chlorophyll is normally 3-6 times per year (May-September) but it ranges from 1-12 per year. Spatial replication depends on lake size with more stations on larger lakes. More than three samples should be used for assessment. Reference values of chlorophyll are detailed in the Water Framework Directive Intercalibration Technical Report – Part 2: Lakes (Poikane 2009).

Chlorophyll boundary values are taken from values agreed for IC phase 1. The chlorophyll *a* EQR were calculated using Equation 1 below, where CHL_{ref} is the Finnish chlorophyll reference value in µg/l and the CHL_{obs} is the observed growing season (June-September) median value in µg/l. The Finnish reference values and class boundaries of chlorophyll *a* for the lake types are presented in Table A.2.

$$CHL\ EQR = CHL_{ref} / CHL_{obs} \qquad \text{Equation 1}$$

Total biomass (total biovolume) (mg/l)

Finland uses phytoplankton total biomass (total biovolume) as the second biomass metric for lake phytoplankton. This metric has a long tradition and good quality assurance in the Nordic countries (e.g. Olrik et al. 1998). Integrated samples from the depth of 0-2 m are taken from mid-lake stations (from the deepest part of the lake). Sampling frequency depends on the lake, and ranges from 1-9 times per year. For sites with one sample per year the sampling is generally done in mid-August. Spatial replication depends on lake size with more stations on larger lakes. More than three samples should be used for assessment. Lugol preserved phytoplankton samples are counted using the Utermöhl technique and total biovolume is calculated from the sum of the biovolumes of each taxon in the sample (cell number x specific cell volume) (CEN 2006). Total biomass (total biovolume) of phytoplankton is automatically calculated for each analysed phytoplankton sample in the phytoplankton data base of the HERTTA database of SYKE.

The reference values and the class boundaries are derived from FI reference lakes. The total biovolume EQR were calculated using Equation 2 below, where BIO_{ref} is the Finnish total biomass reference value in mg/l and the BIO_{obs} is the observed growing season median value in mg/l (June-August). The Finnish reference values and class boundaries of total biomass for the lake types are presented in Table A.2.

$$BIO\ EQR = BIO_{ref} / BIO_{obs} \qquad \text{Equation 2}$$

Phytoplankton trophic index (TPI)

Finland uses phytoplankton trophic index TPI as a composition metric. TPI has been originally developed in Sweden (Willén 2007), and additional species scores have been added into the list of Finnish indicator taxa (e.g. Tikkanen 1986). Assessment is based on the quantitative phytoplankton data that is taken and also used for the calculation of the total biomass metric (see sampling and analysis there). TPI index value is automatically calculated for each analysed phytoplankton sample in the phytoplankton database of the HERTTA database of SYKE. Quantitative phytoplankton analysis has a long tradition and good quality assurance in the Nordic countries (e.g. Olrik et al. 1998). More than three samples should be used for assessment. Assessment is based on the scores of indicator taxa ranging from -3 to 3 as based on the occurrence of taxa in the oligotrophication-eutrophication gradient. The list of FI indicator taxa and their scores (indicator values) are given in Table A.2. Calculation of the TPI index is described in more detail in Willén (2007), and it is based on the Equation 3, where n is the number of taxa with indicator value in

the lake sample, I is indicator value of the taxon i, and B is the biomass (biovolume) of the taxon i:

$$TPI = \frac{\sum_{i=1}^{n} I_{taxon\ i} * B_{taxon\ i}}{\sum_{i=1}^{n} B_{taxon\ i}}$$ (Willén 2007) Equation 3

The reference values and the class boundaries are derived from FI reference lakes. The TPI EQR were calculated using Equation 4 below, where TPI_{ref} is the Finnish TPI reference value (unitless) and TPI_{obs} is the observed median TPI value (unitless). $TPI_{upper\ anchor}$ is the highest ("worst") TPI value for the respective lake type which is rarely exceeded in lakes. The Finnish reference values and class boundaries of TPI for the lake types are presented in Table A.1.

$$TPI\ EQR = (TPI_{obs} - TPI_{upper\ anchor}) / (TPI_{ref} - TPI_{upper\ anchor})$$ Equation 4

Percentage of cyanobacteria (%)

Finland uses percentage of harmful cyanobacteria (bloom forming and potentially toxic cyanobacteria) as another phytoplankton composition metric. Assessment is based on the quantitative phytoplankton data that is taken and also used for the calculation of the total biovolume and TPI metrics (see sampling and analysis there).

Percentage of the biomass of harmful cyanobacteria of the total biomass of phytoplankton is calculated automatically for each analysed phytoplankton sample in the phytoplankton database of the HERTTA database of SYKE. Quantitative phytoplankton analysis, incl. the reliable identification of cyanobacteria, has a long tradition and good quality assurance in the Nordic countries (e.g. Olrik et al. 1998). More than three samples should be used for assessment. The harmful cyanobacterial genera included for the calculation of the metric are listed in Table A.4.

The reference values and the class boundaries are derived from FI reference lakes. The CYA% EQR were calculated using Equation 5 below, where $CYA\%_{ref}$ is the Finnish reference value of the percentage of harmful cyanobacteria (%) and $CYA\%_{obs}$ is the observed median percentage of harmful cyanobacteria of the lake (%). $CYA\%_{upper\ anchor}$ is the highest (worst) %-value for the share of harmful cyanobacteria (100%). The Finnish reference values and class boundaries of CYA% for the lake types are presented in Table A.2.

$$CYA\%\ EQR = (TPI_{upper\ anchor} - TPI_{obs}) / (TPI_{upper\ anchor} - TPI_{ref})$$ Equation 5

Percentage of harmful cyanobacteria also takes into account cyanobacterial bloom intensity, as also does the TPI index with high indicator scores for the bloom-forming cyanobacteria. Additional information on algal blooms in lakes is obtained weekly in June-August (September) by visual observations of the algal bloom monitoring, coordinated by SYKE (www.jarviwiki.fi).

Calculation of EQR for each metric

EQR calculation for the metrics has been presented above in Equations 1, 2, 4 and 5. The EQRs for the biomass metrics (chlorophyll *a* and total biomass) are calculated by dividing reference value with the observed value. For the composition metrics (TPI and % of harmful cyanobacteria) an upper anchor approach is used. Upper anchor is a maximum value of each metric, which is rarely exceeded in lakes. For % of harmful cyanobacteria the upper anchor value for each lake type is 100%, whereas for TPI the value is 3.0 for most FI lake types (see Table A.2). The use of upper anchor provides more even class widths.

Normalisation of EQR for each metric

In order to allow combination of all metrics to a whole BQE assessment, each metric EQR are converted to the normalized scale with equal class widths and standardized class boundaries, where the HG, GM, MP, and PB boundaries are 0.8, 0.6, 0.4, 0.2, respectively. This is done by piecewise linear transformation.

Combination of metrics to whole quality element results

Median was used to combine single metrics to a whole quality element results (see also Figure A.1).

Reference values and class boundaries for each type

Reference values

Reference conditions for the Finnish lake types have been set using data from existing near-natural reference sites. Reference lakes cover the whole area of Finland. For the selection of reference lakes, mainly the following pressure criteria were used: <10% agriculture (of the total catchment area), and no major point sources, originally mainly judged from visual observation of the GIS land-use and population data, and later checked with the CORINE land-use data. In addition, experts from the regional environment centres (Centres for Economic Development, Transport and the Environment) were used in the final decision making. For some lakes historical data have also been used. The criteria used thus consisted of pressure data, impact data, knowledge of biology and chemistry, land-use data in conjunction with expert judgement. Table A.2 gives the Finnish reference values and class boundaries for the lake types.

The metrics' reference values and boundaries were calculated using aggregated data from multiple sampling/survey occasions in time, and if available, from aggregated data from multiple spatial replicates. The time periods for metrics were: chlorophyll *a*: 1976-2006 (June-September), phytoplankton biomass 1980-2006 (June-August) and TPI 1980-2010 (June-August), and harmful cyanobacteria percentage 1980-2006 (July-August).

Median value (50^{th} percentile) has been used for reference site characterization for all FI phytoplankton metrics and lake types. A reference value of a metric for each type is the

median of the median values of reference lakes belonging to the type. The number of phytoplankton observations differs in lakes between the years and the sampling sites. Therefore, to reduce the weight of one year in the calculation: first, yearly medians were calculated for each site, then site medians for each lake, and finally lake medians.

Class boundaries for each type and metric

Statistical analysis of lake reference data sets in national types, and the analysis of lake properties were used to set the Finnish boundary values. The obtained metric boundaries were studied against the type-specific statistical distributions of chlorophyll of reference lakes, and later compared to response curves of taxonomic indicators (biomass of cyanobacteria, and the ratio of sensitive to tolerant phytoplankton species). Figure A.2 shows an example for the LN2a lake type.

The H/G boundaries were set from the 75th %ile of the reference lake distribution for each lake type, as based on the statistical analysis of reference lakes of the type. The HG boundaries were compared with response plots of taxonomic indicators to check that there was in general little or no change in the indicator groups between the reference value and the HG boundary Figure A.2).

Statistical distribution of reference lakes was also used to set the GM boundaries for chlorophyll *a*, phytoplankton total biomass, and the percentage of cyanobacteria: (95 % of the median values of the reference lakes + (the reference values/2)). For % of harmful cyanobacteria, also preliminary boundary values derived from the first intercalibration phase were used to set the final boundaries. For TPI, the GM boundary represents 95th %-tile of the reference lakes of each type. GM boundaries have been checked for breakpoints in the response plots of cyanobacterial biomass and tolerant to sensitive phytoplankton species (Fig. 2). Below the "breakpoint", there should be only slight changes from near-natural reference conditions, and above, there should be a more rapid increase in the impact taxa. The final boundary values were sometimes derived by slightly adjusting the values derived.

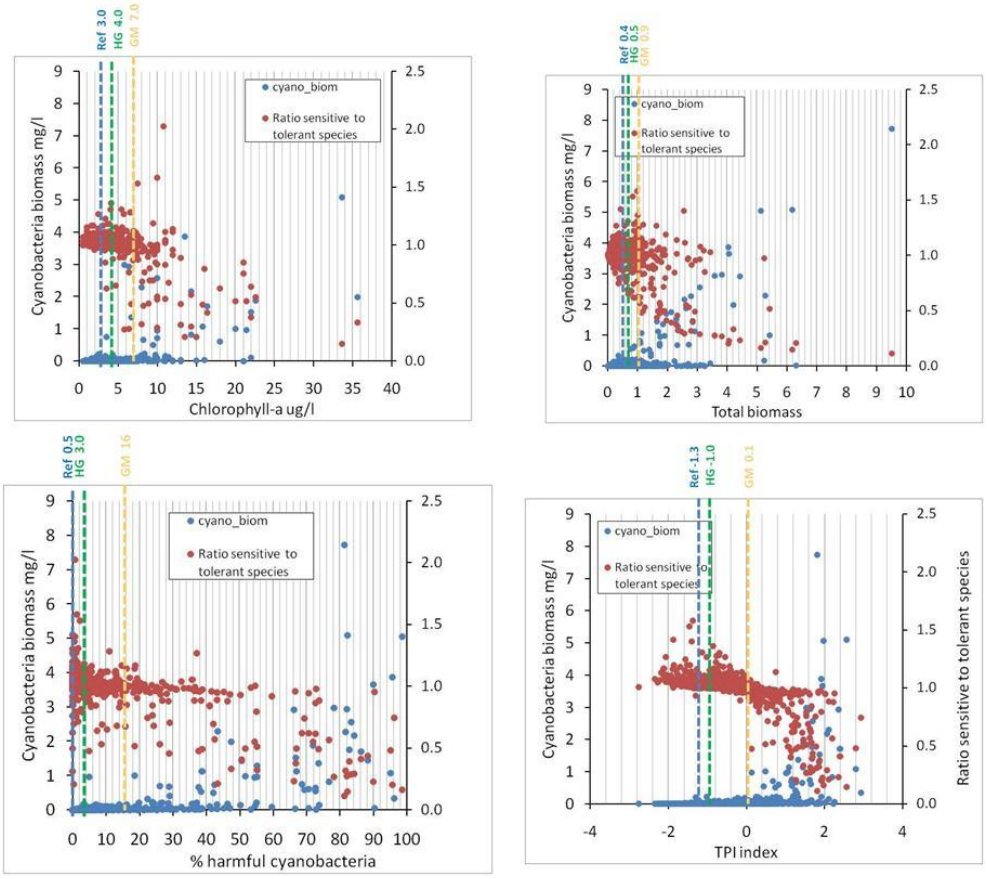

Figure A.2 Reference values (blue line) and H/G (green line) and G/M (orange line) class boundaries of the Finnish lake phytoplankton metrics against cyanobacteria biomass and the ratio of sensitive to tolerant species in the LN2a lake type.

Table A.2 Finnish reference values and class boundaries for each lake type and each metric after intercalibration phase 2.

		Value					EQR			
Type	Classes	Chla	Biovolume	TPI_{FI}	impact Cyano		Chla	Biomass	TPI_{FI}	impact Cyano
		µg/l	mg/l		%		µg/l	mg/l		%
L-N1	Ref value	3	0,50	-1,30	0,5		1,00	1,00	1,00	1,00
	HG	4	0,61	-1,00	3,0		0,75	0,82	0,93	0,97
	GM	7	1,30	0,10	16		0,43	0,38	0,67	0,84
	MP	14	2,60	1,10	33		0,21	0,19	0,44	0,67
	PB	27	5,00	2,00	66		0,11	0,10	0,23	0,34
	max value	*n.a.*		*3,00*	*100*					
L-N2a	Ref value	3	0,40	-1,30	0,5		1,00	1,00	1,00	1,00
	HG	4	0,50	-1,04	3,0		0,75	0,80	0,94	0,97
	GM	7	0,90	0,10	16		0,43	0,44	0,67	0,84
	MP	14	1,90	1,10	33		0,21	0,21	0,44	0,67
	PB	27	3,80	2,00	66		0,11	0,11	0,23	0,34
	max value	*n.a.*		*3,00*	*100*					
L-N2b	Ref value	2	0,25	-1,50	0,5		1,00	1,00	1,00	1,00
	HG	3	0,35	-1,00	2,5		0,67	0,71	0,88	0,98
	GM	5	0,75	0,00	12		0,40	0,33	0,63	0,88
	MP	10	1,50	1,00	24		0,20	0,17	0,38	0,76
	PB	20	3,00	2,00	48		0,10	0,08	0,13	0,52
	max value	*n.a.*		*2,50*	*100*					
L-N5	Ref value	2	0,25	-1,50	0,5		1,00	1,00	1,00	1,00
	HG	3	0,35	-1,00	2,5		0,67	0,71	0,88	0,98
	GM	5	0,75	0,00	12		0,40	0,33	0,63	0,88
	MP	10	1,50	1,00	24		0,20	0,17	0,38	0,76
	PB	20	3,00	2,00	48		0,10	0,08	0,13	0,52
	max value	*n.a.*		*2,50*	*100*					
L-N3a	Ref value	4,5	0,60	-1,30	3,5		1,00	1,00	1,00	1,00
	HG	6	0,75	-1,00	5,0		0,75	0,80	0,93	0,98
	GM	11	1,50	0,20	20		0,41	0,40	0,65	0,83
	MP	20	3,00	1,00	40		0,23	0,20	0,47	0,62
	PB	40	6,00	2,00	70		0,11	0,10	0,23	0,31
	max value	*n.a.*		*3,00*	*100*					
L-N6a	Ref value	3,5	0,70	-1,30	3,5		1,00	1,00	1,00	1,00
	HG	6	0,90	-1,00	5,0		0,58	0,72	0,93	0,98
	GM	9	1,70	0,20	20		0,39	0,40	0,65	0,83
	MP	20	3,40	1,00	40		0,18	0,21	0,47	0,62
	PB	41	6,70	2,00	70		0,09	0,10	0,23	0,31
	max value	*n.a.*		*3,00*	*100*					
L-N8a	Ref value	5	0,70	-1,00	3,5		1,00	1,00	1,00	1,00
	HG	7	0,90	-0,50	5,0		0,71	0,78	0,88	0,98
	GM	12	1,70	1,00	20		0,42	0,41	0,50	0,83
	MP	24	3,40	2,00	40		0,21	0,21	0,25	0,62
	PB	48	6,80	2,50	70		0,10	0,10	0,13	0,31
	max value	*n.a.*		*3,00*	*100*					

Table A.3 Phytoplankton taxa scores used for the calculation of FI TPI index. Negative index scores (-3, -2, -1) indicate taxa with preference to nutrient poor conditions. Positive index scores (1, 2, 3) indicate taxa with preference to nutrient-rich conditions (see Willén 2007).

Taxon	Class	Score
Bitrichia longispina	Chrysophyceae	-3
Bitrichia ollula	Chrysophyceae	-3
Bitrichia phaseolus	Chrysophyceae	-3
Chrysolykos skujae	Chrysophyceae	-3
Dinobryon cylindricum	Chrysophyceae	-3
Dinobryon cylindricum var. alpinum	Chrysophyceae	-3
Dinobryon cylindricum var. palustre	Chrysophyceae	-3
Dinobryon njakajaurense	Chrysophyceae	-3
Dinobryon pediforme	Chrysophyceae	-3
Dinobryon sociale var. americanum	Chrysophyceae	-3
Gymnodinium pituus <10 µm	Dinophyceae	-3
Isthmochloron trispinatum	Xanthophyceae	-3
Kephyrion spp.	Chrysophyceae	-3
Mallomonas hamata	Chrysophyceae	-3
Pseudokephyrion spp.	Chrysophyceae	-3
Pseudopedinella spp.	Dictyochophyceae	-3
Pseudosphaerocystis lacustris	Chlorophyceae	-3
Tabellaria flocculosa var. teilingii	Bacillariophyceae	-3
Aulacoseira alpigena	Bacillariophyceae	-2
Bitrichia spp.	Chrysophyceae	-2
Bitrichia chodatii	Chrysophyceae	-2
Chlamydocapsa spp.	Chlorophyceae	-2
Chrysidiastrum catenatum	Chrysophyceae	-2
Chrysochromulina spp.	Prymnesiophyceae	-2
Chrysococcus spp.	Chrysophyceae	-2
Chrysolykos sp.	Chrysophyceae	-2
Chrysolykos planctonicus	Chrysophyceae	-2
Coenocystis spp.	Chlorophyceae	-2
Cyclotella spp. <10 µm	Bacillariophyceae	-2
Dinobryon borgei	Chrysophyceae	-2
Dinobryon crenulatum	Chrysophyceae	-2
Gloeocystis spp.	Chlorophyceae	-2
Mallomonas akrokomos	Chrysophyceae	-2
Mallomonas akrokomos var. parvula	Chrysophyceae	-2
Merismopedia tenuissima	Cyanophyceae	-2

Taxon	Class	Score
Merismopedia warmingiana	Cyanophyceae	-2
Monoraphidium griffithii	Chlorophyceae	-2
Oocystis submarina var. variabilis	Chlorophyceae	-2
Spiniferomonas spp.	Chrysophyceae	-2
Staurastrum lunatum & var. planctonicum	Conjugatophyceae	-2
Staurodesmus cuspidatus	Conjugatophyceae	-2
Staurodesmus sellatus	Conjugatophyceae	-2
Stichogloea spp.	Chrysophyceae	-2
Chroococcus turgidus	Cyanophyceae	-1
Crucigeniella rectangularis	Chlorophyceae	-1
Cyclotella kuetzingiana	Bacillariophyceae	-1
Dinobryon acuminatum	Chrysophyceae	-1
Dinobryon bavaricum	Chrysophyceae	-1
Dinobryon divergens	Chrysophyceae	-1
Dinobryon sertularia	Chrysophyceae	-1
Gymnodinium uberrimum	Dinophyceae	-1
Mallomonas allorgei	Chrysophyceae	-1
Mallomonas tonsurata	Chrysophyceae	-1
Peridinium inconspicuum	Dinophyceae	-1
Plagioselmis nannoplanctica, P. lacustris / Rhodomonas lacustris, R. minuta	Cryptophyceae	-1
Quadrigula pfitzeri	Chlorophyceae	-1
Willea spp.	Chlorophyceae	-1
Anabaena lemmermannii	Cyanophyceae	1
Aulacoseira ambigua	Bacillariophyceae	1
Aulacoseira islandica	Bacillariophyceae	1
Aulacoseira subarctica	Bacillariophyceae	1
Chlorotetraedron incus	Chlorophyceae	1
Chroococcus dispersus	Cyanophyceae	1
Closteriopsis longissima	Chlorophyceae	1
Closterium acutum var. variabile	Conjugatophyceae	1
Closterium gracile	Conjugatophyceae	1
Closterium limneticum	Conjugatophyceae	1
Closterium macilentum	Conjugatophyceae	1
Closterium pronum	Conjugatophyceae	1
Cosmarium punctulatum	Conjugatophyceae	1
Cyclostephanos dubius	Bacillariophyceae	1
Cyclotella meneghiniana	Bacillariophyceae	1
Diatoma tenuis	Bacillariophyceae	1
Dictyosphaerium ehrenbergianum	Chlorophyceae	1

Taxon	Class	Score
Dictyosphaerium elegans	Chlorophyceae	1
Dictyosphaerium pulchellum	Chlorophyceae	1
Dictyosphaerium tetrachotomum	Chlorophyceae	1
Dimorphococcus lunatus	Chlorophyceae	1
Gonium pectorale	Chlorophyceae	1
Kirchneriella lunaris	Chlorophyceae	1
Kirchneriella obesa	Chlorophyceae	1
Monoraphidium contortum	Chlorophyceae	1
Nitzschia acicularis	Bacillariophyceae	1
Pandorina charkowiensis	Chlorophyceae	1
Pandorina morum	Chlorophyceae	1
Pediastrum biradiatum	Chlorophyceae	1
Peridiniopsis penardiforme	Dinophyceae	1
Peridiniopsis polonicum	Dinophyceae	1
Peridinium bipes	Dinophyceae	1
Peridinium pusillum	Dinophyceae	1
Peridinium umbonatum var. goslaviense	Dinophyceae	1
Peridinium willei	Dinophyceae	1
Planktothrix isothrix, P. mougeotii	Cyanophyceae	1
Scenedesmus denticulatus	Chlorophyceae	1
Scenedesmus magnus	Chlorophyceae	1
Staurastrum tetracerum	Conjugatophyceae	1
Staurodesmus triangularis	Conjugatophyceae	1
Tetraëdriella spinigera	Xanthophyceae	1
Tetraedron spp.	Chlorophyceae	1
Tetrastrum spp.	Chlorophyceae	1
Westella botryoides	Chlorophyceae	1
Actinastrum aciculare	Chlorophyceae	2
Actinastrum spp.	Chlorophyceae	2
Actinocyclus spp.	Bacillariophyceae	2
Anabaena circinalis	Cyanophyceae	2
Anabaena curva	Cyanophyceae	2
Anabaena ellipsoides	Cyanophyceae	2
Anabaena flos-aquae	Cyanophyceae	2
Anabaena fusca	Cyanophyceae	2
Anabaena macrospora	Cyanophyceae	2
Anabaena manguinii	Cyanophyceae	2
Anabaena mendotae	Cyanophyceae	2
Anabaena mucosa	Cyanophyceae	2

Taxon	Class	Score
Anabaena planctonica	Cyanophyceae	2
Anabaena smithii	Cyanophyceae	2
Anabaena solitaria	Cyanophyceae	2
Anabaena suora	Cyanophyceae	2
Aulacoseira granulata	Bacillariophyceae	2
Ceratium furcoides	Dinophyceae	2
Cryptomonas suuri >40 µm	Cryptophyceae	2
Fragilaria crotonensis	Bacillariophyceae	2
Lagerheimia spp.	Chlorophyceae	2
Micractinium pusillum	Chlorophyceae	2
Monoraphidium minutum	Chlorophyceae	2
Pediastrum privum	Chlorophyceae	2
Pediastrum tetras	Chlorophyceae	2
Planktothrix agardhii	Cyanophyceae	2
Pseudanabaena limnetica	Cyanophyceae	2
Scenedesmus armatus	Chlorophyceae	2
Scenedesmus bicaudatus	Chlorophyceae	2
Scenedesmus opoliensis	Chlorophyceae	2
Scenedesmus quadricauda	Chlorophyceae	2
Scenedesmus spinosus (spinosi-ryhmä)	Chlorophyceae	2
Scenedesmus subspicatus	Chlorophyceae	2
Staurastrum chaetoceras	Conjugatophyceae	2
Staurastrum lapponicum	Conjugatophyceae	2
Staurastrum smithii	Conjugatophyceae	2
Stephanodiscus spp.	Bacillariophyceae	2
Strombomonas spp.	Euglenophyceae	2
Surirella spp.	Bacillariophyceae	2
Syncrypta spp.	Chrysophyceae	2
Tetrastrum staurogeniaeforme	Chlorophyceae	2
Trichormus catenula	Cyanophyceae	2
Ulnaria acus	Bacillariophyceae	2
Ulnaria ulna	Bacillariophyceae	2
Actinocyclus normanii f. subsalsus	Bacillariophyceae	3
Anabaena crassa	Cyanophyceae	3
Anabaena kierteinen rihma	Cyanophyceae	3
Anabaena spiroides	Cyanophyceae	3
Aphanizomenon spp.	Cyanophyceae	3
Aulacoseira granulata var. angustissima	Bacillariophyceae	3
Coelastrum spp.	Chlorophyceae	3

Taxon	Class	Score
Cyanodictyon spp.	Cyanophyceae	3
Diplopsalis acuta	Dinophyceae	3
Euglena spp.	Euglenophyceae	3
Lepocinclis spp.	Euglenophyceae	3
Limnothrix spp.	Cyanophyceae	3
Microcystis aeruginosa	Cyanophyceae	3
Microcystis botrys	Cyanophyceae	3
Microcystis flos-aquae	Cyanophyceae	3
Microcystis viridis	Cyanophyceae	3
Microcystis wesenbergii	Cyanophyceae	3
Pediastrum boryanum	Chlorophyceae	3
Pediastrum duplex	Chlorophyceae	3
Pediastrum duplex var. gracillimum	Chlorophyceae	3
Phacus spp.	Euglenophyceae	3
Planktolyngbya spp.	Cyanophyceae	3
Quadricoccus ellipticus	Chlorophyceae	3
Scendesmus acutodesmus-ryhmä: S. acutis, S. acuminatus, S. obtusiusculus ja varieetit	Chlorophyceae	3
Scenedesmus acuminatus	Chlorophyceae	3
Scenedesmus acutus f. alternans	Chlorophyceae	3
Scenedesmus acutus f. tetradesmiformis	Chlorophyceae	3
Scenedesmus dimorphus	Chlorophyceae	3
Scenedesmus obtusus	Chlorophyceae	3
Staurosira berolinensis	Bacillariophyceae	3
Trachelomonas spp.	Euglenophyceae	3
Treubaria triappendiculata	Chlorophyceae	3

Table A.4 Cyanobacteria taxa that are used to calculate the Finnish lake phytoplankton metric: percentage of harmful cyanobacteria (Vuori et al. 2010).

Anabaena affinis f. vigueri (Denis&Fremy) Kom.	*Anabaena sp. "straight"*
Anabaena augstumnalis v. incrassata (Nyg.) Geitl.	*Anabaena sp. "twisted"*
Anabaena flos-aquae f. treleasii (Born.&Flah.) El.	*Anabaena sp.*
Anabaena scheremetievii v. incurvata El.	*Aphanizomenon flos-aquae f. gracile (Lemm.) El.*
Anabaena aequalis Borge	*Aphanizomenon flexuosum Komarek&Kobacik*
Anabaena affinis Lemm.	*Aphanizomenon flos-aquae (L.) Ralfs*

Anabaena aphanizomenoides Forti	*Aphanizomenon gracile (Lemm.) Lemm.*
Anabaena augstumnalis Schmidle	*Aphanizomenon issatschenkoi (Usacev) Proshk.-Lavr.*
Anabaena baltica Schmidt	*Aphanizomenon klebanii*
Anabaena circinalis Rab.	*Aphanizomenon ovalisporum Forti*
Anabaena crassa (Lemm.) Kom.-Legn. & Cronb.	*Aphanizomenon paraflexuosum Watanabe*
Anabaena curva Hill	*Aphanizomenon skujae Kom.-Legn.&Cronb.*
Anabaena cylindrica Lemm.	*Aphanizomenon yezoense Watanabe*
Anabaena elliptica Lemm.	*Aphanizomenon sp.*
Anabaena flos-aquae (Lyngn.) Breb.	*Microcystis aeruginosa (Kutz.) Kutz.*
Anabaena fusca Hill	*Microcystis botrys Teil.*
Anabaena halbfassii Bachm.	*Microcystis densa G.S.West*
Anabaena hieronymusii Lemm.	*Microcystis firma (Kutz.) Schmidle*
Anabaena hungarica	*Microcystis flos-aquae (Wittrock) Kirchner*
Anabaena inaequalis (Kutz.) Born.&Flah. *Anabaena jonssonii Boye-Pet.*	*Microcystis ichthyoblebe Kutz.* *Microcystis marginata (Menegh.) Kutz.*
Anabaena lapponica Borge	*Microcystis natans Lemm.*
Anabaena lemmermannii P.Richter	*Microcystis novacekii (Kom.) Comp.*
Anabaena levanderi Lemm.	*Microcystis reinboldii (Richter) Forti*
Anabaena macrospora Kleb.	*Microcystis robusta (Clark) Nyg.*
Anabaena mendotea Trelease	*Microcystis wesenbergii (Kom.) Starm.*
Anabaena minderi Hub.-Pest.	*Microcystis viridis (A.Braun) Lemm.*
Anabaena miniata Skuja	*Microcystis sp.*
Anabaena mucosa Legn.&Elor.,1992	*Planktothrix agardhii (Gom.) Anagnostidis&Kom.*
Anabaena oscillarioides Bory	*Planktothrix mougeotii (Bory) Anagn.&Kom.*
Anabaena perturbata	*Planktothrix raciborskii (Wolosz.) Anagn.&Kom.*
Anabaena planctonica Brunnthaler	*Planktothrix rubescens (DeCandolle ex Gomont)*
Anabaena smithii Kom.	*Anagn.&Kom.*
Anabaena solitaria Kleb.	*Planktothrix sp.*
Anabaena spiroides Kleb.	*Woronichinia compacta (Lemm.) Kom.&Hind.*
Anabaena torulosa (Carm.) Lagerh.	*Woronichinia elorantae Kom. & Kom.-Legn.*
Anabaena utermoehlii Geitl.	*Woronichinia karelica Kom. & Kom.-Legn.*
Anabaena variabilis Kutz.	*Woronichinia naegeliana (Unger) Elenkin*
Anabaena volzii Lemm.	*Woronichinia sp.*
Anabaena zinserlingii Kos.	

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A.2 Ireland: Irish classification method for phytoplankton in lakes.

Summary

This document outlines how status is assigned for the biological quality element phytoplankton and how boundaries were initially assigned in Ireland. Through the intercalibration process these boundaries may be adjusted to within 0.25 of a status class from the agreed boundary. Both chlorophyll *a* and the composition metric boundaries were set separately with respect to the normative definitions of the WFD at points of ecological change. In addition the boundaries of the IE lake phytoplankton index, used for final assessment of the BQE, were tested against predictions of the reduction in depth of macrophyte colonisation.

Introduction

In the Republic of Ireland, status for the biological quality element (BQE) phytoplankton is assessed using two parameters: chlorophyll *a* as a measure of phytoplankton biomass and a taxonomic composition metric. These parameters are normalised so that their boundaries and class widths are on the same scale and then averaged (Figure A.3). This document summarises the methods and the process of boundary setting for four NGIG types intercalibrated by Ireland (Table A.5).

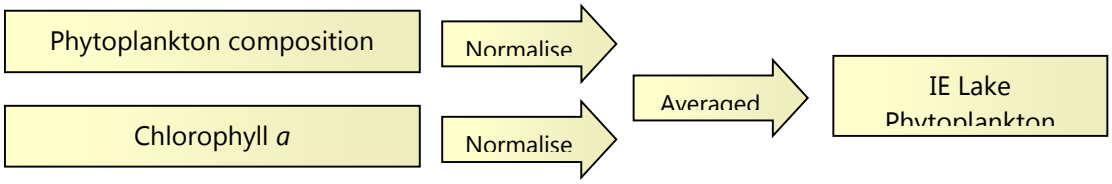

Figure A.3 Phytoplankton composition and chlorophyll a parameters are normalised and averaged annually to provide an IE Lake Phytoplankton Index value.

Table A.5 NGIG lake types intercalibrated by Ireland.

Type	Lake Characterisation	Altitude (m)	Mean depth (m)	Alkalinity (meq l^{-1})	Colour (mg l^{-1} PtCo)
L-N1	Lowland, shallow, moderate alkalinity, clear	<200	3 - 15	0.2 - 1	< 30
L-N2a	Lowland, shallow, low alkalinity, clear	<200	3 - 15	< 0.2	< 30
L-N3a	Lowland, shallow, low alkalinity, meso-humic	<200	3 - 15	< 0.2	30 - 90
L-N8a	Lowland, shallow, moderate alkalinity, meso-humic	<200	3 - 15	0.2 - 1	30 - 90

Metrics included in the Irish phytoplankton assessment system

Chlorophyll a

Sub-surface samples are taken from mid-lake stations. Chlorophyll *a* is determined following extraction using spectrophotometric analysis. Sampling frequency ranges from a maximum of 12 times per year to a minimum of 4 times per year between January and December. Spatial replication depends on lake size with more stations on larger lakes. Reference values and boundaries for L-N types are listed in Table A.6 Reference values were decided at GIG level and are detailed in the Water Framework Directive Intercalibration Technical Report - Part 2: Lakes (Poikane, 2008) and in the Intercalibration decision (EC, 2008).

The approach to setting chlorophyll *a* boundaries for lakes within the NGIG types was previously outlined on pages 61-63 of Poikane (2008) and also in pages 126-7 of Annex E Part 4 (Poikane, 2008). Following the application of reference values and boundaries, the chlorophyll *a* EQR is normalised per lake type using Equation 1 below where the max EQR is set to 2.14.[1]

[1] Where chl *a* is lower than the reference value this results in an EQR >1. This can distort the dataset when chlorophyll a is very low. To deal with this we set the upper EQR of the high class to the 10th percentile of the parameter value (towards high status). For chlorophyll *a* the lower 10% of the GIG data classified as high status was 1.6375. So 3.5 (ref)/ 1.6375 = 2.14 we used this as max EQR and this should improve the distribution generally but there is a need to truncate occasional EQR values >1.

Equation 1:

$$\frac{(EQR - lower\ EQR\ boundary) * (normalised\ upper\ boundary - normalised\ lower\ boundary)}{(upper\ EQR\ boundary - lower\ EQR\ boundary)} + normalised\ lower\ boundary$$

Table A.6 The boundaries of IE status classes for chlorophyll a µg l^{-1} for NGIG lake types.

	Reference	High/Good	Good/Moderate	Moderate/Poor	Poor/Bad
L-N1 Chl a	3.00	6.00	9.09	17.65	37.50
L-N1 EQR		0.50	0.33	0.17	0.08
L-N2a Chl a	2.50	5.00	8.62	16.67	35.71
L-N2a EQR		0.50	0.29	0.15	0.07
L-N3a Chl a	3.00	6.00	9.09	17.65	37.50
L-N3a EQR		0.50	0.33	0.17	0.08
L-N8a Chl a	3.20	5.82	10.00	20.00	40.00
L-N8a EQR		0.55	0.32	0.16	0.08

Phytoplankton composition metric

The phytoplankton composition metric provides an indication of the state of community composition and abundance in relation to the eutrophication pressure gradient. Assessment is based on two summer (1st June to 7th of September) mid-lake sub-surface samples taken annually over a three year monitoring period. Phytoplankton are counted following the Utermöhl technique. Assessment is based on nine groups or genera of indicator taxa, each of which is awarded a score ranging from 1 to 0.1 based on abundance. Sample chlorophyll *a* is also awarded a score ranging from 1 to 0.1. The scores are averaged to produce a phytoplankton composition metric value. See Table 4.10 in Free *et al*. (2006) for scores and further information.

In order to establish a reference value for the composition metric an average metric value of 15 lake 'years' (10 lakes in total) was taken from a set of lakes in reference status. The reference lakes selected were those confirmed as being in reference condition by a palaeolimnological study of 34 candidate reference lakes (Taylor et al., 2006). These lakes had similar assemblages from a comparison of top and bottom core samples (a squared chord distance of 0.40 was used). The lakes chosen were Loughs Barfinnihy, Bunny, Doo, Dunglow, Keel, Kiltooris, Nahasleam, O'Flynn, Upper Lough Veagh and Upper. Lough McNean, although confirmed to be in reference status, was excluded owing to its high TP concentration (24 µg l^{-1}). The average reference composition metric value for these lakes was 0.9383. This was used as a denominator to generate an EQR following guidance document 10 (Tool 3 page 53, REFCOND (2003)).

Boundary setting for the NGIG lakes was based on responses in lakes of alkalinity between 0.4 and 2 meq l^{-1} comprising IE types 5,6,7,8. This only partly overlaps with the gradient of types L-N1 and L-N8a. For the other types < 0.2 meq l^{-1} there was an insufficient pressure gradient in the Irish dataset to assess boundaries or develop specific metrics. Free *et al*. (2006) found only 3 low alkalinity lakes with a TP > 20 µg l^{-1} in a survey of 157 lakes.

Figure A.4, taken from Free *et al*. (2006), shows the response of three phytoplankton taxa to TP in lakes of alkalinity between 0.4 and 2 meq l^{-1}. Generally at TP values less than 10 µg l^{-1} there is an absence or low abundance of eutrophic taxa such as *Pediastrum* or *Scenedesmus*. Whereas between 10 and 25 µg l^{-1} TP some slight changes occur such as an increase in the presence and abundance of *Scenedesmus*. At concentrations greater than 25 µg l^{-1} *Pediastrum* occurs more frequently in higher abundance and, in line with normative definitions for moderate status, the biomass increases (chlorophyll *a* indicated by green smoothed line). This can be related to a 'significant undesirable disturbance in the condition of other biological quality elements' (Annex 5, WFD). This is visible in the accompanying graphs for macrophytes that show after 25 µg l^{-1} TP there is a significant loss of charophytes and also that there is an increased absence of isoetid taxa (including the widely distributed *Littorella*) (Figure A.4). This 25 µg l^{-1} concentration could therefore be used to indicate where a boundary for good/moderate status in the phytoplankton composition metric lies. Poor status may be difficult to decide but could be around 70 µg l^{-1} TP where there is a complete absence of charophytes.

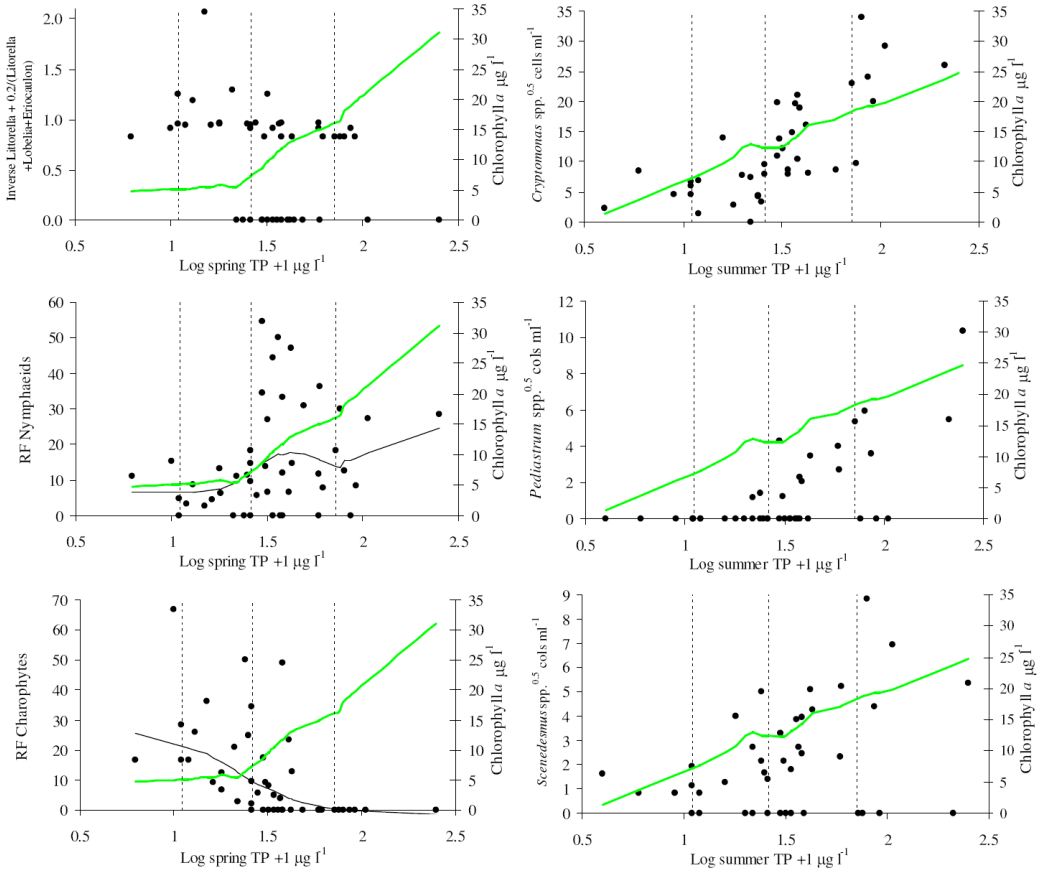

Figure A.4 Relationship between TP (Spring or Summer) and selected macrophyte metrics (left) and phytoplankton taxa (right) for lakes between 0.4 and 2 meq l^{-1} alkalinity. The lowess smoothed relationship between TP and summer

chlorophyll a is overlain (──). Dashed lines represent concentrations of 10, 25 and 70 µg l^{-1} TP.

A nonparametric multiplicative regression (NPMR) model was used to model the response and predict the phytoplankton composition metric values for given TP concentrations. The model's xR^2 was 0.69 and was significant ($p < 0.001$). This model was then used to predict the phytoplankton composition metric values for a given range of TP concentrations of relevance for boundary setting (Table A.7). It is important to realise that the TP boundaries are not being used directly to assess boundary status classes, rather it is the TP concentrations from points of ecological change (Figure A.4) that are being used to estimate the metric values by NPMR. This will serve to inform the national position until such boundaries are formally intercalibrated through the EU intercalibration exercise. The phytoplankton composition metric EQR is then normalised per type using Equation 1 above.

Table A.7 The boundaries of IE status classes for the phytoplankton composition metric. National boundaries (metric 1) and intercalibration boundaries (metric 2 using biovolume data) are for NGIG types L-N 1,2a, 3a and 8a.

	Reference	High/Good	Good/Moderate	Moderate/Poor	Poor/Bad
Composition metric 1	0.9383	0.9160	0.7540	0.4050	0.2476
EQR metric 1		0.9760	0.8040	0.4320	0.2640
Composition metric 2	0.8421	0.8240	0.6923	0.4087	0.2808
EQR metric 2		0.9785	0.8221	0.4853	0.3330

Bloom metric

A separate metric was not developed for phytoplankton blooms. This was because the existing IE lake phytoplankton index is already correlated with the biovolume of cyanophytes and including an additional metric based on cyanophytes did not increase the ability to detect responses to pressure. For additional information please see Appendix in the end of the description of IE assessment method.

Combination Rules

Two parameters are combined to provide an assessment of the BQE: chlorophyll *a* as a measure of phytoplankton biomass and the phytoplankton composition metric. These parameters are normalised using Equation 1 above so that their boundaries and class widths are on the same scale and then averaged to give an annual value of the IE lake phytoplankton index. A mean value and confidence is then calculated from three years of data.

Method performance

The r^2 between the composition metric and log transformed TP was 0.67 for 129 Irish lakes (Free *et al.*, 2006). The r^2 between log transformed chlorophyll *a* and TP was 0.58 for 31 Irish lakes (Irvine, 2001). The final IE lake phytoplankton index for the intercalibrated types had an r^2 ranging from 0.28 to 0.82 depending on type (Table A.9). The low r^2 for L-N2a was likely owing to the limited pressure gradient for these soft water lakes with only 3 lakes > 20 µg l^{-1} TP.

Table A.8 Regressions between the IE lake phytoplankton index and Log TP for L-N 1, 2a, 3a and 8a. Standard error (s.e.) of coefficients are shown. LCB data included for information only. The results for the L-CB GIG are included for information only.

Type	n	r^2	Intercept	s.e.	Log TP	s.e.	p
L-N1	98	0.74	1.35697	0.04053	-0.56511	0.03426	≤0.0001
L-N2a	91	0.28	1.06358	0.0477	-0.312325	0.05334	≤0.0001
L-N3a	107	0.48	1.12968	0.04003	-0.373842	0.03797	≤0.0001
L-N8a	59	0.82	1.38096	0.05066	-0.585679	0.03594	≤0.0001

Boundary setting

Overview of the approach to boundary setting in the Republic of Ireland

The broad approach to defining the good/moderate boundary in the Republic of Ireland is based on the secondary effects of an increase in total phosphorus and chlorophyll *a* on macrophyte diversity in the context of normative definitions for moderate status outlined in Annex 5 of the WFD (Figure A.5) (Council of the European Communities, 2000). The good/moderate boundary was taken to be approximately 25 µg l^{-1} TP on the basis that it corresponds with normative definitions in that it is the point where macrophyte diversity starts to decrease therefore resulting in an 'undesirable disturbance to the balance of organisms'. The increase in diversity between 10 and 25 µg l^{-1} TP may correspond to normative definitions of good status in that the change is not an 'undesirable' one.

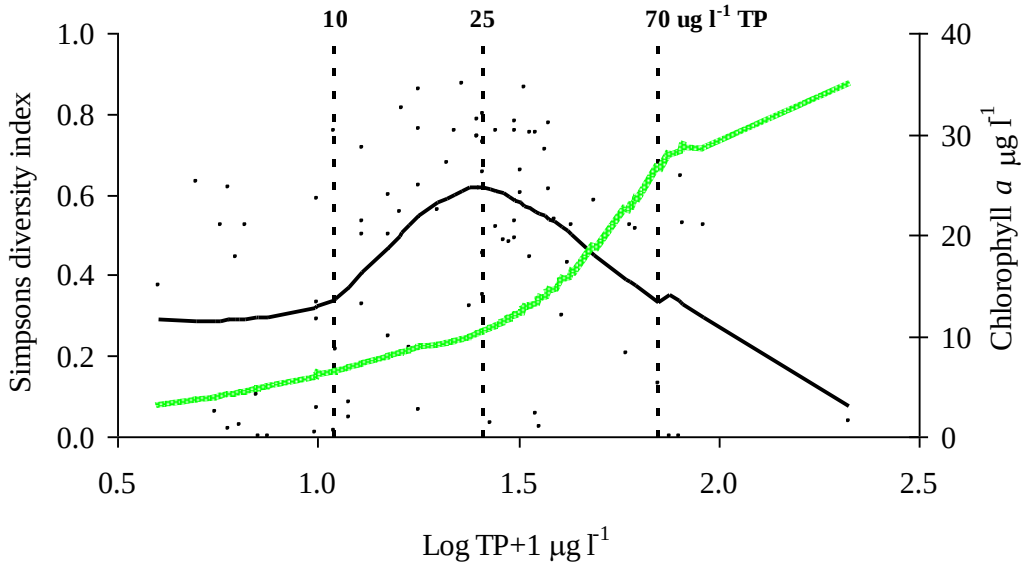

Figure A.5 Relationship between macrophyte diversity (Simpson's diversity index with lowess smoothed line: ——), and transformed (Log x+1) TP. Smoothed relationship of chlorophyll a with transformed (Log x+1) TP is overlain (——). Graph refers to lakes > 0.4 meq l^{-1} only. Selection of TP concentrations, measured mostly in Spring are overlain (- - -).

Updating boundary setting for the second round of intercalibration

In the second round of intercalibration it is necessary to ensure that the final IE lake phytoplankton index boundaries are once again set at points relevant to the normative definitions. The approach to this was to set boundaries of chlorophyll *a* and the composition metric in line with points of ecological change relevant to the normative definitions (see above). However, as boundary setting for the two parameters was done separately (chlorophyll *a* in the 1st round and the composition metric in the 2nd), additional validation is desirable for the combined assessment as new boundaries are essentially formed when both normalised parameters are joined to give a final assessment of the BQE phytoplankton. To achieve this, the boundaries of the IE lake phytoplankton index were checked against a model to predict the depth of colonisation of macrophytes. The depth of colonisation responds to a large degree to the increased attenuation of light owing to higher abundance of phytoplankton with eutrophication.

To estimate the reduction in depth of macrophyte colonisation (Zc) with declining status from an NEQR of 1 a sequence of predictive models were applied (Table A.9, Table A.10). The chlorophyll *a* concentration at each boundary was predicted for each type using a regression with the IE lake phytoplankton index. This chlorophyll *a* at the boundary was then used to predict transparency (for a colour of 30 or 60 mg l^{-1} PtCo depending on type) which was used to predict the depth of colonisation (Table A.9, Table A.10).

The models for the clear lake types L-N1 and L-N2a estimated that the depth of colonisation of angiosperms would decrease from 4.38 and 4.49 m for an NEQR of 1 to

3.55 and 3.56 m at the good/moderate boundary. Charophyte depth of colonisation was predicted to decline from 5.20 and 5.46 m for an NEQR of 1 to 3.59 and 3.61 m at the good/moderate boundary. The good/moderate boundary represented a point where there is estimated to be a loss of a third (31-34%) in the depth of colonisation (Table A.11).

Table A.9 Models used to predict Zc. Sources: 1&2: intercalibration NGIG data: 3: Free (2002), 4: Equation 4 Chambers and Kalff (1985), 5: Blindow (1992). A colour of 30 mg l^{-1} PtCo was assumed for L-N1 and L-N2a and 60 mg l^{-1} PtCo for L-N3a and L-N8a. LCB data included for information only.

Source	Dependent variable	r^2	Model
1c	Log chlorophyll *a* ・g l^{-1} at L-CB1 boundaries	0.89	1.99197+IE lake phytoplankton index*-1.81268
2c	Log chlorophyll *a* ・g l^{-1} at L-CB2 boundaries	0.90	2.10221+ IE lake phytoplankton index *-1.95045
1a	Log chlorophyll *a* ・g l^{-1} at L-N1 boundaries	0.88	2.01878+ IE lake phytoplankton index *-1.75973
1b	Log chlorophyll *a* ・g l^{-1} at L-N2a boundaries	0.67	2.19103+ IE lake phytoplankton index *-2.05993
2a	Log chlorophyll *a* ・g l^{-1} at L-N3a boundaries	0.77	2.11947+ IE lake phytoplankton index *-1.97524
2b	Log chlorophyll *a* ・g l^{-1} at L-N8a boundaries	0.92	1.89514+ IE lake phytoplankton index *-1.50561
3	Log 1+Secchi depth (m)	0.82	1.34495 -0.414109 log (x + 1) colour -0.205299 log (x + 1) chlorophyll *a* ・g l^{-1}
4	Zc Angiosperms$^{0.5}$		1.33 log Secchi depth + 1.4
5	Log Zc Charophyta	0.83	1.03 log Secchi depth + 0.18

The models for the humic lake types L-N3a and L-N8a estimated that the depth of colonisation of angiosperms would decrease from 3.61 and 3.37 m for an NEQR of 1 to 2.71 and 2.64 m at the good/moderate boundary. Charophyte depth of colonisation was predicted to decline from 3.68 and 3.29 m for an NEQR of 1 to 2.35 and 2.26 m at the good/moderate boundary. The good/moderate boundary represented a point where there is estimated to be a loss of a third (31-36%) in the depth of colonisation (Table A.10).

Table A.10 Predicted reduction in depth of macrophyte colonisation (Zc) with declining status from an EQR of 1 for lake types L-N 1, 2a, 3a and 8a. Sequential predictions are based on application of models (see Table A.9) for L-N1: 1a, 3, 4, 5; L-N2a: 1b, 3, 4, 5; L-N3a: 2a, 3, 4, 5; L-N8a 2b, 3, 4, 5. A colour of 30 mg l^{-1} PtCo was assumed for L-N1 and L-N2a and 60 mg l^{-1} PtCo for L-N3a and L-N8a. LCB data included for information only.

Type	Boundary	nEQR	Predicted Chl *a* at nEQR boundary	Predicted Zc Angiosperms	Predicted Zc Charophytes	Predicted % loss of Zc Charophytes from reference
LCB1	EQR1	1.0	1.51	4.45	5.37	0
LCB1	High/Good	0.8	3.48	4.08	4.57	15
LCB1	Good/Moderate	0.6	8.02	3.63	3.73	31
LCB1	Moderate/Poor	0.4	18.49	3.14	2.93	45
LCB1	Poor/Bad	0.2	42.60	2.62	2.23	58
LCB2	EQR1	1.0	1.42	4.48	5.42	0
LCB2	High/Good	0.8	3.48	4.08	4.57	16
LCB2	Good/Moderate	0.6	8.55	3.59	3.66	32
LCB2	Moderate/Poor	0.4	20.99	3.06	2.82	48
LCB2	Poor/Bad	0.2	51.54	2.50	2.09	62
LN1	EQR1	1.0	1.82	4.38	5.20	0
LN1	High/Good	0.8	4.08	4.00	4.41	15
LN1	Good/Moderate	0.6	9.18	3.55	3.59	31
LN1	Moderate/Poor	0.4	20.65	3.07	2.84	46
LN1	Poor/Bad	0.2	46.43	2.56	2.17	58
LN2a	EQR1	1.0	1.35	4.49	5.46	0
LN2a	High/Good	0.8	3.49	4.08	4.57	16
LN2a	Good/Moderate	0.6	9.02	3.56	3.61	34
LN2a	Moderate/Poor	0.4	23.28	3.00	2.73	50
LN2a	Poor/Bad	0.2	60.12	2.40	1.97	64
LN3a	EQR1	1.0	1.39	3.61	3.68	0
LN3a	High/Good	0.8	3.46	3.21	3.04	18
LN3a	Good/Moderate	0.6	8.60	2.71	2.35	36
LN3a	Moderate/Poor	0.4	21.35	2.16	1.72	53
LN3a	Poor/Bad	0.2	53.02	1.58	1.17	68
LN8a	EQR1	1.0	2.45	3.37	3.29	0
LN8a	High/Good	0.8	4.91	3.03	2.77	16
LN8a	Good/Moderate	0.6	9.81	2.64	2.26	31
LN8a	Moderate/Poor	0.4	19.63	2.22	1.77	46
LN8a	Poor/Bad	0.2	39.27	1.77	1.34	59

Translation of intercalibrated boundaries into national types

The NGIG typology is not directly comparable with the Irish typology. The alkalinity bands and depth bands differ and the Irish typology does not type lakes by colour. Consequently, the EQRs from NGIG types will be applied to the Irish lake types that have maximum overlap and comparability, particularly in relation to alkalinity. Applicability of those EQRs to the Irish situation will be explored at a national level.

The Irish typology has two groups of low and moderate alkalinity lakes, those < 0.4 meq l^{-1} and those between 0.4 and 2 meq l^{-1} that overlap with NGIG types. Most of the work on boundaries has taken place in the latter as soft water lakes < 0.4 meq l^{-1} are typically located in catchments without significant eutrophication pressure, mostly peatland catchments. The intercalibration process should therefore be helpful in validating boundary setting in such situations through extending the pressure gradient available for analysis.

The predicted response of the IE lake phytoplankton index to TP indicates that alkalinity seemed the most relevant in determining the response. The low alkalinity types LN2a and LN3a were similar in slope and intercept (Table A.8, Figure A.6). The response of these types to pressure was distinct to that of the moderate alkalinity types LN1 and LN8a. These types were also very similar in slope and intercept (Table A.8, Figure A.6). Colour may therefore not be a strong typological parameter in this analysis.

The potential translation of the intercalibraed types into national types is laid out in Table A.11. There are no or only rare lakes with mean depth > 15 m in Ireland. All lakes > 200 m altitude are small with an area less than 0.5 km^2.

Table A.11 List of IE lake types and intercalibration types. The intercalibration types will inform boundaries to be applied at national level. CBGIG types are included for information.

IE type	Altitude (m)	Alkalinity (meq l^{-1})	Mean depth (m)	Area (km^2)	GIG Type
1	<200	<0.4	<4	<0.5	LN1, LN2a, LN3a, LN8a
2	<200	<0.4	<4	>0.5	LN1, LN2a, LN3a, LN8a
3	<200	<0.4	>4	<0.5	LN1, LN2a, LN3a, LN8a
4	<200	<0.4	>4	>0.5	LN1, LN2a, LN3a, LN8a
5	<200	0.4 - 2	<4	<0.5	LN1, LN8a, L-CB2
6	<200	0.4 - 2	<4	>0.5	LN1, LN8a, L-CB2
7	<200	0.4 - 2	>4	<0.5	LN1, LN8a, L-CB1
8	<200	0.4 -2	>4	>0.5	LN1, LN8a, L-CB1
9	<200	>2	<4	<0.5	L-CB2
10	<200	>2	<4	>0.5	L-CB2

11	<200	>2	>4	<0.5	L-CB1
12	<200	>2	>4	>0.5	L-CB1
13	>200	-	-	-	

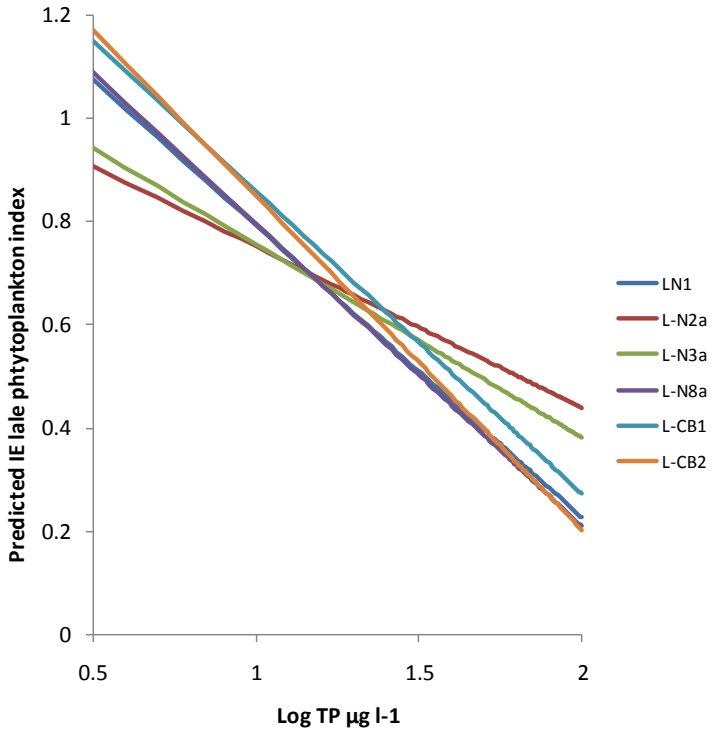

Figure A.6 Predicted IE lake phytoplankton index and TP from models in Table A.8. Predictions are based on relationships with GIG data.

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Appendix The applicability of existing IE phytoplankton metrics in reflecting blooms

Introduction

The metric used in Ireland uses chlorophyll *a* as an indicator of biomass. The composition metric uses a list of indicator taxa that includes cyanophytes and is scored based on abundance or biovolume. Further details are provided on the WISER website (http://www.wiser.eu/) and in Free *et al.* (2006). Both the biomass and composition parameters are normalised and then averaged to give an EQR.

In order to examine the potential for the existing IE metric to reflect the 'bloom' aspect of the BQE it was decided to follow two approaches:

- To carry out a correlation analysis between the national metric normalised EQR and the sum of Cyanophyte biovolume.
- To carry out a multiple regression using TP as a dependent variable and the national EQR and Cyanophyte biovolume as predictors. This should indicate whether Cyanophytes are significant in explaining additional variation in the BQE along the pressure gradient.

The data from the Central Baltic GIG was used to carry out the analysis. The IE metric was calculated for 283 LCB1 lake years and for 148 LCB2 lake years.

Results and Discussion

The IE phytoplankton EQR was significantly ($p \leq 0.0001$) correlated with log (x+1) transformed sum of cyanophytes for both LCB1 ($r^2 = 0.29$) and 2 ($r^2 = 0.32$) (Figure A.7). The dataset contained many values close to zero for cyanophyte biovolume despite transformation. The non-parametric spearman rank correlation coefficients for the relationship were -0.59 for LCB1 and -0.61 for LCB2 ($p<0.0001$). Given the significant relationship between the IE metric and the sum of cyanophytes the bloom aspect

represented by cyanophytes is likely to be reflected to some degree in the existing IE metric.

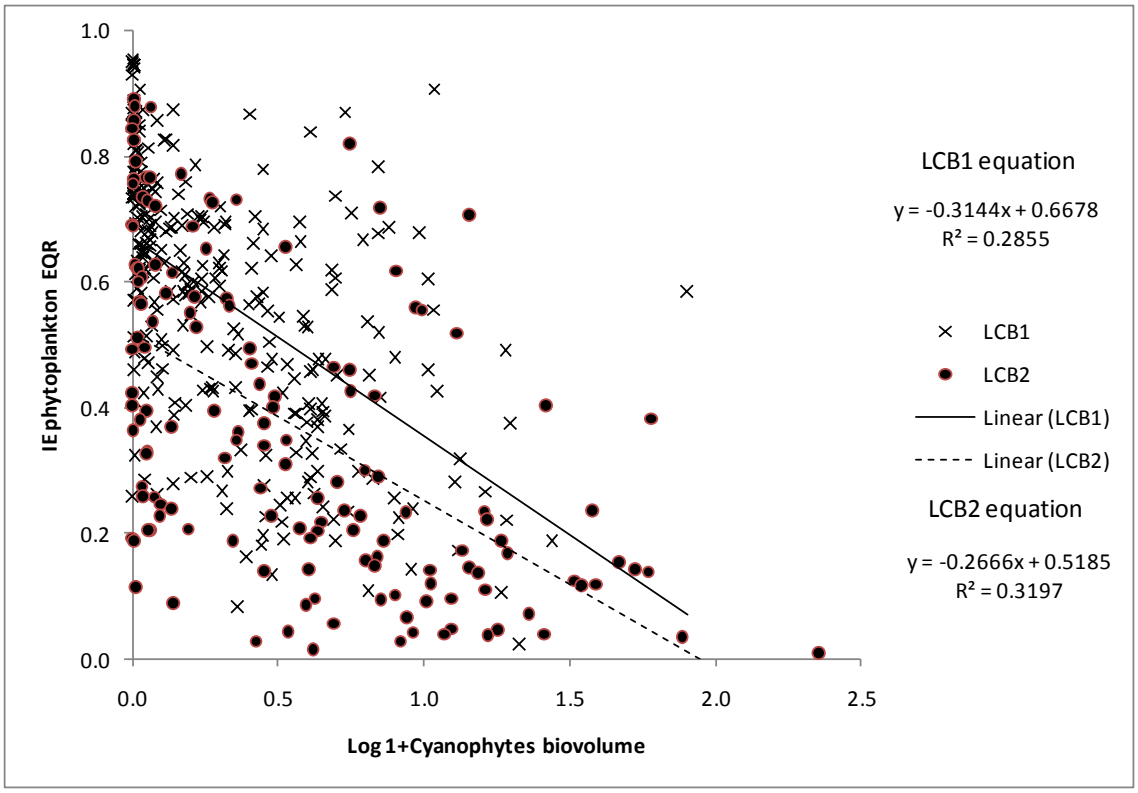

Figure A.7 Relationship between the Log x+1 transformed sum of cyanophytes and the IE phytoplankton metric for both LCB1 and LCB2.

Mischke *et al.* (2010) suggested a value of 10 mm^3 ml^{-1} of Cyanophyte biovolume, derived from the WHO levels for cyanophyte abundance, as a useful medium risk threshold. Using the data for both LCB1 and 2 the existing IE metric would classify 97.5% of lakes as being of moderate class or lower that had in excess of 10 mm^3 ml^{-1} of cyanophyte biovolume. This provides reasonably strong support that the existing IE metric already detects bloom events and correctly identifies the need for a programme of measures.

Stepwise multiple regression using TP as a dependent variable and the IE EQR and transformed (log x+1) cyanophyte biovolume as predictors was carried out for both LCB1 and 2. Cyanophyte biovolume was not significant in explaining additional variation in the pressure gradient (TP) alongside the existing IE metric for both LCB1 ($p = 0.23$) and LCB2 ($p = 0.41$) (Table A.12 and Table A.13). There are likely to be a couple of explanations for this, the first is that the existing IE metric already reflects cyanophyte biomass as indicated by the correlation analysis above and the second is that cyanophytes alone are unreliable as an indicator of pressure. Transformed (log x+1) cyanophytes had a low r^2 with Log TP for LCB1 (0.12, $p \leq 0.0001$) and LCB2 lakes (0.09, $p \leq 0.0001$).

In conclusion the existing IE metric is already correlated with the biovolume of cyanophytes and including an additional metric based on cyanophytes would not increase the ability to detect responses to pressure.

Table A.12 Multiple regression for log TP (µg l-1) for LCB1 lakes. n = 262.

Step	Variable	R^2	Model
1	IE NEQR	0.40	Log TP = 2.19949 – 1.09375 · IE NEQR
2	Log 1+cyanophyte biovolume	0.41	Log TP = 2.13894 – 1.02903 · IE NEQR + 0.0718895 Log 1+cyanophyte biovolume

Table A.13 Multiple regression for log TP (µg l^{-1}) for LCB2 lakes. n = 131.

Step	Variable	R^2	Model
1	IE NEQR	0.34	Log TP = 2.36318 – 1.1751 · IE NEQR
2	Log 1+cyanophyte biovolume	0.34	Log TP = 2.43147 – 1.25786 · IE NEQR - 0.0665084 Log 1+cyanophyte biovolume

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A.3 Norway: Norwegian classification method for phytoplankton in lakes.

Summary

This document outlines how status is assigned for the biological quality element phytoplankton and how boundaries have been assigned in Norway. The metrics included in the Norwegian phytoplankton assessment method are the biomass metrics chlorophyll a and total biovolume, the taxonomic composition metric PTI_{NO} and the bloom intensity metric maximum Cyanobacteria biovolume. The reference value and HG boundary for each metric and each type were set from the median and the 90th %ile of the Norwegian or NGIG reference sites (lake-years) respectively. The GM, MP and PB metric boundaries were set separately with respect to the normative definitions of the WFD at points of

ecological change, as reflected by changes in the proportions of sensitive and tolerant taxa along the trophic gradient.

Introduction

In Norway, the ecological status for the biological quality element (BQE) lake phytoplankton is assessed using four parameters: the biomass metrics chlorophyll a and total biovolume, the taxonomic composition metric, $PTI_{NO,}$ and the bloom intensity metric maximum Cyanobacteria biovolume, $Cyano_{max}$. The EQRs for these parameters are normalised so that their boundaries and class widths are on the same scale and then combined by first taking the average of the two biomass metrics, and then averaging that with the PTI_{NO} and the $Cyano_{max}$ Figure A.8 If the $Cyano_{max}$ shows a better status (i.e. has a higher normalised EQR) than the average of the other metrics, then it is not used for assessment. This document summarises the metrics and the process of boundary setting giving examples for the NGIG types LN1 and LN2a (Table A.14).

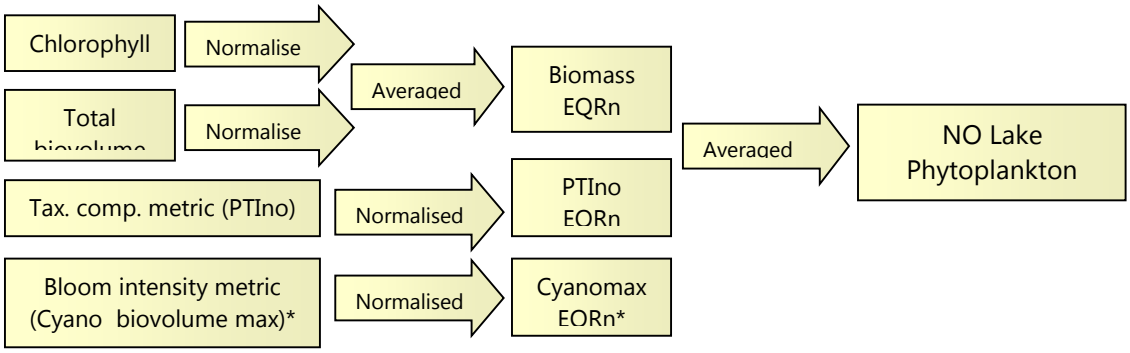

*Figure A.8 Phytoplankton biomass, composition and bloom intensity metrics are normalised and averaged to provide an NO Lake Phytoplankton Index value (as EQRn). * The Cyano-metric is only used if its EQRn is lower than the average of the other metrics.*

Table A.14 NGIG lake types intercalibrated by Norway

Type	Lake Characterisation	Altitude m	Mean depth m	Alkalinity meq l^{-1}	Colour mg l^{-1} PtCo
L-N1	Lowland, shallow, moderate alkalinity, clear	<200	3 - 15	0.2 - 1	< 30
L-N2a	Lowland, shallow, low alkalinity, clear	<200	3 - 15	< 0.2	< 30
L-N2b	Lowland, deep, low alkalinity, clear	<200	3 - 15	< 0.2	< 30
L-N3a	Lowland, shallow, low alkalinity, meso-humic	<200	3 - 15	< 0.2	30 - 90
L-N8a	Lowland, shallow, moderate alkalinity, meso-humic	<200	3 - 15	0.2 - 1	30 - 90
L-N5a	Mid-altitude, shallow, low alkalinity, clear	200-800	3 - 15	< 0.2	< 30

L-N6a	Mid-altitude, shallow, moderate alkalinity, meso-humic	200-800	3 - 15	< 0.2	30 - 90

Metric description: sampling, analyses, principles for setting reference value and boundaries

Chlorophyll a (µg/l)

Integrated samples of euphotic water column are taken from mid-lake stations. Chlorophyll *a* is determined following extraction using spectrophotometric analysis. Sampling frequency is normally 6 times per year (monthly), but ranges from a maximum of 24 times per year to a minimum of 4 times per year between May and October. Spatial replication depends on lake size with more stations on larger lakes. Reference values were decided as ranges at GIG level and are detailed in the Water Framework Directive Intercalibration Technical Report - Part 2: Lakes (Poikane, 2009) and in the Intercalibration decision (EC, 2008). Norway has chosen the lower end of the range of reference values, due to the cold and humid climate in Norway compared to the NGIG average.

The approach to setting chlorophyll *a* boundaries for lakes within the NGIG types was previously outlined on pages 61-63 of Poikane (2009) and also in pages 126-7 of Annex E Part 4 (Poikane, 2009). The chlorophyll *a* EQR is calculated using Equation 1 below where the **$Chla_{ref}$** is the Norwegian chlorophyll reference value in µg/l and the **$Chla_{obs}$** is the observed growing season mean chlorophyll value in µg/l.

Equation 1: $ChlaEQR = Chla_{ref}/Chla_{obs}$

Total biovolume (mg/l)

Norway has chosen to include total biovolume as a second biomass metric for phytoplankton. This metric has a long tradition in the Nordic countries and provides a better basis to compare with the methods used in Sweden and Finland. Moreover, the total biovolume brings little additional work, as it is simply calculated from the sum of the biovolumes for each taxon, which is anyway needed to calculate the taxonomic composition metric (see below). Integrated samples of euphotic water column are taken from mid-lake stations. Sampling frequency is normally 6 times per year (monthly), but ranges from a maximum of 24 times per year to a minimum of 4 times per year between May and October. Spatial replication depends on lake size with more stations on larger lakes. Phytoplankton samples are counted using the Utermöhl technique and total biovolume is calculated from the sum of the biovolumes of each taxon in the sample (cell number x specific cell volume). The reference values and the class boundaries for total biovolume were set from the chla : biovolume regression of the whole NGIG, using the chla boundaries to read off the biovolume boundaries (Figure A.9).

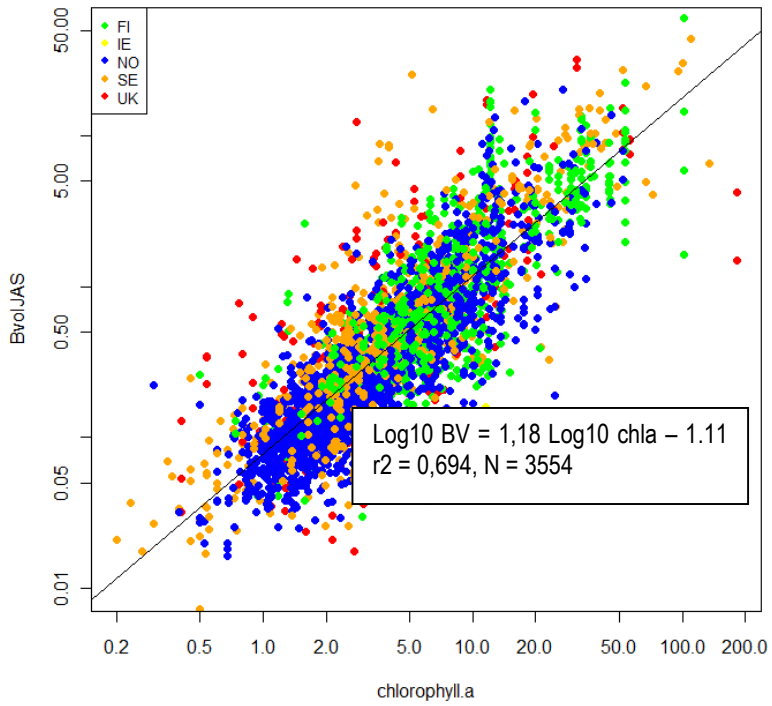

Figure A.9 Biovolume (mg/l) versus chlorophyll a (µg/l) regression for NGIG lakes. Dots are mean values from July-September data for each year. Plot and regression equation made by Geoff Phillips, Environment Agency for England and Wales.

The regression equation is given in Equation 2 below, showing the intercept with 95%iles :

Equation 2 Log BV = 1.18(Log Chla) -1.11(±0.5)

where BV = total biovolume and Chla = chlorophyll a

Phytoplankton composition metric (PTI_{NO})

The phytoplankton composition metric provides an indication of the state of community composition and relative abundance in relation to the eutrophication pressure gradient. Assessment is based on May-October mean values from integrated samples of the euphotic water column taken from mid-lake stations at least monthly (CEN standard). Spatial replication depends on lake size with more stations on larger lakes. Phytoplankton samples are counted following the Utermöhl technique (CEN standard)[2]. Assessment is based on an index called PTI_{no} (Phytoplankton Trophic Index, modified from Ptacnik et al. 2009), which is a weighted average of indicator values for each taxon present in the sample (see equation 3 below). The index values for taxa can range from

[2] Analysts are subject to regular ring tests to ensure that their competence level is maintained

1-5, and the index value for samples can range from 1.5-4.0. See Appendix 1 below for taxa scores (indicator values).

Equation 3:

$$PTI = \frac{\sum_{j=1}^{n} a_j s_j}{\sum_{j=1}^{n} a_j}$$

a_j = proportion of *j*th taxon in the sample

s_j= indicator value of *j*th taxon in the sample (see Appendix 1)

The PTI is well correlated with pressure, measured as Total-P and also clearly distinguish reference lakes from impacted lakes (Figure A.10, extracted from Ptacnik 2009).

Boundary setting for the Norwegian taxonomic composition metric (PTI_{NO}) was done by using a combination of discontinuities of sensitive and tolerant taxa and statistical distribution of reference sites. Identification of sensitive and tolerant taxa was done according to the indicator values of each taxon (see Appendix 1), grouping the taxa into very sensitive, sensitive, tolerant and very tolerant taxa groups. The technique used for this grouping is described in Phillips et al. 2010. The boundaries were also checked against the biovolume of Cyanobacteria to ensure that they were related to discontinuities in the relationship of PTI vs. Cyanobacteria.

Reference value for each type was set from the median-value of the PTI_{NO} for Norwegian sample data from validated reference lakes for each type (see list of validated reference lakes in Appendix 3 in the NGIG final M6 report, Dec.2011). The H/G boundary was set from the 90th %ile of Norwegian sample data from reference lakes for each type. For the humic lake types, the reference value and/or the HG boundary were adjusted 0.1 PTI unit up or down from the median and 90th %ile to allow an equal distance of 0.2 PTI units between the reference value and the HG boundary for all types. These adjustments were also ensuring more stringent values for deep lakes than for shallow lakes, and more stringent values for the low alkalinity clear-water types than for the moderate alkalinity and humic types, in line with general limnological knowledge of differences in phytoplankton species composition in different lake types.

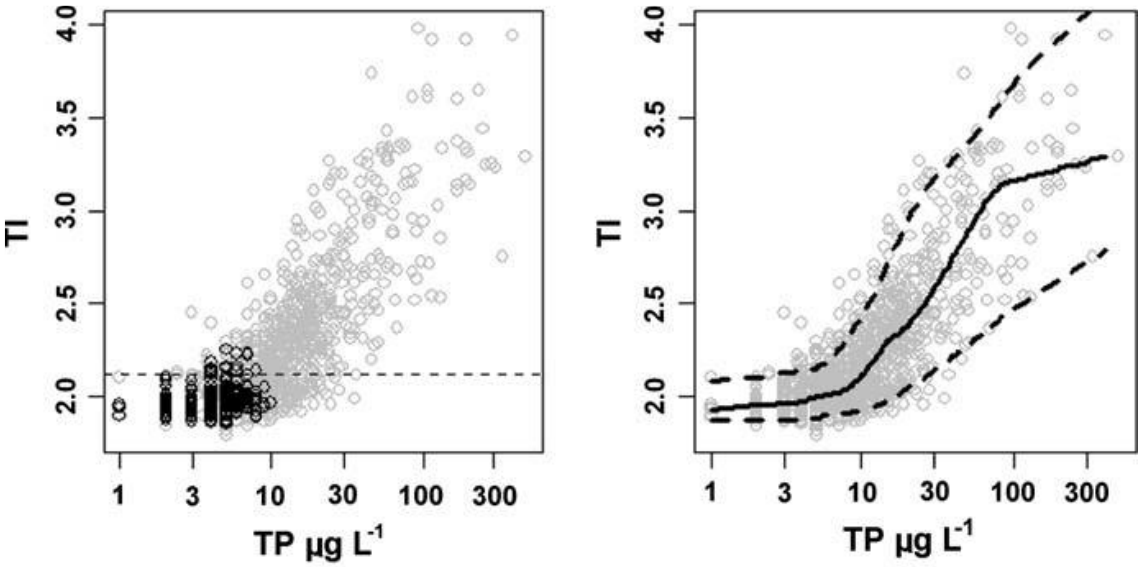

Figure A.10 Trophic index (TI) as a function of total phosphorus (TP). Left: Black dots represent samples from reference lakes, grey dots are impacted lakes. Horizontal dashed line gives the upper 95th percentile of the TI from reference lakes (= 2.11). Right: Same data, with quantile regression, showing the median (bold line) as well as the 5th and 95th percentiles (dashed lines). Note the low variability and steady median seen in TI on the left side of the gradient. From Ptacnik et al. 2009.

The G/M boundary was set from the combination of breakpoints in response curves of very sensitive taxa vs. PTI, very tolerant taxa vs. PTI and Cyano biovolume vs. PTI (see Figure A.11 and Figure A.12 for LN1 and Appendix 2 for the other types). For LN1 lakes, the GM boundary value for PTI separates lakes where the median Cyano biovolume is <0.2 mg/l (WHO vigilance level, see bloom intensity metric description below) from those with where higher biovolumes may occur. The GM boundary value also separates lakes where the median fraction of very sensitive taxa is >30% and the very tolerant taxa is < 10% from those with less sensitive and more tolerant taxa.

The same approach was used for the other lake types. Finally, the GM boundaries were slightly adjusted to obtain an equal distance of 0.2 PTI units from the HG boundary and 0.4 PTI units from the reference value for each type.

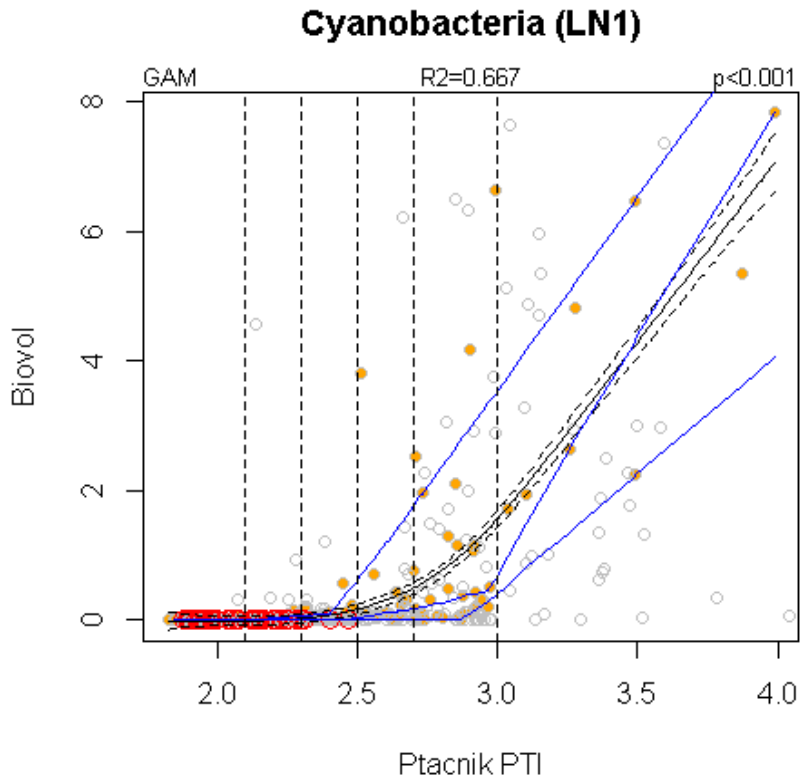

Figure A.11 *PTI_{NO} (Ptacnik et al. 2009) vs. Biovolume of Cyanobacteria as mg/l for the lake type L-N1. The orange dots are Norwegian sample data. The red circles are reference lakes. The black curve with dotted lines is the GAM regression curve with confidence intervals based on the Norwegian sample data, and the blue lines are the quantile regression lines for the 10^{th}, 25^{th}, 50^{th}, 75^{th} and 90^{th} quantiles. The vertical lines are from left to right the reference value, the HG, GM, MP and PB boundaries. Plot and regression analyses made by Geoff Phillips, UK Environment Agency.*

The M/P boundary was set to separate lakes with median Cyano biovolume < 0.5 mg/l from those with higher biovolumes, and also where the proportion of very sensitive taxa is ca. 10% and the very tolerant taxa is ca. 30%. The P/B boundary was set at a value separating lakes where the Cyanobacteria biovolume is sometimes < 1 mg/l from those where the biomass of Cyanobacteria is always > 1mg/l (which is equivalent to the WHO low risk threshold, see bloom intensity metric description below) (Figure A.11). Beyond this value of PTI the relative biomass of very sensitive taxa is close to 0% and the median fraction of very tolerant taxa is > 50% (Figure A.12).

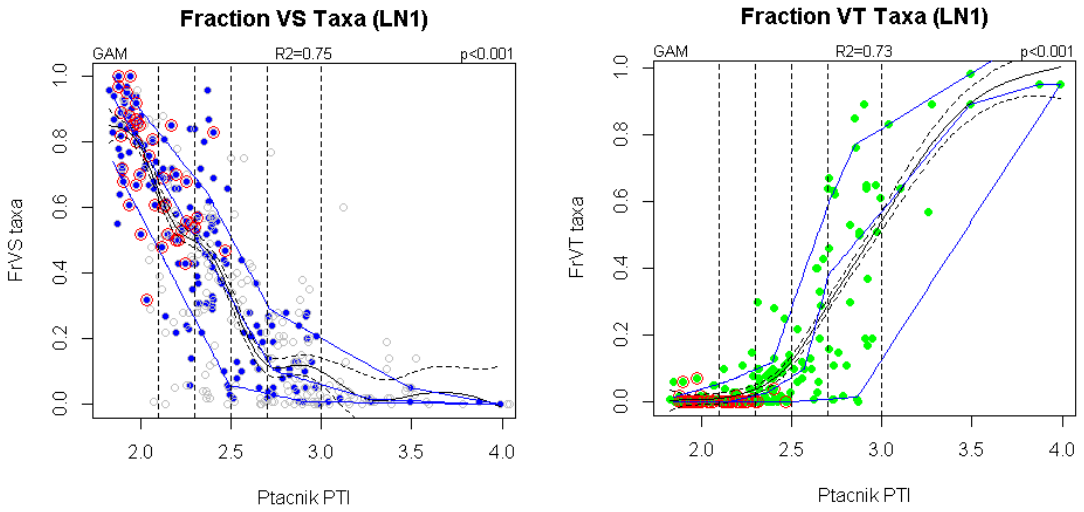

Figure A.12 *PTI_{NO} (Ptacnik et al. 2009) vs. the fraction of very sensitive taxa (left) and very tolerant taxa (right) for the lake type L-N1. The coloured dots are Norwegian sample data. The red circles are reference lakes. The black curve with dotted lines is the GAM regression curve with confidence intervals based on the Norwegian sample data, and the blue lines are the quantile regression lines for the 10^{th}, 25^{th}, 50^{th}, 75^{th} and 90^{th} quantiles. The vertical lines are from left to right in each plot the reference value, the HG, GM, MP and PB boundaries. Plot and regression equation made by Geoff Phillips, UK Environment Agency.*

Bloom intensity: Cyanobacteria maximum biovolume ($Cyano_{max}$) (mg/l)

The WFD Annex V requires that the assessment of lake phytoplankton should include an assessment of the frequency and intensity of algal blooms. It does not define an algal bloom, but a definition emerging from the intercalibration process is that it refers to an elevated biomass of harmful taxa such as Cyanobacteria. Cyanobacteria are associated with enriched conditions in lakes and can produce a high biomass of potentially toxic algae which can restrict the use of a lake. This is a clear case of "undesirable disturbance" as defined by the WFD (European Commission 2009). While bloom frequency is difficult to measure with current sampling techniques used in normal monitoring programmes in lakes, bloom intensity can be assessed by using the maximum biovolume of Cyanobacteria recorded during the late summer period from July-September, when such blooms are most commonly occurring. The Norwegian classification method therefore includes maximum cyanobacterial biomass as a measure of bloom intensity.

Reference value for all types was set from the max-value of Cyanobacteria biovolume (mg/l) for NGIG sample data from validated reference lakes (see list of validated reference lakes in Appendix 3 in the NGIG final M6 report, Dec.2011), and was found to be very close to zero for all types. As this metric is meant to reflect "undesirable disturbance" of phytoplankton communities, the boundary setting protocol was linked to the World Health Organisation's risk levels (WHO 1999). The cyanobacteria metric assesses

"undesirable disturbance" by indicating the risk of cyanobacterial blooms occurring. Thus the different risk levels defined by the World Health Organisation (WHO) were used to set the boundaries. The WHO defines the "vigilance level", as well as low and medium risk thresholds as 4,000, 20,000 and 100,000 cells ml^{-1} respectively (Who 1999). These values were converted to bio-volume thresholds of 0.2, 1 and 5 mm^3 l^{-1} (or mg/l) by multiplication of a typical cell volume (based on a spherical cell such as *Microcystis* with a cell diameter of 4.5µm; Hillebrand *et al.* 1999).

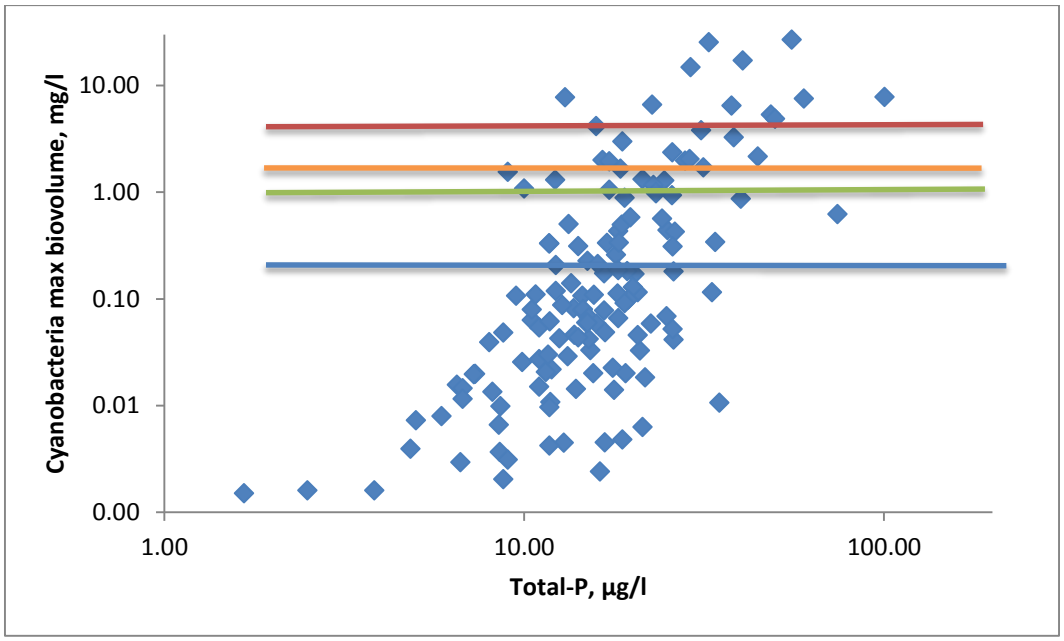

Figure A.13 *Cyanobacteria maximum biovolume in July-September against total P for all NGIG LN1 lakes. The horizontal lines are the boundaries: 0,16 mg/l for HG (blue), 1 mg/l for GM (green), 2 mg/l for MP (orange), and 5 mg/l for PB (red).*

Thus, the HG boundary was set at 0.16 mg/l, which is below the WHO "vigilance" level of 0.2 mg/l, the Good/Moderate boundary at 1 mg/l corresponding to the WHO low risk threshold. The PB boundary was set at twice the GM boundary, so at 2 mg/l, and the BP boundary at 5 mg/l corresponding to the WHO medium risk threshold. The boundaries and the relationship with pressure (as Total-P) are shown in Figure A.13. These boundaries were used for all lake types.

Calculation of EQR and normalised EQR for all metrics.

EQR-calculations for total biovolume, PTI and Cyanobacteria biovolume

With the exception of chlorophyll a, where the EQR was calculated according to the results from the intercalibration phase 1 (Poikane 2009) (see equation 1 above), the other three metrics applied an upper anchor (i.e. a maximum value of each metric, which is rarely exceeded in lakes, according to the NGIG dataset compiled in the WISER EU project, see the final NGIG M6 report) to calculate the EQR value according to equation 4. This method is recommended in the Intercalibration guidance (check this) because it

provides more even class widths, and better precision when converting to normalised (or transformed) EQRs.

Equation 4: $$EQR = \frac{Obs - Max}{Ref - Max}$$

where

Obs = observed metric value

Ref = reference value of metric

Max = maximum value of metric

For PTI the maximum value is set to 4.0 for all lake types, and for Cyanobacteria biovolume the maximum value is set to 10 mg/l for all types.

For total biovolume the maximum value is type-specific and is given in Table A.15 below. Any sample that exceeds the maximum value will become negative and therefore is set by default to EQR = zero.

Table A.15 Maximum values of total biovolume (mg/l) for Norwegian lakes in different NGIG lake types.

Lake type	Maximum total biovolume (mg/l)
LN1	6,0
LN2a	4,0
LN2b	3,6
LN5	3,0
LN3a	6,0
LN6a	3,6
LN8a	7,0

Normalisation of EQR for each metric

In order to allow combination of all metrics to a whole BQE assessment, each metric EQR has to be converted to the normalised scale with equal class widths and standardised class boundaries, where the HG, GM, MP, and PB boundaries are 0.8, 0.6, 0.4, 0.2 respectively (Figure A.14). This is done by piecewise linear transformation according to equation 5 below.

Equation 5: $$EQR_{Norm} = \left[\left(\frac{EQR - LowerBoundary}{ClassWidth}\right) \times 0.2\right] + LowerBoundary_{Norm}$$

EQR_{Norm} = Normalised EQR (in fig. 8: 0.73)

EQR = non-normalised EQR (see eq. 1 for chla and eq. 4 for other metrics) (in Figure A.14: 0.75)

LowerBoundary = lower non-normalised EQR class boundary for the relevant class (in Figure A.14: 0.55)

LowerBoundary$_{Norm}$ = lower normalised EQR class boundary for the relevant class (in Figure A.14: 0.60)

ClassWidth = Class width of non-normalised scale (i.e. upper minus lower non-normalised EQR class boundaries, in Figure A.14: 0.85-0.55)

0.2 = standardised class width of normalised scale (i.e. upper minus lower normalised EQR class boundaries, example in Figure A.14: 0.80-0.60, the same class width of 0.2 applies for all classes)

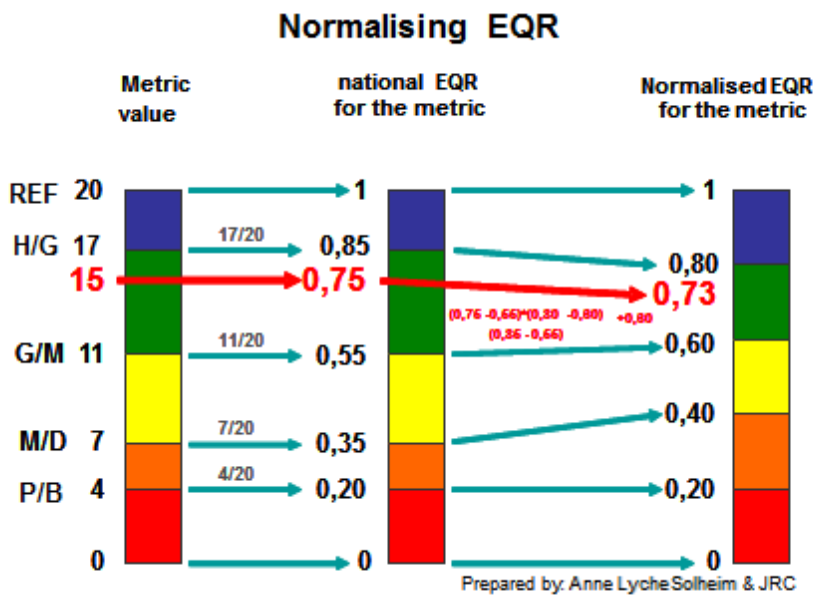

Figure A.14 Conversion of metric values to EQR and to normalised EQR.

Combination of metrics to whole quality element result

The following process is used to combine single metrics to a whole quality element results for lake phytoplankton (to be done for a whole growing season only, not for single samples):

1. Average the normalised EQRs of chlorophyll a and total biovolume (two biomass metrics). This is important to avoid too heavy weight on the biomass metric relative to the other metrics.
2. Average the normalised EQRs for the biomass metrics from point 1 with the normalised EQRs of the PTI and of the Cyanobacteria maximum biovolume (Cyano$_{max}$). If the bloom metric (Cyano$_{max}$) has a higher normalised EQR than the

biomass metrics and the PTI, then the bloom metric should not be used. The rational for this is that a bloom should be used to downgrade a lake to a worse class, but the absence of a bloom should not be used to upgrade a lake to a better class than it would get from the other metrics.

Reference values and class boundaries for each type

Table A.16 gives all the reference values and class boundaries for the Norwegian classification system for each metric both as absolute values and as EQRs (non-normalised). The final whole BQE class boundaries are not very informative, as they are simply the normalised boundaries: 0.8, 0.6, 0.4, 0.2 for the HG, GM, MP, PB boundaries respectively.

The boundaries were intercalibrated with other countries in NGIG against a common metric (see Appendix 3 in the final NGIG M6 report), and boundaries of the single metrics were originally too stringent, causing Norway to be way above the bias band for both the HG and GM boundaries for most types. In the final stage of intercalibration the boundaries of the single metrics were adjusted to bring Norway within the bias band for all types and both boundaries, yet still ensuring that the final adjusted boundaries were still in line with the boundary setting protocol and the normative definitions.

Table A.16 Norwegian reference values and class boundaries for each type and each metric after intercalibration phase 2.

Absolute values (changes from phase 1 to 2 highlighted in blue)								EQR values (non-normalised)				
Type	class	chla (phase 1)	chla (phase 2)	bio-volum	PTI	Cyano max	class	chla (phase 1)	chla (phase 2)	bio-volum	PTI	Cyano max
		µg/L	µg/L	mg/L		mg/L						
LN1	ref	2,5	3,0	0,28	2,10	0,00	ref					
	HG	5,0	6,0	0,64	2,30	0,16	HG	0,50	0,50	0,94	0,89	0,98
	GM	7,5	9,0	1,04	2,50	1,00	GM	0,33	0,33	0,87	0,79	0,90
	MP	15	18	2,35	2,70	2,00	MP	0,17	0,17	0,64	0,68	0,80
	PB	30	36	5,33	3,00	5,00	PB	0,08	0,08	0,12	0,53	0,50
	max value (upper anchor)			6,00	4,00	10,00						
Type	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max
LN2a	ref	1,5	2,0	0,18	2,00	0,00	ref					
	HG	3,0	4,0	0,40	2,20	0,16	HG	0,5	0,50	0,94	0,90	0,98
	GM	5,0	6,0	0,64	2,40	1,00	GM	0,29	0,30	0,88	0,80	0,90
	MP	10	13	1,60	2,60	2,00	MP	0,15	0,15	0,63	0,70	0,80
	PB	20	27	3,79	2,80	5,00	PB	0,08	0,08	0,05	0,60	0,50
	max value (upper anchor)			4,00	4,00	10,00						
Absoluttverdier (endret fra fase 1 til fase 2 markert med blått)								**EQR verdier**				
Type	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max
LN2b	ref	1,3	1,3	0,11	1,90	0,00	ref					
	HG	2,5	2,0	0,18	2,10	0,16	HG	0,50	0,65	0,98	0,90	0,98
	GM	4,0	4,0	0,40	2,30	1,00	GM	0,33	0,33	0,92	0,81	0,90
	MP	7,0	7,0	0,77	2,50	2,00	MP	0,19	0,19	0,81	0,71	0,80
	PB	15	15	1,90	2,70	5,00	PB	0,09	0,09	0,49	0,62	0,50
	max value (upper anchor)			3,60	4,00	10,00						
Type	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max
LN5	ref	1,0	1,3	0,11	1,80	0,00	ref					
	HG	2,0	2,0	0,18	2,00	0,16	HG	0,5	0,65	0,98	0,91	0,98
	GM	3,0	4,0	0,40	2,20	1,00	GM	0,33	0,33	0,90	0,82	0,90
	MP	7,0	7,0	0,77	2,40	2,00	MP	0,14	0,19	0,77	0,73	0,80
	PB	15	15	1,90	2,60	5,00	PB	0,07	0,09	0,38	0,64	0,50
	max value (upper anchor)			3,00	4,00	10,00						
Absoluttverdier (endret fra fase 1 til fase 2 markert med blått)								**EQR verdier**				
Type	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max
LN3a	ref	2,5	**2,7**	0,30	2,10	0,00	ref					
	HG	5,0	**5,4**	0,60	2,30	0,16	HG	0,50	0,50	0,95	0,89	0,98
	GM	7,5	**9,0**	1,00	2,50	1,00	GM	0,30	0,30	0,88	0,79	0,90
	MP	15	**16**	2,00	2,70	2,00	MP	0,17	0,17	0,70	0,68	0,80
	PB	30	**32**	4,60	3,00	5,00	PB	0,08	0,08	0,25	0,53	0,50
	max value (upper anchor)			6,00	4,00	10,00						
Type	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max
LN6a	ref	2,0	2,0	0,18	2,00	0,00	ref					
	HG	4,0	4,0	0,40	2,20	0,16	HG	0,50	0,50	0,93	0,90	0,98
	GM	6,0	6,0	0,64	2,40	1,00	GM	0,33	0,33	0,86	0,80	0,90
	MP	12	12	1,46	2,60	2,00	MP	0,17	0,17	0,63	0,70	0,80
	PB	25	25	3,46	2,80	5,00	PB	0,08	0,08	0,04	0,60	0,50
	max value (upper anchor)			3,60	4,00	10,00						
Type	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max	Klasse	chla (fase 1)	chla (fase 2)	bio-volum	PTI	Cyano max
LN8a	ref	3,5	3,5	0,34	2,25	0,00	ref					
	HG	7,0	7,0	0,77	2,45	0,16	HG	0,50	0,50	0,94	0,89	0,98
	GM	10,5	10,5	1,24	2,65	1,00	GM	0,33	0,33	0,86	0,77	0,90
	MP	20	20	2,66	2,85	2,00	MP	0,18	0,18	0,65	0,66	0,80
	PB	40	40	6,03	3,25	5,00	PB	0,09	0,09	0,15	0,43	0,50
	max value (upper anchor)			7,00	4,00	10,00						

Correlation of Norwegian combined whole BQE phytoplankton method against pressure (total-P)

The Norwegian combined whole BQE phytoplankton method is well correlated with pressure (Total-P) for all NGIG lake types (see main NGIG final M6 report appendix 7). The r^2 vary from 0.4 to 0.7 with best correlation for the moderate alkalinity lake types LN1 and LN8a, where the pressure gradient is longest, and least good for LN6a (mid-altitude, low alkalinity, humic).

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Appendix 1 Indicator values of single phytoplankton taxa. From supplementary data for Ptacnik 2009.

Ln-transformed total phosphorus concentrations (TP µg L^{-1}) were used as a proxy for eutrophication in order to estimate taxa optima relative to eutrophication. For each taxon, a trophic optimum was calculated by weighted averaging of TP concentrations from all sites where this taxon occurred (N obs), using the taxon's square-root transformed proportional biomass as weight. We calculated optima both at the species and at the genus level. In the latter case, species were aggregated at the genus level. The optimum given as Ln(TP) is the indicator value for each taxon that are used in the PTI formula.

RebeccaID	Taxon	Optima, as Ln(TP)	Optima as TP, µg/l	Records
R0016	Acanthoceras zachariasii	2.699	14.9	22
R0117	Achnanthes	1.84	6.3	143
R1574	Achroonema	3.5	33.1	93
R0471	Actinastrum hantzschii	4.986	146.3	10
R1667	Amphidinium	2.174	8.8	11

RebeccaID	Taxon	Optima, as Ln(TP)	Optima as TP, µg/l	Records
R1548	Anabaena	3.273	26.4	13
R1531	Anabaena circinalis	3.268	26.3	59
R1536	Anabaena flos-aquae	2.962	19.3	335
R1539	Anabaena lemmermannii	3.345	28.4	51
R1544	Anabaena planctonica	3.276	26.5	183
R1549	Anabaena spiroides	4.461	86.6	61
R0477	Ankistrodesmus bibraianus	4.137	62.6	11
R0480	Ankistrodesmus falcatus	3.301	27.1	117
R0486	Ankistrodesmus spiroides	2.361	10.6	11
R0489	Ankyra judayi	3.417	30.5	51
R0490	Ankyra lanceolata	2.401	11.0	365
R1558	Aphanizomenon flos-aquae	3.537	34.4	75
R1560	Aphanizomenon gracile	2.942	19.0	28
R1414	Aphanocapsa elachista	4.007	55.0	12
R1420	Aphanocapsa reinboldii	3.656	38.7	26
R1432	Aphanothece	3.271	26.3	49
R1427	Aphanothece clathrata	3.99	54.1	11
R0135	Asterionella formosa	2.399	11.0	814
R0019	Aulacoseira alpigena	2.06	7.8	497
R0020	Aulacoseira ambigua	3.159	23.5	82
R0021	Aulacoseira distans	1.911	6.8	30
R0023	Aulacoseira granulata	4.515	91.4	17
R0028	Aulacoseira italica	3.328	27.9	218
R0033	Aulacoseira subarctica	1.946	7.0	57
R1351	Aulomonas purdyi	2.27	9.7	107
R0464	Bicosoeca	2.167	8.7	58
R0462	Bicosoeca planctonica	2.064	7.9	27
R1155	Bitrichia chodatii	1.759	5.8	814
R1159	Bitrichia ollula	1.567	4.8	11
R0493	Botryococcus braunii	2.072	7.9	360
R0923	Carteria	2.19	8.9	267
R1671	Ceratium furcoides	3.706	40.7	40
R1672	Ceratium hirundinella	2.401	11.0	340
R1367	Chilomonas	3.188	24.2	12
R0941	Chlamydomonas	2.36	10.6	841
R1008	Chromulina	1.89	6.6	1360
R1007	Chromulina nebulosa	3.613	37.1	59
R1443	Chroococcus minutus	2.801	16.5	83

RebeccaID	Taxon	Optima, as Ln(TP)	Optima as TP, µg/l	Records
R1375	Chroomonas	2.118	8.3	1636
R1163	Chrysidiastrum catenatum	2.196	9.0	67
R1818	Chrysochromulina parva	2.149	8.6	901
R1019	Chrysococcus	2.01	7.5	32
R1011	Chrysococcus cordiformis	2.136	8.5	93
R1012	Chrysococcus furcata	1.168	3.2	13
R1015	Chrysococcus minutus	2.011	7.5	23
R1018	Chrysococcus rufescens	2.031	7.6	33
R1166	Chrysolykos planctonicus	1.806	6.1	167
R1167	Chrysolykos skujae	1.555	4.7	841
R1171	Chrysophyceae	1.924	6.8	4577
R1062	Chrysosphaerella longispina	2.575	13.1	11
R1201	Closterium	2.81	16.6	40
R1178	Closterium acutum	2.919	18.5	158
R1191	Closterium limneticum	3.995	54.3	45
R0523	Coelastrum astroideum	3.694	40.2	43
R0527	Coelastrum microporum	3.247	25.7	68
R0530	Coelastrum reticulatum	3.16	23.6	24
R0532	Coelastrum sphaericum	4.195	66.4	24
R0533	Coenochloris fottii	2.716	15.1	41
R1233	Cosmarium	2.452	11.6	93
R1209	Cosmarium depressum	2.439	11.5	102
R1214	Cosmarium granatum	3.438	31.1	11
R1217	Cosmarium margaritiferum	2.525	12.5	11
R1221	Cosmarium phaseolus	3.067	21.5	11
R1225	Cosmarium pygmaeum	2.665	14.4	45
R2084	Cosmarium sphagnicolum	2.024	7.6	84
R1235	Cosmarium subcostatum	3.214	24.9	31
R0546	Crucigenia quadrata	2.223	9.2	112
R0550	Crucigenia tetrapedia	2.167	8.7	176
R0552	Crucigeniella apiculata	2.8095	16.6	28
R0555	Crucigeniella rectangularis	2.079	8.0	81
R1803	Cryptaulax vulgaris	1.761	5.8	162
R1394	Cryptomonas	2.364	10.6	1815
R1377	Cryptomonas curvata	3.0925	22.0	872
R1378	Cryptomonas erosa	2.911	18.4	593
R1382	Cryptomonas marssonii	2.206	9.1	1293

RebeccaID	Taxon	Optima, as Ln(TP)	Optima as TP, µg/l	Records
R1387	Cryptomonas parapyrenoidifera	3.315	27.5	66
R1389	Cryptomonas pyrenoidifera	3.894	49.1	12
R0053	Cyclotella	1.899	6.7	570
R0042	Cyclotella comensis	2.279	9.8	34
R0045	Cyclotella iris	1.614	5.0	11
R0047	Cyclotella meneghiniana	1.792	6.0	36
R0051	Cyclotella radiosa	1.878	6.5	420
R0052	Cyclotella rossii	2.549	12.8	100
R2572	Cylindrotheca gracilis	3.633	37.8	41
R0189	Diatoma tenuis	2.673	14.5	194
R0571	Dictyosphaerium pulchellum	3.088	21.9	146
R0575	Dictyosphaerium subsolitarium	1.852	6.4	316
R1086	Dinobryon	1.847	6.3	692
R1066	Dinobryon bavaricum	2.277	9.7	343
R1068	Dinobryon borgei	1.751	5.8	691
R1069	Dinobryon crenulatum	1.663	5.3	888
R1070	Dinobryon cylindricum	1.669	5.3	314
R1073	Dinobryon divergens	2.226	9.3	329
R1076	Dinobryon korshikovii	1.753	5.8	96
R1081	Dinobryon sertularia	2.569	13.1	51
R1083	Dinobryon sociale	1.819	6.2	517
R1089	Dinobryon suecicum	1.779	5.9	326
R2058	Discostella glomerata	1.725	5.6	465
R0598	Elakatothrix	1.921	6.8	804
R0599	Elakatothrix viridis	2.79	16.3	90
R1092	Epipyxis polymorpha	2.016	7.5	60
R1262	Euastrum	2.048	7.8	29
R0963	Eudorina elegans	2.553	12.8	79
R1726	Euglena	3.799	44.7	60
R1714	Euglena acus	3.433	31.0	14
R1721	Euglena oxyuris	3.964	52.7	14
R0204	Eunotia bilunaris	1.995	7.4	25
R0214	Eunotia zasuminensis	2.781	16.1	49
R0238	Fragilaria	2.54	12.7	974

RebeccaID	Taxon	Optima, as Ln(TP)	Optima as TP, µg/l	Records
R2520	Fragilaria capucina ssp. rumpens	3.196	24.4	58
R0223	Fragilaria crotonensis	3.21	24.8	204
R0231	Fragilaria nanana	2.981	19.7	17
R0611	Franceia ovalis	3.574	35.7	10
R0891	Gloeocystis	1.96	7.1	120
R1403	Goniomonas truncata	2.808	16.6	112
R0967	Gonium sociale	3.2	24.5	22
R1824	Gonyostomum semen	2.954	19.2	77
R1654	Gymnodinium	1.86	6.4	715
R1643	Gymnodinium albulum	1.651	5.2	55
R1646	Gymnodinium fuscum	2.044	7.7	30
R1647	Gymnodinium helveticum	1.91	6.8	369
R1649	Gymnodinium lacustre	1.817	6.2	1331
R1660	Gymnodinium uberrimum	1.902	6.7	476
R1792	Gyromitus cordiformis	2.058	7.8	452
R0280	Hannaea arcus	1.77	5.9	31
R1055	Hydrurus foetidus	1.922	6.8	18
R1860	Isthmochloron trispinatum	1.574	4.8	57
R1404	Katablepharis ovalis	2.05	7.8	1966
R1037	Kephyrion	1.618	5.0	51
R1021	Kephyrion boreale	1.701	5.5	259
R1029	Kephyrion littorale	1.329	3.8	108
R0633	Kirchneriella	2.859	17.4	14
R0631	Kirchneriella obesa	4.409	82.2	11
R0637	Koliella	2.14	8.5	401
R0635	Koliella longiseta	3.024	20.6	28
R0649	Lagerheimia genevensis	2.997	20.0	26
R1109	Mallomonas	2.125	8.4	615
R1097	Mallomonas akrokomos	2.113	8.3	608
R1099	Mallomonas allorgei	2.401	11.0	88
R1100	Mallomonas caudata	2.349	10.5	311
R1101	Mallomonas crassisquama	2.178	8.8	223
R1108	Mallomonas punctifera	2.411	11.1	67
R1111	Mallomonas tonsurata	3.014	20.4	14
R0062	Melosira varians	3.272	26.4	10
R1479	Merismopedia tenuissima	1.759	5.8	388
R0660	Micractinium pusillum	3.389	29.6	66
R1482	Microcystis aeruginosa	4.04	56.8	125

RebeccaID	Taxon	Optima, as Ln(TP)	Optima as TP, µg/l	Records
R1499	Microcystis wesenbergii	3.46	31.8	32
R1116	Monochrysis agilissima	1.814	6.1	22
R0663	Monoraphidium arcuatum	2.34	10.4	64
R0665	Monoraphidium contortum	2.534	12.6	366
R0667	Monoraphidium dybowskii	1.974	7.2	874
R0670	Monoraphidium griffithii	1.645	5.2	473
R0673	Monoraphidium komarkovae	1.85	6.4	257
R0675	Monoraphidium minutum	3.643	38.2	101
R0677	Monoraphidium nanum	3.692	40.1	13
R0683	Monoraphidium tortile	4.094	60.0	18
R1003	Mougeotia	1.888	6.6	24
R0335	Navicula	2.862	17.5	15
R0690	Nephrocytium agardhianum	2.24	9.4	22
R0692	Nephrocytium lunatum	2.458	11.7	20
R0394	Nitzschia	3.917	50.2	66
R1120	Ochromonas	1.893	6.6	2284
R0697	Oocystis lacustris	3.013	20.3	78
R0698	Oocystis marssonii	2.731	15.3	91
R0701	Oocystis parva	3.176	24.0	84
R0703	Oocystis rhomboidea	2.251	9.5	22
R0704	Oocystis solitaria	3.016	20.4	17
R0706	Oocystis submarina	1.726	5.6	1005
R0971	Pandorina morum	3.169	23.8	120
R1806	Paramastix conifera	1.927	6.9	225
R0906	Paulschulzia pseudovolvox	2.6	13.5	112
R0908	Paulschulzia tenera	2.918	18.5	11
R0713	Pediastrum boryanum	3.734	41.8	129
R0716	Pediastrum duplex	3.951	52.0	92
R0721	Pediastrum privum	3.027	20.6	26
R0725	Pediastrum tetras	3.107	22.4	67
R2116	Peridiniopsis cunningtonii	3.658	38.8	16
R1678	Peridiniopsis edax	4.046	57.2	60
R1679	Peridiniopsis elpatiewskyi	3.488	32.7	58
R1680	Peridiniopsis penardiforme	2.389	10.9	34
R1682	Peridiniopsis polonicum	2.795	16.4	21
R1699	Peridinium	2.09	8.1	266

RebeccaID	Taxon	Optima, as Ln(TP)	Optima as TP, µg/l	Records
R1684	Peridinium aciculiferum	2.971	19.5	12
R1687	Peridinium cinctum	2.546	12.8	50
R1691	Peridinium inconspicuum	1.887	6.6	974
R1698	Peridinium raciborskii	2.277	9.7	106
R2131	Peridinium umbonatum var. goslaviense	2.524	12.5	66
R1704	Peridinium willei	2.276	9.7	143
R0975	Phacotus lenticularis	2.826	16.9	11
R1748	Phacus	3.689	40.0	11
R2617	Picoplankton	1.911	6.8	2295
R2711	Plagioselmis	2.094	8.1	1921
R1609	Planktolyngbya contorta	3.797	44.6	18
R1613	Planktothrix agardhii	3.653	38.6	162
R2594	Planktothrix compressa	2.376	10.8	49
R1621	Pseudanabaena limnetica	3.719	41.2	27
R2134	Pseudogoniochloris tripus	4.464	86.8	11
R1051	Pseudokephyrion	1.624	5.1	66
R1044	Pseudokephyrion alaskanum	1.633	5.1	127
R1046	Pseudokephyrion attenatum	1.692	5.4	15
R1047	Pseudokephyrion entzii	1.598	4.9	792
R1052	Pseudokephyrion taeniatum	1.718	5.6	83
R1053	Pseudokephyrion tatricum	1.985	7.3	11
R1154	Pseudopedinella	1.869	6.5	166
R0742	Quadrigula korshikovii	2.07	7.9	11
R0744	Quadrigula pfitzeri	2.107	8.2	138
R0750	Raphidocelis subcapitata	2.527	12.5	125
R0811	Scenedesmus	3.119	22.6	294
R0754	Scenedesmus acuminatus	3.597	36.5	29
R2442	Scenedesmus arcuatus	2.997	20.0	40
R0762	Scenedesmus armatus	3.728	41.6	141
R0763	Scenedesmus bicaudatus	3.639	38.1	22
R0775	Scenedesmus denticulatus	2.564	13.0	127
R0777	Scenedesmus dimorphus	3.455	31.7	11
R0781	Scenedesmus ecornis	3.033	20.8	155
R0799	Scenedesmus opoliensis	3.929	50.9	55
R0806	Scenedesmus quadricauda	3.667	39.1	136

RebeccaID	Taxon	Optima, as Ln(TP)	Optima as TP, µg/l	Records
R0813	Scenedesmus spinosus	3.451	31.5	41
R0820	Schroederia setigera	2.964	19.4	28
R0987	Scourfieldia cordiformis	1.826	6.2	257
R1510	Snowella lacustris	2.374	10.7	299
R1814	Spermatozopsis exsultans	3.721	41.3	12
R0993	Sphaerocystis schroeteri	2.38	10.8	362
R1130	Spiniferomonas bourrellyi	1.697	5.5	472
R1273	Spondylosium planum	2.06	7.8	66
R1309	Staurastrum	2.717	15.1	23
R1275	Staurastrum anatinum	2.051	7.8	11
R1282	Staurastrum chaetoceras	3.745	42.3	50
R1283	Staurastrum cingulum	2.002	7.4	12
R1288	Staurastrum gracile	2.278	9.8	112
R1293	Staurastrum luetkemuelleri	2.361	10.6	16
R1295	Staurastrum lunatum	2.413	11.2	37
R1300	Staurastrum paradoxum	3.039	20.9	219
R1304	Staurastrum planctonicum	2.757	15.8	90
R1305	Staurastrum pseudopelagicum	2.337	10.4	36
R1315	Staurodesmus cuspidatus	2.146	8.6	55
R1321	Staurodesmus indentatus	1.796	6.0	109
R1324	Staurodesmus mamillatus	2.505	12.2	25
R1330	Staurodesmus triangularis	1.934	6.9	44
R2516	Staurosira berolinensis	4.69	108.9	15
R1364	Stelexomonas dichotoma	2.123	8.4	69
R0079	Stephanodiscus hantzschii	3.541	34.5	261
R1057	Stichogloea doederleinii	1.847	6.3	187
R1138	Syncrypta	2.661	14.3	15
R1144	Synura splendida	2.378	10.8	13
R1145	Synura uvella	2.566	13.0	251
R0440	Tabellaria fenestrata	2.388	10.9	418
R0442	Tabellaria flocculosa	2.141	8.5	411
R1333	Teilingia granulata	2.416	11.2	29
R1855	Tetraëdriella patiens	1.45	4.3	18
R0843	Tetraedron caudatum	3.113	22.5	72
R0848	Tetraedron minimum	2.228	9.3	392
R2038	Tetraselmis	1.769	5.9	42
R0871	Tetrastrum staurogeniaeforme	3.478	32.4	19

RebeccaID	Taxon	Optima, as Ln(TP)	Optima as TP, µg/l	Records
R0874	Thelesphaera alpina	2.302	10.0	54
R1765	Trachelomonas hispida	4.767	117.6	14
R1776	Trachelomonas volvocina	3.596	36.5	99
R0880	Treubaria triappendiculata	3.847	46.9	28
R2179	Trichormus catenula	3.325	27.8	42
R1634	Tychonema bornetii	2.478	11.9	13
R2175	Ulnaria ulna	2.769	15.9	286
R1147	Uroglena americana	2.259	9.6	367
R2548	Urosolenia eriensis	1.985	7.3	126
R2549	Urosolenia longiseta	1.992	7.3	306
R1521	Woronichinia compacta	2.68	14.6	18
R1525	Woronichinia naegeliana	2.827	16.9	194
R1345	Xanthidium antilopaeum	2.166	8.7	11

A.4 Sweden

Introduction

Changes in the water's nutrient status are rapidly reflected in biomass and species composition of phytoplankton. Phytoplankton are therefore used as an indicator in order e.g. to monitor the recovery process after a nutrient reduction, to monitor an acidification process or as an early sign of increasing nutrient load. Phytoplankton respond rapidly to environmental changes and are a good "early warning signal" (Table A.17).

Table A.17 Metrics included in the Swedish phytoplankton assessment system

Parameter	Shows primarily effects of	How often do measurements need to be taken?	At what time of the year?
Total biomass	Nutrient impact	Once a year, but 3-year mean value	July-August
TPI (trophic plankton index)	Nutrient impact	Once a year, but 3-year mean value	July-August
Proportion of cyanobacteria	Nutrient impact	Once a year, but 3-year mean value	July-August
Number of species	Acidity	Once a year, but 3-year mean value	July-August
Chlorophyll	Nutrient impact	Once a year, but 3-year mean value	July-August

Phytoplankton communities have a marked dynamic in their population development, in which weather and wind have overall importance. Despite this, the proportion of

cyanobacteria is a good indicator of increasing nutrient levels. Certain individual species of other phytoplankton groups that can develop in nutrient-poor water are an exception. These species normally do not have gas vacuoles and hence do not rise to the surface. For example the clear link between the relative cyanobacterial biomass and increasing nutrients levels does not apply in lakes with the raphidophycean flagellate *Gonyostomum semen*. Lakes containing a lot of *Gonyostomum* are found mainly in southern Sweden and are of a humic nature. The *Gonyostomum* share of the total biomass in a lake must be at least 5% for it to be regarded as dominant.

Chlorophyll measurements are a comparatively quick and simple method to obtain an overview of the total phytoplankton biomass in a water body, but since the amount of chlorophyll a varies between different plankton groups, this method can be used only as an indication of the current situation. The method is applicable for screening, and to give indications of possible changes in the phytoplankton biomass in a water body. Where there are doubts, a complete phytoplankton analysis should always be carried out to verify results. Moreover, in certain situations a chlorophyll analysis does not give the whole truth about the current situation in a water body. For example, in mountain lakes where the water is clear, a relatively large proportion of the primary production is produced on the lake bottoms by benthic organisms like periphytic algae or higher vegetation. In such cases, reliance exclusively on chlorophyll a, or phytoplankton data, can lead to the false conclusion that the biomass of primary producers is less than is actually the case. Even in humic lakes, it is possible to be misled into the belief that the phytoplankton biomass is less than is the case if one relies solely on chlorophyll analyses. That is because in these systems phytoplankton biomass can in varying degrees consist of heterotrophic and/or mixotrophic plankton organisms, which can be poorly pigmented since these in varying degrees live on dead organic material.

Input parameters

For classification of phytoplankton as a quality factor in a trophic gradient, the following parameters must be used:

- **Total biomass of phytoplankton.** Total biomass can be expressed both as a volume unit or as a mass in which phytoplankton are assumed to have the same density as water i.e. 1 g cm^{-3}. Total biomass can then be expressed as mg l^{-1} or µg l^{-1} and if the concept of 'total volume' is used, the corresponding units are mm3 l^{-1}. The term 'total biomass' is used in these assessment criteria.
- **Proportion of cyanobacteria** (blue-green algae). I.e. the cyanobacterial biomass as a percentage of the total biomass.
- **Trophic plankton index** (TPI) based on indicator species on a scale from – 3 to 3.
- **Chlorophyll** (primarily as a screening method in the absence of phytoplankton analysis). The biomass of planktonic algae can be gauged in a general way by analysing the algae's chlorophyll *a* content. However, this analysis gives no detailed information about structures in the phytoplankton community.

Requirements for supporting data

If the assessment criteria for phytoplankton in lakes are to be applicable, the tests must be taken during the period July-August and the analysis must be conducted in accordance with standard SS-EN 15204:2006 or by another method that gives an equally good result. At least three years' data must be used for the classification. The sample should preferably represent the upper layer of the water above the ther¬mocline (epilimnion). It is also possible to use the top metre(s) of this layer, particu¬larly in humic lakes since parts of the supporting material has been derived from these levels. Since the plankton in humic water seek the surface, at least during daylight hours, the majority of organisms are to be found in the upper metres of these lakes. In clear lakes, on the other hand, the greatest biomass can be found a little way down in the water mass, because the plankton organisms can be damaged by excessive light radiation at the surface. To obtain the best possible comparison, it is therefore best if the sample represents approximately 75% of the epilimnion. The sample is analysed and the taxa counted in accordance with the Utermöhl method (Utermöhl 1958), preferably using the technical procedure described in the Swedish EPA's survey type 'Phytoplankton in lakes'. It is particularly important to use this method of analysis when classifying the number of species. In cases where only the most frequently occurring taxa have been counted, expert assessments may be made based on the index values, such as the total biomass and the proportion of cyanobac¬teria, even though that does not give the same precision as using a more detailed analytical method. As regards the use of the trophic plankton index for samples counting a limited number of species, a number of such tests from a survey of 1000 or so lakes in 1972 corresponded well with results from the material which consti¬tuted the basis for the construction of the TPI index. It is, however, important not to limit the count to only 4-5 taxa if there is no mass development, but to count at least 20 or more taxa, with exception made for lakes in the mountain region which are much more species-poor.

If fewer than four species with an indicator number have been found in a lake, the TPI cannot be calculated and the classification of nutrient conditions must be based solely on total biomass and the proportion of cyanobacte¬ria. Where there is a lack of supporting data even to make a classification of total biomass and proportion of cyanobacteria, a classification based solely on chlorophyll may be made. As regards chlorophyll, the Swedish standard methods that apply for tests and analysis are SS 02 81 46 and 02 81 70 or equivalent methods.

Typology

For the classification of phytoplankton, lakes in Sweden are divided into five types with different reference values (Table A.18). For the trophic plankton index, no distinction is made between clear and humic lakes in Norrland (northern Sweden). The types are based on the ecoregions given in the Swedish EPA's Regu¬lations on Typology and Analysis (NFS 2006:1), and the humus content of the lakes (water colour). Under the regulations, the lakes are divided into low humus content (h) and high humus content (H) with a boundary of 50 mg Pt/l. For the classification of phytoplankton, however, the boundary

has instead been set at 30 mg Pt/l, which corresponds with that used for intercalibration of classifications among the Nordic countries. In the regulations, there is also a more precise division into limnic types but the other factors for allocation have not been shown to affect the classification of phytoplankton with the supporting data currently available.

All the lakes which match one of the lake types established are given the same reference value for classification of phytoplankton.

Table A.18 Typology of lakes for classification of phytoplankton. Ecoregions and humus class in accordance with the Swedish EPA's Regulations on Typology and Analysis (NFS:2006:1) are also shown.

Lake classifications for phytoplankton	Ecoregion in accordance with NFS 2006:1	Humus class in accordance with NFS 2006:1
Mountains above the tree-line	1	h, H
Norrland clear lakes[1]	2, 3	h[3]
Norrland humic lakes[2]	2, 3	H[3]
Southern Sweden clear lakes	4, 5, 6	h
Southern Sweden humic lakes	4, 5, 6	H

[1]Water colour ≤30mg Pt/l or Abs420/5 ≤0,06 (filtered sample)

[2]Water colour >30mg Pt/l or Abs420/5 >0,06 (filtered sample)

[3]When classifying in accordance with TPI, no distinction is made between clear and humic lakes in Norrland

One type of humic lakes that have high and deviant biomasses (total biomass or chlorophyll) is those dominated by *Gonyostomum semen*. This is revealed only by analysis of the species composition of the phytoplankton community. Here, TPI in combination with proportion of cyanobacteria are the suitable indicators to use unless the lake is acidic, in which case it is instead the number of species that gives the status.

Description of metrics

Total biomass

For samples taken and analysed in accordance with the description above, the total biomass is determined. A mean value of at least three years' data must be used for the classification. The ecological quality ratio (EQR) for biomass is calculated as follows:

EQR = reference value/observed total biomass (mean value)

Reference values and class boundaries are given in SEPA 2010.

Proportion of cyanobacteria

Proportion of cyanobacteria (blue-green algae) shall also be used as an indicator of increasing nutrient levels. The biomass of cyanobacteria is determined and divided by the total phytoplankton biomass in order to ascertain the cyanobacterial proportion. A

mean value of at least three years' data must be used for the classification. The ecological quality ratio (EQR) for cyanobacterial abundance is calculated as follows:

EQR = (100 – observed % cyanobacteria) / (100 – reference value)

Reference values and class boundaries are given in SEPA 2010.

Comments

If one or more of the cyanobacterial taxa shown in Table A.19 dominate, it may be a reason for particular attention as they can often give rise to nuisance or even be potentially toxic.

Table A.19 Cyanobacterial taxa that are often associated with bad water quality as they often massdevelop or can form toxins. When developing en masse, all species can give off a bad odour or make the water taste like raw sewage.

Taxon	Comment
Anabaena	Produces nerve and liver poisons, as well as substances giving rise to bad odour and taste. Toxicity has been verified in samples from Sweden.
Aphanizomenon	Potentially toxic, not verified in Sweden with the species in cultivation, but present in cyanobacteria communities where toxicity has been registered.
Gloeotrichia	The species *echinulata*. Toxin production not verified in Sweden
Limnothrix	Potentially toxic, not verified in Sweden with the species in cultivation, but present in cyanobacteria communities where toxicity has been registered.
Microcystis	Producer of nerve and liver poisons, verified in Sweden. The species *wesenbergii* does not have the genes for toxin production.
Planktothrix	Primarily the species *agardhii* and *prolifica* both producers of liver poisons, verified in Sweden.
Pseudanabaena	Potentially toxic, not verified in Sweden with the species in cultivation.
Woronichinia	Primarily the species *naegeliana*. Gives rise to smell and taste in mass-development.

Trophic plankton index

The trophic plankton index (TPI) is calculated as follows:

TPI lake = $\sum (I_{species\ i} \times B_{species\ i}) / \sum B_{species\ i}$, where

B = biomass per litre for species i

n = the number of species with indicator number in a lake

I = the indicator number for species i

Reference values and class boundaries are given in SEPA 2010.

Chlorophyll

In cases where there is no available data to enable a classification to be made with the parameters stated described above, the water authority will have to make a classification by using chlorophyll alone. The biomass of planktonic algae can be gauged in a general way by analysing the algae's chlorophyll a content. However, this analysis gives no detailed information about the phytoplankton community structure.

The chlorophyll content is determined according to the standard method and the EQR is calculated as follows:

EQR = reference value / observed chlorophyll content

Reference values and class boundaries are given in SEPA 2010.

If a lake is assigned the status 'moderate' or worse, either a supplementary phyto-plankton analysis must be carried out, especially if no other quality factors show a similar classification status, or an expert assessment has to be made. This applies particularly in humic lakes (AbsF420/5 >0.06 or water colour >30 mg Pt l-1) in which the phytoplankton biomass can in certain cases be dominated by the flagellate Gonyostomum semen.

Comments

When evaluating chlorophyll data, it is important to keep in mind that the chloro-phyll content gives only an estimate of the phytoplankton biomass and it cannot completely substitute phytoplankton analyses. These analysis methods are not completely comparable both because of uncertainties in the chlorophyll measure-ments and because different phytoplankton species contain varying quantities of chlorophyll a, and in many cases are also supplemented by other chlorophylls or other pigments. Since chlorophyll analyses are comparatively quick and cheap, they can be a good complement in, for example, screening studies or long-term monitor¬ing. Any changes or divergent contents should nevertheless always be followed up by a supplementary and verifying phytoplankton analysis to investigate the cause of the change or divergence.

In comparisons between classifications as regards chlorophyll a and total phyto¬plankton biomass, it is obvious that the variation is large. As mentioned above, that is because of uncertainties in the chlorophyll analyses and because phytoplankton species contain different amounts of chlorophyll. Another important reason why there is a certain difference is that the analyses have often not been carried out on the same water sample. Chlorophyll analyses are often conducted on surface water samples (0.5 m), while phytoplankton analyses are commonly done on integrated samples that are intended to correspond to the water mass above the thermocline. Since phytoplankton are in general not homogeneously distributed in the water col¬umn, major differences can arise if integrated samples are compared to surface water samples. The difference is perhaps most obvious in calm weather during the sum¬mer when cyanobacteria often tend to accumulate in the surface water and there is then a risk that they are over-represented in a surface sample. Even so, any accumu¬lation of e.g. Gonyostomum at the thermocline can give significantly higher bio¬masses compared with samples taken near the surface. This difference between surface water and integrated samples is

nevertheless unavoidable and indeed reflects well the reality that status classification as regards chlorophyll content will primarily be conducted on surface samples.

A lake must nevertheless not be given the status 'moderate' or worse, however, solely on the classification of chlorophyll and instead supplementary analyses of, for example, phytoplankton must be made to ascertain the cause and guarantee the lake's status before taking any necessary measures to maintain or achieve 'good' status.

Pressure-response relationships of Swedish indices for phytoplankton for Northern Humic lakes approximately corresponding to LN6a lakes

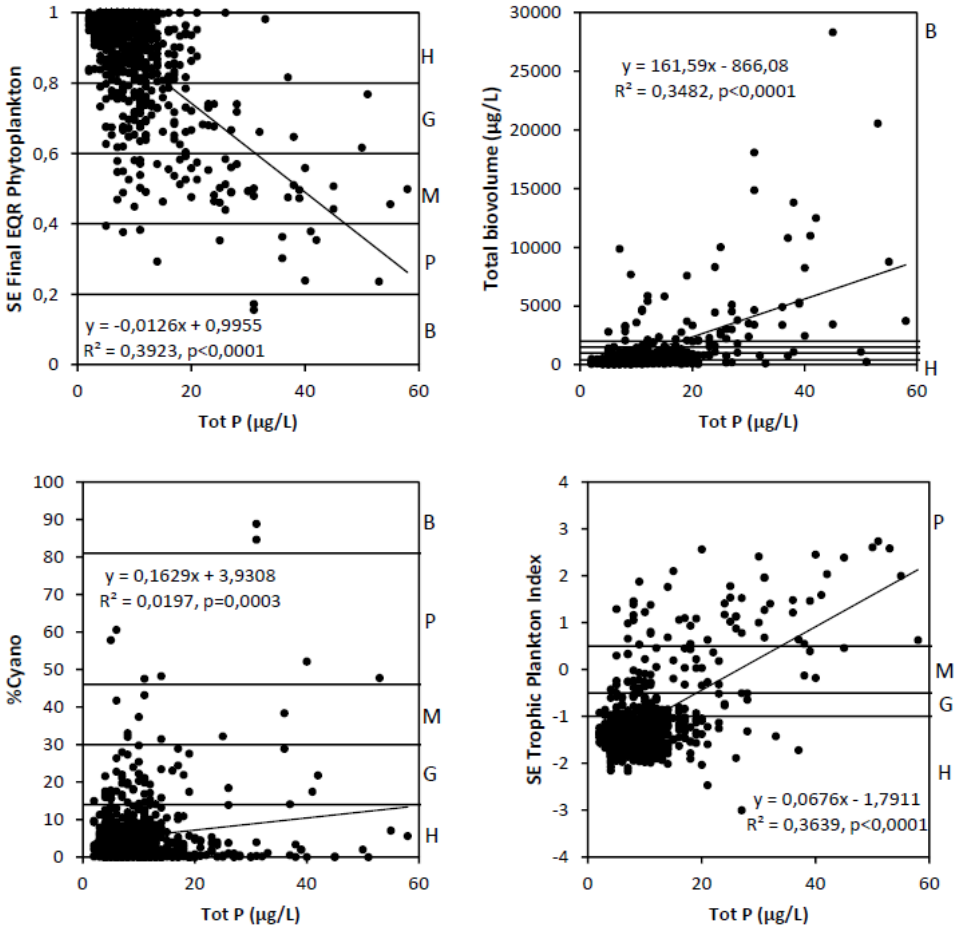


*Figure A.15Response of **a)** Swedish Multimetric Index for Phytoplankton, **b)** total biovolume of phytoplankton, **c)** proportion of cyanobacteria and **d)** SE Trophic Plankton Index, to total phosphorus. The lake type is Swedish Northern Humic lakes, approximately corresponding to type LN6a (also LN3a, LN3b, LN6b, LN8a, and LN8b lakes are found in SE type. 666 data points from 62 lakes 1993-2009. No reference filter were available.*

Weighting of trophic status parameters

When weighted together, the parameters total biomass, trophic plankton index (TPI) and proportion of cyanobacteria, form the basis for the classification of the lake's status as regards nutrients.

Since the TPI can only be used if at least four species in a sample have been assigned an indicator number, there will be lakes where the classification is based solely on total volumes and cyanobacterial proportion. For lakes characterised by *Gonyostomum semen*, the total biomass parameter may be unsuitable, particularly if the biomass is very large, which is not uncommon since this species often develops en masse. Such mass development is not necessarily a sign of eutrophication. It is therefore recommended that *Gonyostomum* lakes should be quality-classed using the TPI value and cyanobacterial proportion instead of by total biomass.

Parameters are weighted together as follows:

Step 1) The weighting must be based on the classified status for total biomass, cyanobacterial proportion and TPI. The status classes are given a numerical value in accordance with Table A.20. A weighted class value for each parameter is calculated before the weighting is conducted in accordance with Step 2.

Table A.20 Division of the status classes in numerical values.

Status	Numerical value
High status	4 - 4.99
Good status	3 - 3.99
Moderate status	2 - 2.99
Poor status	1 - 1.99
Bad status	0 - 0.99

The numerical class (N_{class}) for the respective parameters for the relevant EQR class interval (EQR_{lower}–EQR_{upper}) is calculated as follows:

$(N_{class}) = (N_{lower}) + (EQR_{calculated} - EQR_{lower})/(EQR_{upper} - EQR_{lower})$

Where

(N_{class}) = weighted status value for each parameter

N_{lower} = the first digit (integer) in the numerical values for the status class in accordance with Table 3.12

$EQR_{calculated}$= calculated EQR-value from the classification

EQR_{lower} and EQR_{upper} = EQR for lower and upper class boundary for the corresponding class, taken from Tables 3.3, 3.4 and 3.8 respectively.

EQR_{lower} for bad status = 0 and EQR_{upper} for high status = 1

Step 2) The mean value for the numeric classes (Nclass) of the three parameters is calculated, which becomes the weighted classification of phytoplankton. The status

classification is determined by the mean value for the numerical classification in accordance with Table A.20

Description of boundary setting approach

To set reference values and classes for total biovolume, %cyanobacteria and Trophic Plankton Index (TPI) the following procedure was used. Of a total of 480 lakes, 273 reference lakes were selected that had a Total P less than 10µg/l (for humic lakes a calculated TotP-ref = 5,9 + abs * 39 were used) and less than 10% agricultural land in the drainage area. July and August samples were used and mean values if several years of data. Indicators were separated based on region (south, north, mountainous) and water color (border at 30 mgPt/L or 0.06 $Abs_{420\ nm/5cm\ cuvette}$). *Gonyostomum*- lakes were not included (lakes with > 5% of biomass as *Gonyostomum*). 75th percentiles was used for reference value for each index. These values were reviewed and balanced based on current knowledge of algal group behavior along the trophic gradient. Highest and lowest values of the total dataset were identified and values were distributed between the different classes. Expert knowledge of phytoplankton communities in some of the lakes were also used in the boundary setting. Some of the relationships from the background reports are included here as an example (Figure A.16 and Figure A.17).

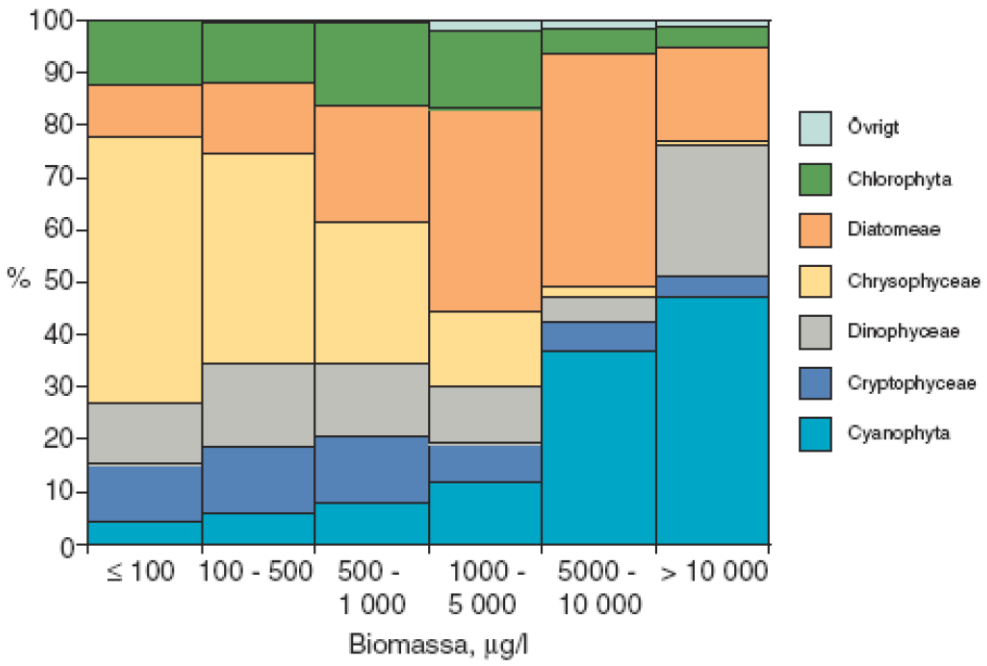
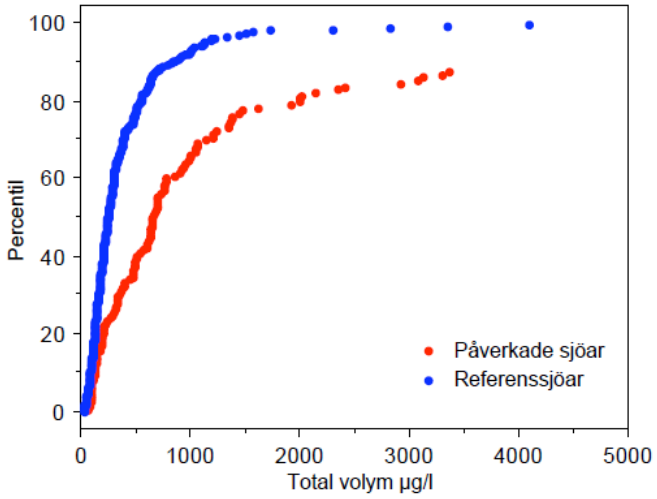
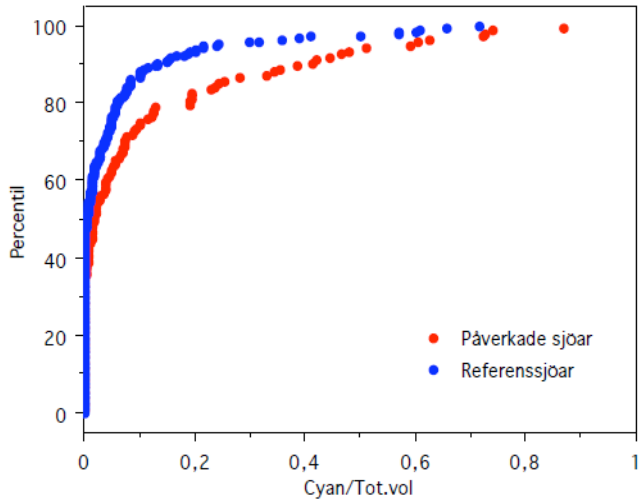


Figure A.16 *Relative proportions of phytoplankton groups in July and August i a gradient with increasing total biomass of phytoplankton (409 lakes). The proportion of cyanobacteria increases and chrysophytes decreses. (From Bedömningsgrunder för sjöar och vattendrag Bilaga A, Swedish EPA, Handbok 2007:4)*



a)



b)

Figure A.17 ***a)*** *Cumulative frequency distribution of total biovolume of phytoplankton in reference lakes (blue dots, Referenssjöar) and impacted lakes, eutrophication gradient (red dots, Påverkade sjöar). Maximum biomass in impacted lakes was 15000 µg/L, but the scale has been truncated for clarity. Median value for references and impacted lakes are 248 and 650µg/L, respectively.*

b) *Cumulative frequency distribution of the ratio between cyanobacteria and total phytoplankton biomass in reference lakes (blue dots, Referenssjöar) and impacted lakes, eutrophication gradient (red dots, Påverkade sjöar). The median ratio was 0.004 and 0.018 respectively, for reference and impacted lakes. Correspondingly, the 90th percentile was 0.13 and 0.40. Data are from 480 lakes of which 273 were reference lakes. From background report (Willén E., 2007, Växtplankton i sjöar, Bedömningsgrunder, Inst f miljöanalys, Rapport 2007:6).*

References

SEPA (2010) Status, potential and quality requirements for lakes, watercourses, coastal and transitional waters – A handbook on how quality requirements in bodies of surface water can be determined and monitored, Swedish Environmental Protection Agency Handbook 2007:4, Naturvårdsverket 2010, ISBN 978-91-620-0174-2, ISSN 1650-2361.

Willén E., 2007, Växtplankton i sjöar, Bedömningsgrunder, Inst f miljöanalys, Rapport 2007:6.

A.5 UK Phytoplankton Assessment System to assess status for the Water Framework Directive.

Summary

Three groups of indicators are used, phytoplankton abundance, taxonomic composition and the likelihood of cyanobacteria blooms.

Phytoplankton abundance is measured by proxy using chlorophyll a as a surrogate. The metric used is the mean[3] annual chlorophyll a concentration, derived from samples collected monthly between January and December[4].

Taxonomic composition is measured using the Plankton Trophic Index (PTI) calculated from samples collected monthly between July and September[5].

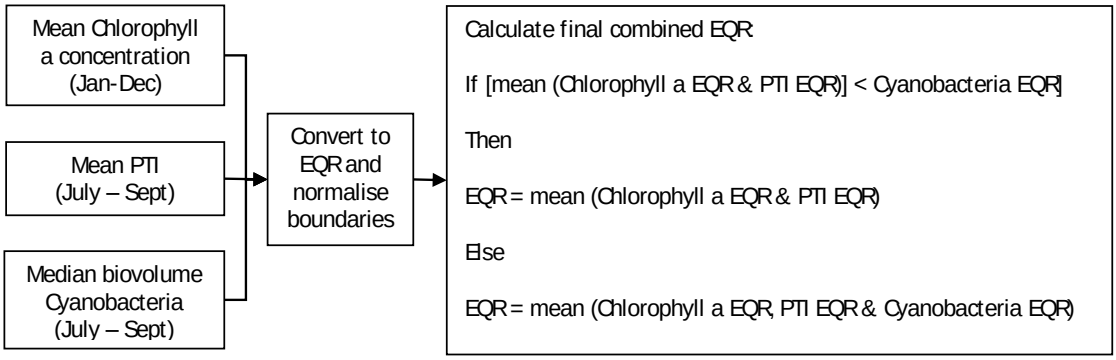
The likelihood of cyanobacteria blooms is calculated from the bio-volume of cyanobacteria present. The metric used is the median bio-volume of cyanobacteria in samples collected monthly between July and September.

Each of these metrics is converted to an EQR, using modelled estimates of reference conditions. These EQR are then normalised, so that the boundaries of each metric are on the same scale (0.8, 0.6, 0.4, 0.2), and then combined by averaging. The cyanobacteria EQR is excluded from the average if it is greater than the average of the chlorophyll and PTI EQR.

[3] Values are log transformed prior to averaging, so that the mean is a geometric mean. This allows uncertainty estimates to be made.

[4] January – December represents the growing season in the UK; in parts of the country significant biomass of phytoplankton are present in the winter months.

[5] July – September represents the late summer which is the most sensitive season for phytoplankton composition response to nutrient enrichment.



Monitoring system

Samples are taken from the lake outflow, or from the shore using throw bottles to sample below the surface. Samples for chlorophyll a are taken monthly throughout the year and are analysed at a central laboratory. Samples for taxanomic composition are taken monthly from July to September and preserved in Lugol's solution and stored in the dark. The cells are counted with an inverted microscope by trained analysts[6]. Identification of taxa is generally to species, using a standardised list of c240 taxa. Size measurements of a sub-sample of cells are taken to calculate bio-volume ($\mu m^3\ ml^{-1}$).

Metric Details

Biomass Metric - Chlorophyll a

The biomass of phytoplankton is assessed by proxy using the chlorophyll a concentration as a surrogate. The annual geometric mean chlorophyll a concentration (*Chl*) is converted to an EQR using a modelled reference value (equation 1)

$$EQR_{Chl} = \frac{Chl_{Ref}}{mean\left(\log_{10}\left(Chl\right)\right)} \qquad \text{equation 1}$$

Reference Chlorophyll

The reference chlorophyll a is predicted from a multiple regression model derived from 59 reference lakes (equation 2a).

$$Chl_{Ref} = 10^{\left(0.223+0.166\times\log(Alk)+0.684\times\sqrt{1/Depth}\right)} \qquad \text{equation 2a}$$

Where

Chl = geometric annual mean chlorophyll a concentration (µg/l)

Alk = reference alkalinity (mEq/l) (minimum value of 0.005)

Depth = reference mean depth (m) (minimum value of 1.0)

[6] Analysts are subject to ring-tests and attend regular training sessions to ensure that their competency level is maintained

The predicted reference chlorophyll a concentration is compared to a range of reference chlorophyll a concentrations which were set during Phase 1 of the intercalibration process (Poikane 2010). Where a value falls outside of this range, it is truncated to the upper or lower range limit. For lake types that have not been intercalibrated, reference chlorophyll values are constrained within the range of 1.3 – 6.0 µg/l.

As the mean reference chlorophyll a values set during intercalibration are arithmetic, they are first transformed[7] to geometric means using a standard deviation estimated from a large EU data set (WISER), see equation 2b

$$GeoChl = ArithChl \Big/ e^{(0.5\times(2.323\times SD)^2)} \qquad \text{equation 2b}$$

Where

GeoChl = Estimated geometric mean reference chlorophyll a defined during intercalibration

ArithChl = Arithmetic mean reference Chlorophyll defined during intercalibration

SD = standard deviation of $\log_{10}$Chl samples for a "typical" lake

= 0.213 for low and moderate alkalinity lakes (estimated from large EU data set)

= 0.285 for high alkalinity lakes (estimated from large EU data set)

Calculation of EQR and boundary setting

The approach to boundary setting is documented in the Phase 1 intercalibration reports, and the chlorophyll a EQR boundaries used here are those determined in that exercise (Table A.21, and Poikane 2008). In the case of low alkalinity lakes (alkalinity < 0.2 mEq/l) the original chlorophyll a EQR boundaries were adjusted during harmonisation, and then normalised using piecewise linear transformation (equation 3)

$$ChlEQR_{Norm} = \left[\left(\frac{EQR_{Chl} - LowerBoundary}{ClassWidth}\right)\times 0.2\right] + LowerBoundary_{Norm} \qquad \text{equation 3}$$

Where

$ChlEQR_{Norm}$ = Normalised EQR (e.g. HG = 0.80, GM = 0.60, MP = 0.40, PB = -0.20)

LowerBoundary =lower un-normalised EQR boundary (see Table A.21)

$LowerBoundary_{Norm}$ = lower normalised EQR boundary of class (e.g for Good = 0.60)

ClassWidth = Class width of non-normalised scale (e.g for Good = 0.55 – 0.32 = 0.23)

[7] For a log normal distribution the arithmetic and geometric means are related by AM = GM x $\exp(0.5SD^2)$

Table A.21 Chlorophyll a EQR boundaries for UK phytoplankton method

Lake Type	UK Type	IC Type (GIG)	Alkalinity (mEq/l)	Mean depth (m)	HG EQR	GM EQR	MP EQR	PB EQR
High alkalinity shallow	HAS	L-CB1	>1.0	3.0 - 15.0	0.55	0.32	0.16	0.05
High alkalinity very shallow	HAVS	L-CB2	>1.0	< 3.0	0.63	0.30	0.15	0.05
Moderate alkalinity deep	MAD		0.2 - 1.0	>15.0	0.50	0.33	0.17	0.05
Moderate alkalinity shallow	MAS	L-N1, L-N8a	0.2 - 1.0	3.0 - 15.0	0.50	0.33	0.17	0.05
Moderate alkalinity very shallow	MAVS		0.2 - 1.0	< 3.0	0.63	0.30	0.15	0.05
Low alkalinity deep	LAD	L-N2b	<0.2	>15.0	0.64	0.33	0.17	0.05
Low alkalinity shallow	LAS	L-N2a L-N3a	<0.2	3.0 - 15.0	0.64	0.29	0.15	0.05
Low alkalinity very shallow	LAVS		<0.2	< 3.0	0.63	0.30	0.15	0.05
Marl shallow	MarlS		>1.0	3.0 - 15.0	0.55	0.32	0.16	0.05
Marl very shallow	MarlVS		>1.0	< 3.0	0.63	0.30	0.15	0.05

Taxonomic Metric – Plankton Trophic Index (PTI)

The Phytoplankton Trophic Index (PTI) was derived from a CCA ordination (univariate analysis) of the taxonomic data constrained by total phosphorus (log transformed). This single variable was most significantly related to the 1st axis of all the constrained ordinations tested and reflects the main pressure of concern in lake management, eutrophication. CCA reduces to a weighted average ordination in the case of a single variable (Braak and Looman 1986), and species axis 1 scores represent the $\log_{10}$ weighted average of total phosphorus. These scores were transformed to values between 0 (low pressure) and 1 (high pressure) by converting all the scores to positive values (by adding the lowest score), then dividing by the resulting maximum score.

The site PTI is calculated for each sample collected between July to September using equation 5; the resulting metric has a good relationship with phosphorus and chlorophyll a (Figure A.18).

$$PTI = \frac{\sum_{j=1}^{n} \log(a_j) s_j}{\sum_{j=1}^{n} \log(a_j)} \qquad \text{equation 5}$$

Where:

a_j = biovolume of jth taxon in the sample ($\mu m^3\ ml^{-1}$) [8]

s_j = optimum of jth taxon in the sample (see table A1)

[8] The units are important due to the log transformation

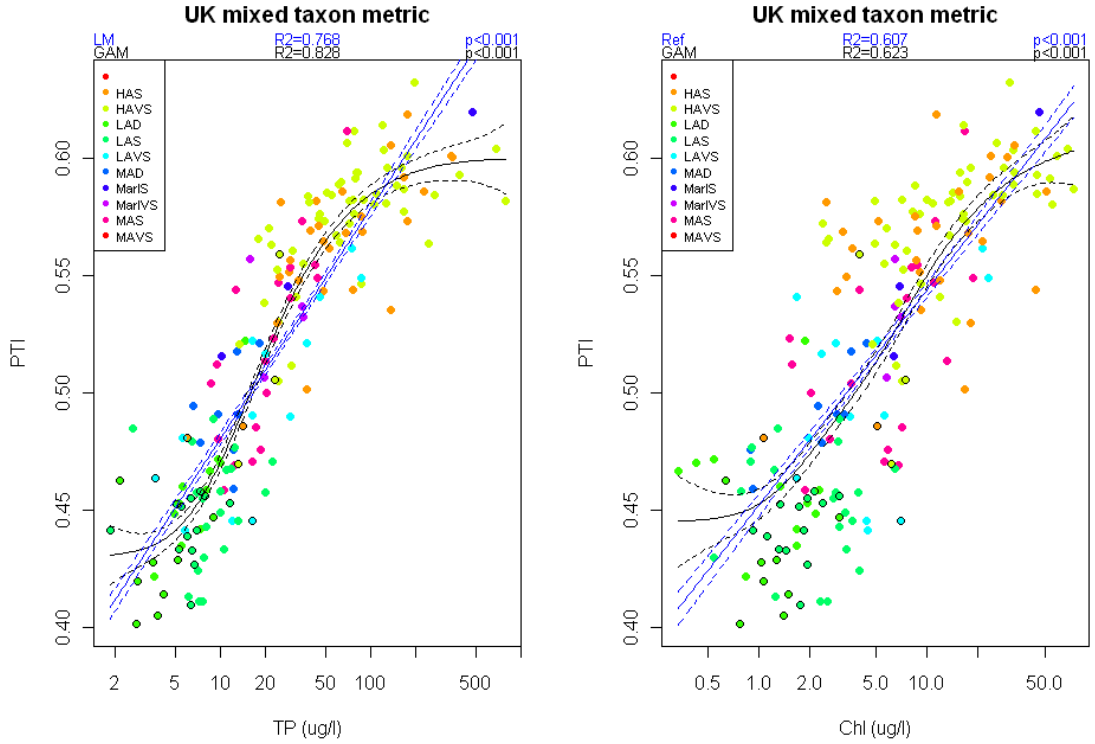


Figure A.18 *Relationship between PTI metric and a) mean annual total phosphorus, b) mean annual chlorophyll a for UK lakes classified by waterbody type. Circles identify reference lakes*

Correction of UK PTI during Intercalibration

The PTI metric calculated for UK sites in the intercalibration (WISER) database were notably different from those calculated for the same sites in the UK database due to the compromises in taxonomic nomenclature that were made for international harmonisation of the common (WISER) database. To compensate for this, NGIG[9] adjusted the PTI values calculated from the WISER intercalibration data set using the relationship between the scores calculated in the UK and those in the WISER database (PTI_{UK} = 0.889 PTI_{WISER} + 0.0589 R^2 = 0.977 $p<0.001$).

Reference PTI

[9] For CBGIG lakes UK EQR values were taken directly from the UK dataset and not from the WISER database.

The reference PTI is predicted from a multiple regression model derived from a sub-set (26) of reference lakes where taxonomic data were available at the time of method development (equation 5).

Reference PTI Model $PTI_{Ref} = 0.028 \times log_{10}MEI + 0.498 \quad R^2 = 0.688$ ...equation 5

Where

MEI = Alk/Depth (Morpho Edaphic Index)

Calculation of EQR_{PTI}

Site specific reference PTI values are calculated for each lake, and then are used to convert the observed sample PTI to an EQR using equation 6

$$EQR_{PTI} = \left(\frac{PTI_{Obs} - PTI_{Max}}{PTI_{\mathrm{Re}f} - PTI_{Max}} \right) \qquad \text{equation 6}$$

Where:

PTI_{Obs} = Sample PTI

PTI_{Max} = Maximum PTI score (*0.75)*

PTI_{Ref} = Reference PTI

Sample EQR_{PTI} are then averaged to obtain a water body EQR_{PTI}

Boundary setting for EQR_{PTI}

EQR boundaries were initially set independently of the lake typology as the reference PTI are site specific and take into account alkalinity and depth (the key variables that have been found to determine the phytoplankton community; Phillips *et al.* 2010). The boundaries were subsequently reviewed in the light of type specific pressure responses and were also adjusted during the intercalibration process to ensure they were consistent with other European countries.

The High/Good EQR boundary was based on the 10th percentile of EQR_{PTI} values for reference lakes (H/G EQR_{PTI} = 0.93). The other EQR boundaries were set using changes in the proportion of taxa sensitivity groups, split according to their nutrient optima and with reference to the bio-volume of eutrophic cyanobacteria taxa. The fractions of very sensitive and very tolerant taxa and the relationships between EQR_{PTI} and eutrophic cyanobacteria were examined and potential boundaries identified using GAM and quantile regression models. The Good/Moderate boundary was initially set at 0.82, the point at which 50% of lakes still have 20% of the very sensitive taxa and 90% of lakes have less than 10% of the very tolerant taxa. Cyanobacteria first show an increase in biomass at an EQR_{PTI} of 0.85 (Figure A.19), a value that is below the proposed High/Good boundary and slightly above the proposed Good/Moderate boundary. At this point the response mainly occurs in high alkalinity lakes and although it represents more than a "slight" change in the phytoplankton community, it is clearly not a significant undesirable impact at this level. It is therefore consistent with good status, although the change in

cyanobacterial response and the associated EQR_{PTI} value indicate that conditions are indeed approaching the Good/Moderate boundary. The Moderate/Poor boundary was initially set at 0.70, the point at which 50% of lakes have more than 5% of very tolerant taxa. The Poor/Bad boundary was set at 0.58, a value which provides the same class width for Poor as for Moderate (see Figure A.20 for all modelled boundaries).

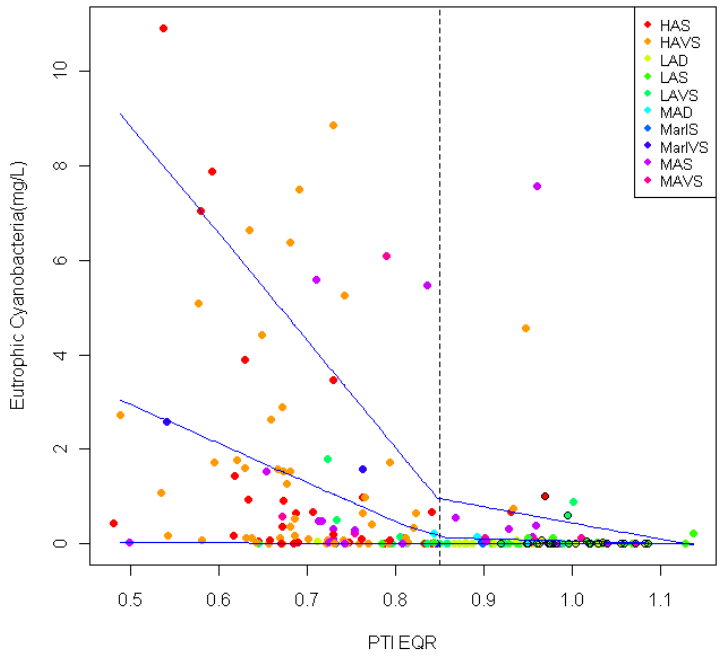


Figure A.19 *The relationship of EQR_{PTI} with the biovolume of eutrophic cyanobacteria. The 90th and 75th quantiles are given, reference sites are outlined and the potential EQR G/M boundary is shown at 0.85.*

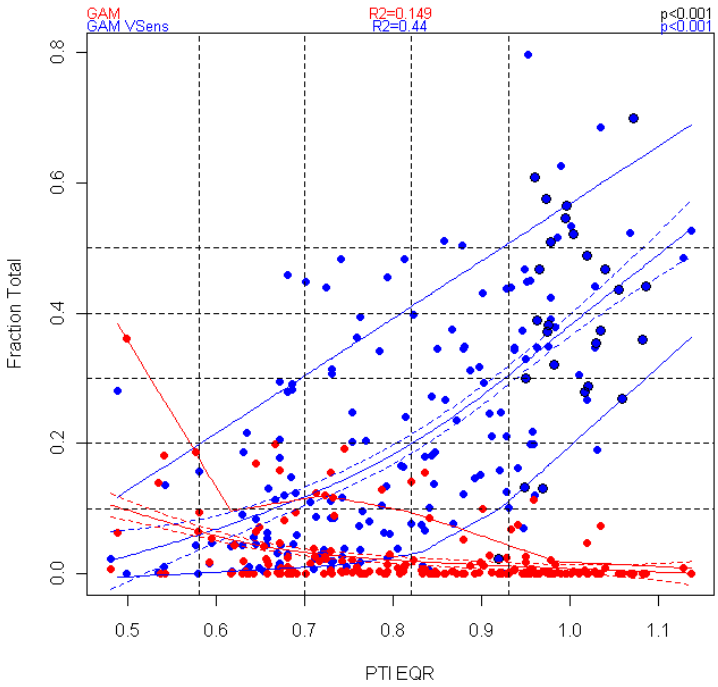


Figure A.20 *The relationship between EQR_{PTI} and the fraction of very sensitive taxa (blue spots) and very tolerant (red spots) together with 90^{th} and 10^{th} quantile regressions and GAM models. Reference sites are outlined and the potential boundaries at EQR_{PTI} 0.93, 0.82, 0.70 and 0.58 are shown.*

Although it was initially intended to apply these EQR boundaries to all lake types, it was observed that the EQR from lakes of different alkalinity types had significantly different relationships with pressure despite the use of a site specific model to determine reference conditions. The importance of alkalinity on the phytoplankton community has also been identified in larger European data sets (Phillips *et al.* 2010). These different relationships were quantified using linear mixed models (Figure A.21) with EQR_{PTI} as dependent variable, log TP as co-variable and type as a random variable. The model revealed significant differences in intercept between types, but not in slope. The model was repeated using fixed slopes and the resulting random effect values due to lake type (i.e. the differences in intercepts) were used to adjust the proposed EQR boundaries (Table A.22).

Table A.22 *Random effect of lake geology type on relationship between PTI EQR and logTP for UK lakes, and the type specific EQR adjustments to account for this effect.*

Lake Geology Type	Random effect of type on intercept of linear model	EQR adjustment
High Alkalinity	-0.021	-0.02
Moderate Alkalinity	-0.004	0.00

Low Alkalinity	+0.022	+0.02
Marl	+0.003	0.00

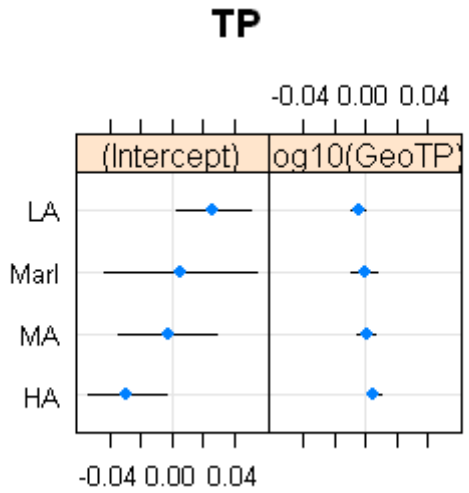


Figure A.21 The range of intercept and slope values for linear mixed models between PTI EQR and logTP. Horizontal lines show confidence limits.

During the intercalibration process these boundaries were adjusted to ensure that the UK method was not less precautionary than other member states with similar lake types. Boundaries for other UK lake types that could not be intercalibrated were adjusted based on those that were. Very shallow lakes were assumed to have less stringent boundaries than shallow lakes and low alkalinity lakes humic lakes to have less stringent boundaries than low alkalinity clear water lakes. The original and final harmonised EQR_{PTI} boundaries are shown in Table A.23.

The EQR_{PTI} is normalised using quadratic functions of the form

$$PTIEQR_{Norm} = A \times EQR_{PTI}^{\ 2} - B \times EQR_{PTI} - C$$

Parameters used for each lake type are also given in Table A.23.

Bloom Frequency Metric – Cyanobacteria bio-volume

The WFD requires that the assessment of lake phytoplankton should include an assessment of the frequency and intensity of algal blooms. It does not define an algal bloom, but a definition emerging from the intercalibration process is that it refers to an elevated biomass of cyanobacteria. Cyanobacteria are associated with enriched conditions in lakes and can produce a high biomass of potentially toxic algae which can restrict the use of a lake. This is a clear case of "undesirable disturbance" as defined by the WFD (European Commission 2009). Although increases in cyanobacteria are indicated by both an elevated biomass (chlorophyll concentration) and an increase in the PTI, the UK method now includes a direct assessment of cyanobacterial biomass using the median biovolume of cyanobacteria.

Table A.23 EQR boundaries for Plankton Trophic Index (PTI). The harmonised boundaries are the final values used in the UK method following intercalibration. Equations for normalisation are also shown.

Lake Type	Humic Type	UK Type	IC Type (GIG)	Type Parameter values			Original Boundaries				Harmonised Boundaries				Normalisation equation
				Alkalinity mEq/l	Mean depth m	Colour mgPt/l	HG EQR	GM EQR	MP EQR	PB EQR	HG EQR	GM EQR	MP EQR	PB EQR	
High alkalinity shallow		HAS	L-CB1	>1.0	3.0 - 15.0	not used	0.91	0.80	0.68	0.56	0.93	0.82	0.70	0.58	$EQR_{Norm} = 1.228 \times EQR^2 - 0.0898 \times EQR - 0.1538$
High alkalinity very shallow		HAVS	L-CB2	>1.0	< 3.0						0.91	0.80	0.68	0.56	$EQR_{Norm} = 1.228 \times EQR^2 - 0.0407 \times EQR - 0.1551$
Moderate alkalinity deep		MAD		0.2 - 1.0	>15.0		0.93	0.82	0.70	0.58	0.95	0.84	0.72	0.60	$EQR_{Norm} = 1.228 \times EQR^2 - 0.1389 \times EQR - 0.1515$
Moderate alkalinity shallow		MAS	L-N1, L-N8a	0.2 - 1.0	3.0 - 15.0										
Moderate alkalinity very shallow		MAVS		0.2 - 1.0	< 3.0						0.93	0.82	0.70	0.58	$EQR_{Norm} = 1.228 \times EQR^2 - 0.0898 \times EQR - 0.1538$
Low alkalinity deep	Clear	LADcl	L-N2b	<0.2	>15.0	≤ 30	0.95	0.84	0.72	0.60	0.98	0.87	0.75	0.63	$EQR_{Norm} = 1.228 \times EQR^2 - 0.2004 \times EQR - 0.147$
Low alkalinity deep humic	Humic	LADhm		<0.2	>15.0	> 30					0.95	0.84	0.72	0.60	$EQR_{Norm} = 1.228 \times EQR^2 - 0.1389 \times EQR - 0.1515$
Low alkalinity shallow	Clear	LAScl	L-N2a	<0.2	3.0 - 15.0	≤ 30					0.98	0.87	0.75	0.63	$EQR_{Norm} = 1.228 \times EQR^2 - 0.2004 \times EQR - 0.147$
Low alkalinity shallow humic	Humic	LAShm	L-N3a	<0.2	3.0 - 15.0	> 30					0.96	0.85	0.73	0.61	$EQR_{Norm} = 1.228 \times EQR^2 - 0.1512 \times EQR - 0.1508$
Low alkalinity very shallow	Clear	LAVScl		<0.2	< 3.0	≤ 30					0.95	0.84	0.72	0.60	$EQR_{Norm} = 1.228 \times EQR^2 - 0.1389 \times EQR - 0.1515$
Low alkalinity very shallow humic	Humic	LAVShm		<0.2	< 3.0	> 30					0.93	0.82	0.70	0.58	$EQR_{Norm} = 1.228 \times EQR^2 - 0.0898 \times EQR - 0.1538$
Marl shallow		MarlS		>1.0	3.0 - 15.0		0.93	0.82	0.70	0.58	0.95	0.84	0.72	0.60	$EQR_{Norm} = 1.228 \times EQR^2 - 0.1389 \times EQR - 0.1515$
Marl very shallow		MarlVS		>1.0	< 3.0						0.93	0.82	0.70	0.58	$EQR_{Norm} = 1.228 \times EQR^2 - 0.0898 \times EQR - 0.1538$

Boundary Setting for Cyanobacteria biomass

The cyanobacteria metric assesses "undesirable disturbance" by indicating the risk of cyanobacterial blooms occurring, using the low and medium risk thresholds defined as by the World Health Organisation as 20,000 and 100,000 cells ml-1 respectively (Who 1999). These values were converted to bio-volume thresholds of 1 and 5 mm3 l-1 by multiplication of a typical cell volume (based on a spherical cell such as Microcystis with a cell diameter of 4.5µm; Hillebrand et al. 1999).

Status boundaries were set in accordance with the Eutrophication Guidance (European Commission 2009). This document proposes an increasing risk of undesirable disturbances, thus at Good status there should be a very low probability of blooms occurring. The likelihood increases through the Moderate class and is high at Poor status. The distribution of cyanobacteria biomass in summer samples can be used to assess how often a particular lake exceeds these thresholds and consequently a classification can be derived. It is proposed that at the High/Good boundary 90% of samples would be below the 1 mm3 l-1 threshold, and at the Good/Moderate 25% of samples would be below this threshold. The Moderate/Poor boundary was set where 75% of samples were above the 1 mm3 l-1 threshold but below 5 mm3 l-1, and the Poor/Bad boundary where 75% of samples exceeded the 5 mm3 l-1 threshold (Figure A.22).

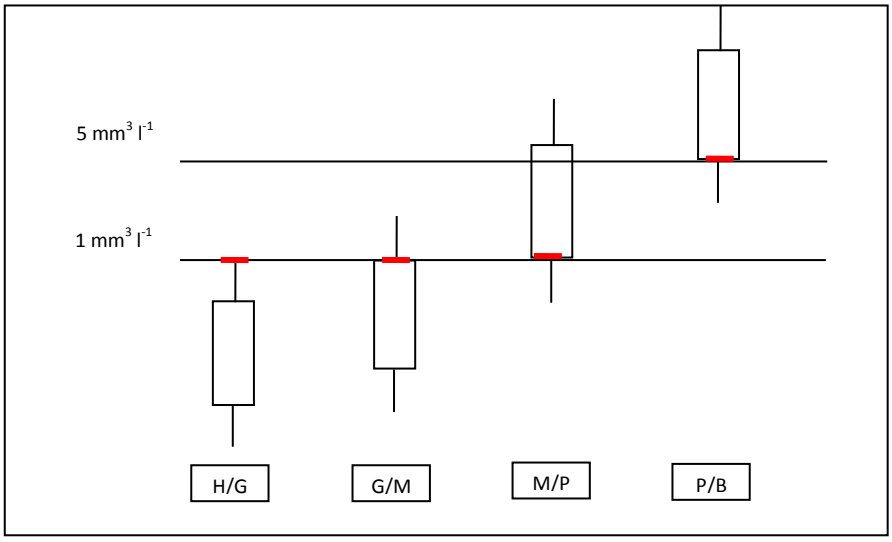


Figure A.22 *Diagram illustrating position of WFD boundaries using different percentiles of cyanobacteria bio-volume. Boxes represent 25th, 75th percentiles, tails 90th percentiles, horizontal line represent the biomass equivalent to the low and medium risk WHO thresholds for blooms. Red lines identify the tested percentile to determine class*

The European (WISER database) lakes were classified according to the distribution of cyanobacteria using the above rules. The median summer cyanobacteria bio-volume (July – September) was calculated for each lake. The distribution of these median values in each class was determined and boundary values for were set at the overlap between the upper and lower 25th percentiles of adjacent classes (Figure A.23 and Table A.24). The High/Good boundary median cyanobacteria biovolume is well below the WHO

"vigilance" level (0.2 mm3 l-1), and the Good/Moderate boundary is below the low risk threshold and is therefore consistent with a low risks of "undesirable disturbance".

Table A.24 Boundary values and EQRs for summer cyanobacteria biomass

Boundary	Cyanobacteria bio-volume (July - September) samples	Median cyanobacteria bio-volume ($mm^3 l^{-1}$)		EQR boundary values	
		Low & Moderate Alkalinity & Marl lakes	High alkalinity lakes	Low & Moderate Alkalinity & Marl lakes	High alkalinity lakes
Reference		0	0.01	1.00	1.00
High/Good	90th percentile < $1mm^3 l^{-1}$	0.08	0.20	0.47	0.63
Good/Moderate	75th percentile < $1mm^3 l^{-1}$	0.56	1.00	0.32	0.43
Moderate/Poor	25th percentile < $1mm^3 l^{-1}$	1.58	2.00	0.23	0.34
Poor/Bad	10th percentile < $1mm^3 l^{-1}$	5.62	5.62	0.13	0.21

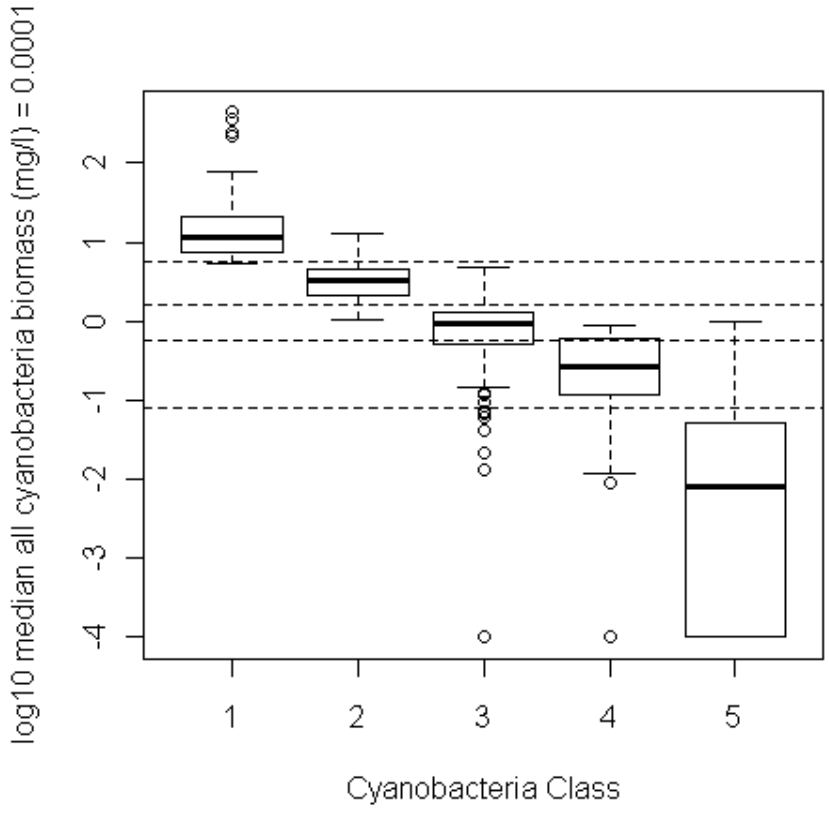


Figure A.23 Distribution of median biomass of cyanobacteria in European lakes in different WFD classes (5 high, 4 good, 3 moderate, 2 poor, 1 bad). Boxes represent upper and lower 25th percentiles, lines 90th percentiles. Horizontal dotted lines mark boundary values for median summer cyanobacteria.

Conversion to EQR

The median cyanobacteria bio-volumes were converted to EQRs using the following equation[10].

$$EQR_{Cyan} = \frac{\log(BV_{Obs} + 0.0001) - \log(BV_{Max} + 0.0001)}{\log(BV_{\mathrm{Re}f} + 0.0001) - \log(BV_{Max} + 0.0001)}$$ equation 7

Where

BV_{Obs} = median bio-volume cyanobacteria ($mm^3\ l^{-1}$) [11]

BV_{Ref} = median bio-volume cyanobacteria in reference lakes ($mm^3\ l^{-1}$)

= 0.01 $mm^3\ l^{-1}$ for high alkalinity lakes

= 0.00 $mm^3\ l^{-1}$ for other lake types

BV_{Max} = maximum median bio-volume (taken as 30.0 $mm^3\ l^{-1}$)

If $BV_{Obs} > BV_{Max}$ then EQR_{Cyan} defaults to 0.0

The EQRCyan is then normalised using equation 8 for combination with other metrics

$$CyanEQR_{Norm} = \left[\left(\frac{EQR_{Cyan} - LowerBoundary}{ClassWidth}\right) \times 0.2\right] + LowerBoundary_{Norm}$$ equation 8

For derivation of terms see equation 3

Combination of metrics

To calculate an overall EQR, the normalised metric EQRs are combined by averaging.

The $ChlEQR_{Norm}$ and the $PTIEQR_{Norm}$ are first averaged to produce an interim EQR ($IntEQR_{Norm}$).

The cyanobacteria metric is only included in order to downgrade a lake status where blooms are likely; the absence of cyanobacteria should not upgrade the status of a lake. Consequently, if the $CyanEQR_{Norm}$ is < $IntEQR_{Norm}$ it is averaged with $IntEQR_{Norm}$, otherwise the cyanobacteria metric is ignored.

The resulting overall EQR represent status on a standard scale with boundaries of HG= 0.80, GM=0.60, MP=0.40 and PB=0.20

Data checking & uncertainty estimation

Classification is normally based on data collected over the preceeding three years. The mean metric values (Chlorophyll a concentration, PTI and Cyanobacteria bio-volume) should be calculated for this period before calculating EQRs.

[10] Logarithms are used to create a realistic class width on the EQR scale

[11] To convert from $\mu m^3\ ml^{-1}$ to $mm^3\ l^{-1}$ divide by 10^6

Samples for Chlorophyll a must be collected evenly throughout the year (i.e. at the same time each month). Twelve monthly samples should be used, but at minimum of 1 sample from each quarter of the year is required to calculate a representative mean.

Phytoplankton counts should be checked by comparing the calculated total sample bio-volume against a value predicted from the sample chlorophyll a value (equation 9). If the total sample bio-volume is outside of the predicted value ±95th percentile of the modelled residuals the sample should be marked as "suspect" and the results compared with other samples from the same lake and time of year, before these sample results for Cyanobacteria and PTI are used.

$$BV_{Pred} = 10^{1.18\times\log(Chl)-1.11)}$$

$$UpperBV_{Pred} = 10^{1.18\times\log(Chl)-1.11+0.5)} \qquad \text{equation 9}$$

$$LowerBV_{Pred} = 10^{1.18\times\log(Chl)-1.11-0.5)}$$

The uncertainty of each metric will be estimated and combined to provide an overall assessment of confidence of class. The method for estimating uncertainty is currently under development.

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Who (1999). Toxic cyanobacteria in water: A guide to their public health consequences, monitoring and management. London, E & F N Spon.

Appendix 1 UK Plankton Trophic Index Optima (for taxa included on standard UK counting list)

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
01000000	TRUE	Unidentified Cyanophyte		0.581	group	
01020000	TRUE	Anabaena		0.568	genus	
01020040	TRUE		Anabaena catenula	0.713	species	
01020042	TRUE		Anabaena catenula var. solitaria	0.701	species	
01020050	TRUE		Anabaena circinalis	0.743	species	
01020090	TRUE		Anabaena flos-aquae	0.652	species	
01020140	TRUE		Anabaena spiroides	0.631	species	
01030000	FALSE	Anabaenopsis		0.729	genus	
01040000	TRUE	Aphanizomenon		0.717	genus	
01040020	TRUE		Aphanizomenon flos-aquae	0.748	species	
01040040	TRUE		Aphanizomenon issatschenkoi	0.717	genus	not in training data
01050000	TRUE	Aphanocapsa		0.539	genus	
01050020	TRUE		Aphanocapsa delicatissima	0.539	genus	not in training data
01050030	TRUE		Aphanocapsa elachista	0.405	species	
01060000	TRUE	Aphanothece		0.459	genus	
01060020	TRUE		Aphanothece clathrata	0.459	genus	not in training data
01060050	TRUE		Aphanothece minutissima	0.301	species	
01130000	TRUE	Chroococcus		0.438	genus	
01130020	TRUE		Chroococcus dispersus	0.438	genus	too few records
01130060	TRUE		Chroococcus minutus	0.349	species	
01150000	TRUE	Coelosphaerium		0.496	genus	
01150010	TRUE		Coelosphaerium kuetzingianum	0.495	species	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
01170000	FALSE	Cyanodictyon		0.325	genus	
01170020	TRUE		Cyanodictyon planctonicum	0.322	species	
01200000	FALSE	Cylindrospermum		0.193	genus	
01300000	FALSE	Gloeothece		0.365	genus	
01310000	FALSE	Gloeotrichia		0.602	genus	
01320000	TRUE	Gomphosphaeria		0.46	genus	
01320010	TRUE		Gomphosphaeria aponina	0.436	species	
01430000	TRUE	Lyngbya		0.71	genus	
01430050	TRUE		Lyngbya contorta	0.71	genus	too few records
01460000	TRUE	Merismopedia		0.48	genus	
01460050	TRUE		Merismopedia warmingiana	0.225	species	
01490000	TRUE	Microcystis		0.672	genus	
01490010	TRUE		Microcystis aeruginosa	0.672	genus	not in training data
01490020	TRUE		Microcystis flos-aquae	0.672	genus	not in training data
01490030	TRUE		Microcystis wesenbergii	0.672	genus	not in training data
01530000	TRUE	Oscillatoria		0.567	genus	
01530010	TRUE		Oscillatoria agardhii	0.552	species	
01530012	TRUE		Oscillatoria agardhii var. isothrix	0.322	species	
01530160	TRUE		Oscillatoria limnetica	0.643	species	
01530170	TRUE		Oscillatoria limosa	0.567	genus	not in training data
01530230	TRUE		Oscillatoria redekei	0.567	genus	not in training data
01550000	FALSE	Phormidium		0.188	genus	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
01580000	TRUE	Pseudanabaena		0.503	genus	
01610000	FALSE	Rhabdoderma		0.211	genus	
01690000	FALSE	Synechococcus		0.458	genus	
01700000	FALSE	Synechocystis		0.337	genus	
01750000	TRUE	Snowella		0.513	genus	
01750010	TRUE		Snowella lacustris	0.639	species	
01750020	TRUE		Snowella septentrionalis	0.309	species	
01750030	TRUE		Snowella atomus	0.311	species	
01760000	FALSE	Radiocystis		0.187	genus	
01780000	TRUE	Woronichinia		0.503	genus	
01780010	TRUE		Woronichinia naegeliana	0.526	species	
04020000	TRUE	Euglena		0.587	genus	
04070000	TRUE	Phacus		0.715	genus	
04090000	TRUE	Strombomonas		0.633	genus	
04100000	TRUE	Trachelomonas		0.621	genus	
05020000	TRUE	Chroomonas		0.544	genus	
05020010	TRUE		Chroomonas acuta	0.502	species	
05040000	TRUE	Cryptomonas		0.547	genus	
05040001	TRUE		Cryptomonas (small) Length <20 µm	0.53	species	
05040002	TRUE		Cryptomonas (medium) Length 20-30 µm	0.533	species	
05040003	TRUE		Cryptomonas (large) Length >30 µm	0.589	species	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
05040030	TRUE		Cryptomonas erosa	0.547	genus	not in training data
05040040	TRUE		Cryptomonas marssonii	0.631	species	
05040050	TRUE		Cryptomonas ovata	0.508	species	
05060000	FALSE	Cyathomonas		0.606	genus	
05100000	TRUE	Rhodomonas		0.539	genus	
05100010	TRUE		Rhodomonas lacustris	0.358	species	
05100012	TRUE		Rhodomonas lacustris var. nannoplanctica	0.473	species	
05109910	TRUE		Rhodomonas lens	0.539	genus	not in training data
05110000	FALSE	Plagioselmis		0.355	genus	
06000000	FALSE	indet. dinoflagellate		0.288	group	
06020000	FALSE	Ceratium		0.505	genus	
06020010	TRUE		Ceratium carolinianum	0.505	genus	not in training data
06020020	TRUE		Ceratium cornutum	0.505	genus	not in training data
06020030	TRUE		Ceratium furcoides	0.644	species	
06020040	TRUE		Ceratium hirundinella	0.493	species	
06050000	TRUE	Glenodinium		0.561	genus	
06070000	TRUE	Gymnodinium		0.46	genus	
06070110	TRUE		Gymnodinium helveticum	0.479	species	
06100000	FALSE	Peridiniopsis cf. elpatiewskyi		0.406	genus	
06110000	TRUE	Peridinium		0.485	genus	
06110050	TRUE		Peridinium cinctum	0.485	genus	not in training data

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
06110090	TRUE		Peridinium inconspicum	0.229	species	
06110100	TRUE		Peridinium willei	0.332	species	
07010000	FALSE	Gonyostomum		0.297	genus	
07010010	TRUE		Gonyostomum semen	0.297	genus	not in training data
08010000	TRUE	Chrysochromulina		0.341	genus	
08010010	TRUE		Chrysochromulina parva	0.348	species	
08040000	TRUE	Prymnesium		0.838	genus	
09000000	TRUE	Chrysophyceae		0.324	genus	
09030000	TRUE	Bitrichia		0.288	genus	
09030010	TRUE		Bitrichia chodatii	0.235	species	
09030020	TRUE		Bitrichia longispina	0.288	genus	not in training data
09050000	TRUE	Chromulina		0.41	genus	
09050030	TRUE		Chromulina nebulosa	0.41	genus	not in training data
09060000	TRUE	Chrysamoeba		0.256	genus	
09080000	TRUE	Chrysidiastrum		0.276	genus	
09080010	TRUE		Chrysidiastrum catenatum	0.267	species	
09130000	TRUE	Chrysococcus		0.427	genus	
09150000	TRUE	Chrysolykos		0.233	genus	
09150010	TRUE		Chrysolykos planctonicus	0.245	species	
09230000	TRUE	Dinobryon		0.411	genus	
09230010	TRUE		Dinobryon bavaricum	0.328	species	
09230030	TRUE		Dinobryon crenulatum	0.201	species	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
09230040	TRUE		Dinobryon cylindricum	0.211	species	
09230050	TRUE		Dinobryon divergens	0.392	species	
09230052	TRUE		Dinobryon divergens var. schauninslandii	0.318	species	
09230070	TRUE		Dinobryon sertularia	0.411	genus	not in training data
09230080	TRUE		Dinobryon sociale	0.41	species	
09230090	TRUE		Dinobryon suecicum	0.233	species	
09230110	TRUE		Dinobryon borgei	0.205	species	
09250000	TRUE	Epipyxis		0.411	genus	
09290000	FALSE	Kephyrion		0.434	genus	
09310000	TRUE	Mallomonas		0.452	genus	
09310030	TRUE		Mallomonas akrokomos	0.473	species	
09310080	TRUE		Mallomonas caudata	0.346	species	
09330000	FALSE	Monochrysis		0.23	genus	
09350000	TRUE	Ochromonas		0.409	genus	
09370000	TRUE	Phaeaster		0.252	genus	
09430000	TRUE	Pseudokephyrion		0.345	genus	
09450000	TRUE	Spiniferomonas		0.211	genus	
09480000	TRUE	Stichogloea		0.293	genus	
09530000	TRUE	Synura		0.365	genus	
09540000	TRUE	Uroglena		0.443	genus	
09550000	FALSE	Pseudopedinella		0.372	genus	
09559910	TRUE		Pseudopedinella (small <5um)	0.471	species	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
09559920	TRUE		Pseudopedinella (big >5um)	0.37	species	
10050000	TRUE	Centritractus		0.326	genus	
10090000	TRUE	Goniochloris		0.764	genus	
10110000	TRUE	Isthmochloron		0.184	genus	
10140000	TRUE	Ophiocytium		0.545	genus	
10160000	TRUE	Pseudostaurastrum		0.714	genus	
10180000	FALSE	Tetraedriella		0.138	genus	
10190000	FALSE	Tribonema		0.366	genus	
10220000	FALSE	Gloeobotrys		0.312	genus	
12000000	FALSE	Bacillariales		0.571	group	
12000001	TRUE		Small centric diatom (5 - <10 µm diam.)	0.573	group	
12000002	TRUE		Medium centric diatom (10-20 µm diam.)	0.568	group	
12000003	TRUE		Large centric diatom (>20 µm diam.)	0.599	group	
12000004	TRUE		Very small centric diatom (<5 µm diam.)	0.574	group	
12010000	FALSE	Acanthoceras		0.721	genus	
12010010	TRUE		Acanthoceras zachariasi	0.716	species	
12030000	TRUE	Aulacoseira		0.606	genus	
12030020	TRUE		Aulacoseira ambigua	0.606	genus	not in training data
12030060	TRUE		Aulacoseira granulata	0.717	species	
12030062	TRUE		Aulacoseira granulata var. angustissima	0.719	species	
12030080	TRUE		Aulacoseira italica	0.475	species	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
12030084	TRUE		Aulacoseira italica v.tenuissima	0.435	species	
12030150	TRUE		Aulacoseira subarctica	0.563	species	
12040000	FALSE	Chaetoceros		1	genus	
12040010	TRUE		Chaetoceros muelleri	1	genus	not in training data
12070000	TRUE	Cyclotella		0.355	genus	
12110000	TRUE	Melosira		0.71	genus	
12110080	TRUE		Melosira varians	0.722	species	
12160000	FALSE	Skeletonema		0.8	genus	
12180000	TRUE	Stephanodiscus		0.634	genus	
12200000	TRUE	Urosolenia		0.3	genus	
12200010	TRUE		Urosolenia eriensis	0.258	species	
12200020	TRUE		Urosolenia longiseta	0.346	species	
13000000	FALSE	Pennate diatoms		0.418	group	
13000001	TRUE		Small pennate diatom <10 µm diam	0.356	group	
13000002	TRUE		Medium pennate diatom 10-20 µm diam	0.349	group	
13000003	TRUE		Large pennate diatom >20 µm diam	0.379	group	
13050000	FALSE	Amphora		0.305	genus	
13080000	FALSE	Asterionella		0.492	genus	
13080010	TRUE		Asterionella formosa	0.491	species	
13200000	FALSE	Cylindrotheca		1	genus	
13210000	FALSE	Cymatopleura		0.57	genus	
13260000	TRUE	Diatoma		0.567	genus	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
13260040	TRUE		Diatoma tenuis	0.573	species	
13280000	FALSE	Didymosphaenia sp.		0.203	genus	
13370000	TRUE	Fragilaria		0.44	genus	
13370030	TRUE		Fragilaria capucina	0.534	species	
13370040	TRUE		Fragilaria crotonensis	0.467	species	
13420000	FALSE	Gyrosigma		0.712	genus	
13520000	TRUE	Navicula		0.497	genus	
13540000	TRUE	Nitzschia		0.628	genus	
13540020	TRUE		Nitzschia acicularis	0.673	species	
13770000	FALSE	Staurosira		0.35	genus	
13770013	TRUE		Fragilaria construens	0.347	species	
13810000	TRUE	Synedra		0.506	genus	
13810010	TRUE		Synedra acus	0.544	species	
13810120	TRUE		Synedra nana	0.506	genus	not in training data
13810180	TRUE		Synedra ulna	0.381	species	
13820000	TRUE	Tabellaria		0.327	genus	
13820010	TRUE		Tabellaria fenestrata	0.297	species	
13820020	TRUE		Tabellaria flocculosa	0.295	species	
13820022	TRUE		Tabellaria flocculosa var. asterionelloides	0.333	species	
15030000	FALSE	Monomastix		0.305	genus	
15050000	FALSE	Neproselsmis pyriformis		0.402	genus	
15110000	FALSE	Pyramimonas		0.503	genus	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
15120000	FALSE	Scourfeldia		0.529	genus	
16000000	FALSE	Unidentified green		0.285	genus	
16020000	FALSE	Asterococcus		0.313	genus	
16060000	TRUE	Carteria		0.586	genus	
16170000	FALSE	Chlamydocapsa		0.275	genus	
16180000	TRUE	Chlamydomonas		0.511	genus	
16190000	TRUE	Chlorogonium		0.492	genus	
16260000	FALSE	Eudorina		0.544	genus	
16260010	TRUE		Eudorina elegans	0.539	species	
16330000	TRUE	Gonium		0.292	genus	
16470000	TRUE	Pandorina		0.683	genus	
16470010	TRUE		Pandorina morum	0.652	species	
16490000	FALSE	Paulschulzia		0.304	genus	
16590010	TRUE		Pseudosphaerocystis lacustris	0.299	species	
16600000	TRUE	Pteromonas		0.902	genus	
16680000	FALSE	Pyrobotrys		0.582	genus	
16740000	FALSE	Tetraspora		0.448	genus	
16770000	FALSE	Volvocales		0.544	genus	
16770010	TRUE		Volvox aureus	0.664	species	
17000000	TRUE	Chlorococcales		0.503	genus	
17020000	FALSE	Actinastrum		0.803	genus	not in training data
17020010	TRUE		Actinastrum hantzschii	0.789	species	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
17050000	TRUE	Ankistrodesmus		0.425	genus	
17050030	TRUE		Ankistrodesmus falcatus	0.482	species	
17050050	TRUE		Ankistrodesmus fusiformis	0.348	species	
17050060	TRUE		Ankistrodesmus spiralis	0.443	species	
17060000	TRUE	Ankyra lanceolata		0.627	genus	
17060020	TRUE		Ankyra judayi	0.625	species	
17080000	TRUE	Botryococcus		0.313	genus	
17080010	TRUE		Botryococcus braunii	0.344	species	
17170000	TRUE	Closteriopsis		0.696	genus	
17170010	TRUE		Closteriopsis acicularis	0.696	genus	not in training data
17170020	TRUE		Closteriopsis longissima	0.484	species	
17200000	TRUE	Coelastrum		0.699	genus	
17200010	TRUE		Coelastrum astroideum	0.726	species	
17200020	TRUE		Coelastrum microporum	0.718	species	
17200070	TRUE		Coelastrum sphaericum	0.699	genus	not in training data
17210000	FALSE	Coenochloris		0.437	genus	
17210010	TRUE		Coenochloris fottii	0.437	genus	not in training data
17220000	FALSE	Coenococcus		0.13	genus	
17230000	FALSE	Coenocystis		0.247	genus	
17230020	TRUE		Coenocystis planctonica	0.247	genus	not in training data
17250000	TRUE	Crucigenia		0.552	genus	
17250030	TRUE		Crucigenia tetrapedia	0.535	species	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
17260000	TRUE	Crucigeniella		0.504	genus	
17300000	FALSE	Dichotomococcus		0.452	genus	
17330000	TRUE	Dictyosphaerium		0.556	genus	
17330040	TRUE		Dictyosphaerium pulchellum	0.618	species	
17340000	TRUE	Didymocystis		0.424	genus	
17350020	TRUE		Didymogenes palatina	0.492	genus	too few records
17410000	FALSE	Franceia		0.593	genus	
17420000	TRUE	Gloeocystis		0.82	genus	
17430000	TRUE	Golenkinia		0.618	genus	
17430020	TRUE		Golenkinia radiata	0.618	genus	not in training data
17440000	FALSE	Golenkiniopsis		0.337	genus	
17440020	TRUE		Golenkiniopsis longispina	0.337	genus	not in training data
17500000	FALSE	Keratococcus		0.337	genus	
17510000	TRUE	Kirchneriella		0.605	genus	
17530000	TRUE	Korshikoviella		0.601	genus	
17540000	TRUE	Lagerheimia		0.778	genus	
17540040	TRUE		Lagerheimia genevensis	0.767	species	
17570000	TRUE	Micractinium		0.629	genus	
17570010	TRUE		Micractinium pusillum	0.629	genus	not in training data
17580000	TRUE	Monoraphidium		0.538	genus	
17580010	TRUE		Monoraphidium arcuatum	0.713	species	
17580020	TRUE		Monoraphidium contortum	0.596	species	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
17580030	TRUE		Monoraphidium convolutum	0.685	species	
17580040	TRUE		Monoraphidium griffithii	0.553	species	
17580050	TRUE		Monoraphidium irregulare	0.64	species	
17580070	TRUE		Monoraphidium komarkovae	0.614	species	
17580080	TRUE		Monoraphidium minutum	0.623	species	
17580120	TRUE		Monoraphidium tortile	0.538	genus	not in training data
17580130	TRUE		Monoraphidium dybowskii	0.419	species	
17630000	FALSE	Nephrocytium		0.436	genus	
17640000	TRUE	Oocystis		0.54	genus	
17640050	TRUE		Oocystis lacustris	0.542	species	
17640120	TRUE		Oocystis parva	0.432	species	
17670000	FALSE	Palmodictyon		0.223	genus	
17680000	TRUE	Pediastrum		0.686	genus	
17680020	TRUE		Pediastrum biradiatum	0.686	genus	not in training data
17680030	TRUE		Pediastrum boryanum	0.706	species	
17680050	TRUE		Pediastrum duplex	0.726	species	
17680080	TRUE		Pediastrum simplex	0.686	genus	not in training data
17680090	TRUE		Pediastrum tetras	0.628	species	
17690010	TRUE		Planktosphaeria gelatinosa	0.309	species	
17780000	TRUE	Quadrigula		0.271	genus	
17780020	TRUE		Quadrigula pfitzeri	0.186	species	
17800000	TRUE	Raphidocelis		0.511	genus	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
17810000	TRUE	Scenedesmus		0.616	genus	
17810080	TRUE		Scenedesmus armatus	0.603	species	
17810160	TRUE		Scenedesmus communis	0.701	species	
17810220	TRUE		Scenedesmus falcatus	0.859	species	
17810340	TRUE		Scenedesmus opoliensis	0.817	species	
17830000	FALSE	Schroederia		0.748	genus	
17830020	TRUE		Schroederia robusta	0.683	species	
17830030	TRUE		Schroederia setigera	0.757	species	
17860000	TRUE	Selenastrum		0.723	genus	
17870000	FALSE	Siderocelis		0.257	genus	
17910000	TRUE	Sphaerocystis		0.558	genus	
17910020	TRUE		Sphaerocystis schroeteri	0.479	species	
17960000	TRUE	Tetraedron		0.621	genus	
17960010	TRUE		Tetraedron caudatum	0.633	species	
17960030	TRUE		Tetraedron minimum	0.581	species	
17970000	FALSE	Tetrastrum		0.658	genus	
17970010	TRUE		Tetrastrum elegans	0.658	genus	not in training data
17970040	TRUE		Crucigenia quadrata	0.358	species	
17970050	TRUE		Tetrastrum staurogeniaeforme	0.834	species	
17970060	TRUE		Tetrastrum triangulare	0.658	genus	not in training data
18010000	FALSE	Treubaria		0.666	genus	
18010010	TRUE		Treubaria setigera	0.666	genus	not in training data

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
18030000	FALSE	Westella		0.442	genus	
24170000	TRUE	Gloeotila		0.264	genus	
24340000	FALSE	Stichococcus		0.365	genus	
24380000	FALSE	Ulothrix		0.305	genus	
25010000	TRUE	Elakatothrix		0.437	genus	
25010010	TRUE		Elakatothrix gelatinosa	0.436	species	
25010020	TRUE		Elakatothrix genevensis	0.342	species	
25030000	TRUE	Koliella		0.439	genus	
25030010	TRUE		Koliella longiseta	0.53	species	
25030020	TRUE		Koliella spiculiformis	0.271	species	
27040000	TRUE	Closterium		0.592	genus	
27040030	TRUE		Closterium aciculare	0.613	species	
27040040	TRUE		Closterium acutum	0.594	species	
27040044	TRUE		Closterium acutum var. variabile	0.579	species	
27040340	TRUE		Closterium kuetzingii	0.316	species	
27040500	TRUE		Closterium parvulum	0.499	species	
27050000	TRUE	Cosmarium		0.456	genus	
27051650	TRUE		Cosmarium punctulatum	0.388	species	
27052120	TRUE		Cosmarium subcrenatum	0.205	species	
27060000	FALSE	Cosmocladium		0.33	genus	
27070000	FALSE	Cylindrocystis		0.193	genus	
27110000	TRUE	Euastrum		0.367	genus	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
27120000	FALSE	Genicularia		0.232	genus	
27130000	TRUE	Gonatozygon		0.203	genus	
27180000	FALSE	Hyalotheca		0.23	genus	not in training data
27230000	FALSE	Netrium		0.19	genus	
27280000	FALSE	Pleurotaenium		0.183	genus	
27360040	TRUE		Spondylosium planum	0.339	species	
27380000	TRUE	Staurastrum		0.458	genus	
27380060	TRUE		Staurastrum anatinum	0.458	genus	not in training data
27380330	TRUE		Staurastrum cingulum	0.451	species	
27380840	TRUE		Staurastrum longipes	0.388	species	
27380860	TRUE		Staurastrum lunatum	0.338	species	
27381030	TRUE		Staurastrum paradoxum	0.412	species	
27381110	TRUE		Staurastrum pingue	0.309	species	
27381120	TRUE		Staurastrum planctonicum	0.27	species	
27381160	TRUE		Stauratsrum pseudopelagicum	0.249	species	
27381460	TRUE		Staurastrum tetracerum	0.458	genus	not in training data
27390000	TRUE	Staurodesmus		0.251	genus	
27390130	TRUE		Staurodesmus cuspidatus	0.255	species	
27390440	TRUE		Staurodesmus triangularis	0.169	species	
27400000	FALSE	Teilingia		0.271	genus	
27420000	FALSE	Tetmemorus		0.188	genus	
27430000	TRUE	Xanthidium		0.34	genus	

Code	UK Counter List	Genus	Species	Optima	Optima type	Reason for use of genus or group optima
27430020	TRUE		Xanthidium antilopaeum	0.302	species	
27440000	FALSE	Zygnema		0.202	genus	
90000000	TRUE	Picoplankton - unidentified single cells <2 µm diam.		0.539	genus	
90000003	TRUE	Nanoplankton - unidentified single cells 2-20 µm diameter		0.532	group	
90000004	TRUE	Unidentified cells >20 µm diam.		0.6	group	
90000005	TRUE	Nanoplankton - unidentified flagellates 2-20 µm diameter		0.519	group	

B. Overview of NGIG reference value and class boundaries for all metrics and types for each country

Table B.1 Finnish reference values and class boundaries for phytoplankton in lakes October 2011

Type	Classes	Values					EQRs				
		Chla µg/l	Biovolume mg/l	Chla/BV	TPI_{FI}	impact Cyano %	Classes	Chl-a	Biovolume	TPI_{FI}	Impact Cyano
L-N1	Ref value	3	0.50	0.60%	-1.30	0.5	Ref value	1.00	1.00	1.00	1.00
	HG	4	0.61	0.66%	-1.00	3.0	HG	0.75	0.82	0.93	0.97
	GM	7	1.30	0.54%	0.10	16	GM	0.43	0.38	0.67	0.84
	MP	14	2.60	0.54%	1.10	33	MP	0.21	0.19	0.44	0.67
	PB	27	5.00	0.54%	2.00	66	PB	0.11	0.10	0.23	0.34
	max value (upper anchor)	*n.a.*			*3.00*	*100*					
L-N2a	Ref value	3	0.40	0.75%	-1.30	0.5	Ref value	1.00	1.00	1.00	1.00
	HG	4	0.50	0.80%	-1.04	3.0	HG	0.75	0.80	0.94	0.97
	GM	7	0.90	0.78%	0.10	16	GM	0.43	0.44	0.67	0.84
	MP	14	1.90	0.74%	1.10	33	MP	0.21	0.21	0.44	0.67
	PB	27	3.80	0.71%	2.00	66	PB	0.11	0.11	0.23	0.34
	max value (upper anchor)	*n.a.*			*3.00*	*100*					

Type	Classes	Values					EQRs				
		Chla µg/l	Biovolume mg/l	Chla/BV	TPI_{FI}	impact Cyano %	Classes	Chl-a	Biovolume	TPI_{FI}	Impact Cyano
L-N2b	Ref value	2	0.25	0.80%	-1.50	0.5	Ref value	1.00	1.00	1.00	1.00
	HG	3	0.35	0.86%	-1.00	2.5	HG	0.67	0.71	0.88	0.98
	GM	5	0.75	0.67%	0.00	12	GM	0.40	0.33	0.63	0.88
	MP	10	1.50	0.67%	1.00	24	MP	0.20	0.17	0.38	0.76
	PB	20	3.00	0.67%	2.00	48	PB	0.10	0.08	0.13	0.52
	max value (upper anchor)	*n.a.*			*2.50*	*100*					
L-N5	Ref value	2	0.25	0.80%	-1.50	0.5	Ref value	1.00	1.00	1.00	1.00
	HG	3	0.35	0.86%	-1.00	2.5	HG	0.67	0.71	0.88	0.98
	GM	5	0.75	0.67%	0.00	12	GM	0.40	0.33	0.63	0.88
	MP	10	1.50	0.67%	1.00	24	MP	0.20	0.17	0.38	0.76
	PB	20	3.00	0.67%	2.00	48	PB	0.10	0.08	0.13	0.52
	max value (upper anchor)	*n.a.*			*2.50*	*100*					
L-N3a	Ref value	4.5	0.60	0.75%	-1.30	3.5	Ref value	1.00	1.00	1.00	1.00
	HG	6	0.75	0.80%	-1.00	5.0	HG	0.75	0.80	0.93	0.98
	GM	11	1.50	0.73%	0.20	20	GM	0.41	0.40	0.65	0.83
	MP	20	3.00	0.67%	1.00	40	MP	0.23	0.20	0.47	0.62

Type	Classes	Values					EQRs				
		Chla µg/l	Biovolume mg/l	Chla/BV	TPI_{FI}	impact Cyano %	Classes	Chl-a	Biovolume	TPI_{FI}	Impact Cyano
	PB	40	6.00	0.67%	2.00	70	PB	0.11	0.10	0.23	0.31
	max value (upper anchor)	*n.a.*			*3.00*	*100*					
L-N6a	Ref value	3.5	0.70	0.50%	-1.30	3.5	Ref value	1.00	1.00	1.00	1.00
	HG	6	0.90	0.67%	-1.00	5.0	HG	0.58	0.72	0.93	0.98
	GM	9	1.70	0.53%	0.20	20	GM	0.39	0.40	0.65	0.83
	MP	20	3.40	0.59%	1.00	40	MP	0.18	0.21	0.47	0.62
	PB	41	6.70	0.61%	2.00	70	PB	0.09	0.10	0.23	0.31
	max value (upper anchor)	*n.a.*			*3.00*	*100*					
L-N8a	Ref value	5	0.70	0.71%	-1.00	3.5	Ref value	1.00	1.00	1.00	1.00
	HG	7	0.90	0.78%	-0.50	5.0	HG	0.71	0.78	0.88	0.98
	GM	12	1.70	0.71%	1.00	20	GM	0.42	0.41	0.50	0.83
	MP	24	3.40	0.71%	2.00	40	MP	0.21	0.21	0.25	0.62
	PB	48	6.80	0.71%	2.50	70	PB	0.10	0.10	0.13	0.31
	max value (upper anchor)	*n.a.*			*3.00*	*100*					

Table B.2 Irish reference values and class boundaries for phytoplankton in lakes (November 2011)

Type	Classes	Chla µg/l	Composition Metric	Classes	Chla EQR	Composition Metric EQR
L-N1	Ref value	3	0.84	Ref value	1.00	1.00
	HG	6	0.82	HG	0.50	0.98
	GM	9	0.69	GM	0.33	0.82
	MP	18	0.41	MP	0.17	0.49
	PB	38	0.28	PB	0.08	0.33
	max value (upper anchor)	*n.a.*				
L-N2a	Ref value	2.5	0.84	Ref value	1.00	1.00
	HG	5.0	0.82	HG	0.50	0.98
	GM	9	0.69	GM	0.29	0.82
	MP	17	0.41	MP	0.15	0.49
	PB	36	0.28	PB	0.07	0.33
	max value (upper anchor)	*n.a.*				
L-N3a	Ref value	3.0	0.84	Ref value	1.00	1.00
	HG	6.0	0.82	HG	0.50	0.98
	GM	9.1	0.69	GM	0.33	0.82
	MP	17.7	0.41	MP	0.17	0.49
	PB	37.5	0.28	PB	0.08	0.33
	max value (upper anchor)	*n.a.*				

Type	Classes	Chla µg/l	Composition Metric	Classes	Chla EQR	Composition Metric EQR
L-N8a	Ref value	3.5	0.84	Ref value	1.00	1.00
	HG	5.8	0.82	HG	0.60	0.98
	GM	10.0	0.69	GM	0.35	0.82
	MP	20.0	0.41	MP	0.18	0.49
	PB	40.0	0.28	PB	0.09	0.33
	max value (upper anchor)	*n.a.*				

Table B.3 Norwegian reference values and class boundaries for phytoplankton in lakes (November 2011)

Type	Classes	Chla µg/l	Biovolume mg/l	Chla/BV	PTI_{No}	Cyano-biovol (max Jul-Sep) mg/l		Classes	Chla EQR	BiovolumeEQR	PTI_{NO} EQR	Cyano-max EQR
L-N1	Ref value	3	0.28	1.07%	2.10	0.00		Ref value	1.00	1.00	1.00	1.00
	HG	6	0.64	0.94%	2.30	0.16		HG	0.50	0.94	0.89	0.98
	GM	9	1.04	0.87%	2.50	1.00		GM	0.33	0.87	0.79	0.90
	MP	18	2.35	0.77%	2.70	2.00		MP	0.17	0.64	0.68	0.80
	PB	36	5.33	0.68%	3.00	5.00		PB	0.08	0.12	0.53	0.50
	max value (upper anchor)	*n.a.*	*6.00*		*4.00*	*10.00*						
L-N2a	Ref value	2	0.18	1.14%	2.00	0.00		Ref value	1.00	1.00	1.00	1.00
	HG	4	0.40	1.00%	2.20	0.16		HG	0.50	0.94	0.90	0.98
	GM	6	0.64	0.93%	2.40	1.00		GM	0.33	0.88	0.80	0.90

Type	Classes	Chla µg/l	Biovolume mg/l	Chla/BV	PTI_{No}	Cyano-biovol (max Jul-Sep) mg/l		Classes	Chla EQR	BiovolumeEQR	PTI_{NO} EQR	Cyano-max EQR
	MP	13	1.60	0.81%	2.60	2.00		MP	0.15	0.63	0.70	0.80
	PB	27	3.79	0.71%	2.80	5.00		PB	0.07	0.05	0.60	0.50
	max value (upper anchor)	*n.a.*	*4.00*		*4.00*	*10.00*						
L-N2b	Ref value	1.3	0.11	1.23%	1.90	0.00		Ref value	1.00	1.00	1.00	1.00
	HG	2	0.18	1.14%	2.10	0.16		HG	0.65	0.98	0.90	0.98
	GM	4	0.40	1.00%	2.30	1.00		GM	0.33	0.92	0.81	0.90
	MP	7	0.77	0.91%	2.50	2.00		MP	0.19	0.81	0.71	0.80
	PB	15	1.90	0.79%	2.70	5.00		PB	0.09	0.49	0.62	0.50
	max value (upper anchor)	*n.a.*	*3.60*		*4.00*	*10.00*						
L-N5	Ref value	1.3	0.11	1.23%	1.80	0.00		Ref value	1.00	1.00	1.00	1.00
	HG	2	0.18	1.14%	2.00	0.16		HG	0.65	0.98	0.91	0.98
	GM	4	0.40	1.00%	2.20	1.00		GM	0.33	0.90	0.82	0.90
	MP	7	0.77	0.91%	2.40	2.00		MP	0.19	0.77	0.73	0.80
	PB	15	1.90	0.79%	2.60	5.00		PB	0.09	0.38	0.64	0.50
	max value (upper anchor)	*n.a.*	*3.00*		*4.00*	*10.00*						
L-N3a	Ref value	2.7	0.30	0.90%	2.10	0.00		Ref value	1.00	1.00	1.00	1.00

Type	Classes	Chla µg/l	Biovolume mg/l	Chla/BV	PTI_{No}	Cyano-biovol (max Jul-Sep) mg/l		Classes	Chla EQR	BiovolumeEQR	PTI_{NO} EQR	Cyano-max EQR
	HG	5.4	0.60	0.90%	2.30	0.16		HG	0.50	0.95	0.89	0.98
	GM	9	1.00	0.90%	2.50	1.00		GM	0.30	0.88	0.79	0.90
	MP	16	2.00	0.80%	2.70	2.00		MP	0.17	0.70	0.68	0.80
	PB	32	4.60	0.70%	3.00	5.00		PB	0.08	0.25	0.53	0.50
	max value (upper anchor)	*n.a.*	*6.00*		*4.00*	*10.00*						
L-N6a	Ref value	2	0.18	1.14%	2.00	0.00		Ref value	1.00	1.00	1.00	1.00
	HG	4	0.40	1.00%	2.20	0.16		HG	0.50	0.93	0.90	0.98
	GM	6	0.64	0.93%	2.40	1.00		GM	0.33	0.86	0.80	0.90
	MP	12	1.46	0.82%	2.60	2.00		MP	0.17	0.63	0.70	0.80
	PB	25	3.46	0.72%	2.80	5.00		PB	0.08	0.04	0.60	0.50
	max value (upper anchor)	*n.a.*	*3.60*		*4.00*	*10.00*						
L-N8a	Ref value	3.5	0.34	1.03%	2.25	0.00		Ref value	1.00	1.00	1.00	1.00
	HG	7	0.77	0.91%	2.45	0.16		HG	0.50	0.94	0.89	0.98
	GM	10.5	1.24	0.84%	2.65	1.00		GM	0.33	0.86	0.77	0.90
	MP	20	2.66	0.75%	2.85	2.00		MP	0.18	0.65	0.66	0.80
	PB	40	6.03	0.66%	3.25	5.00		PB	0.09	0.15	0.43	0.50
	max value (upper anchor)	*n.a.*	*7.00*		*4.00*	*10.00*						

Table B.4 Swedish reference values and class boundaries for phytoplankton in lakes (November 2011)

Type	Classes	Chla µg/l	Biovolume	chla/BV	TPI_{SE}	all Cyano %		Classes	Chla EQR	BiovolumeEQR	TPI_{SE} EQR	all Cyano EQR
L-N1	Ref value	2.5	0.2	1.25%	-1.25	5		Ref value	1.00	1.00	1.00	1.00
	HG	5	0.5	1.00%	-0.90	10		HG	0.50	0.40	0.50	0.95
	GM	8.5	1.0	0.85%	1.00	24		GM	0.30	0.20	0.13	0.80
	MP	17	2.2	0.77%	2.00	43		MP	0.15	0.09	0.10	0.60
	PB	33	4.8	0.69%	n.a.	81		PB	0.08	0.04	0.00	0.20
	max value (upper anchor)	*n.a.*				*100*						
L-N2a	Ref value	2.5	0.2	1.25%	-1.25	5		Ref value	1.00	1.00	1.00	1.00
	HG	5	0.5	1.00%	-0.90	10		HG	0.50	0.40	0.50	0.95
	GM	8.5	1.0	0.85%	1.00	24		GM	0.30	0.20	0.13	0.80
	MP	17	2.2	0.77%	2.00	43		MP	0.15	0.09	0.10	0.60
	PB	33	4.8	0.69%	n.a.	81		PB	0.08	0.04	0.00	0.20
	max value (upper anchor)	*n.a.*				*100*						

Type	Classes	Chla µg/l	Biovolume	chla/BV	TPI_{SE}	all Cyano %		Classes	Chla EQR	BiovolumeEQR	TPI_{SE} EQR	all Cyano EQR
L-N2b	Ref value	2.5	0.2	1.25%	-1.25	5		Ref value	1.00	1.00	1.00	1.00
	HG	5	0.5	1.00%	-0.90	10		HG	0.50	0.40	0.50	0.95
	GM	7.5	0.8	0.94%	1.00	24		GM	0.30	0.25	0.13	0.80
	MP	17	2.2	0.77%	2.00	43		MP	0.15	0.09	0.10	0.60
	PB	33	4.8	0.69%	n.a.	81		PB	0.08	0.04	0.00	0.20
	max value (upper anchor)	*n.a.*				*100*						
L-N5	Ref value	2	0.2	1.00%	-1.5	5		Ref value	1.00	1.00	1.00	1.00
	HG	4	0.4	1.00%	-1.0	10		HG	0.50	0.50	0.50	0.95
	GM	6	0.65	0.92%	-0.50	24		GM	0.33	0.31	0.33	0.80
	MP	12	1.5	0.80%	0.50	43		MP	0.17	0.13	0.20	0.60
	PB	24	3.3	0.73%	n.a.	81		PB	0.08	0.06	0.00	0.20
	max value (upper anchor)	*n.a.*				*100*						
L-N3a	Ref value	3	0.3	1.00%	-1.0	7		Ref value	1.00	1.00	1.00	1.00
	HG	6	0.6	1.00%	-0.5	14		HG	0.50	0.50	0.50	0.92
	GM	10	1.2	0.83%	1.00	30		GM	0.30	0.25	0.20	0.75
	MP	20	2.7	0.74%	2.00	44		MP	0.15	0.11	0.14	0.60
	PB	40	6.0	0.67%	n.a.	81		PB	0.08	0.05	0.00	0.20
	max value (upper anchor)	*n.a.*				*100*						

Type	Classes	Chla µg/l	Biovolume	chla/BV	TPI_{SE}	all Cyano %		Classes	Chla EQR	BiovolumeEQR	TPI_{SE} EQR	all Cyano EQR
L-N6a	Ref value	2.5	0.2	1.25%	-1.5	7		Ref value	1.00	1.00	1.00	1.00
	HG	5	0.5	1.00%	-1.0	14		HG	0.50	0.40	0.50	0.92
	GM	7.5	0.8	0.94%	-0.50	30		GM	0.33	0.25	0.33	0.75
	MP	17	2.2	0.77%	0.50	44		MP	0.15	0.09	0.20	0.60
	PB	33	4.8	0.69%	n.a.	81		PB	0.08	0.04	0.00	0.20
	max value (upper anchor)	*n.a.*				*100*						
L-N8a	Ref value	3	0.3	1.00%	-1.0	7		Ref value	1.00	0.67	1.00	1.00
	HG	6	0.6	1.00%	-0.5	14		HG	0.50	0.33	0.50	0.92
	GM	10	1.2	0.83%	1.00	30		GM	0.30	0.17	0.20	0.75
	MP	20	2.7	0.74%	2.00	44		MP	0.15	0.07	0.14	0.60
	PB	40	6.0	0.67%	n.a.	81		PB	0.08	0.03	0.00	0.20
	max value (upper anchor)	*n.a.*				*100*						

Table B.5 UK reference values and class boundaries for phytoplankton in lakes (November 2011)

Note: UK Ref Chl and Ref PTI is modelled and is lake specific.

Type	Classes	Chla µg/l	PTI_{UK}	Cyano-biovol (mean Jul-Sep) mg/l		Classes	Chla EQR µg/l	PTI_{UK} EQR	Cyano-mean EQR mg/l
L-N1	Ref value	2.9	site-spec	0.00		Ref value			1.00

Type	Classes	Chla µg/l	PTI_{UK}	Cyano-biovol (mean Jul-Sep) mg/l		Classes	Chla EQR µg/l	PTI_{UK} EQR	Cyano-mean EQR mg/l
	HG	6		0.08		HG	0.50	0.95	0.47
	GM	9		0.56		GM	0.33	0.84	0.32
	MP	17		1.58		MP	0.17	0.72	0.23
	PB	58		5.62		PB	0.05	0.60	0.13
	max value (upper anchor)	*n.a.*	*0.75*	*30.00*					
L-N2a	Ref value	2.2	site-spec	0.00		Ref value			1.00
	HG	3.4		0.08		HG	0.64	0.98	0.47
	GM	7.6		0.56		GM	0.29	0.87	0.32
	MP	15		1.58		MP	0.15	0.75	0.23
	PB	44		5.62		PB	0.05	0.63	0.13
	max value (upper anchor)	*n.a.*	*0.75*	*30.00*					
L-N2b	Ref value	2	site-spec	0.00		Ref value			1.00
	HG	3		0.08		HG	0.64	0.98	0.47
	GM	6		0.56		GM	0.33	0.87	0.32
	MP	12		1.58		MP	0.17	0.75	0.23
	PB	40		5.62		PB	0.05	0.63	0.13
	max value (upper anchor)	*n.a.*	*0.75*	*30.00*					
L-N3a	Ref value	2.8		0.00		Ref value			1.00
	HG	6		0.08		HG	0.50	0.96	0.47

Type	Classes	Chla µg/l	PTI_{UK}	Cyano-biovol (mean Jul-Sep) mg/l		Classes	Chla EQR µg/l	PTI_{UK} EQR	Cyano-mean EQR mg/l
	GM	9		0.56		GM	0.29	0.85	0.32
	MP	19		1.58		MP	0.15	0.73	0.23
	PB	56		5.62		PB	0.05	0.61	0.13
	max value (upper anchor)	*n.a.*	*0.75*	*30.00*					
L-N8a	Ref value	3.8		0.00		Ref value			1.00
	HG	8		0.08		HG	0.50	0.95	0.47
	GM	12		0.56		GM	0.33	0.84	0.32
	MP	22		1.58		MP	0.17	0.72	0.23
	PB	76		5.62		PB	0.05	0.60	0.13
	max value (upper anchor)	*n.a.*	*0.75*	*30.00*					

C. List of NGIG reference lakes, including coordinates and pressure data

Table C.1 List of NGIG reference lakes, including coordinates and pressure data (October 2011)

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N1	FI	Iso-Roine	61.2095	24.5931	0.98	5.09	6.35	87.6	6.8	5.8	13.5	0.37
L-N1	FI	Kukkia	61.3277	24.6736	0.56	1.34	4.63	93.5	3.3	3.6	10.2	0.32
L-N1	FI	Pyhäjärvi	67.0401	27.2397	0.82	0.00	0.00	99.2	2.8	4.6	12.9	0.21
L-N2a	FI	Ala-Keitele	62.5725	25.8557	0.48	1.49	3.84	94.2	4.5	5.2	9.6	0.35
L-N2a	FI	Alvajärvi	63.4065	25.4310	0.29	4.24	5.24	90.2	3.0	7.1	12.3	0.37
L-N2a	FI	Iso Hietajärvi	63.1610	30.7136	0.00	0.00	0.00	100.0	0.0	2.4	6.4	0.20
L-N2a	FI	Iso-Kisko	60.1822	23.4598	0.00	0.00	3.90	96.1	1.2	3.5	8.3	0.27
L-N2a	FI	Juojärvi	62.7940	28.4999	0.30	0.50	2.41	96.8	3.3	2.9	5.4	0.36
L-N2a	FI	Konnevesi	62.6261	26.6142	0.62	1.67	4.18	93.5	7.0	4.0	8.2	0.34
L-N2a	FI	Kuohijärvi	61.1975	24.9038	0.26	1.34	2.86	95.5	2.1	3.0	8.1	0.38
L-N2a	FI	Kuolimo	61.2184	27.5719	0.53	0.21	2.60	96.7	4.1	2.1	4.4	0.34
L-N2a	FI	Kuusvesi	62.4233	26.0484	0.64	2.04	4.68	92.6	7.1	4.7	9.6	0.36
L-N2a	FI	Puruvesi	61.8884	29.5246	0.53	1.42	2.23	95.8	6.9	2.7	7.6	0.25
L-N2a	FI	Pyhäjärvi	63.7112	25.9886	0.61	1.14	3.89	94.4	7.7	4.7	12.6	0.41
L-N2a	FI	Rautjärvi	61.1069	26.3419	0.00	0.00	0.60	99.4	0.2	2.2	4.5	0.36
L-N2a	FI	Suontee	61.6727	26.5389	0.16	0.13	3.23	96.5	1.8	2.1	4.4	0.28
L-N2b	FI	Vuohijärvi	61.1867	26.7020	0.51	0.47	3.76	95.3	4.5	2.6	5.2	0.39
L-N3a	FI	Haukijärvi	63.0395	27.0862	0.00	0.00	1.48	98.5	0.3	5.1	9.8	0.36
L-N3a	FI	Haukivesi	62.0608	28.3417	0.70	2.27	3.50	93.5	9.5	9.2	14.8	0.48
L-N3a	FI	Jormasjärvi	64.0514	28.1638	0.00	0.21	1.36	98.4	0.7	5.2	13.8	0.43

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N3a	FI	Kolima	63.2032	25.9027	0.43	3.03	4.48	92.1	3.2	12.3	18.1	0.52
L-N3a	FI	Kyyvesi	61.8942	27.2107	0.55	0.78	5.07	93.6	3.9	8.7	15.1	0.51
L-N3a	FI	Lentua	64.2321	29.5116	0.00	0.03	0.61	99.4	0.5	4.4	11.5	0.32
L-N3a	FI	Nilakka	63.0848	26.5531	0.30	2.00	4.29	93.4	3.5	9.3	15.2	0.44
L-N3a	FI	Ontojärvi-Nurmesjärvi	64.0973	29.0183	0.16	0.03	0.83	99.0	2.0	7.2	17.7	0.34
L-N3a	FI	Orivesi	62.0920	29.8976	0.53	1.44	2.17	95.9	7.8	6.1	11.8	0.38
L-N3a	FI	Pielavesi	63.2359	26.7151	0.29	2.15	4.75	92.8	3.8	6.7	11.1	0.41
L-N3a	FI	Pielinen	62.9222	30.2027	0.27	0.82	1.54	97.4	3.8	4.9	10.8	0.40
L-N3a	FI	Pihlajavesi	61.5232	28.4823	0.70	2.15	3.49	93.7	9.4	3.7	8.3	0.38
L-N3a	FI	Punelia	60.6684	24.2069	0.00	0.00	0.62	99.4	1.4	4.2	10.4	0.28
L-N3a	FI	Puula	61.6565	27.0657	0.45	0.55	3.81	95.2	4.2	6.3	10.7	0.43
L-N3a	FI	Takkajärvi	64.9496	28.2195	0.00	0.00	0.00	100.0	0.0	2.9	6.8	0.28
L-N5	FI	Inarijärvi l. Anarjävri	68.8074	27.6072	0.09	0.00	0.03	99.9	0.4	1.3	4.9	0.17
L-N5	FI	Iso Venejärvi	66.9849	25.9722	0.00	0.00	0.00	100.0	0.1	2.6	8.8	0.17
L-N6a	FI	Kontojärvi	66.7729	25.3067	0.00	0.00	0.00	100.0	0.2	3.5	14.4	0.25
L-N6a	FI	Miekojärvi	66.6028	24.3677	0.03	0.00	0.62	99.4	0.7	7.0	16.6	0.32
L-N6a	FI	Mukkajärvi	66.8076	25.2765	0.00	0.00	0.00	100.0	0.2	4.0	15.6	0.32
L-N6a	FI	Pesiöjärvi	64.9310	28.6581	0.00	0.00	0.65	99.4	1.9	7.8	14.9	0.33
L-N6a	FI	Piispajärvi	65.2946	29.0549	0.00	0.00	0.00	100.0	0.8	5.9	13.1	0.34
L-N6a	FI	Pöyliöjärvi	66.4505	25.8005	0.00	0.00	0.00	100.0	0.2	5.0	12.3	0.35
L-N6a	FI	Simojärvi	66.0763	27.2198	0.00	0.11	0.88	99.0	0.5	4.5	7.9	0.26
L-N8a	FI	Ala-Keitele (N60+99.50)	62.5725	25.8557	0.48	1.49	3.84	94.2	4.5	3.7	7.6	0.33
L-N8a	FI	Höytiäinen	62.7409	29.7667	0.36	3.64	4.31	91.7	4.6	4.1	9.7	0.42

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N2a	IE	Doo	53.6508	-9.7636	0.00	0.00	0.00	100.0	0.1	2.8	15.0	
L-N1	NO	Andsvatnet	69.0661	18.4214	0.00	0.00	0.00	100.0	2.5	1.1	1.7	0.12
L-N1	NO	Drevvatnet	66.0535	13.3815	0.00	0.04	1.09	98.9	5.4	1.8	2.5	0.13
L-N1	NO	Hostovatnet	63.1913	9.5683	0.00	0.00	0.00	100.0	0.4	5.5	5.8	0.25
L-N1	NO	Langvatnet	62.8981	7.1880	0.00	0.00	0.00	100.0	0.4	2.2	7.7	0.24
L-N1	NO	Nosvatnet	62.9066	7.3705	0.00	3.73	2.77	93.5	0.2	3.2	8.1	0.31
L-N1	NO	Røyrbakvatnet	68.9576	17.7507	0.00	0.00	4.15	95.9	0.1	1.4	3.3	0.09
L-N1	NO	Sagelvvatnet	69.1907	19.0956	0.00	3.93	0.53	95.5	0.1	2.2	6.8	0.14
L-N1	NO	Øvrevatnet	68.8680	17.9511	0.00	0.01	0.86	99.1	0.6	1.1	2.7	0.10
L-N2a	NO	Breidflå	58.5516	7.7938	0.00	0.04	0.53	99.4	0.1	1.1	4.0	0.23
L-N2a	NO	Eidsvatnet	64.5418	12.1222	0.00	0.20	2.57	97.2	7.3	1.8	5.4	0.19
L-N2a	NO	Fetvatnet	62.3235	6.5972	0.00	0.06	3.80	96.1	0.1	1.7	5.3	0.16
L-N2a	NO	Gagnåsvatnet	63.2753	9.6597	0.00	0.20	3.06	96.7	5.6	2.6	5.3	0.22

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N2a	NO	Hafstadvatnet	62.8247	8.3367	0.00	0.00	0.00	100.0	0.7	1.7	3.5	0.14
L-N2a	NO	Hetlandsvatnet	59.1754	6.1164	0.00	0.00	0.00	100.0	5.6	2.1	5.7	0.75
L-N2a	NO	Hjartsjåvatnet	59.6041	8.7360	0.00	0.96	2.79	96.3	0.3	0.9	5.5	0.26
L-N2a	NO	Kvitebergsvatnet	60.0285	5.8592	0.00	0.00	0.00	100.0	0.8	1.9	6.1	0.35
L-N2a	NO	Lønavatnet	60.6895	6.4820	0.00	0.05	2.09	97.9	0.1	1.2	5.5	0.15
L-N2a	NO	Nome	59.2962	9.1685	0.09	0.09	1.19	98.6	0.2	1.6	5.5	0.24
L-N2a	NO	Nordre Storavatn	59.8915	5.3231	0.00	0.00	0.00	100.0	0.2	2.8	5.3	0.42
L-N2a	NO	Nordre Storavatnet	59.3686	5.5595	0.00	0.01	0.16	99.8	2.9	2.7	8.1	0.44
L-N2a	NO	Nøklevann	59.8765	10.8773	0.40	0.00	0.00	99.6	6.0	2.8	5.5	0.28
L-N2a	NO	Sigernessjøen	60.1173	12.0470	0.00	0.00	0.53	99.5	0.2	2.8	5.5	0.33
L-N2a	NO	Skagestadvatnet	58.0653	7.5899	0.00	0.00	2.06	97.9	5.9	2.3	6.3	0.60
L-N2a	NO	Stølsvatnet	62.8841	8.2056	0.00	0.00	0.00	100.0	0.2	1.7	4.6	0.20
L-N2a	NO	Søndre Storavatn	59.7837	5.4206	0.00	0.04	1.16	98.8	1.0	1.1	4.4	0.42

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N2b	NO	Aksdalsvatnet	59.4181	5.4293	0.00	0.00	0.00	100.0	2.8	2.3	6.1	0.55
L-N2b	NO	Askevatnet	60.4921	5.1696	0.00	0.00	0.00	100.0	2.0	1.3	3.0	0.36
L-N2b	NO	Bandak	59.4133	8.1984	0.07	0.07	0.85	99.0	2.3	1.4	4.8	0.23
L-N2b	NO	Bjøreimsvatnet	59.0674	5.9911	0.00	0.35	3.52	96.1	3.9	1.4	4.4	0.45
L-N2b	NO	Breimsvatnet	61.7315	6.3916	0.00	0.12	5.64	94.2	0.1	2.1	5.3	0.19
L-N2b	NO	Byrkjelandsvatnet	58.7127	6.1997	0.00	0.65	5.57	93.8	0.3	1.4	4.6	0.38
L-N2b	NO	Eidsfjordvatnet	60.4546	7.1039	0.00	0.00	0.00	100.0	2.8	1.1	4.5	0.15
L-N2b	NO	Endestadvatnet	61.6037	5.5668	0.00	0.00	0.00	100.0	0.1	3.9	7.6	0.16
L-N2b	NO	Engsetvatnet	62.5334	6.6328	0.00	0.00	0.03	100.0	5.0	2.4	4.8	0.18
L-N2b	NO	Evangervatnet	60.6496	6.1045	0.11	0.00	4.83	95.1	0.5	2.1	6.3	0.17
L-N2b	NO	Flåvatnet	59.3053	8.9087	0.06	0.08	1.03	98.8	2.6	1.7	4.1	0.25
L-N2b	NO	Gjønavatnet	60.2592	5.8498	0.00	0.00	11.12	88.9	7.3	1.3	2.7	0.32
L-N2b	NO	Hafslovatnet	61.3059	7.1666	0.00	0.09	1.54	98.4	2.9	1.8	5.8	0.14

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N2b	NO	Henangervatn	60.2076	5.8313	0.00	0.00	4.49	95.5	0.2	3.2	8.2	0.36
L-N2b	NO	Hofreistævatnet	58.6761	6.1699	0.00	0.56	5.26	94.2	2.8	1.3	3.1	0.36
L-N2b	NO	Holsavatnet	61.4201	6.1346	0.00	0.00	0.00	100.0	2.6	2.5	5.7	0.17
L-N2b	NO	Hovlandsdalsvatnet	61.2477	5.4193	0.00	0.00	0.00	100.0	1.4	2.7	7.3	0.17
L-N2b	NO	Hovlandsvatnet	61.2678	5.3666	0.00	0.00	0.00	100.0	1.0	2.2	8.3	0.17
L-N2b	NO	Hovsvatnet	58.4923	6.4936	0.00	4.83	0.00	95.2	0.5	1.4	5.0	0.40
L-N2b	NO	Hurdalssjøen	60.3240	11.1004	0.17	0.24	2.97	96.6	5.3	1.8	3.5	0.42
L-N2b	NO	Hæstadfjorden	61.3302	5.9259	0.00	0.06	0.88	99.1	0.8	1.9	4.7	0.15
L-N2b	NO	Krøderen	60.1573	9.7187	0.20	2.33	0.00	97.5	2.0	2.5	8.6	0.23
L-N2b	NO	Lovatnet	61.8525	6.8965	0.00	0.00	0.00	100.0	0.0	1.9	6.2	0.14
L-N2b	NO	Lundevatnet	58.4434	6.5656	0.07	0.91	0.00	99.0	0.0	1.7	5.1	0.31
L-N2b	NO	Lygne	58.4764	7.2048	0.00	0.00	16.54	83.5	0.6	2.0	8.0	0.36
L-N2b	NO	Lykkjebøvatnet	61.6167	5.5843	0.00	0.00	0.91	99.1	0.7	4.0	8.2	0.16

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N2b	NO	Movatnet	61.4362	5.9680	0.00	0.12	1.30	98.6	0.2	2.5	7.1	0.19
L-N2b	NO	Norsjø	59.3527	9.2216	0.20	0.14	2.06	97.6	1.1	2.3	6.9	0.38
L-N2b	NO	Sandvinvatnet	60.0271	6.5577	0.00	0.02	0.62	99.4	0.2	0.8	5.0	0.18
L-N2b	NO	Seljordvatnet	59.4371	8.7479	0.11	0.08	2.21	97.6	0.1	1.8	4.8	0.29
L-N2b	NO	Selura	58.3129	6.6958	0.22	0.72	4.59	94.5	0.8	0.8	4.5	0.39
L-N2b	NO	Snåsavatnet	64.2002	12.0567	0.00	0.14	2.03	97.8	0.5	1.9	4.7	0.26
L-N2b	NO	Sundkilen	59.3780	8.5196	0.07	1.14	0.00	98.8	0.5	2.3	7.5	0.30
L-N2b	NO	Svardalsvatnet	61.5342	5.4484	0.00	0.00	0.00	100.0	0.5	3.2	7.3	0.16
L-N2b	NO	Tinnsjø	59.9553	8.8425	0.09	0.02	0.19	99.7	5.6	1.5	3.6	0.38
L-N2b	NO	Tyrivatnet	59.2648	9.1386	0.09	0.07	1.05	98.8	0.7	1.4	3.5	0.47
L-N2b	NO	Vangsvatnet, øvre basseng	60.6205	6.3941	0.17	0.06	3.50	96.3	0.4	2.1	7.3	0.15
L-N2b	NO	Vassbygdvatnet	60.8709	7.2708	0.00	0.03	0.40	99.6	0.8	1.2	5.1	0.16
L-N2b	NO	Veitastrondvatnet	61.3381	7.0919	0.00	0.00	0.00	100.0	0.2	1.4	5.4	0.12

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N2b	NO	Viksdalsvatnet	61.3225	5.9828	0.00	0.06	0.95	99.0	0.3	2.0	5.3	0.13
L-N2b	NO	Årdalsvatnet, hovedstasjon	61.2686	7.7581	0.06	0.00	1.78	98.2	0.5	1.6	6.1	0.12
L-N3a	NO	Dølisjøen	60.2863	11.7837	0.00	5.91	0.00	94.1	0.4	4.3	9.1	0.40
L-N3a	NO	Gjerstadvatnet	58.8554	9.0745	0.00	0.00	2.28	97.7	0.3	1.1	6.1	0.38
L-N3a	NO	Heimsvatnet	63.4195	9.0561	0.00	0.38	3.81	95.8	3.3	2.5	5.0	0.22
L-N3a	NO	Hukusjøen	60.5201	11.9386	0.00	0.00	8.06	91.9	4.1	2.5	7.2	0.34
L-N3a	NO	Nugguren	60.3060	12.0879	0.10	0.28	3.41	96.2	1.9	2.3	8.3	0.35
L-N3a	NO	Tinnå	59.6103	9.2782	0.07	0.03	0.36	99.5	0.0	1.4	3.9	0.42
L-N3a	NO	Trævatn	58.4964	8.5900	0.00	0.00	0.00	100.0	0.2	1.3	6.4	0.41
L-N3a	NO	Venneslafjorden	58.2755	7.9583	0.05	0.77	0.00	99.2	0.2	1.3	5.5	0.26
L-N5	NO	Bergsjøen	60.2422	9.7766	0.00	1.39	0.00	98.6	0.3	2.2	5.5	0.27
L-N5	NO	Espedalsvatnet	61.3833	9.6101	0.00	0.06	1.94	98.0	4.3	1.8	4.7	0.15
L-N5	NO	Fustvatnet	65.9045	13.3822	0.00	0.00	0.00	100.0	1.0	1.3	2.5	0.10

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N5	NO	Grungevatnet	59.7115	7.7487	0.00	0.03	0.40	99.6	1.1	1.9	4.6	0.17
L-N5	NO	Hartevatnet	59.5383	7.3555	0.00	0.00	0.00	100.0	0.0	0.8	2.5	0.18
L-N5	NO	Heggefjorden	61.1369	9.0687	0.00	2.06	0.00	97.9	0.8	2.0	6.8	0.38
L-N5	NO	Holsfjorden	60.6117	8.3022	0.02	0.07	0.80	99.1	1.6	1.8	5.9	0.18
L-N5	NO	Hovsfjorden	60.6132	8.2456	0.00	0.05	0.59	99.4	0.0	1.4	5.3	0.17
L-N5	NO	Langsjøen	62.1601	11.6010	0.00	0.00	0.00	100.0	3.7	2.2	6.5	0.18
L-N5	NO	Langvatnet ved Sulitjelma	67.1350	16.0401	0.00	2.67	0.00	97.3	0.3	0.7	3.2	0.10
L-N5	NO	Lenglingen	64.2249	13.8005	0.00	0.07	1.14	98.8	0.2	1.5	3.0	0.18
L-N5	NO	Lysvatnet	69.3907	17.8314	0.00	0.02	0.42	99.6	5.2	0.9	1.8	0.07
L-N5	NO	Narsjøen	62.3544	11.4826	0.00	0.00	0.28	99.7	1.3	2.5	5.0	0.18
L-N5	NO	Oftevatn	59.4906	8.2054	0.13	1.78	0.00	98.1	0.4	2.5	7.3	0.26
L-N5	NO	Olstappen	61.5062	9.4002	0.00	0.00	1.14	98.9	0.1	1.6	6.7	0.18
L-N5	NO	Sandnesvatnet	67.8576	15.9652	0.00	0.00	0.00	100.0	0.8	1.1	1.8	0.10

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N5	NO	Skjelbreidvatnet	64.4936	13.3703	0.00	0.17	1.59	98.2	0.9	1.5	3.0	0.17
L-N5	NO	Skogsfjordvatnet	69.9557	19.1568	0.00	0.00	0.00	100.0	0.6	0.9	1.3	0.07
L-N5	NO	Skredvatnet	59.3284	8.1266	0.06	0.03	0.49	99.4	8.8	1.3	5.0	0.24
L-N5	NO	Skurdalsvatnet	59.5720	8.3097	0.00	0.02	0.48	99.5	3.9	1.7	6.8	0.18
L-N5	NO	Steinsetfjorden	61.0555	9.4223	0.00	0.00	0.00	100.0	0.1	1.7	6.0	0.23
L-N5	NO	Strandafjorden	60.6136	8.5251	0.08	0.92	0.00	99.0	1.7	2.4	8.1	0.19
L-N5	NO	Sudndalsfjorden	60.6354	8.0641	0.00	0.02	0.22	99.8	0.2	1.1	6.5	0.16
L-N5	NO	Sæbufjorden	61.0237	9.1980	0.00	2.47	1.00	96.5	0.4	1.5	7.4	0.33
L-N5	NO	Ulen	64.1554	13.8631	0.00	0.04	0.87	99.1	0.9	1.1	3.3	0.15
L-N5	NO	Ustedalsfjorden	60.5230	8.1766	0.04	0.00	0.32	99.6	1.0	1.1	7.1	0.16
L-N5	NO	Vinjevatnet	59.6172	7.8409	0.00	0.03	0.47	99.5	0.2	1.1	4.0	0.18
L-N5	NO	Ørevatn	58.5579	7.3879	0.00	0.02	0.31	99.7	5.1	1.5	6.0	0.33
L-N6a	NO	Vermunden	60.7010	12.3785	0.00	0.00	0.15	99.8	0.8	2.9	9.1	0.32

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N8a	NO	Storvatnet	63.6083	9.6391	0.00	0.00	0.00	100.0	8.0	3.7	8.8	0.23
L-N2a	SE	Västra Solsjön	59.1015	12.2788	0.00	2.33	0.00	97.7	1.3	1.6	4.8	0.33
L-N3a	SE	Fiolen	57.0922	14.5325	0.00	2.06	15.14	82.8	4.8	6.5	12.7	0.56
L-N5	SE	Abiskojaure	68.3075	18.6567	0.00	0.00	0.00	100.0	0.0	0.8	4.3	0.19
L-N5	SE	Båtkåjaure	66.9160	16.6148	0.00	0.00	0.00	100.0	0.0	0.8	3.7	0.19
L-N5	SE	Louvvajaure	66.3945	18.1733	0.00	0.00	0.00	100.0	0.0	0.8	3.9	0.19
L-N5	SE	Pahajärvi	66.7723	23.3578	0.00	0.00	0.00	100.0	0.0	3.8	9.8	0.24
L-N5	SE	Valkeajärvi	67.5978	21.7945	0.00	0.00	0.00	100.0	0.0	1.8	5.0	0.22
L-N6a	SE	Degervattnet	63.8738	16.2327	0.13	0.59	0.58	98.7	0.2	2.1	5.9	0.27
L-N6a	SE	Dunnervattnet	64.2847	14.6948	0.00	0.00	0.08	99.9	0.0	1.3	4.1	0.20
L-N6a	SE	Fjätsjön Övre	62.2355	12.7677	0.00	0.00	0.21	99.8	0.0	1.7	6.2	0.22
L-N6a	SE	Jutsajaure	67.0603	19.9478	0.18	0.00	0.72	99.1	0.0	1.9	6.7	0.24
L-N6a	SE	Remmarsjön	63.8632	18.2763	0.12	0.21	0.34	99.3	0.3	2.1	10.2	0.28
L-N6a	SE	Sangen	61.9277	14.8968	0.00	0.00	0.00	100.0	0.0	2.5	8.6	0.25
L-N6a	SE	Stensjön	61.6435	16.5787	0.00	0.00	0.00	100.0	0.0	2.4	6.7	0.27
L-N6a	SE	Vuolgamjaure	65.6647	18.5600	0.00	0.00	0.24	99.8	0.0	1.8	4.7	0.22
L-N8a	SE	Vaimok	67.0095	16.9343	0.00	0.00	0.00	100.0	0.0	0.8	2.5	0.23
L-N2a	UK	Llyn Bodlyn	52.7960	-4.0060	0.00	0.00	0.26	99.7	0.0	1.7	3.2	0.22
L-N2a	UK	Loch Eilt	56.8802	-5.5925	0.00	0.00	2.15	97.8	2.3	1.8	5.3	
L-N2a	UK	Loch Tarff	57.1535	-4.6053	0.00	0.00	9.88	90.1	0.0	3.2	10.0	0.12
L-N2b	UK	Buttermere	54.5306	-3.2646	0.05	0.23	4.45	95.3	0.1	1.6	1.9	0.32
L-N2b	UK	Loch Bad a' Ghaill	58.0392	-5.2610	0.00	0.00	0.83	99.2	0.0	1.9	4.1	
L-N2b	UK	Loch Maree	57.6865	-5.4732	0.02	0.00	3.09	96.9	0.3	1.6	3.9	0.09

ICtype		Waterbody Name	Latitude	Longitude	Artificial Land Use (%)	Intensive Agriculture (%)	Low Intensity Agriculture (%)	Natural Land Use (%)	Population Density (pe/km2)	Chl a (mean), µg/l	Total P, µg/l	Total N, mg/l
L-N2b	UK	Loch Muick	56.9331	-3.1704	0.00	0.00	1.27	98.7	0.0	2.0	9.8	
L-N2b	UK	Wast Water	54.4416	-3.2927	0.28	0.09	7.84	91.8	2.4	1.2	2.0	0.42
L-N3a	UK	Llyn Teifi	52.2926	-3.7852	0.00	0.00	7.66	92.3	0.0	3.1	6.2	0.25
L-N3a	UK	Loch a' Bhaid-luachraich	57.8148	-5.5505	0.00	0.00	2.52	97.5	0.0	2.0	3.5	
L-N3a	UK	Loch a' Ghriama	58.1978	-4.7396	0.00	0.00	1.17	98.8	0.0	4.7	7.3	
L-N3a	UK	Loch Craggie	58.4347	-4.3726	0.00	0.00	6.75	93.3	0.0	2.3	8.1	
L-N3a	UK	Loch Lee	56.9039	-2.9502	0.03	0.02	0.70	99.3	0.0	2.2	12.3	0.57
L-N3a	UK	Loch Meadie	58.3322	-4.5599	0.00	0.00	0.14	99.9	0.0	2.1	9.4	
L-N3a	UK	Loch Merkland	58.2417	-4.7454	0.00	0.00	1.17	98.8	0.0	5.4	7.7	
L-N3a	UK	Loch Naver	58.2945	-4.3653	0.00	0.00	4.04	96.0	0.2	2.3	5.7	0.14
L-N3a	UK	Loch of Girlsta	60.2518	-1.2199	0.00	0.00	3.26	96.7	0.0	3.6	9.3	
L-N3a	UK	Loch Stack	58.3367	-4.9245	0.00	0.00	8.77	91.2	0.5	2.4	6.3	0.09
L-N3a	UK	Lochindorb	57.4044	-3.7129	0.00	0.00	3.24	96.8	0.0	3.8	7.2	0.17

D. A description of phytoplankton communities at reference conditions and ecological class boundaries for NGIG lake types LN3a and LN2a

Introduction

Two requirements for a boundary description are required by the intercalibration process: page 15 of the guidance:

1. Description of type-specific reference/biological benchmark communities of common IC type at GIG level, considering possible biogeographical differences.
2. Description of type-specific biological communities of common IC type at GIG level representing moderate deviation from reference conditions (good-moderate boundary), including associated environmental conditions. With more detail on page p31 of the guidance: "Similar to the benchmarking step the biological communities representing the "borderline" conditions between good and moderate ecological status have to be described. This shall be done using sites of the common dataset that fall into a selected boundary range (e.g. harmonisation band of national good-moderate boundaries expressed in common metric scale)."

The common metric was formed by averaging the chlorophyll *a* normalised EQR, using boundaries agreed during the first round of intercalibration, with a composition metric based on taxa - TP weighted averages. The N-GIG used a mixed linear model, now referred to as "Continuous Benchmarking" to standardise the common metric. It was decided to use Indicator species analysis to provide an objective numeric description of the change in taxa composition and abundance across the common metric EQR scale with pressure.

Methods

Data that were used to assign values of the common metric and also national classifications in the NGIG were extracted on 20/9/11 from the database (File: NGIGTaxaForGary.xls). Average boundaries on the common metric scale were taken from the files sent on 20/9/11 and 11/10/11 by Geoff Phillips (Table D.1 and Table D.2).

Indicator species analysis (Dufrene and Legendre, 1997) for groups across the trophic scale centred on class boundaries was carried out using the software PC-ORD (McCune and Mefford, 1999). Groups were defined using boundaries provided (Geoff Phillips) for the common metric for LN3a as H/G: 0.832, G/M: 0.618, and M/P: 0.400. The P/B boundary was estimated as halfway between poor and zero: 0.200. As continuous benchmarking was used the description of reference condition followed a similar approach assigning a boundary value of 1. The lakes in this group represent a benchmark towards reference condition, in line with the benchmarking approach. Lakes were selected as groups that were within plus and minus 0.25 as a proportion of class width from these boundaries. The same approach was followed for type LN2a using the boundaries in Table D.2.

Three components of indicator species analysis were presented to summarise the changes in taxonomic composition and abundance for class boundaries:

1. RELATIVE ABUNDANCE in group, % of perfect indication (average abundance of a given taxon in a given group of lakes over the average abundance of that taxon in all lakes expressed as a %).
2. RELATIVE FREQUENCY in group, % of perfect indication (% of lakes in given group where a given taxon is present)
3. INDICATOR VALUES (% of perfect indication, based on combining the above values for relative abundance and relative frequency).

*Table D.1 Boundaries on the common metric scale for LN3a. * set at ½ M/P.*

Boundary	LN2a common metric boundaries
H/G	0.832
G/M	0.618
M/P	0.400
P/B	0.200*

*Table D.2 Boundaries on the common metric scale for LN2a * set at ½ M/P.*

Boundary	LN2a common metric boundaries
H/G	0.828
G/M	0.640
M/P	0.451
P/B	0.226*

Results LN3a Lowland, mesohumic, shallow, low alkalinity lakes

Indicator species analysis was carried out for LN3a on 250 taxa. The requirements of intercalibration include a description of reference (or alternative benchmark) as well as a description of the good/moderate boundary. The indicator values produced provide a composite value of abundance and frequency of occurrence for each taxon at each boundary (Table D.3). This should provide an objective description of the changes in phytoplankton across the proposed boundaries for LN3a. Indicator values for taxa that were indicative of reference condition and the good moderate boundary were also compared with their WISER optima (a score based on a weighted averaging analysis of taxa developed for the FP7 project WISER).

LN3a 'Reference condition' (Lakes with EQR of common metric equal to 1 ± 0.25 class)

Eleven taxa had a maximum indicator value (IV) recorded in the 'EQR1' group that was greater than 20. These were cross checked against WISER optima (file circulated 21/2/2011) with values placed in brackets where available. Taxa are highlighted where their indicator value and WISER optima agree: Botryococcus (-0.96), Bitrichia (-1.43), Chroococcus (0.49), Staurastrum1 (no optima), Merismopedia (-1.16), Dinophyceae (-1.25), Fragilaria (0.29), Cyclotella (no optima), Rhabdogloea (-1.75), Kephyrion (-1.01) and

Radiocystis (-0.73). Thirty-three other taxa had their maximum IV recorded in the reference group but were weaker indicators (Table D.3).

LN3a Good/Moderate boundary (Lakes with EQR of common metric equal to G/M boundary value ± 0.25 class)

Taxa that had a maximum indicator value (IV) recorded in the 'G/M' group that was greater than 20 were: Ankyra (0.09), Tabellaria (-0.67), Chlamydomonas (0.19), Gonyostomum
(-0.12), Elakatothrix (-0.94), Melosira (1.37), Tribonema (1.2), Aulacoseira it.is.grp (no optima), Monochrysis (-1.07), Asterionella (-0.14), Pseudosphaerocystis (-0.19), Koliella (-0.69), Pennales (1.03), Cosmarium2 (no optima), Micractinium (1.38), Pseudanabaena (1.76), Ulothrix (1.62) and Schroederia (1.77). Thirty-two other taxa had their maximum IV recoded in the good/moderate group but were weaker indicators (Table D.3).

Table D.3 Results of indicator species analysis carried out for LN3a lakes. Groups were defined by lakes occurring within ±0.25 of proposed common metric class boundaries for EQR 1, High/Good, Good/Moderate, Moderate/Poor, Poor/Bad. Taxa are grouped from EQR1 to poor/bad depending on what class they were most indicative of (had their maximum IV in). Within each group taxa are ranked by IV. A horizontal line indicates the transition between groups. Number of lakes per group: EQR1=52, H/G=72, G/M=14, M/P=6, P/B=2

	Relative abundance					Relative Frequency					Indicator values				
	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B
Botryococcus	72	20	2	4	2	87	89	79	83	100	62	17	2	4	2
Bitrichia	78	21	0	0	0	60	60	57	17	0	47	12	0	0	0
Chroococcus	91	1	1	6	2	38	26	36	83	50	35	0	0	5	1
Staurastrum1	62	32	1	3	2	48	44	71	83	100	30	14	1	2	2
Merismopedia	49	6	45	0	0	58	31	29	0	0	28	2	13	0	0
Dinophyceae	91	3	1	5	0	31	46	50	33	0	28	1	1	2	0
Fragilaria	76	8	14	1	1	35	47	86	67	100	26	4	12	1	1
Cyclotella1	58	16	6	16	4	40	53	79	83	50	23	8	5	13	2
Rhabdogloea	91	0	8	0	0	25	1	7	0	0	23	0	1	0	0
Kephyrion	58	41	0	0	0	38	51	29	50	0	22	21	0	0	0
Radiocystis	69	30	0	0	0	31	14	21	0	0	21	4	0	0	0
Pseudokephyrion	31	30	39	0	0	56	47	29	0	0	17	14	11	0	0
Epipyxis	100	0	0	0	0	17	25	29	0	0	17	0	0	0	0
Stichogloea	38	53	10	0	0	42	24	21	0	0	16	12	2	0	0
Tetrastrum1	99	0	0	1	0	15	18	21	67	0	15	0	0	1	0
Tetraedron	97	0	0	2	1	13	21	0	50	50	13	0	0	1	0
Nephrocytium	100	0	0	0	0	12	7	14	0	0	12	0	0	0	0
Chrysostephanosphaera	54	46	0	0	0	17	8	0	0	0	9	4	0	0	0
Isthmochloron	97	3	0	0	0	10	1	0	0	0	9	0	0	0	0

	Relative abundance					Relative Frequency					Indicator values				
	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B
Chrysolykos	57	43	0	0	0	15	15	0	0	0	9	7	0	0	0
Chromulinales	56	44	0	0	0	13	7	0	0	0	8	3	0	0	0
Carteria	94	6	0	0	0	8	1	0	0	0	7	0	0	0	0
Nitzschia	41	57	0	1	0	17	11	50	50	0	7	6	0	0	0
Pyramimonas	100	0	0	0	0	6	0	0	0	0	6	0	0	0	0
Crucigeniella	98	0	0	2	0	6	6	21	33	0	6	0	0	1	0
Chlorophyta	90	10	0	0	0	6	3	0	0	0	5	0	0	0	0
Navicula	99	1	0	0	0	4	1	7	0	0	4	0	0	0	0
Tetrasporales	60	40	0	0	0	6	3	0	0	0	3	1	0	0	0
Achnanthes	88	0	12	0	0	4	0	7	0	0	3	0	1	0	0
Monoraphidium2	50	50	0	0	0	6	4	7	0	0	3	2	0	0	0
Phaeaster	100	0	0	0	0	2	0	0	0	0	2	0	0	0	0
Lyngbya	100	0	0	0	0	2	0	0	0	0	2	0	0	0	0
Tetrastrum2	100	0	0	0	0	2	1	0	0	0	2	0	0	0	0
Westella	100	0	0	0	0	2	0	0	0	0	2	0	0	0	0
Cryptophyceae	100	0	0	0	0	2	0	0	0	0	2	0	0	0	0
Woloszynskia	100	0	0	0	0	2	0	0	0	0	2	0	0	0	0
Frustulia	100	0	0	0	0	2	0	0	0	0	2	0	0	0	0
Netrium	100	0	0	0	0	2	0	0	0	0	2	0	0	0	0
Pteromonas	100	0	0	0	0	2	0	0	0	0	2	0	0	0	0
Cocconeis	100	0	0	0	0	2	0	0	0	0	2	0	0	0	0
Genicularia	100	0	0	0	0	2	0	0	0	0	2	0	0	0	0

	Relative abundance					Relative Frequency					Indicator values				
	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B
Gomphonema	95	5	0	0	0	2	1	0	0	0	2	0	0	0	0
Romeria	61	39	0	0	0	2	3	14	17	50	1	1	0	0	0
Spiniferomonas	2	95	1	1	1	71	89	71	67	50	1	84	0	1	1
Dinobryon	6	84	4	6	0	94	96	93	67	0	6	81	3	4	0
Pseudopedinella	8	72	5	13	3	85	97	86	100	50	6	70	5	13	1
Monomastix	1	98	0	1	0	38	67	71	67	50	0	65	0	1	0
Urosolenia	10	57	22	11	0	48	89	79	100	0	5	51	17	11	0
Chrysochromulina	35	49	5	11	1	69	93	93	100	50	24	45	4	11	1
Centrales	2	88	5	4	0	12	49	36	33	0	0	43	2	1	0
Cosmarium1	4	91	1	1	2	44	43	43	50	50	2	39	0	0	1
Oocystis	9	49	2	26	15	90	81	79	67	100	8	39	1	17	15
Closterium	0	89	2	8	0	19	43	93	100	0	0	38	2	8	0
Monoraphidium3	0	99	1	0	0	25	36	79	67	0	0	36	0	0	0
Didymocystis	0	84	2	11	3	8	42	57	100	50	0	35	1	11	1
Plagioselmis	6	36	19	22	16	85	96	86	100	100	5	34	16	22	16
Cyanodictyon	0	98	0	1	0	10	33	36	50	0	0	33	0	1	0
Dictyosphaerium	1	80	3	11	4	27	40	79	33	50	0	32	3	4	2
Staurodesmus	43	57	0	0	0	60	51	36	50	50	26	29	0	0	0
Chrysidiastrum	2	91	0	1	6	23	29	21	17	50	0	27	0	0	3
Scourfieldia	53	47	0	0	0	37	56	71	50	0	19	26	0	0	0
Chrysococcus	1	97	0	0	2	37	24	14	17	50	0	23	0	0	1
Planktothrix arg.grp	0	75	22	3	0	2	31	57	33	0	0	23	13	1	0

	Relative abundance					Relative Frequency					Indicator values				
	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B
Gloeotila	31	69	0	0	0	17	28	7	17	0	5	19	0	0	0
Chrysosphaerella	4	79	3	14	0	6	24	7	17	0	0	19	0	2	0
Scenedesmus2	52	44	0	3	0	31	39	57	100	50	16	17	0	3	0
Monas	21	39	24	16	0	15	42	36	33	0	3	16	9	5	0
Fragilariopsis	0	94	6	0	0	6	15	7	0	0	0	14	0	0	0
Oscillatoriales	0	93	1	6	0	4	15	50	50	0	0	14	0	3	0
Cyanophyceae	0	91	0	0	9	10	14	7	0	50	0	13	0	0	4
Planktothrix grp	0	100	0	0	0	4	11	7	0	0	0	11	0	0	0
Sphaerocystis	4	85	2	8	0	29	13	21	17	0	1	11	0	1	0
Achnanthidium	0	100	0	0	0	4	10	7	0	0	0	10	0	0	0
Paulschulzia	0	100	0	0	0	0	7	7	0	0	0	7	0	0	0
Raphidocelis	17	83	0	0	0	4	8	21	0	0	1	7	0	0	0
Bacillariales	0	99	0	0	0	2	7	21	17	0	0	7	0	0	0
Eunotia	16	70	14	0	0	6	10	14	0	0	1	7	2	0	0
Spondylosium	51	48	1	0	0	10	14	50	33	50	5	7	0	0	0
Tetraëdriella	29	45	26	0	0	10	14	7	0	0	3	6	2	0	0
Planktosphaeria	0	62	38	0	0	0	10	14	0	0	0	6	5	0	0
Surirella	0	100	0	0	0	0	6	7	0	0	0	6	0	0	0
Gloeobotrys	0	100	0	0	0	2	6	7	0	0	0	6	0	0	0
Ankistrodesmus	28	69	0	3	1	6	7	14	67	50	2	5	0	2	0
Staurosira	0	100	0	0	0	2	4	7	0	0	0	4	0	0	0
Ochromonas	1	99	0	0	0	13	4	14	0	0	0	4	0	0	0

	Relative abundance					Relative Frequency					Indicator values				
	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B
Willea	0	99	1	0	0	8	4	7	0	0	0	4	0	0	0
Discostella	43	57	0	0	0	2	6	0	0	0	1	3	0	0	0
Chromulina	0	99	0	0	0	21	3	7	0	0	0	3	0	0	0
Cyanonephron	0	100	0	0	0	0	3	0	0	0	0	3	0	0	0
Merismopedia2	0	100	0	0	0	2	3	0	0	0	0	3	0	0	0
Keratococcus	0	100	0	0	0	0	1	0	0	0	0	1	0	0	0
Siderocelis	0	100	0	0	0	0	1	0	0	0	0	1	0	0	0
Microcystis1	0	100	0	0	0	0	1	0	0	0	0	1	0	0	0
Hyalotheca	0	100	0	0	0	0	1	0	0	0	0	1	0	0	0
Centritractus	0	100	0	0	0	0	1	0	0	0	0	1	0	0	0
Oscillatoria	0	99	1	0	0	0	1	7	0	0	0	1	0	0	0
Limnothrix	0	100	0	0	0	0	1	0	0	0	0	1	0	0	0
Chlorella	0	100	0	0	0	0	1	0	0	0	0	1	0	0	0
Cyclotella2	0	100	0	0	0	0	1	0	0	0	0	1	0	0	0
Sphaerellopsis	0	100	0	0	0	0	1	0	0	0	0	1	0	0	0
Merotricha	0	100	0	0	0	0	1	0	0	0	0	1	0	0	0
Gloeocystis	27	73	0	0	0	2	1	0	0	0	1	1	0	0	0
Cymbella	42	58	0	0	0	2	1	0	0	0	1	1	0	0	0
Ankyra	0	0	100	0	0	17	35	79	50	0	0	0	78	0	0
Tabellaria	4	17	78	2	0	69	85	93	33	0	3	14	72	1	0
Chlamydomonas	0	10	86	1	2	63	68	79	67	100	0	7	68	1	2
Gonyostomum	3	17	70	10	0	23	61	93	83	0	1	10	65	8	0

	Relative abundance					Relative Frequency					Indicator values				
	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B
Elakatothrix	17	35	49	0	0	75	71	93	67	50	12	25	45	0	0
Melosira	0	1	99	0	0	0	6	43	0	0	0	0	42	0	0
Tribonema	0	0	98	2	0	0	1	43	17	0	0	0	42	0	0
Aulacoseira it.is.grp	0	3	45	36	16	19	47	93	83	50	0	1	42	30	8
Monochrysis	0	4	96	0	0	21	50	43	33	0	0	2	41	0	0
Asterionella	29	6	43	22	0	42	86	86	100	0	12	5	37	22	0
Pseudosphaerocystis	6	22	72	0	0	6	14	50	0	0	0	3	36	0	0
Koliella	0	30	70	0	0	13	38	43	17	0	0	11	30	0	0
Pennales	11	9	64	16	0	12	29	43	17	0	1	3	28	3	0
Cosmarium2	1	4	78	17	0	2	3	29	17	0	0	0	22	3	0
Micractinium	0	0	100	0	0	0	0	21	0	0	0	0	21	0	0
Pseudanabaena	0	0	100	0	0	2	0	21	17	0	0	0	21	0	0
Ulothrix	0	0	100	0	0	0	1	21	0	0	0	0	21	0	0
Schroederia	0	0	100	0	0	0	0	21	0	0	0	0	21	0	0
Euastrum	34	3	63	0	0	12	3	29	0	0	4	0	18	0	0
Quadrigula	0	16	83	1	0	37	43	21	33	50	0	7	18	0	0
Scenedesmus1	0	39	60	0	0	2	8	29	0	0	0	3	17	0	0
Eudorina	2	32	47	19	0	4	11	36	17	0	0	4	17	3	0
Picoplankton	20	2	50	23	5	46	22	29	50	50	9	0	14	12	3
Microcystis2	0	0	100	0	0	0	0	14	0	0	0	0	14	0	0
Gyrosigma	0	0	100	0	0	0	0	14	0	0	0	0	14	0	0
Spermatozopsis	0	3	97	0	0	2	1	14	0	0	0	0	14	0	0

	Relative abundance					Relative Frequency					Indicator values				
	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B
Merismopedia1	0	10	90	0	0	13	31	14	17	0	0	3	13	0	0
Synechococcus	0	0	56	44	0	0	0	14	17	0	0	0	8	7	0
Xanthidium	16	31	53	0	0	6	4	14	0	0	1	1	8	0	0
Entomoneis	0	0	100	0	0	0	1	7	0	0	0	0	7	0	0
Ulotrichales	0	0	100	0	0	0	1	7	0	0	0	0	7	0	0
Dimorphococcus	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Pseudopediastrum	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Lemmermanniella	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Tetrachlorella	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Hormidium	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Polyedriopsis	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Stichococcus	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Golenkinia	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Syncrypta	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Achroonema	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Klebsormidium	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Pandorina	0	0	100	0	0	0	0	7	0	0	0	0	7	0	0
Eupodiscales	0	5	95	0	0	0	3	7	0	0	0	0	7	0	0
Chlamydocapsa	0	14	86	0	0	0	4	7	0	0	0	1	6	0	0
Ophiocytium	0	15	85	0	0	0	4	7	0	0	0	1	6	0	0
Chroomonas	43	17	40	0	0	12	3	14	0	0	5	0	6	0	0
Colacium	32	0	68	0	0	2	0	7	0	0	1	0	5	0	0

	Relative abundance					Relative Frequency					Indicator values				
	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B
Cyclostephanos	0	34	66	0	0	0	1	7	0	0	0	0	5	0	0
Diatoma	0	61	39	0	0	0	4	7	0	0	0	3	3	0	0
Synura	1	5	20	74	0	21	51	93	83	0	0	2	19	62	0
Pediastrum	0	1	5	67	28	0	22	57	83	100	0	0	3	56	28
Anabaena lem.grp	0	0	0	100	0	21	19	36	50	0	0	0	0	50	0
Treubaria	0	0	3	97	0	2	0	14	50	0	0	0	0	49	0
Phacus	0	0	0	87	13	6	1	0	50	50	0	0	0	43	7
Chroococcales	1	6	8	85	0	13	46	64	50	0	0	3	5	42	0
Aulacoseira alp.grp	13	8	27	41	10	54	58	86	100	50	7	5	23	41	5
Stephanodiscus	0	0	12	82	6	0	3	50	50	50	0	0	6	41	3
Acanthoceras	0	4	35	61	0	2	26	79	67	0	0	1	28	40	0
Ulnaria	5	7	28	56	4	10	40	43	67	50	0	3	12	37	2
Scenedesmus3	0	0	4	96	0	4	1	7	33	0	0	0	0	32	0
Mallomonas	11	19	22	48	0	90	99	100	67	0	10	19	22	32	0
Peridinium	12	23	15	38	13	73	78	93	83	50	9	18	14	31	7
Nephrochlamys	0	0	0	93	7	0	0	0	33	50	0	0	0	31	4
Uroglena	7	30	3	60	0	33	79	79	50	0	2	24	2	30	0
Volvocales	1	8	9	82	0	8	24	50	33	0	0	2	5	27	0
Aphanocapsa	2	3	14	81	0	21	31	64	33	0	0	1	9	27	0
Aphanothece	8	14	29	49	0	25	46	64	50	0	2	6	18	25	0
Crucigenia	8	14	9	70	0	27	43	50	33	0	2	6	5	23	0
Pediastrum privum	3	23	7	46	22	10	42	50	50	50	0	10	3	23	11

	Relative abundance					Relative Frequency					Indicator values				
	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B
Monoraphidium1	25	21	12	34	7	87	94	79	67	100	22	20	9	23	7
Kirchneriella	0	3	8	68	21	4	4	14	33	50	0	0	1	23	10
Coelastrum	0	2	22	53	24	2	11	43	33	50	0	0	9	18	12
Pseudogoniochloris	0	0	0	100	0	0	0	0	17	0	0	0	0	17	0
Quadricoccus	0	0	0	100	0	0	0	0	17	0	0	0	0	17	0
Nephroselmis	2	3	2	94	0	2	1	7	17	0	0	0	0	16	0
Staurastrum2	7	0	0	93	0	2	0	0	17	0	0	0	0	16	0
Cryptomonadales	0	4	4	91	0	4	7	29	17	0	0	0	1	15	0
Rhizochrysis	0	11	0	89	0	0	3	0	17	0	0	0	0	15	0
Lagerheimia	1	0	20	78	0	2	1	29	17	0	0	0	6	13	0
Coelosphaerium	0	15	20	65	0	0	1	7	17	0	0	0	1	11	0
Heterotrophic, biflag	11	13	16	60	0	6	7	21	17	0	1	1	3	10	0
Heterotrophic, flag	6	10	29	56	0	6	8	21	17	0	0	1	6	9	0
Teilingia	19	6	24	50	0	2	7	7	17	0	0	0	2	8	0
Aphanizomenon	0	0	1	11	88	15	40	71	83	100	0	0	1	9	88
Woronichinia	0	3	4	6	87	40	71	79	83	100	0	2	3	5	87
Anabaena grp	1	0	6	7	86	19	57	79	83	100	0	0	5	6	86
Pseudostaurastrum	0	2	17	0	81	0	1	29	0	100	0	0	5	0	81
Planktolyngbya	0	0	0	22	78	4	0	0	17	100	0	0	0	4	78
Microcystis3	0	0	3	28	69	10	10	50	83	100	0	0	2	23	69
Trachelomonas	0	4	2	29	64	23	28	50	67	100	0	1	1	19	64
Aulacoseira gran.grp	0	2	13	23	62	13	24	43	83	100	0	0	6	19	62

	Relative abundance					Relative Frequency					Indicator values				
	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B	EQR1	H/G	G/M	M/P	P/B
Ceratium	0	2	3	44	50	37	57	57	83	100	0	1	2	36	50
Goniochloris	0	0	0	0	100	2	0	0	0	50	0	0	0	0	50
Anabaena flos.grp	0	0	0	0	100	10	10	29	0	50	0	0	0	0	50
Phacotus	0	1	0	0	99	2	1	0	0	50	0	0	0	0	49
Chlorogonium	0	1	0	0	99	0	1	0	0	50	0	0	0	0	49
Peridiniopsis	0	2	0	0	98	0	3	0	0	50	0	0	0	0	49
Cryptomonas	4	8	11	34	43	96	100	100	100	100	3	8	11	34	43
Euglena	0	0	0	58	42	0	7	21	67	100	0	0	0	38	42
Chrysophyceae	18	9	10	25	37	79	53	50	50	100	14	5	5	13	37
Snowella	55	1	1	6	37	42	71	64	83	100	23	0	1	5	37
Mougeotia	4	6	32	0	59	17	21	57	0	50	1	1	18	0	29
Gymnodinium	14	18	22	18	28	88	89	86	50	100	12	16	19	9	28
Chlorococcales	19	10	7	41	22	85	72	86	50	100	16	7	6	20	22
Rhabdoderma	0	86	0	0	14	0	1	0	0	50	0	1	0	0	7

Taxa characteristic of other boundaries may be seen in Table D.3. Taxa are grouped from EQR1 to poor/bad depending on what class they were most indicative of (had their maximum IV in). Within each group, taxa are ranked by IV.

A description of the environmental conditions associated with boundaries is required by the guidance, specifically for the good/moderate boundary. Boxplots of TP, TN and chlorophyll *a* and associated summary statistics are presented in Figure D.1, Table D.4, Table D.5 and Table D.6 for LN3a.

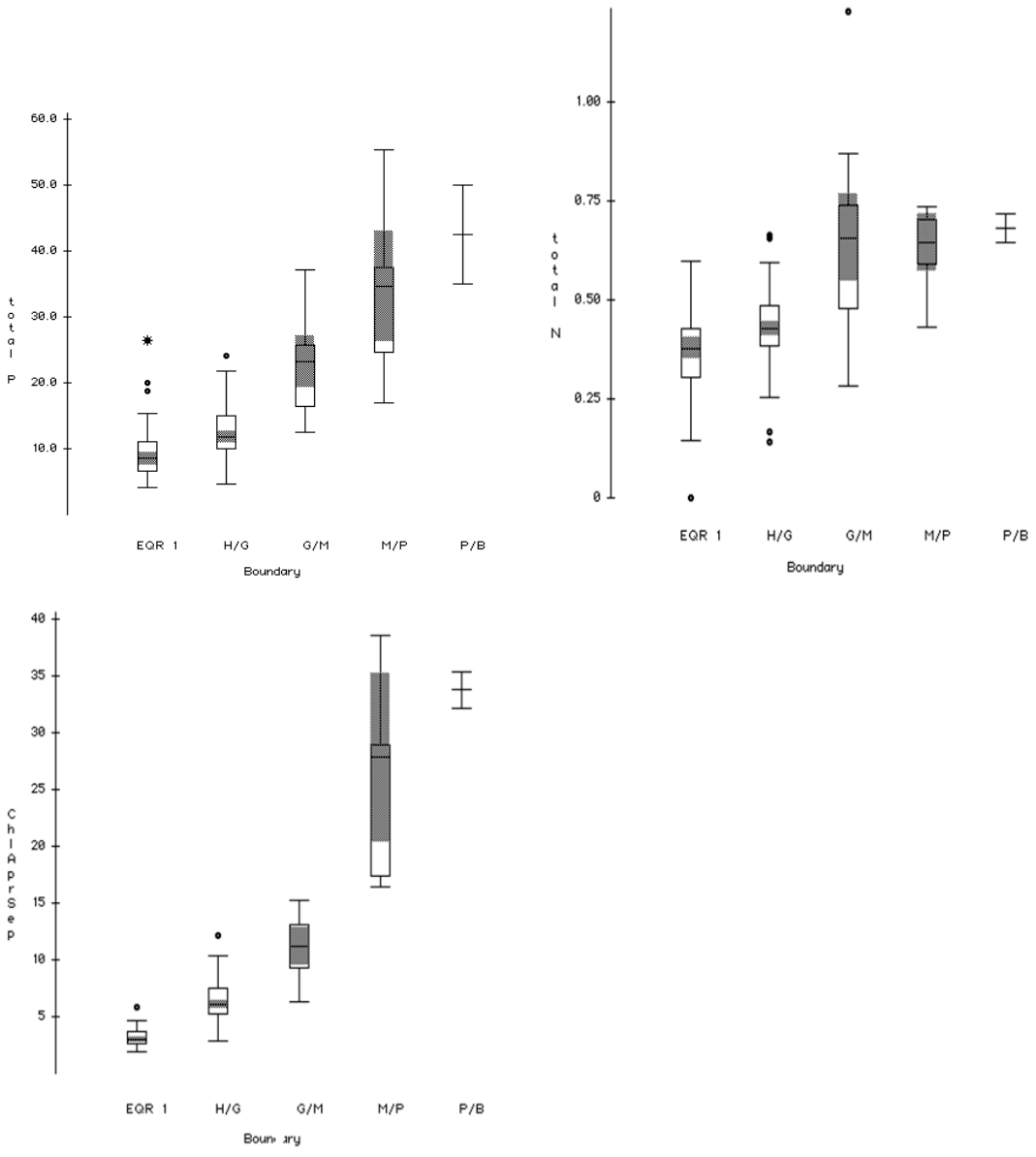

Figure D.1 Box plot of TP µg l-1 , TN mg l-1 and Chlorophyll a µg l-1 (April-September) for LN3a lakes occurring within ±0.25 of proposed common metric class boundaries. Shaded areas are 95% C.I. for comparing medians

Table D.4 Summary statistics of Chlorophyll a µg l^{-1} for LN3a boundary groups (boundary ±0.25 class)

Group	Count	Mean	Median	StdDev	Lower 25%tile	Upper 75%tile
EQR1	52	3.13	2.94	0.77	2.52	3.58
High/Good	72	6.38	6.13	1.75	5.36	7.53
Good/Moderate	14	11.10	11.25	2.51	9.31	13.16
Moderate/Poor	6	26.23	27.90	8.22	17.48	29.00
Poor/Bad	2	33.83	33.83	2.23	32.25	35.40

Table D.5 Summary statistics of TP µg l^{-1} for LN3a boundary groups (boundary ±0.25 class).

Group	Count	Mean	Median	StdDev	Lower 25%tile	Upper 75%tile
EQR1	52	9.4	8.4	4.2	6.5	11.0
High/Good	72	12.6	11.9	4.0	10.0	14.9
Good/Moderate	14	22.9	23.3	6.9	16.5	25.9
Moderate/Poor	6	34.1	34.7	13.2	24.7	37.7
Poor/Bad	2	42.5	42.5	10.6	35.0	50.0

Table D.6 Summary statistics of TN mg l^{-1} for LN3a boundary groups (boundary ±0.25 class).

Group	Count	Mean	Median	StdDev	Lower 25%tile	Upper 75%tile
EQR1	52	0.38	0.38	0.12	0.31	0.43
High/Good	72	0.43	0.43	0.09	0.39	0.49
Good/Moderate	14	0.67	0.66	0.23	0.48	0.74
Moderate/Poor	6	0.63	0.65	0.11	0.59	0.70
Poor/Bad	2	0.68	0.68	0.05	0.65	0.72

Results LN2a, Lowland, clear-water, shallow, low alkalinity lakes

Indicator species analysis was carried out for LN2a on 209 taxa. The requirements of intercalibration include a description of reference (or alternative benchmark) as well as a description of the good/moderate boundary. The indicator values produced provide a composite value of abundance and frequency of occurrence for each taxon at each boundary (Table D.7). This should provide an objective description of the changes in phytoplankton across the proposed boundaries for LN2a. Indicator values for taxa that were indicative of reference condition and the good moderate boundary were also compared with their WISER optima (a score based on a weighted averaging analysis of taxa developed for the FP7 project WISER).

LN2a 'Reference condition' (EQR of common metric equal to 1 ± 0.25 class)

Nineteen taxa that had a maximum indicator value (IV) recorded in the 'EQR1' group that was greater than 20. These were cross checked against WISER optima (file circulated 21/2/2011) with values placed in brackets where available. Taxa are highlighted where their indicator value and WISER optima agree: Chrysophyceae (-1.34), Kephyrion (-1.01), Staurastrum1 (no optima), Chlamydomonas (0.19), Chroococcus (0.49), Crucigenia (0.06), Chroomonas (-0.82), Chrysolykos (-1.91), Merismopedia1 (no optima), Sphaerocystis (-0.16), Pseudokephyrion (-1.72), Uroglena (-0.66), Aphanocapsa (0.7), Cyclotella1 (no optima), Ceratium (0.66), Anabaena grp (no optima), Stichogloea (-1.38), Tetraedron (0.57), Merismopedia (-1.16). Sixty-three other taxa had their maximum IV recorded in the reference group but were weaker indicators (Table D.7).

LN2a Good/Moderate boundary

Taxa that had a maximum indicator value (IV) recorded in the 'G/M' group that was greater than 20 were: Dinobryon (-0.75), Mallomonas (-0.65), Monoraphidium1 (no optima), Spiniferomonas (-1.37), Gonyostomum (-0.12), Snowella (-0.02), Cryptomonas (0.2), Chrysochromulina (-0.44), Plagioselmis (-0.58), Gymnodinium (-1.07), Aulacoseira gran.grp (no optima), Elakatothrix (-0.94), Fragilaria (0.29), Tabellaria (-0.67), Picoplankton (-1.3), Dictyosphaerium (0.1), Monoraphidium3 (no optima), Staurodesmus (-1.1), Quadrigula (-0.66), Monomastix (-0.82), Planktothrix arg.grp (no optima), Synura (-0.27), Ochromonas (-1.27). Fourty-two other taxa had their maximum IV recoded in the good/moderate group but were weaker indicators (Table D.7).

Taxa characteristic of the high/good boundary may be seen in Table D.7. Taxa are grouped from EQR1 to good/moderate depending on what class they were most indicative of (had their maximum IV in). Within each group taxa are ranked by IV. Too few lakes were in Moderate/Poor and Poor/Bad status for analysis for this type.

A description of the environmental conditions associated with boundaries is required by the guidance, specifically for the good/moderate boundary. Boxplots of TP, TN and chlorophyll a and associated summary statistics are presented in Figure D.2, Table D.8, Table D.9 and Table D.10 for LN2a.

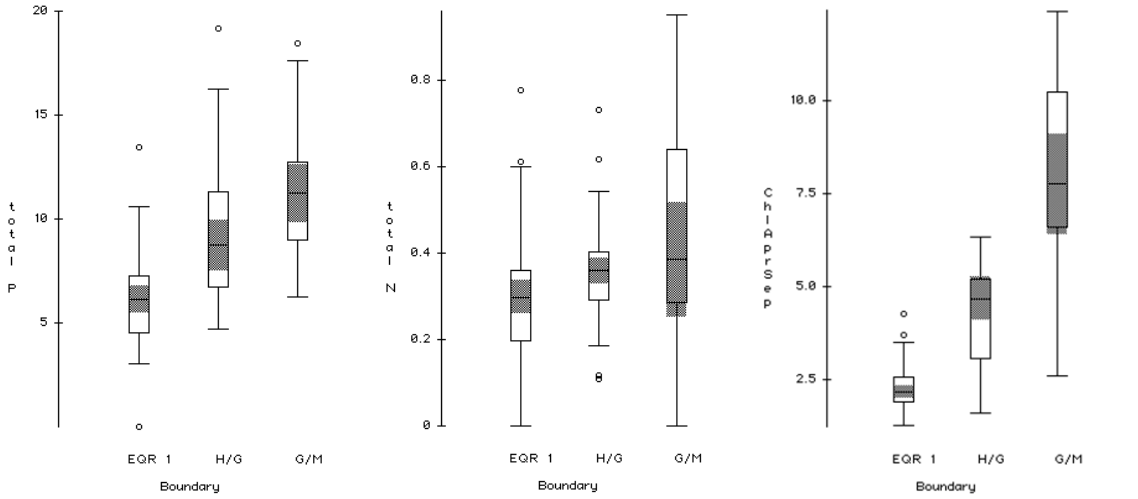

Figure D.2 Box plot of TP µg l-1 , TN mg l-1 and Chlorophyll a µg l-1 (April-September) for LN2a lakes occurring within ±0.25 of proposed common metric class boundaries. Shaded areas are 95% C.I. for comparing medians. Boundaries were significantly different in Scheffe post hoc tests (p<0.03).

Table D.7 Results of indicator species analysis carried out for LN2a lakes. Groups were defined by lakes occurring within ±0.25 of proposed common metric class boundaries for EQR 1, High/Good, Good/Moderate, too few lakes were in Moderate/Poor, Poor/Bad status were present for analysis. Taxa are grouped from EQR1 to poor/bad depending on what class they were most indicative of (had their maximum IV in). Within each group taxa are ranked by IV. A horizontal line indicates the transition between groups. Number of lakes per group: EQR1=44, H/G=34, G/M=18, M/P=0, P/B=0.

	Relative abundance			Relative Frequency			Indicator values		
	EQR 1	H/G	G/M	EQR 1	H/G	G/M	EQR 1	H/G	G/M
Chrysophyceae	79	11	10	66	68	72	52	8	7
Kephyrion	100	0	0	50	47	28	50	0	0
Staurastrum1	97	0	2	50	47	78	49	0	2
Chlamydomonas	99	0	0	48	59	56	47	0	0
Chroococcus	99	1	0	41	44	17	41	0	0
Crucigenia	100	0	0	39	21	50	39	0	0
Chroomonas	96	3	1	36	29	39	35	1	0
Chrysolykos	100	0	0	34	29	6	34	0	0
Merismopedia1	100	0	0	32	35	17	32	0	0
Sphaerocystis	98	0	1	32	26	44	31	0	1

	Relative abundance			Relative Frequency			Indicator values		
	EQR 1	H/G	G/M	EQR 1	H/G	G/M	EQR 1	H/G	G/M
Pseudokephyrion	57	0	43	52	41	39	30	0	17
Uroglena	65	9	26	45	56	83	30	5	22
Aphanocapsa	99	0	0	27	21	17	27	0	0
Cyclotella1	83	12	6	32	47	44	26	5	3
Ceratium	63	29	8	41	62	33	26	18	3
Anabaena grp	61	5	34	41	32	28	25	2	9
Stichogloea	65	23	12	36	21	22	23	5	3
Tetraedron	100	0	0	20	15	0	20	0	0
Merismopedia	98	1	1	20	24	39	20	0	0
Scenedesmus2	60	39	1	32	38	28	19	15	0
Cosmarium1	52	4	44	36	21	39	19	1	17
Chrysococcus	73	25	1	25	24	22	18	6	0
Epipyxis	99	0	0	18	21	11	18	0	0
Ulnaria	94	3	3	18	26	17	17	1	1
Centrales	57	43	0	30	29	0	17	13	0
Mougeotia	100	0	0	16	3	11	16	0	0
Tetrastrum1	100	0	0	16	12	6	16	0	0
Monoraphidium2	100	0	0	14	6	0	14	0	0
Xanthidium	100	0	0	14	3	0	14	0	0
Cyanophyceae	99	1	0	14	6	17	13	0	0
Chromulinales	49	30	21	27	18	22	13	5	5
Chlorophyta	91	8	0	14	6	6	12	0	0
Aphanizomenon	95	3	2	11	24	17	11	1	0
Monas	66	34	0	16	21	0	11	7	0
Pennales	50	41	10	20	15	6	10	6	1
Achnanthes	100	0	0	9	3	0	9	0	0
Eunotia	100	0	0	9	6	17	9	0	0
Chrysidiastrum	47	25	27	18	24	11	9	6	3
Radiocystis	48	52	0	16	12	0	8	6	0
Euastrum	81	19	0	9	9	0	7	2	0
Rhabdogloea	61	39	0	11	9	0	7	3	0
Microcystis3	100	0	0	7	9	6	7	0	0
Rhabdoderma	100	0	0	7	0	0	7	0	0
Kirchneriella	100	0	0	7	9	6	7	0	0
Chrysostephanosphaera	100	0	0	7	3	0	7	0	0
Phytoplankton, unid	43	54	4	16	12	6	7	6	0
Oscillatoria	50	50	0	11	9	11	6	4	0

	Relative abundance			Relative Frequency			Indicator values		
	EQR 1	H/G	G/M	EQR 1	H/G	G/M	EQR 1	H/G	G/M
Bacillariales	80	20	0	7	6	0	5	1	0
Euglena	100	0	0	5	9	6	5	0	0
Heterotrophic, biflag.	100	0	0	5	12	0	5	0	0
Romeria	100	0	0	5	0	0	5	0	0
Cyanonephron	98	2	0	5	3	0	4	0	0
Willea	100	0	0	5	9	0	5	0	0
Cymbella	100	0	0	5	3	0	5	0	0
Phormidium	100	0	0	5	3	0	5	0	0
Pinnularia	100	0	0	5	0	0	5	0	0
Isthmochloron	90	10	0	5	3	0	4	0	0
Tetmemorus	91	9	0	5	3	0	4	0	0
Eupodiscales	85	15	0	5	3	0	4	0	0
Oscillatoriales	67	0	33	5	0	6	3	0	2
Coenochloris	67	33	0	5	6	0	3	2	0
Tetrastrum3	100	0	0	2	0	17	2	0	0
Navicula	100	0	0	2	0	0	2	0	0
Tetrastrum2	100	0	0	2	0	0	2	0	0
Schroederia	100	0	0	2	0	0	2	0	0
Phacus	100	0	0	2	0	0	2	0	0
Gomphosphaeria	100	0	0	2	0	0	2	0	0
Cosmarium3	100	0	0	2	0	0	2	0	0
Cyclostephanos	100	0	0	2	0	0	2	0	0
Lepochromulina	100	0	0	2	0	0	2	0	0
Asterococcus	100	0	0	2	0	0	2	0	0
Gonium	100	0	0	2	0	0	2	0	0
Closteriopsis	100	0	0	2	0	0	2	0	0
Leptolyngbya	100	0	0	2	0	0	2	0	0
Pleurotaenium	100	0	0	2	0	0	2	0	0
Euglenophyceae	100	0	0	2	0	0	2	0	0
Ulotrichales	100	0	0	2	0	0	2	0	0
Ulothrix	100	0	0	2	0	0	2	0	0
Actinastrum	100	0	0	2	0	0	2	0	0
Limnothrix	100	0	0	2	0	0	2	0	0
Gloeothece	100	0	0	2	0	0	2	0	0
Zygnematales	100	0	0	2	0	0	2	0	0
Oocystis	1	97	3	89	71	61	1	68	2
Urosolenia	21	77	2	34	62	56	7	47	1

	Relative abundance			Relative Frequency			Indicator values		
	EQR 1	H/G	G/M	EQR 1	H/G	G/M	EQR 1	H/G	G/M
Bitrichia	43	57	0	73	82	61	31	47	0
Botryococcus	42	58	1	59	74	50	25	42	0
Scourfieldia	0	94	6	20	41	28	0	39	2
Aulacoseira alp.grp	0	92	8	23	41	56	0	38	4
Peridinium	43	45	13	80	82	67	34	37	8
Pediastrum privum	2	97	2	14	35	17	0	34	0
Dinophyceae	28	68	4	43	47	17	12	32	1
Asterionella	50	46	4	48	59	89	24	27	3
Pseudopedinella	22	36	42	64	74	61	14	27	26
Chlorococcales	34	41	25	64	62	72	21	25	18
Woronichinia	51	48	1	18	50	39	9	24	0
Nephrocytium	0	98	2	16	24	6	0	23	0
Didymocystis	10	84	6	11	26	6	1	22	0
Gloeotila	5	95	0	7	24	0	0	22	0
Cyanodictyon	0	100	0	16	21	0	0	21	0
Phytoplankton, flag.	21	39	41	52	47	28	11	18	11
Ankyra	0	100	0	14	18	28	0	18	0
Anabaena lem.grp	6	78	17	7	21	11	0	16	2
Aphanothece	44	45	12	27	35	17	12	16	2
Volvocales	14	86	0	9	15	0	1	13	0
Closterium	55	45	0	18	26	17	10	12	0
Cryptomonadales	1	99	0	5	12	0	0	12	0
Phytoplankton, biflag.	4	96	0	7	12	0	0	11	0
Crucigeniella	45	55	0	20	18	22	9	10	0
Monochrysis	13	36	51	25	26	6	3	9	3
Gloeocystis	1	76	24	5	12	17	0	9	4
Heterotrophic, flag.	25	75	0	5	12	0	1	9	0
Scenedesmus1	0	97	3	11	9	17	0	9	0
Nitzschia	0	39	61	9	21	11	0	8	7
Coelastrum	21	53	26	11	15	11	2	8	3
Diatoma	54	46	0	7	15	0	4	7	0
Raphidocelis	30	70	0	5	9	0	1	6	0
Trachelomonas	0	100	0	2	6	17	0	6	0
Cosmarium2	0	100	0	7	6	6	0	6	0
Pyramimonas	0	100	0	0	6	0	0	6	0
Planktothrix grp	8	92	0	5	6	0	0	5	0
Stephanodiscus	0	59	41	0	9	11	0	5	5

	Relative abundance			Relative Frequency			Indicator values		
	EQR 1	H/G	G/M	EQR 1	H/G	G/M	EQR 1	H/G	G/M
Gloeobotrys	32	68	0	2	6	0	1	4	0
Phacotus	36	64	0	2	6	0	1	4	0
Staurastrum2	49	51	0	2	6	6	1	3	0
Achnanthidium	40	50	9	7	6	6	3	3	1
Westella	0	100	0	0	3	0	0	3	0
Nephroselmis	0	100	0	0	3	0	0	3	0
Entomoneis	0	100	0	0	3	0	0	3	0
Pseudostaurastrum	0	100	0	0	3	0	0	3	0
Paulschulzia	0	99	1	0	3	6	0	3	0
Dimorphococcus	0	100	0	0	3	0	0	3	0
Achroonema	0	100	0	0	3	0	0	3	0
Tychonema	0	100	0	0	3	0	0	3	0
Centritractus	0	100	0	0	3	0	0	3	0
Lyngbya	0	100	0	0	3	0	0	3	0
Didymosphenia	0	100	0	0	3	0	0	3	0
Gomphonema	0	100	0	0	3	0	0	3	0
Gonatozygon	0	100	0	0	3	0	0	3	0
Lemmermanniella	0	100	0	0	3	0	0	3	0
Staurosira	0	100	0	0	3	0	0	3	0
Lagerheimia	0	100	0	0	3	0	0	3	0
Microcystis2	14	86	0	2	3	0	0	3	0
Tetrasporales	21	79	0	2	3	0	0	2	0
Cylindrocystis	28	72	0	7	3	6	2	2	0
Dinobryon	2	1	97	98	85	100	2	1	97
Mallomonas	5	4	91	82	88	83	4	4	76
Monoraphidium1	1	1	98	84	74	72	1	1	71
Spiniferomonas	0	0	99	57	53	61	0	0	61
Gonyostomum	0	1	99	5	18	61	0	0	61
Snowella	25	0	75	52	59	78	13	0	58
Cryptomonas	15	35	50	100	97	100	15	34	50
Chrysochromulina	35	1	64	61	76	78	21	1	50
Plagioselmis	18	40	43	89	94	100	16	37	43
Gymnodinium	40	19	41	91	85	89	36	16	37
Aulacoseira gran.grp	0	7	93	5	18	39	0	1	36
Elakatothrix	42	16	42	68	71	83	29	12	35
Fragilaria	34	14	52	32	56	61	11	8	32
Tabellaria	34	24	43	61	74	72	21	17	31

	Relative abundance			Relative Frequency			Indicator values		
	EQR 1	H/G	G/M	EQR 1	H/G	G/M	EQR 1	H/G	G/M
Picoplankton	27	33	40	50	56	72	14	19	29
Dictyosphaerium	15	33	52	23	18	50	3	6	26
Monoraphidium3	33	16	51	39	21	50	13	3	26
Staurodesmus	33	22	45	41	41	56	14	9	25
Quadrigula	55	5	40	36	35	61	20	2	24
Monomastix	32	0	68	27	35	33	9	0	23
Planktothrix arg.grp	0	0	100	0	21	22	0	0	22
Synura	1	36	63	16	24	33	0	9	21
Ochromonas	26	35	39	34	35	50	9	12	20
Carteria	5	16	79	7	6	22	0	1	18
Chromulina	30	41	29	36	35	56	11	14	16
Spondylosium	0	6	94	14	18	17	0	1	16
Anabaena flos.grp	28	29	43	14	26	33	4	8	14
Discostella	8	32	60	7	18	22	1	6	13
Chrysosphaerella	15	8	76	2	6	17	0	0	13
Pediastrum	4	23	73	7	12	17	0	3	12
Planctococcus	0	0	100	0	0	11	0	0	11
Phaeaster	0	0	100	5	0	11	0	0	11
Fragilariopsis	1	0	99	2	0	11	0	0	11
Pandorina	0	1	99	0	3	11	0	0	11
Koliella	49	3	47	18	32	22	9	1	11
Pseudanabaena	22	32	46	14	9	22	3	3	10
Aulacoseira it.is.grp	86	1	13	9	18	67	8	0	9
Ankistrodesmus	16	44	40	18	18	22	3	8	9
Acanthoceras	0	49	51	0	9	17	0	4	8
Chlamydocapsa	4	25	71	2	3	11	0	1	8
Eudorina	5	26	68	2	9	11	0	2	8
Teilingia	0	35	65	2	12	11	0	4	7
Golenkinia	0	0	100	0	0	6	0	0	6
Keratococcus	0	0	100	0	0	6	0	0	6
Micractinium	0	0	100	0	0	6	0	0	6
Nephrochlamys	0	0	100	0	0	6	0	0	6
Merotricha	0	0	100	0	0	6	0	0	6
Rhizochrysis	0	0	100	0	0	6	0	0	6
Chlorogonium	0	0	100	0	0	6	0	0	6
Chaetoceros	0	0	100	0	0	6	0	0	6
Coccomyxa	0	0	100	0	0	6	0	0	6

	Relative abundance			Relative Frequency			Indicator values		
	EQR 1	H/G	G/M	EQR 1	H/G	G/M	EQR 1	H/G	G/M
Netrium	0	0	100	2	0	6	0	0	6
Prorocentrum	0	0	100	0	0	6	0	0	6
Chroococcales	0	0	100	18	32	6	0	0	6
Tetraëdriella	2	49	50	2	6	11	0	3	6
Coelosphaerium	2	0	98	2	0	6	0	0	5
Planktosphaeria	7	0	93	2	3	6	0	0	5
Glenodinium	0	6	94	0	3	6	0	0	5
Synechococcus	12	0	88	2	0	6	0	0	5
Treubaria	0	13	87	0	3	6	0	0	5
Pseudosphaerocystis	0	27	73	0	15	6	0	4	4
Cyclotella2	0	34	66	0	6	6	0	2	4
Frustulia	37	1	62	5	3	6	2	0	3
Scenedesmus3	35	15	50	5	9	6	2	1	3
Chrysamoeba	58	0	42	2	0	6	1	0	2

Table D.8 Summary statistics of Chlorophyll a µg l-1 for LN2a boundary groups (boundary ±0.25 class).

Group	Count	Mean	Median	StdDev	Lower 25%tile	Upper 75%tile
EQR1	44	2.25	2.14	0.61	1.89	2.55
High/Good	34	4.28	4.70	1.27	3.07	5.22
Good/Moderate	18	7.94	7.78	2.62	6.63	10.25
Moderate/Poor	0					
Poor/Bad	0					

Table D.9 Summary statistics of TP µg l-1 for LN2a boundary groups (boundary ±0.25 class).

Group	Count	Mean	Median	StdDev	Lower 25%tile	Upper 75%tile
EQR1	44	6.2	6.2	2.2	4.6	7.3
High/Good	34	9.2	8.8	3.5	6.8	11.3
Good/Moderate	18	11.5	11.3	3.5	9.0	12.8
Moderate/Poor	0					
Poor/Bad	0					

Table D.10 Summary statistics of TN mg l-1 for LN2a boundary groups (boundary ±0.25 class).

Group	Count	Mean	Median	StdDev	Lower 25%tile	Upper 75%tile
EQR1	44	0.30	0.30	0.16	0.21	0.36
High/Good	34	0.35	0.36	0.13	0.29	0.40
Good/Moderate	18	0.43	0.39	0.25	0.29	0.64
Moderate/Poor	0					
Poor/Bad	0					

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E. Standardisation of national metrics

Standardization of national metrics

In addition to standardising the common metric it is necessary to standardise the national metrics to make allowances for bio-geographic differences. This could be achieved by comparing the EQRs for each national method in the reference sites (Figure E.1).

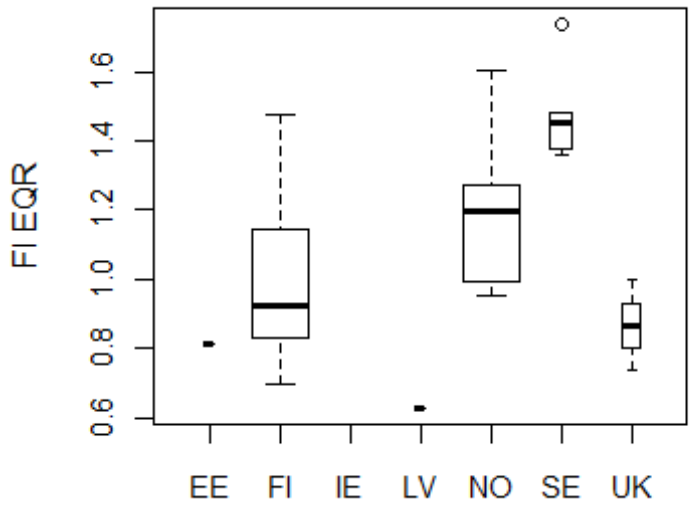


Figure E.1 Range of Finland final EQR values when applied to L-N2a reference lake populations for each country from NGIG (note some CBGIG Lakes included from EE and LV).

With this approach the median value of each national metric derived from each national set of reference sites can be used to standardise the national metrics, by subtracting the median value for all reference sites from the median value in reference sites from each country (Table E.1). In this example the Finland method produces lower EQRs in the UK and higher values in NO. The reasons are not clear, but they are assumed to be a result of climatic and other factors which influence the phytoplankton community. The resulting off-set values are used to standardise the national metric by either subtracting or dividing by the national offset. Subtraction is used where it is assumed that the national differences remain constant across the pressure gradient, division is used where the differences reduce with pressure.

Table E.1 Median value for Finland EQR for L-N2a reference lakes and resulting country off-set.

	Median	Offset
EE	0.810	-0.267
FI	0.924	-0.153
IE		
LV	0.627	-0.450
NO	1.197	0.119
SE	1.454	0.377
UK	0.863	-0.214
All	1.077	

To determine whether the country specific differences are constant or reduce across the pressure gradient final EQRs for each country method were plotted against total phosphorus. An example for Finland is shown ion Figure E.2. This plot does not suggests that country specific differences reduce with pressure and it is not easy to identify the differences. This contrasts with the UK method (Figure E.2) where a clear difference can be seen. When the UK method is applied to lakes in Finland it produces significantly higher EQRs than when the same method is applied to lakes in Norway. The apparent differences shown by comparing the median values of metrics from the reference population (Table E.1) are artefacts from the distribution of reference sites across the phosphorus gradient. For this reason country effects were assessed using continuous benchmarking, where data from the whole pressure gradient is used to detect country effects.

Continuous Benchmarking

A linear mixed model with the national EQR as the dependent variable, log total phosphorus as covariable and country as a random factor were fitted to each countries method for each lake type. The model was applied to the linear region of the EQR v TP relationship and outliers were excluded where appropriate. The random factors from the model are the country offset values and are subtracted from the EQR for each national method. Figure E.3 shows the resulting regression relationships for the UK method and the offsets are shown in Table E.2. Offsets for other countries methods are shown in Figure E.4. It is important to note that when comparing the standardised national EQR with the common metric the national boundary values also need to be adjusted by the offset value. Thus for L-N2a lakes when the NO method is applied to lakes in NO a value of 0.012 is subtracted from the NO EQR and the NO G/M boundary of 0.6 becomes (0.60 – 0.012) 0.588. A simpler approach is to adjust each of the national off-set values to be relative to the country method. These values are shown in Table E.2b, so for NO the offset relative to NO becomes 0 but other country offsets for the NO method are decreased by 0.012. This avoids the need to adjust the national boundary values when comparing with the common metric.

Table E.2 National off-set values for L-N2a lakes, a)value relative to all lakes, b)value relative to national method

National off-set relative to all methods

	FI	IE	NO	SE	UKv2
EE	0.000		-0.001	0.000	-0.027
FI	0.000	0.027	0.004	0.000	0.066
IE	0.000	-0.012	-0.014	0.000	-0.004
LV	0.000		0.002	0.000	-0.028
NO	0.000	-0.015	0.012	0.000	-0.053
SE	0.000	0.000	-0.003	0.000	0.046
UK	0.000	-0.012	-0.014	0.000	-0.004

National off-set relative to national method

	FI	IE	NO	SE	UKv2
EE	0.000		-0.013	0.000	-0.022
FI	0.000	0.040	-0.007	0.000	0.070
IE	0.000	0.000	-0.026	0.000	0.000
LV	0.000		-0.009	0.000	-0.023
NO	0.000	-0.003	0.000	0.000	-0.049
SE	0.000	0.013	-0.014	0.000	0.050
UK	0.000	0.000	-0.026	0.000	0.000

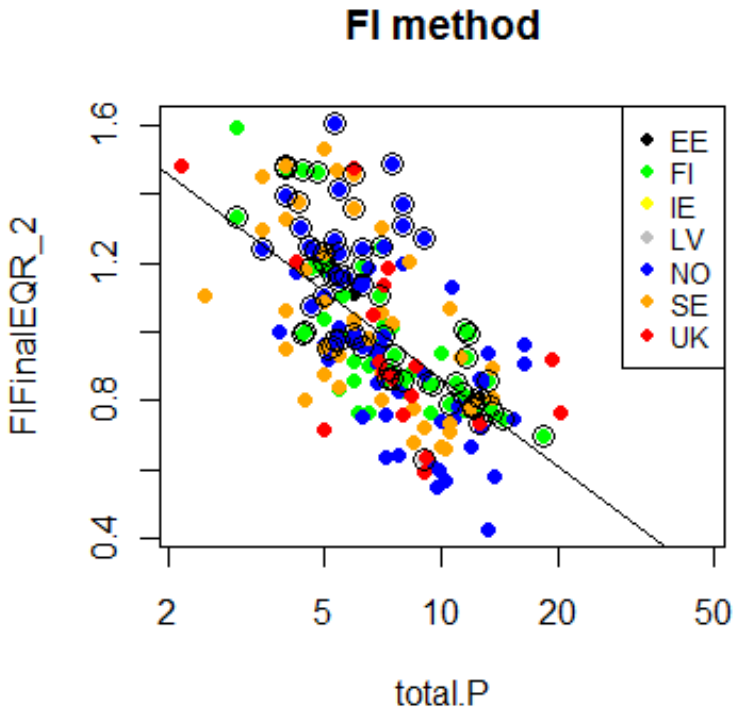


Figure E.2 Relationship between Finland EQR for L-N2a lakes and total P. Points with open circles are reference sites, line shown linear regression for all data

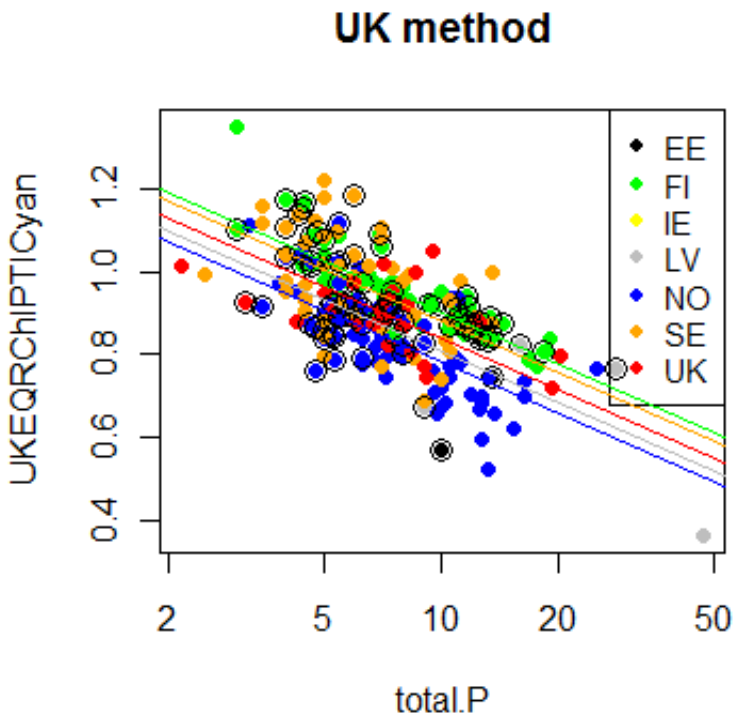


Figure E.3 Relationship between UK EQR for L-N2a lakes and total P. Points with open circles are reference sites, lines shown linear mixed model regressions for all data

Note that there were insufficient lakes from Ireland in the data set to determine a country off-set value for Ireland. To overcome this it was assumed that Ireland would use the same offset as the UK as the two countries have similar sampling strategies and are in the same ecoregion.

With this approach it can be seen that the methods from Finland and Sweden are not sensitive to country, while methods from Norway, UK and Ireland are. Results for NO, SE and IE are shown in Figure E.5 for information.

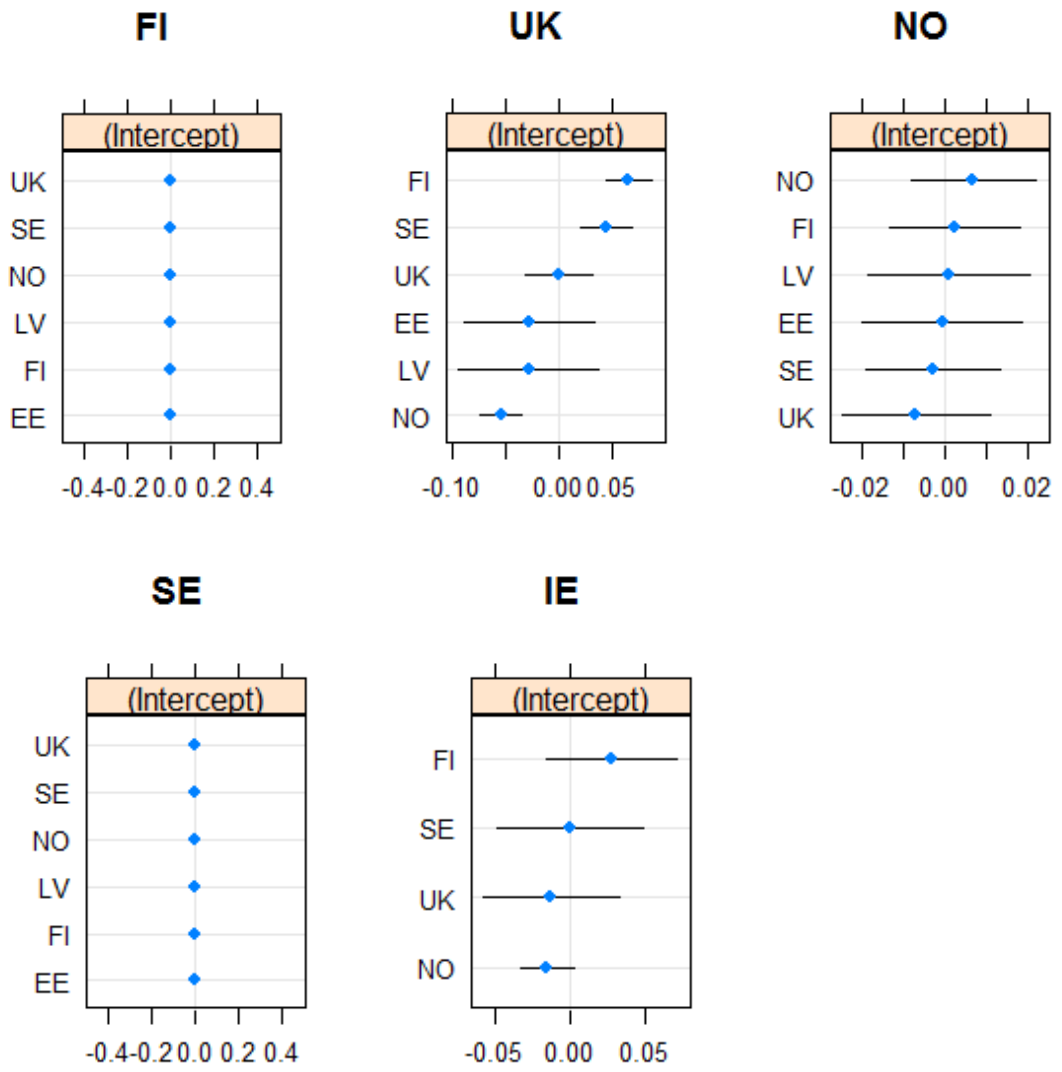


Figure E.4 Random factors (±SE) for National EQRs applied to whole population of L-N2a lakes, values used as national off-sets for standardisation.

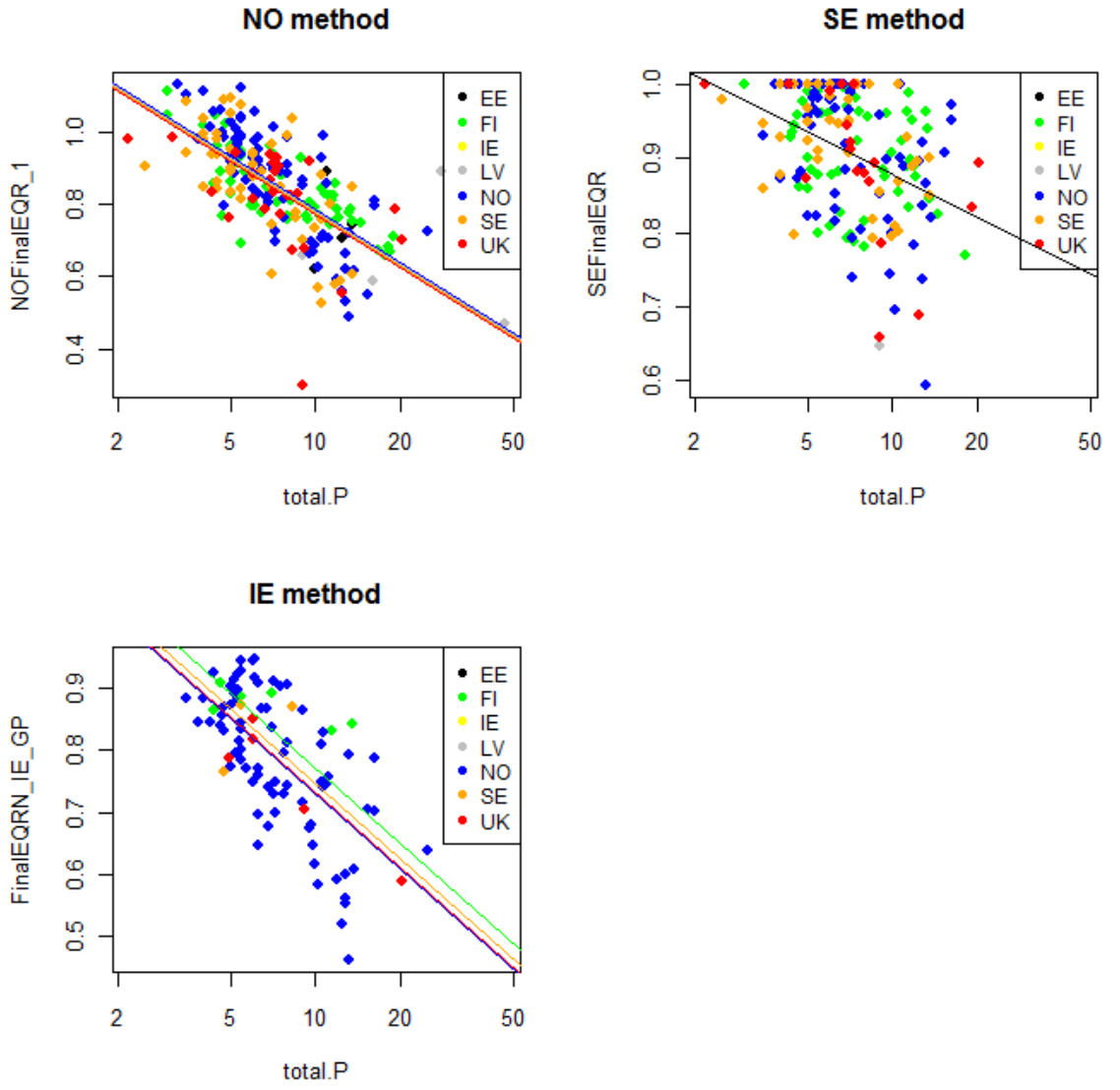


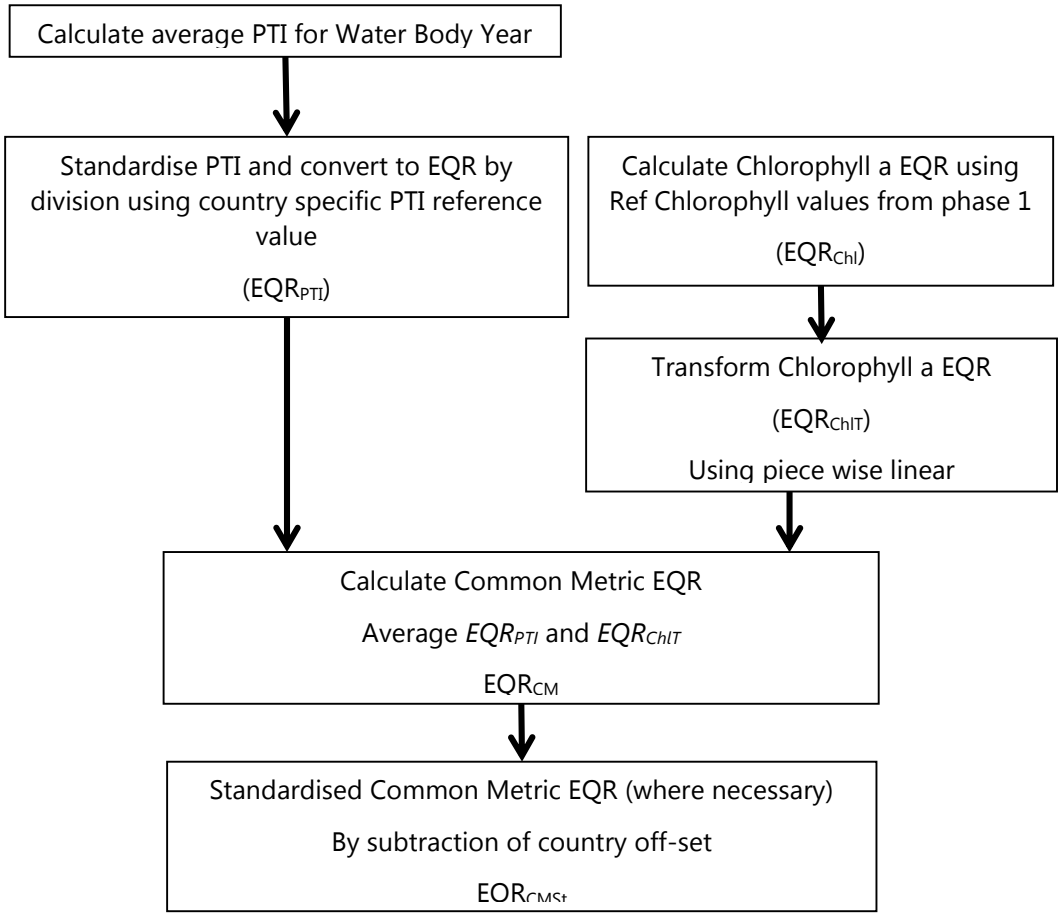
Figure E.5 Relationship between a) NO EQR, b)SE EQR and IE EQR for L-N2a lakes and total P. Lines show linear mixed model relationships

F. Common Metric used for NGIG methods comparisons

Summary

The common metric used by NGIG was an average of the EQRs for chlorophyll a and the WISER PTI. This was a similar approach to that used by the CGIG phytoplankton group, but differed in detail in the approach used to standardise the WISER PTI.

A summary of the approach is shown below



Note that in this approach the PTI metric is standardised for country specific bio-geographical differences before it is combined with chlorophyll a. Two alternative approaches for standardisation, division and subtraction, are described in the intercalibration guidance (Birk *et al.* 2011). For the low and moderate alkalinity lakes compared in the NGIG the convergent relationship between PTI and pressure required division to be used. This enabled the PTI metric to be converted to an EQR during the standardisation process. For high alkalinity lakes, compared in the CBGIG the PTI pressure relationship did not converge and thus subtraction was used for standardisation and conversion to EQR required an additional step.

Having standardised the PTI to allow for country effects it was expected that the final common metric EQR would not require further standardisation. However, this was

checked and for some lake types an additional standardisation was required prior to comparison with national methods. Details of the constituent metrics used in the common metric are given below.

Metric - Chlorophyll a

Chlorophyll a EQR values were calculated using equation 1, the approach agreed in the phase 1 IC process

$$EQR_{Chl} = \frac{Chl_{Ref}}{Chl} \qquad (1)$$

Where:

Chl = observed mean chlorophyll for the growing season (March – October)

Chl_{Ref}= reference chlorophyll

Reference chlorophyll values and EQR boundaries for high good and good moderate were based on those agreed in the phase 1 decision (Poikane 2010). As the relationship between total phosphorus and the chlorophyll EQR calculated in this way is not linear, the EQR was transformed so that boundaries were 0.8, 0.6, 0.4, 0.2 using piece-wise linear transformations (equation 2). To do this it was necessary to make assumptions about the moderate/poor and poor/bad boundaries, which were taken to be factors of 0.5 and 0.25 the agreed Good Moderate boundaries (Table F.1).

$$EQR_T = (EQR_{NT} - LB_{NT})/(UB_{NT} - LB_{NT}) \times (UB_T - LB_T) + LB_T \qquad (2)$$

Where:

EQR_T = Transformed EQR (0.8, 0.6, 0.4, 0.2)

EQR_{NT} = Untransformed EQR (calculated from Equation 1)

UB_{NT} = Upper boundary of the untransformed EQR (Table F.1)

LB_{NT} = Lower boundary of the untransformed EQR (Table F.1)

UB_T = Upper boundary of the transformed EQR

LB_T = Lower boundary of the transformed EQR

Note that (UB_T – LB_T) simplifies to 0.2

It was assumed that the UB_T for High status was 1.00

Calculations were done in spreadsheets for each type using lookup tables for each GIG type.

Table F.1 Reference chlorophyll a and EQR boundaries used for the chlorophyll a common metric.

Lake Type	Ref Chl a	HG EQR	GM EQR	MP EQR	PB EQR
L-N1	3.0	0.50	0.33	0.17	0.08

L-N2a	2.0	0.50	0.30	0.15	0.08
L-N2b	2.0	0.64	0.33	0.17	0.08
L-N5	1.5	0.50	0.30	0.15	0.08
L-N3a	3.0	0.50	0.30	0.15	0.08
L-N6a	2.5	0.50	0.33	0.15	0.08
L-N8a	4.0	0.50	0.33	0.17	0.08

Metric - WISER common metric Plankton Trophic Index (PTI)

Following proposals in the draft WISER report (Phillips *et al.* 2010) a Plankton Trophic Index value (PTI) has been used to represent the taxonomic component of the phytoplankton. This was calculated using equation 3

$$PTI = \frac{\sum_{j=1}^{n} a_j s_j}{\sum_{j=1}^{n} a_j} \qquad (3)$$

Where:

a_j = proportion of *j*th taxon in the sample

s_j= optimum of *j*th taxon in the sample (see below for details)

The WISER metric was developed using summer data (July-September) so the metric is only applicable to samples from this time window. Sample PTI scores are calculated, then averaged for each Water Body Year, from which an EQR is determined using equation 4

$$EQR_{PTI} = \left(\frac{PTI_{Obs} - PTI_{Max}}{PTI_{\mathrm{Re}f} - PTI_{Max}} \right) \qquad (4)$$

Where:

PTI_{Obs} = mean sample PTI for each lake year

PTI_{Max} = Maximum PTI score for type, the upper (worst) anchor. (1.3 for low alkalinity, 1.5 for moderate alkalinity)

PTI_{Ref} = Expected or reference PTI for type and country, the lower (best) anchor (see below for details of country specific values)

(If $PTI_{Obs} > PTI_{Max}$ then EQR_{PTI} is set to 0)

Taxa Optima used to calculate PTI

The draft WISER report provided sets of genus optima derived from an anlysis of the full data set and for various subsets derived from different GIGs. For NGIG optima derived from the Northern and Central Baltic GIGs were used (Table F.3). These optima were derived from the 1st axis of a CCA ordination constrained by Log TP using the vegan package in R(Oksanen *et al.* 2010). At a WISER project board meeting some concerns

were raised that some genera covered a wide range of nutrient conditions and that this could limit the usefulness of the metric. To explore this an additional series of ordinations were performed using species level data. As time was limited this analysis only used NGIG and CBGIG data and as for the previous work the CCA ordination was constrained by Log TP. The sample PTIs derived from both the species and generic optima were then compared with TP and Chl, using both linear and GAM models. As the species optima were only marginally better than those using the generic values GIG members agreed that in general species optima were less appropriate for use as a common metric. However it was felt that some some genera could be split into groups. Data were tabulated and where species optima for a given genus had a large range, and the numbers of samples used to generate the optima were sufficient, the genera were split into sub-groups. The following genera were split, *Anabeana*, *Aulacosira*, *Cosmarium*, *Cyclotella*, *Merismopedia*, *Mycrocystis*, *Monoraphidium*, *Planktothrix*, *Scendesmus*, *Staurastrum* and *Tetrastrum*. Each sub-group was then allocated an optima based on the weighted average of the species optima within the sub-group, the weight being the number of records for each species in the sub-group (Table F.4).

Finally all of the taxa listed in the WISER database, which were sufficiently common to be included in the analysis were allocated a generic or generic group optima (Available as an Excel File NGIG_CBGIG_WISER_Optima.xls). This allows sample PTIs to be calculated quickly without the need to combine taxa at generic level.

All samples from the lake types intercalibrated in NGIG have had a sample PTI and PTI EQR calculated.

Standardisation to remove country effects, relationship between WISER common metric and Pressure

The relationship between PTI and TP for all lakes (allocated to an alkalinity type) in Northern and Central Baltic GIGs is shown in Figure F.1. GAM models (Wood 2006) demonstrated that the relationship is linear below a TP of 100 μgl^{-1} (Phillips *et al.* 2010) and linear mixed models (Bates *et al.* 2011) with PTI as dependent variable, logTP as covariable and alkalinity type as a random variable demonstrated that alkalinity type was the most significant typological factor influencing this relationship (Figure F.1). In the NGIG, where low and moderate alkalinity lakes dominate it was also clear that the relationship between PTI and TP was dependent on country (Figure F.2). These differences were quantified using linear mixed models for all low and then moderate alkalinity lakes. The models were set up with PTI as dependent variable with logTP as a co-variable and country as a random factor. The resulting coefficients of the models are shown in Figure F.3 and Table F.2. The effect of country was most significant for low alkalinity lakes, but in both low and moderate alkalinity lakes Norway has lower PTI values than either the UK or Finland for the same concentration of total phosphorus, demonstrating the need for standardisation. It was not possible to identify the reason for these differences, but the data suggest that samples from Norway tended to have fewer taxa with high optima relative to the level of enrichment with phosphorus. This difference was also noted when the Norwegian and UK taxonomic metrics were applied

to the GIG data and may be a climatic effect, but can also be caused by UK sampling of littoral or outflow, where the likelihood to get benthic taxa with higher nutrient optima is higher.

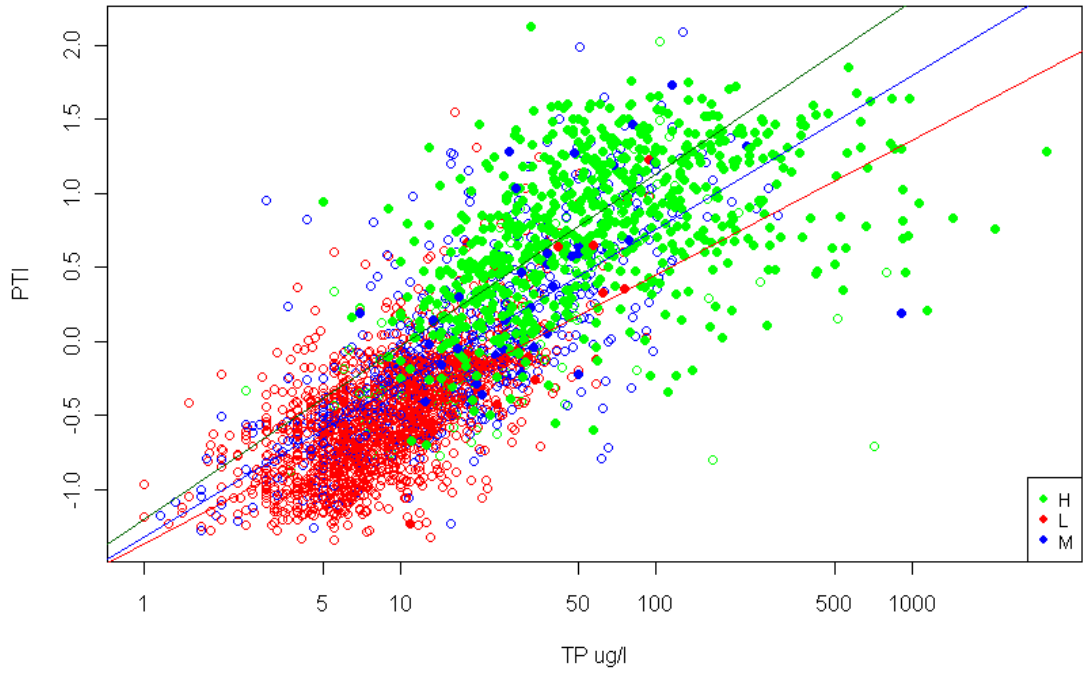


Figure F.1 Relationship between mean growing season TP and PTI, linear mixed models fitted to high (H), moderate (M) and low (L) alkalinity lake types in NGIG and CBGIG (TP<100 µgl-1). Open circles NGIG lakes, closed circles CBGIG lakes

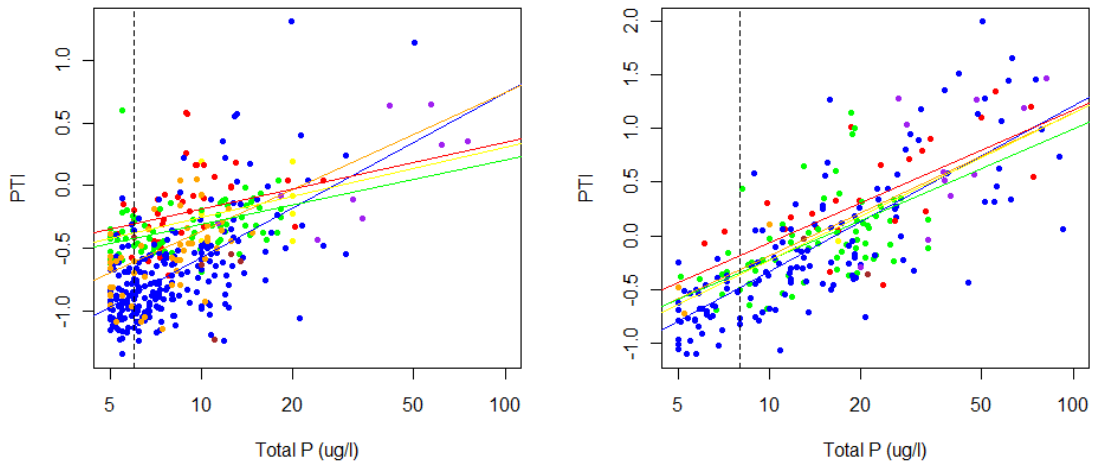


Figure F.2 Relationship between PTI and total phosphorus for a) low and b) moderate alkalinity lakes in Northern GIG. Points and lines (linear mixed model with country as random factor) identified by country, NO blue, SE orange, FI green, Ireland yellow, UK red. Vertical line total P value used to estimate country specific reference PTI (LA = 6µgl^{-1}, MA = 8 µgl^{-1}).

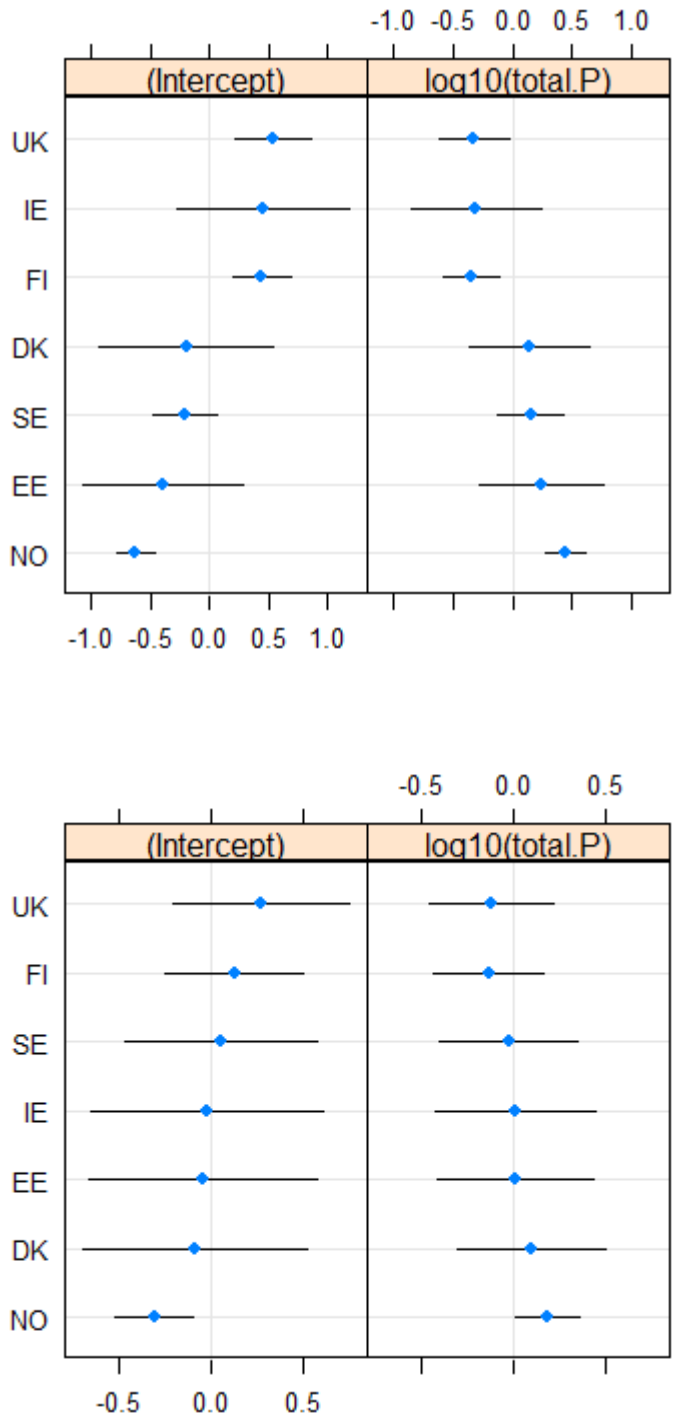


Figure F.3 Parameters for linear mixed model relationship between PTI and log10 Total P in a)low and b) moderate alkalinity lakes from northern and central GIGs. Horizontal lines represent confidence intervals of coefficients. TP in range of 5-100 µgl^{-1}

Standardisation of PTI to create an EQR using continuous benchmarking

PTI values are country dependent and thus require standardisation before they can be used as a component of a common metric. As the relationship between the metric value and pressure clearly converges (Figure F.2) it is appropriate to standardise by division (Birk *et al.* 2011). Division will normally convert a metric score to an EQR, although in the case of the PTI, where the metric value increases with pressure the EQR needs to be inverted (see equation 4 above). Thus the PTI metric was converted to an EQR and standardised in the same step, by using a country specific PTI reference value.

In NGIG it would be theoretically possible to determine a reference PTI value by calculating a summary statistic from all reference sites, such as the median. However, even in the NGIG the number of reference sites for any particular type is limited and the distribution of reference lake total phosphorus concentrations by country is not uniform. A more robust approach is to use the linear mixed models (Table F.2) to predict a country specific reference PTI from a fixed TP concentration or benchmark. The exact value of the benchmark is not a critical factor as the resulting common metric EQR is only used as a relative scale, however benchmark values for TP of 6 and 8 μgl^{-1} TP were used for low and moderate alkalinity lakes respectively. The same country specific reference values for low and moderate alkalinity lakes were used for both clear water and humic lake types.

Table F.2 Parameters from linear mixed models used to predict country specific reference PTI values for low and moderate alkalinity lakes. TP in range of 5-100 μgl^{-1}

Country	Low alkalinity lakes			Moderate alkalinity lakes		
	Intercept	Slope	Est PTI Ref	Intercept	Slope	Est PTI Ref
DK	-1.461	1.011	-0.674	-1.666	1.456	-0.351
EE	-1.662	1.111	-0.797	-1.621	1.370	-0.383
FI	-0.824	0.516	-0.423	-1.450	1.222	-0.347
IE	-0.816	0.560	-0.380	-1.597	1.369	-0.360
NO	-1.895	1.316	-0.871	-1.885	1.543	-0.492
SE	-1.474	1.020	-0.680	-1.524	1.333	-0.320
UK	-0.730	0.545	-0.307	-1.306	1.236	-0.190
All	-1.266	0.868	-0.591	-1.266	0.868	-0.482

Combination of Chlorophyll and PTI EQR values to form a single common metric and final standardisation.

The final common metric was derived by averaging the normalised chlorophyll a EQR and the PTI EQR. Initially an attempt was made to normalise the EQR_{PTI}, by setting boundaries and applying a piece wise linear transformation. However, this produced a final common metric EQR which had a worse relationship with the national metrics than averaging the raw EQR_{PTI}. As normalisation requires boundaries to be set independently

on the PTI scale, which is not a requirement of a common metric, the PTI EQR was not normalised. The final common metric EQR had a better relationship with pressure (TP) than either of the constituent metrics (EQR_{Chl} and EQR_{PTI}) demonstrating the benefits of incorporating both biomass and taxonomic components (Figure F.4).

For each of the NGIG lake types the common metric was tested to check if further standardisation was required. This followed the same procedure as the standardisation of the national metrics. The relationship between the common metric EQR and log of TP was determined and a linear mixed model with Country as a random factor was fitted within the linear range. Where the resulting random factors were significantly different, the Common Metric EQR was adjusted by subtracting the random factor (the relative country off-set). Subtraction was used as there was no evidence, based on the scatter plots, that relationships converged. The results of the standardisation for each lake type are shown in the type specific excel sheets used to make comparisons.

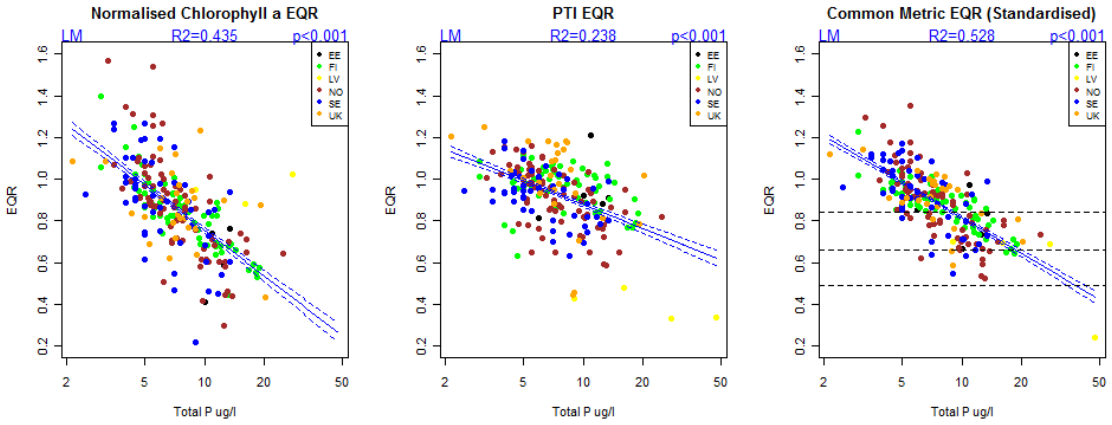


Figure F.4 Relationship between components of the common metric, a)EQR_{Chla}, b)EQR_{PTI} and c)the standardised common metric EQR_{CMSt} for low alkalinity shallow lakes (type L-N2a) . Horizontal lines show final intercarlibrated boundaries on common metric scale

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Table F.3 List of taxon optima used to derive PTI score for Common Metric

Taxon	Optima	Records
Acanthoceras	0.401	167
Achnanthes	-0.590	95
Achnanthidium	-0.437	17
Achroonema	1.156	43
Actinastrum	2.867	102
Actinocyclus	3.672	49
Amphora	1.757	41
Anabaena	1.022	917
Anabaena flos-aquae group	1.280	592
Anabaena lemmermannii group	-0.010	305
Anabaenopsis	2.864	33
Ankistrodesmus	0.666	208
Ankyra	0.085	360
Aphanizomenon	1.700	559
Aphanocapsa	0.695	370
Aphanothece	0.231	333
Asterionella	-0.142	856
Aulacoseira	0.787	853
Aulacoseira alpigena group	-0.410	217
Aulacoseira granulata group	1.420	522
Bitrichia	-1.430	620
Botryococcus	-0.958	619
Carteria	-0.341	140
Centrales	1.286	410
Centritractus	0.811	36
Ceratium	0.655	771
Chlamydocapsa	0.361	12
Chlamydomonas	0.185	835
Chlorella	1.237	27
Chlorococcales	-0.423	704
Chlorogonium	2.334	18
Chlorophyceae	1.896	123
Chlorotetraedron	1.619	16
Chromulina	-1.184	409

Taxon	Optima	Records
Chroococcales	0.881	249
Chroococcus	0.486	445
Chroomonas	-0.823	510
Chrysidiastrum	-1.288	143
Chrysochromulina	-0.440	727
Chrysococcus	-0.374	264
Chrysolykos	-1.910	310
Chrysophyceae	-1.337	862
Chrysosphaerella	-0.751	56
Chrysostephanosphaera	-1.472	28
Closteriopsis	1.859	49
Closterium	0.976	632
Cocconeis	1.327	62
Coelastrum	1.746	305
Coelosphaerium	0.864	116
Coenochloris	0.293	52
Coenococcus	-0.973	8
Coenocystis	0.351	8
Colacium	0.068	12
Cosmarium	0.000	558
Cosmarium bioculatum group	0.560	81
Cosmarium formosulum/humile	1.830	18
Crucigenia	0.058	423
Crucigeniella	0.130	188
Cryptomonadales	0.479	73
Cryptomonas	0.204	1539
Cryptophyceae	1.518	63
Cyanodictyon	0.294	207
Cyanonephron	0.545	15
Cyanophyceae	1.672	162
Cyclostephanos	2.337	89
Cyclotella	-0.480	751
Cyclotella meneghiniana group	1.320	201
Cylindrospermopsis	1.871	42
Cylindrotheca	1.566	13
Cymatopleura	1.665	12
Cymbella	1.117	43
Diatoma	1.314	158
Dictyosphaerium	0.102	461

Taxon	Optima	Records
Didymocystis	0.226	146
Dinobryon	-0.749	1208
Dinophyceae	-1.250	471
Diplochloris	3.689	23
Discostella	-1.456	216
Elakatothrix	-0.941	786
Epipyxis	-1.085	129
Erkenia	0.819	20
Euastrum	-0.422	73
Eudorina	0.839	118
Euglena	1.646	239
Euglenophyceae	1.819	15
Eunotia	-0.232	98
Fragilaria	0.290	837
Franceia	1.274	19
Frustulia	-1.341	13
Glenodinium	0.193	41
Gloeocystis	-1.099	57
Gloeotila	-1.210	126
Golenkinia	1.601	40
Gomphonema	1.640	24
Gomphosphaeria	1.623	53
Goniochloris	2.451	58
Gonium	0.973	12
Gonyostomum	-0.120	243
Gymnodinium	-1.072	1042
Gyrosigma	1.440	23
Isthmochloron	-1.922	25
Katodinium	-0.716	10
Kephyrion	-1.011	415
Keratococcus	0.404	11
Kirchneriella	1.145	224
Koliella	-0.693	272
Lagerheimia	1.996	136
Limnothrix	1.701	188
Lyngbya	2.224	18
Mallomonas	-0.645	961
Melosira	1.371	48
Merismopedia	-1.163	584

Taxon	Optima	Records
Merismopedia punctata group	1.610	46
Micractinium	1.378	67
Microcystis	1.851	432
Microcystis aeruginosa/wesenbergii	1.490	429
Microcystis flos-aquae/viridis	1.920	94
Microsystis botrys/novacekii	0.460	33
Monochrysis	-1.074	167
Monomastix	-0.822	270
Monomorphina	1.976	40
Monoraphidium	-0.699	1182
Monoraphidium contortum group	1.290	982
Monoraphidium dybowskii/griffithii	-1.130	1011
Mougeotia	0.186	253
Navicula	1.174	148
Nephrochlamys	2.327	22
Nephrocytium	-0.406	100
Nephroselmis	0.560	21
Nitzschia	1.892	438
Ochromonadales	-1.670	257
Ochromonas	-1.270	591
Oocystis	-0.539	1088
Ophiocytium	0.612	20
Oscillatoria	1.533	164
Oscillatoriales	1.477	70
Pandorina	1.707	135
Paulschulzia	-0.107	61
Pediastrum	1.415	596
Pennales	1.025	137
Peridiniopsis	0.625	65
Peridinium	-0.209	1142
Phacotus	1.229	88
Phacus	2.031	157
Phormidium	1.391	14
Picoplankton	-1.297	651
Pinnularia	0.198	16
Plagioselmis	-0.585	1052
Plagioselmis	1.021	196
Planctonema	2.064	28
Planktolyngbya	1.569	221

Taxon	Optima	Records
Planktosphaeria	0.978	46
Planktothrix	1.502	471
Planktothrix isothrix group	-0.250	51
Pseudanabaena	1.757	300
Pseudodictyosphaerium	0.437	10
Pseudogoniochloris	0.891	31
Pseudokephyrion	-1.720	445
Pseudopedinella	-1.116	586
Pseudosphaerocystis	-0.190	68
Pseudostaurastrum	1.842	51
Pteromonas	3.095	39
Puncticulata	0.149	29
Quadricoccus	3.203	17
Quadrigula	-0.662	335
Radiocystis	-0.725	96
Raphidocelis	-0.024	130
Rhabdoderma	-0.267	30
Rhabdogloea	-1.747	33
Rhodomonas	0.866	108
Romeria	1.328	34
Scenedesmus	1.549	798
Scenedesmus ecornis group	0.640	222
Scenedesmus quadricauda group	2.190	744
Schroederia	1.769	75
Scourfieldia	-1.236	339
Siderocelis	2.018	22
Skeletonema	3.064	46
Snowella	-0.021	587
Spermatozopsis	2.028	33
Sphaerocystis	-0.163	307
Spiniferomonas	-1.373	490
Spondylosium	-0.782	126
Staurastrum	0.548	637
Staurastrum cingulum group	-0.570	306
Staurastrum gracile group	0.820	168
Staurodesmus	-1.096	333
Stauroneis	2.986	13
Staurosira	2.115	54
Stephanodiscus	1.622	329

Taxon	Optima	Records
Stichococcus	1.232	18
Stichogloea	-1.375	215
Surirella	1.858	27
Syncrypta	0.718	14
Synechococcus	1.073	38
Synura	-0.274	322
Tabellaria	-0.669	629
Teilingia	-0.584	52
Tetraëdriella	-0.469	57
Tetraedron	0.568	545
Tetraselmis	0.181	18
Tetrastrum	0.727	194
Tetrastrum komarekii/triangulare	0.140	131
Tetrastrum staurogeniaeforme/triacanthum	1.800	68
Thalassiosira	2.482	11
Trachelomonas	1.258	414
Treubaria	1.168	81
Tribonema	1.200	28
Trichormus	1.519	58
Ulnaria	1.003	566
Ulothrix	1.618	14
Uroglena	-0.660	445
Urosolenia	-0.643	499
Volvocales	0.893	162
Volvox	1.564	15
Westella	0.831	12
Willea	-1.011	74
Woronichinia	0.069	393
Xanthidium	-0.143	53

Table F.4 Species allocated to grouped genera (other species in genera take generic score shown in Table F.3)

Rebecca ID	Genus	Genus Group	AcceptedTaxon	Optima	Species Records
R1534	Anabaena	Anabaena lemmermannii group	Anabaena curva	-0.01	11
R1905			Anabaena danica		5
R1539			Anabaena lemmermannii		154
R1540			Anabaena macrospora		40
R1544			Anabaena planctonica		95
R2189		Anabaena flos-aquae group	Anabaena bergii var. limnetica	1.28	5
R2161			Anabaena catenula var. affinis		11
R1531			Anabaena circinalis		63
R1532			Anabaena compacta		12
R1533			Anabaena crassa		41
R1536			Anabaena flos-aquae		330
R1541			Anabaena mendotae		13
R1545			Anabaena smithii		9
R1549			Anabaena spiroides		108
R0019	Aulacoseira	Aulacoseira alpigena group	Aulacoseira alpigena	-0.41	217
R0021			Aulacoseira distans		132
R0033			Aulacoseira subarctica		55
R0034			Aulacoseira tenella		38
R0020		Aulacoseira granulata group	Aulacoseira ambigua	1.42	153
R0023			Aulacoseira granulata		277
R0024			Aulacoseira granulata var. angustissima		92
R1205	Cosmarium	Cosmarium bioculatum group	Cosmarium bioculatum	0.56	25

Rebecca ID	Genus	Genus Group	AcceptedTaxon	Optima	Species Records
R1214			Cosmarium granatum		14
R1215			Cosmarium impressulum		4
R1217			Cosmarium margaritiferum		18
R1222			Cosmarium protractum		5
R1224			Cosmarium punctulatum		3
R1231			Cosmarium reniforme		10
R1245			Cosmarium turpinii		2
R1213		Cosmarium formosulum/humile	Cosmarium formosulum	1.83	10
R2284			Cosmarium humile		8
R0039	Cyclotella	Cyclotella meneghiniana group	Cyclotella atomus	1.32	56
R2195			Cyclotella cyclopuncta		5
R0047			Cyclotella meneghiniana		100
R0048			Cyclotella ocellata		40
R1475	Merismopedia	Merismopedia punctata group	Merismopedia glauca	1.61	8
R1476			Merismopedia minima		18
R1477			Merismopedia punctata		20
R1483	Microcystis	Microsystis botrys/novacekii	Microcystis botrys	0.46	18
R1494			Microcystis novacekii		15
R1482		Microcystis aeruginosa/wesenbergii	Microcystis aeruginosa	1.49	262
R1499			Microcystis wesenbergii		167
R1487		Microcystis flos-aquae/viridis	Microcystis flos-aquae	1.92	50
R1498			Microcystis viridis		44
R0667			Monoraphidium dybowskii	-1.13	709

Rebecca ID	Genus	Genus Group	AcceptedTaxon	Optima	Species Records
R0670	Monoraphidium	Monoraphidium dybowskii/griffithii	Monoraphidium griffithii		302
R0663		Monoraphidium contortum group	Monoraphidium arcuatum	1.29	60
R0664			Monoraphidium circinale		31
R0665			Monoraphidium contortum		442
R0666			Monoraphidium convolutum		24
R0672			Monoraphidium irregulare		20
R0673			Monoraphidium komarkovae		179
R0675			Monoraphidium minutum		191
R0676			Monoraphidium mirabile		11
R0677			Monoraphidium nanum		3
R0683			Monoraphidium tortile		21
R2147	Planktothrix	Planktothrix isothrix group	Planktothrix isothrix	-0.25	49
R1616			Planktothrix prolifica		2
R0753	Scenedesmus	Scenedesmus ecornis group	Scenedesmus aculeolatus	0.64	11
R0766			Scenedesmus brasiliensis		7
R0781			Scenedesmus ecornis		149
R0760			Scenedesmus obtusus		27
R0810			Scenedesmus serratus		15
R1922			Scenedesmus verrucosus		13
R2552		Scenedesmus quadricauda group	Scenedesmus abundans	2.19	23
R0754			Scenedesmus acuminatus		100
R0763			Scenedesmus bicaudatus		44

Rebecca ID	Genus	Genus Group	AcceptedTaxon	Optima	Species Records
R0772			Scenedesmus costato-granulatus		18
R0775			Scenedesmus denticulatus		28
R0777			Scenedesmus dimorphus		60
R0784			Scenedesmus granulatus		9
R0789			Scenedesmus intermedius		20
R0793			Scenedesmus longispina		4
R0794			Scenedesmus magnus		12
R0799			Scenedesmus opoliensis		90
R0806			Scenedesmus quadricauda		279
R0813			Scenedesmus spinosus		33
R0814			Scenedesmus subspicatus		24
R1275	Staurastrum	Staurastrum cingulum group	Staurastrum anatinum	-0.57	39
R1278			Staurastrum avicula		14
R1283			Staurastrum cingulum		63
R2608			Staurastrum cingulum var. obesum		11
R1284			Staurastrum erasum		8
R1291			Staurastrum longipes		19
R1293			Staurastrum luetkemuelleri		19
R1295			Staurastrum lunatum		60
R1303			Staurastrum pingue		34
R1305			Staurastrum pseudopelagicum		34
R1308			Staurastrum smithii		5
R1282		Staurastrum gracile group	Staurastrum chaetoceras	0.82	24

Rebecca ID	Genus	Genus Group	AcceptedTaxon	Optima	Species Records
R1286			Staurastrum furcigerum		5
R1288			Staurastrum gracile		94
R1301			Staurastrum paradoxum var. parvum		32
R1311			Staurastrum tetracerum		13
R0866	Tetrastrum	Tetrastrum komarekii/triangulare	Tetrastrum komarekii	0.14	47
R0873			Tetrastrum triangulare		84
R0871		Tetrastrum staurogeniaeforme/triacanthum	Tetrastrum staurogeniaeforme	1.8	64
R0872			Tetrastrum triacanthum		4

G. Reference conditions, relationships between national method and pressure, relationships between national method and common metric, and box lots for biomass and bloom metrics in each status class

G.1 LN1 lakes

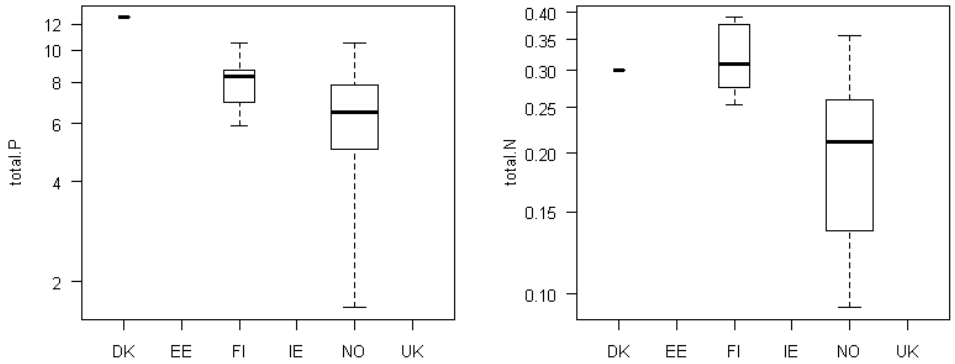
Summary

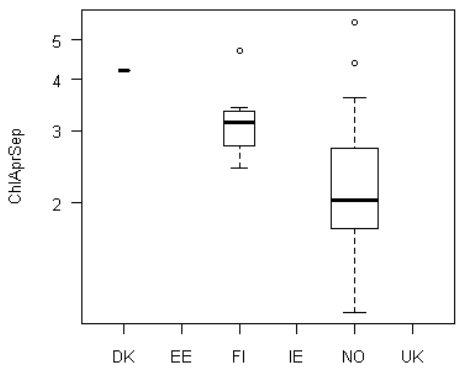
Final version has the following changes:

1. NO and UK combination rule changed so that cyanobacteria only averaged if worse than average of other EQRs;
2. UK PTI boundaries changed back to original UK values;
3. Common metric standardised following advice at validation workshop;
4. NO Reference chlorophyll a changed and standardizations checked.

All countries have a significant relationship with pressure and achieve the required relationship with the common metric. All countries are in the harmonisation band

Reference Conditions





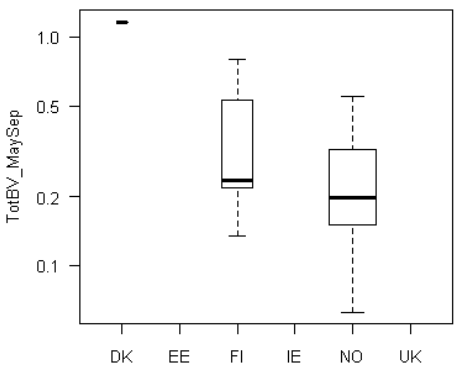


Figure G.1 Distributions of a)TP ug/l, b)TN mg/l, c)Chlorophyll a (Apr –Sept), d) total biovolume mg/l May-Sep in LN1 reference lakes for each country.

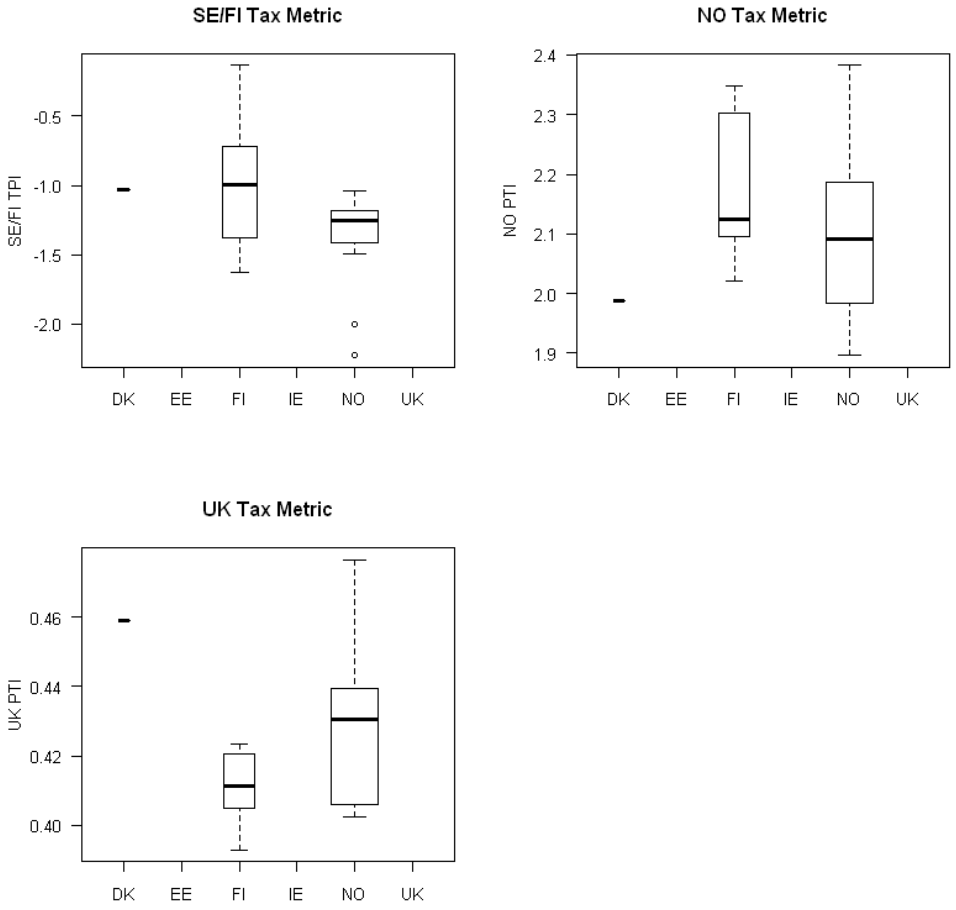


Figure G.2 Distributions of taxonomic metrics a)Swedish TPI index, b)Norwegian PTI index, c)UK PTI index in LN1 reference lakes for each country

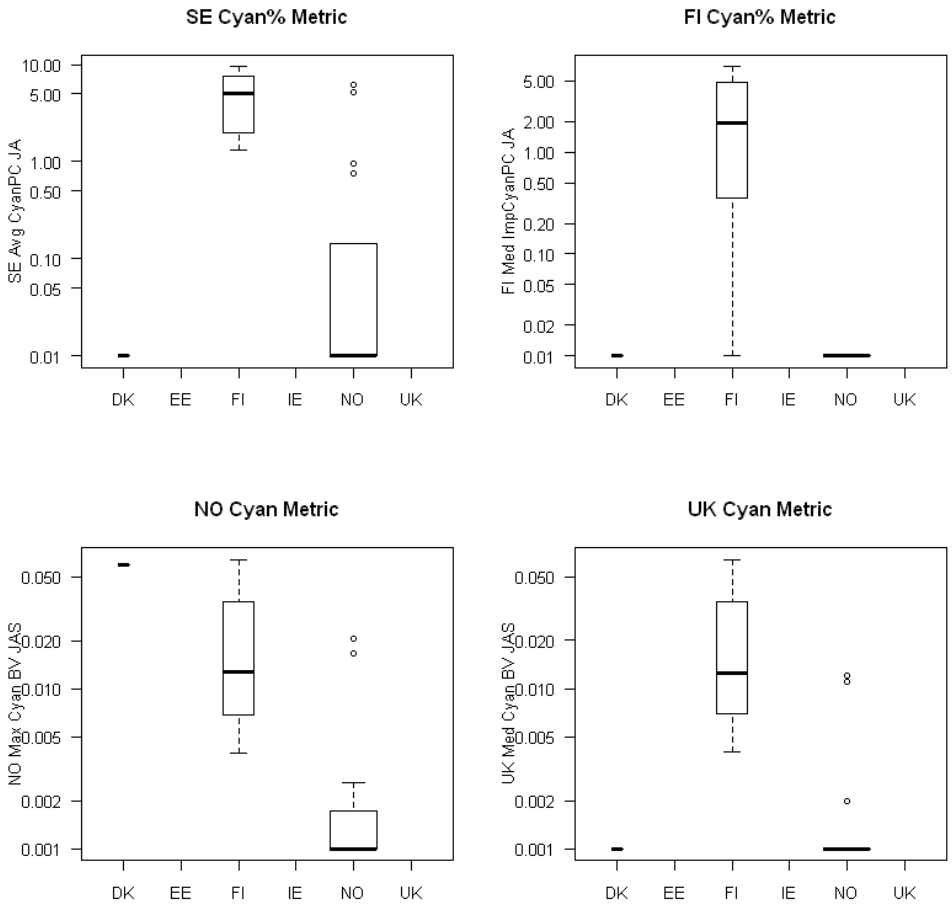


Figure G.3 Distributions of cyanobacteria metrics a)Sweden % cyanobacteria (July & Aug), b)Finland % impact cyanobacteria (July & Aug), c)Norway max cyanobacteria biovolume (mg/l) July-Sept, d)UK median cyanobacteria biovolume (mg/l) July - Sept in LN1 reference lakes for each country

Table G.1 Distributions of metrics for LN1 Reference Lakes

Metric	Country	50%	90%	95%	100%	N
TP	DK	13	13	13	13	1
TP	FI	8	9	10	11	8
TP	NO	7	10	10	11	17
TP	All	7	10	11	13	26
		50%	90%	95%	100%	N
Chl	DK	4.2	4.2	4.2	4.2	1
Chl	FI	3.1	3.8	4.3	4.7	8
Chl	NO	2.0	3.9	4.6	5.5	17
Chl	All	2.6	4.3	4.6	5.5	26
		50%	90%	95%	100%	N
BVol	DK	1.16	1.16	1.16	1.16	1

Metric	Country	50%	90%	95%	100%	N
BVol	FI	0.24	0.66	0.73	0.80	8
BVol	NO	0.20	0.39	0.43	0.55	17
BVol	All	0.23	0.57	0.75	1.16	26
		50%	90%	95%	100%	N
SE TPI	DK	-1.029	-1.029	-1.029	-1.029	1
SE TPI	FI	-0.998	-0.539	-0.337	-0.134	8
SE TPI	NO	-1.253	-1.098	-1.062	-1.035	17
SE TPI	All	-1.226	-0.736	-0.715	-0.134	26
		50%	90%	95%	100%	N
NO PTI	DK	1.989	1.989	1.989	1.989	1
NO PTI	FI	2.124	2.326	2.337	2.348	8
NO PTI	NO	2.092	2.307	2.349	2.383	17
NO PTI	All	2.113	2.329	2.346	2.383	26
		50%	90%	95%	100%	N
UK PTI	DK	0.459	0.459	0.459	0.459	1
UK PTI	FI	0.411	0.423	0.423	0.423	8
UK PTI	NO	0.430	0.450	0.462	0.477	17
UK PTI	All	0.423	0.452	0.459	0.477	26
		50%	90%	95%	100%	N
FI ImpCyanPC	DK	0.00	0.00	0.00	0.00	1
FI ImpCyanPC	FI	1.92	6.73	6.80	6.87	8
FI ImpCyanPC	NO	0.00	0.00	0.00	0.00	17
FI ImpCyanPC		0.00	2.92	5.74	6.87	26
		50%	90%	95%	100%	N
SE CyanPC	DK	0.00	0.00	0.00	0.00	1
SE CyanPC	FI	4.98	8.33	8.91	9.50	8
SE CyanPC	NO	0.00	2.67	5.42	6.14	17
SE CyanPC	All	0.07	6.82	7.74	9.50	26
		50%	90%	95%	100%	N
NO Max CyanBV	DK	0.058	0.058	0.058	0.058	1
NO Max CyanBV	FI	0.012	0.053	0.058	0.063	8
NO Max CyanBV	NO	0.000	0.007	0.016	0.020	17
NO Max CyanBV	All	0.001	0.034	0.056	0.063	26
		50%	90%	95%	100%	N
UK Med CyanBV	DK	0.000	0.000	0.000	0.000	1
UK Med CyanBV	FI	0.012	0.053	0.058	0.063	8
UK Med CyanBV	NO	0.000	0.005	0.010	0.011	17
UK Med CyanBV	All	0.000	0.017	0.041	0.063	26

Based on above results the ratio of the median chlorophyll to 90th percentile chlorophyll for reference lakes is shown in Table G.1

Table G.2 Ratio of median chlorophyll a to 90th percentile chlorophyll a for reference sites. A potential HG EQR boundary.

FI	0.83
NO	0.52
All	0.59

Relationship with Pressure

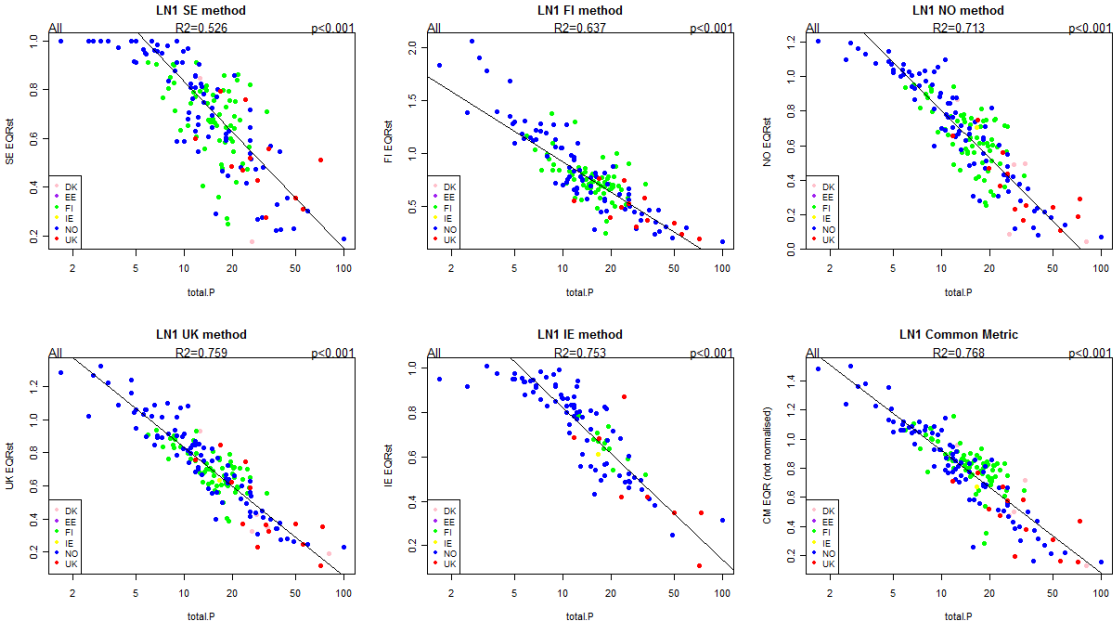


Figure G.4 Relationship between national final EQRs (standardised to remove country effects) and total P. a) SE, b) FI, c) NO, d) UK, e) IE, f) common metric for LN1 lake type

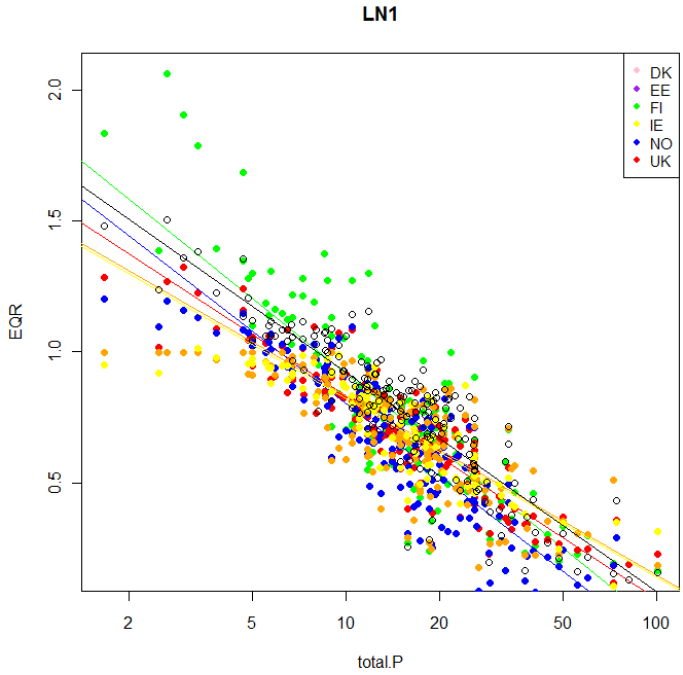


Figure G.5 Relationship between national EQRs (standardised to remove country effects) and total P. Points coloured by national method (applied to all countries data), open black circles are for common metric. (note that SE has not lakes identified as LN1 in the GIG data set, but method has been applied to other MS data)

Table G.3 Regression parameters for relationship between final EQRs (standardised to remove country effects) and total P, based on TP range of 5-50 ug/l

	Intercept	log10(total.P)	adj R2	p
SE	1.517	-0.685	0.522	<0.001
FI	1.871	-0.954	0.635	<0.001
NO	1.723	-0.918	0.711	<0.001
UK	1.610	-0.777	0.758	<0.001
IE	1.506	-0.683	0.750	<0.001

Relationship with Common Metric

For Finland segmented regression demonstrated different linear relationships above and below a break point of FI EQR = 0.55 (see point and bar in fig 5) The regression parameters for the upper segment have been used to determine the FI HG boundary on the common metric scale and the lower segment for the GM boundary.

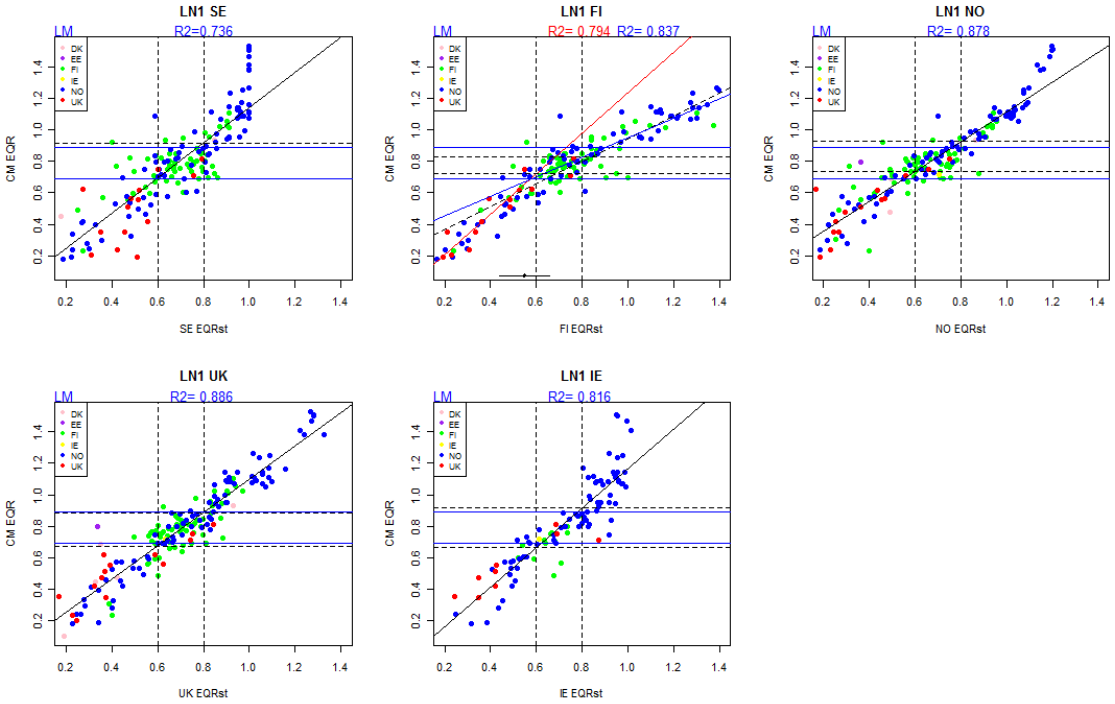


Figure G.6 Relationship between national standardised EQR and common metric EQR. a) SE, b) FI, c) NO, d) UK, e) IE for LN1 lake type. Vertical lines mark boundaries on standardised national scale. Horizontal line in c marks location of segment and error, red line in b is the regression used for GM boundary, the blue line in b is the regression for the HG boundary

Table G.4 Regression parameters for relationship between national and common metric

	UK	NO	IE	SE	FI (Global)	FI GM FI EQR <0.55	FI HG FI EQR >0.55
Intercept	0.04	0.170	-0.08	0.02	0.22	-0.05	0.33
slope	1.06	0.943	1.25	1.12	0.72	1.28	0.61
Pearson's r	0.94	0.94	0.90	0.86	0.94	0.89	0.91
R^2	0.89	0.878	0.816	0.736	0.875	0.794	0.837

Distribution of pressure and biological metrics by common metric class

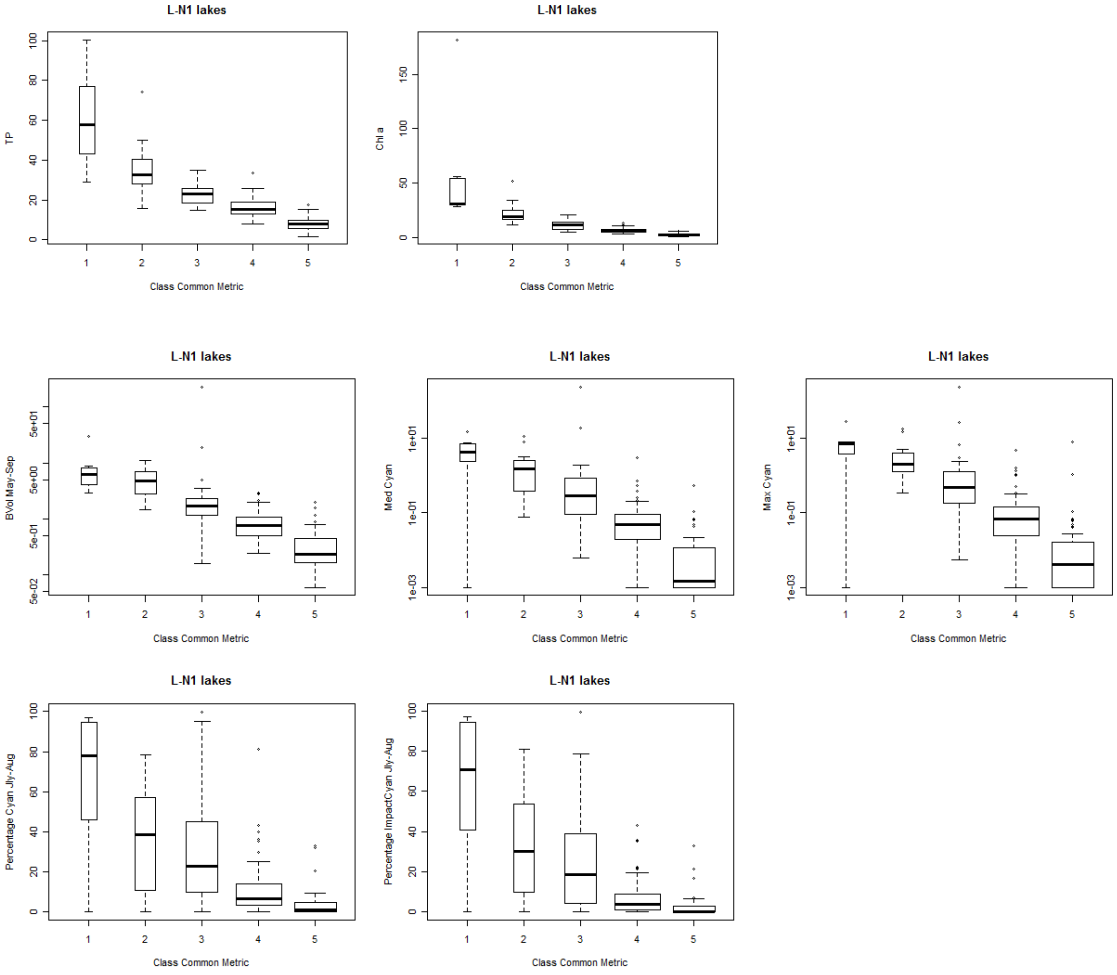


Figure G.7 Distribution of mean (growing season) TP, mean (growing season)Chlorophyll a , mean May-Sep Biovolume, median summer (Jly-Sep) cyanobacteria biovolume, max summer (Jly-Sep) cyanobacteria biovolume, percentage of summer (Jly/Aug) impact cyanobacteria for lakes classified by common metric boundaries for LN1 lake type

G.2 LN2a lakes

Summary

Final (final) version has following changes

1. Changes to NO and UK combination rule, cyanobacteria only averaged if worse than average of other averaged EQR values
2. Change to SE Bio-volume boundaries following email discussion with Anneli Harlen after ECOSTAT
3. UK PTI boundaries harmonized by increasing PTI EQR by 0.03 EQR units.
4. No changes to FI or IE metrics
5. NO PTI boundaries changed to reduce bias, UK PTI EQR increased by additional 0.01 EQR units. (Bilateral discussions UK and NO 11/11/2011)
6. Standardise Common Metric following validation workshop
7. Modify NO Ref Chl and GM EQR

All countries have a significant relationship with pressure and achieve required relationship with common metric, but R^2 for SE is < half the maximum R^2. Despite this, boundaries for SE have been used to set the harmnonisation band. All countries within the harmonisation band.

Reference Conditions

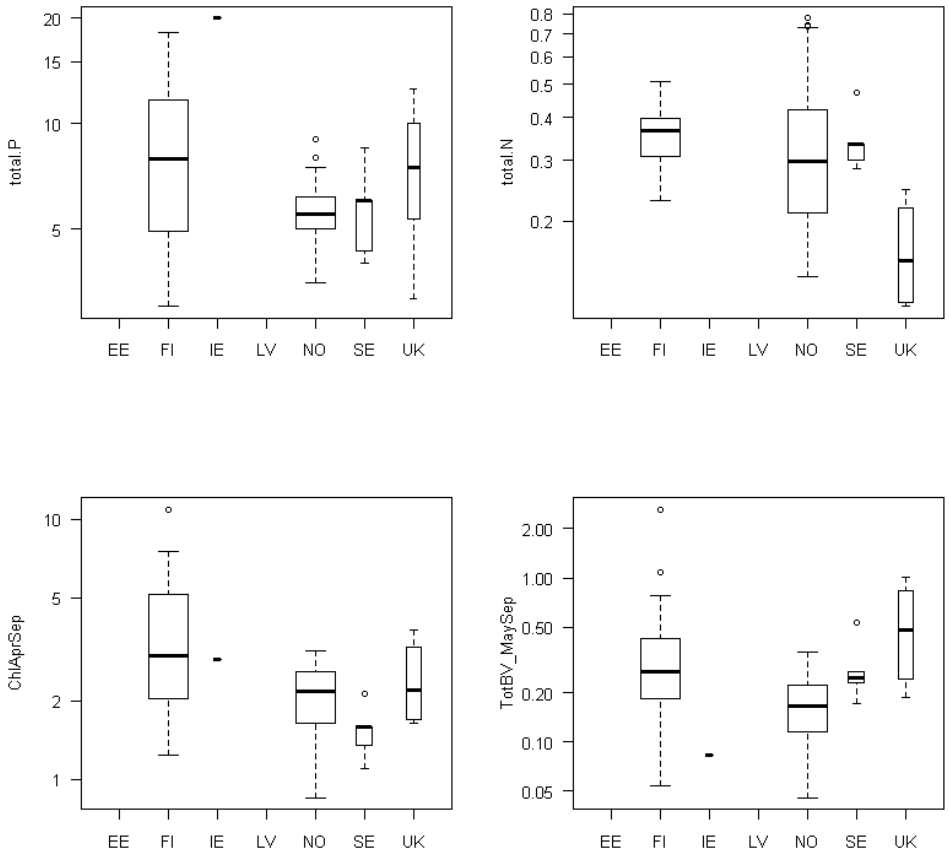


Figure G.8 Distributions of a)TP ug/l, b)TN mg/l, c)Chlorophyll a (Apr –Sept), d)total biovolume mg/l May-Sep in LN1 reference lakes for each country

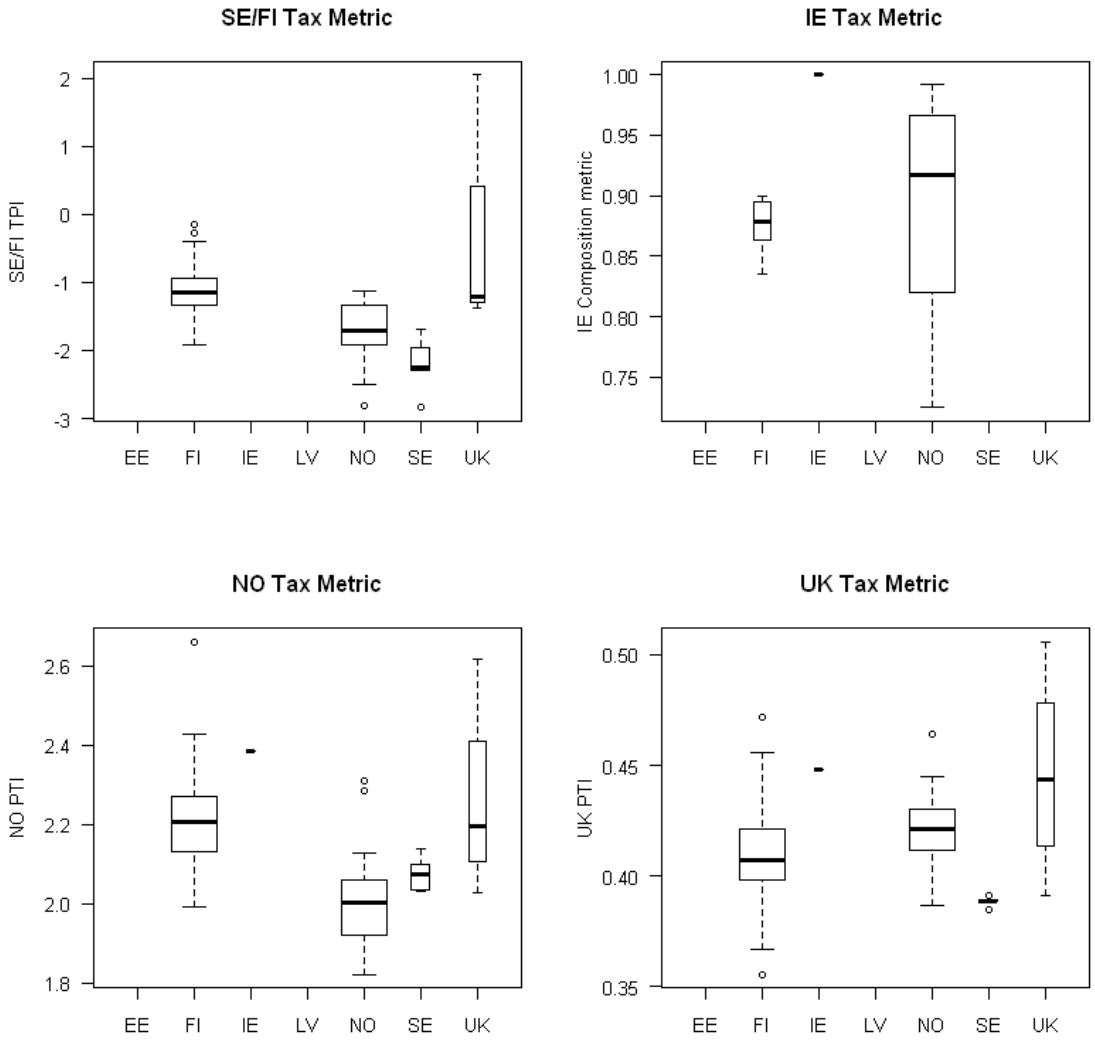


Figure G.9 Distributions of taxonomic metrics a) Finland TPI b) Norwegian PTI index, c) UK PTI index in LN1 reference lakes for each country

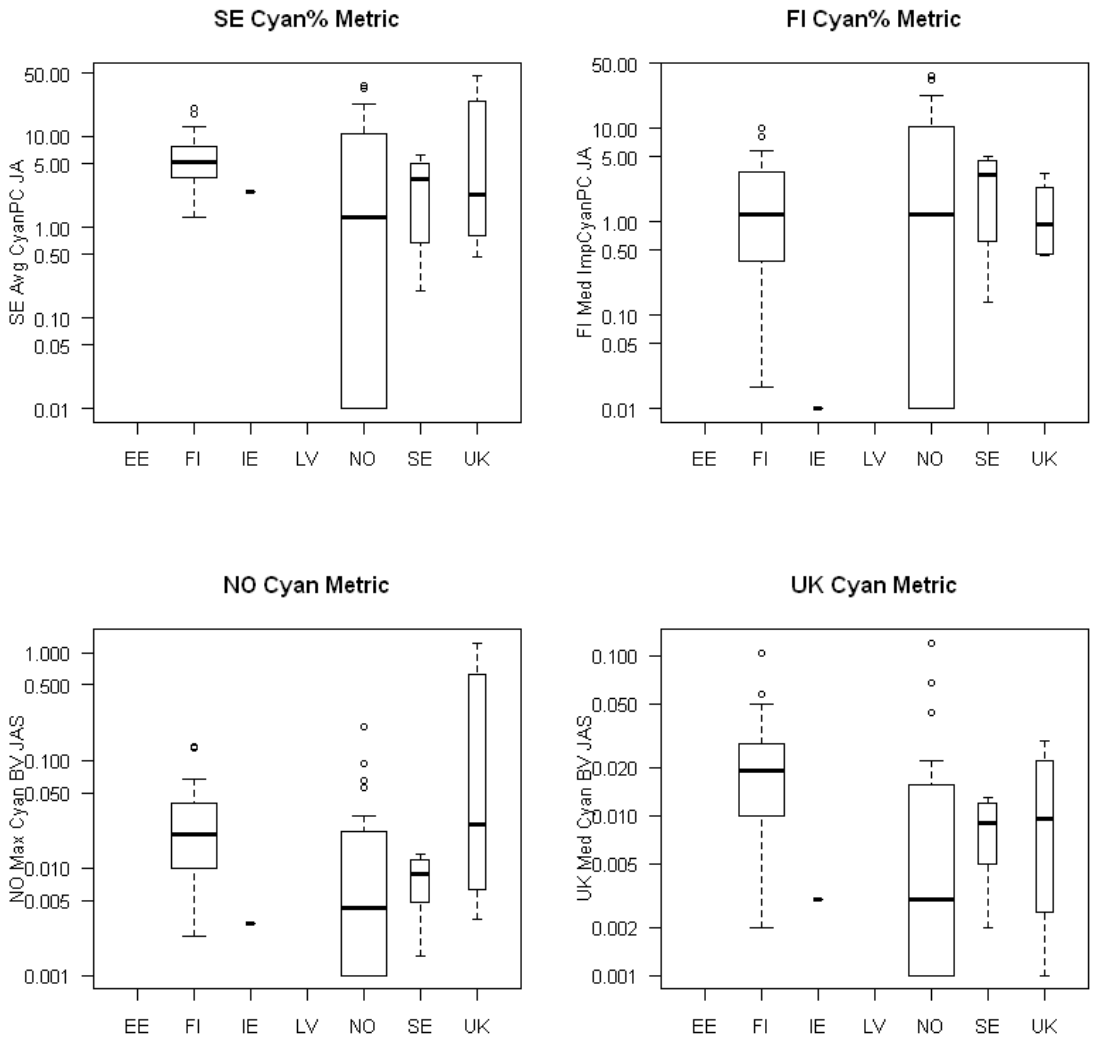


Figure G.10 Distributions of cyanobacteria metrics a) Finland % impact cyanobacteria (July & Aug), b) Norway max cyanobacteria biovolume (mg/l) July-Sept, c) UK median cyanobacteria biovolume (mg/l) July - Sept in LN1 reference lakes for each country

Table G.5 Distributions of metrics for LN2a Reference Lakes

Metric	Country	50%	90%	95%	100%	N
TP	FI	8	13	14	18	31
TP	IE	20	20	20	20	1
TP	NO	6	8	8	9	31
TP	SE	6	8	8	9	5
TP	UK	8	12	12	13	4
	All	6	12	13	20	
		50%	90%	95%	100%	N

Metric	Country	50%	90%	95%	100%	N
Chl	FI	3.0	5.7	6.7	10.9	31
Chl	IE	2.9	2.9	2.9	2.9	1
Chl	NO	2.2	3.0	3.1	3.1	31
Chl	SE	1.6	1.9	2.0	2.1	5
Chl	UK	2.2	3.4	3.6	3.8	4
	All	2.3	5.1	5.7	10.9	
		50%	90%	95%	100%	N
BVol	FI	0.27	0.77	0.93	2.62	31
BVol	IE	0.08	0.08	0.08	0.08	1
BVol	NO	0.17	0.26	0.28	0.36	31
BVol	SE	0.25	0.43	0.48	0.53	5
BVol	UK	0.48	0.90	0.96	1.01	4
	All	0.22	0.53	0.77	2.62	
		50%	90%	95%	100%	N
SE TPI	FI	-1.143	-0.548	-0.335	-0.159	31
SE TPI	IE	NA	NA	NA	NA	1
SE TPI	NO	-1.711	-1.186	-1.136	-1.129	31
SE TPI	SE	-2.248	-1.803	-1.749	-1.695	5
	UK	-1.214	1.396	1.722	2.049	4
	All	-1.357	-0.844	-0.455	2.049	
		50%	90%	95%	100%	N
IE Taxonomic Score	FI	0.879	0.898	0.899	0.900	31
IE Taxonomic Score	IE	1.000	1.000	1.000	1.000	1
IE Taxonomic Score	NO	0.917	0.981	0.988	0.992	31
IE Taxonomic Score	SE	NA	NA	NA	NA	5
IE Taxonomic Score	UK	NA	NA	NA	NA	4
	All	0.900	0.982	0.992	1.000	
		50%	90%	95%	100%	N
NO PTI	FI	yy	2.344	2.407	2.661	31
NO PTI	IE	2.386	2.386	2.386	2.386	1
NO PTI	NO	2.003	2.125	2.206	2.310	31
NO PTI	SE	2.076	2.123	2.131	2.140	5
NO PTI	UK	2.197	2.494	2.555	2.616	4
	All	2.091	2.328	2.385	2.661	
		50%	90%	95%	100%	N
UK PTI	FI	0.407	0.427	0.443	0.472	31
UK PTI	IE	0.448	0.448	0.448	0.448	1
UK PTI	NO	0.421	0.437	0.443	0.464	31
UK PTI	SE	0.389	0.390	0.391	0.391	5

Metric	Country	50%	90%	95%	100%	N
UK PTI	UK	0.443	0.489	0.498	0.506	4
UK PTI	All	0.416	0.440	0.453	0.506	
		50%	90%	95%	100%	N
FI ImpCyanPC	FI	1.2	4.8	7.1	10.0	31
FI ImpCyanPC	IE	0.0	0.0	0.0	0.0	1
FI ImpCyanPC	NO	1.2	23.9	35.0	36.6	31
FI ImpCyanPC	SE	3.2	4.8	4.9	5.0	5
	UK	0.9	2.7	3.0	3.3	4
	All	1.2	10.5	22.7	36.6	
		50%	90%	95%	100%	N
SE Cyan PC	FI	5.1	8.9	15.2	20.3	31
SE Cyan PC	IE	2.4	2.4	2.4	2.4	1
SE Cyan PC	NO	1.3	23.9	35.2	36.6	31
SE Cyan PC	SE	3.4	5.7	5.9	6.2	5
SE Cyan PC	UK	2.3	33.4	39.8	46.3	4
	All	3.8	20.3	28.3	46.3	
		50%	90%	95%	100%	N
	FI	0.019	0.056	0.098	0.134	31
NO Max CyanBV	IE	0.002	0.002	0.002	0.002	1
NO Max CyanBV	NO	0.003	0.054	0.078	0.201	31
NO Max CyanBV	SE	0.008	0.012	0.012	0.012	5
NO Max CyanBV	UK	0.024	0.871	1.049	1.227	4
	All	0.012	0.056	0.109	1.227	
		50%	90%	95%	100%	N
	FI	0.018	0.049	0.056	0.103	31
UK Med CyanBV	IE	0.002	0.002	0.002	0.002	1
UK Med CyanBV	NO	0.002	0.021	0.055	0.119	31
UK Med CyanBV	SE	0.008	0.012	0.012	0.012	5
UK Med CyanBV	UK	0.009	0.024	0.026	0.028	4
	All	0.011	0.043	0.056	0.119	

Based on above results the ratio of the median chlorophyll to 90th percentile chlorophyll for reference lakes is shown in Table G.5.

Table G.6 ratio of median chlorophyll a to 90th percentile chlorophyll a for reference sites. A potential HG EQR boundary.

FI	0.52
IE	1.00
NO	0.73
SE	0.83

UK	0.64
All	0.45

Relationship with Pressure

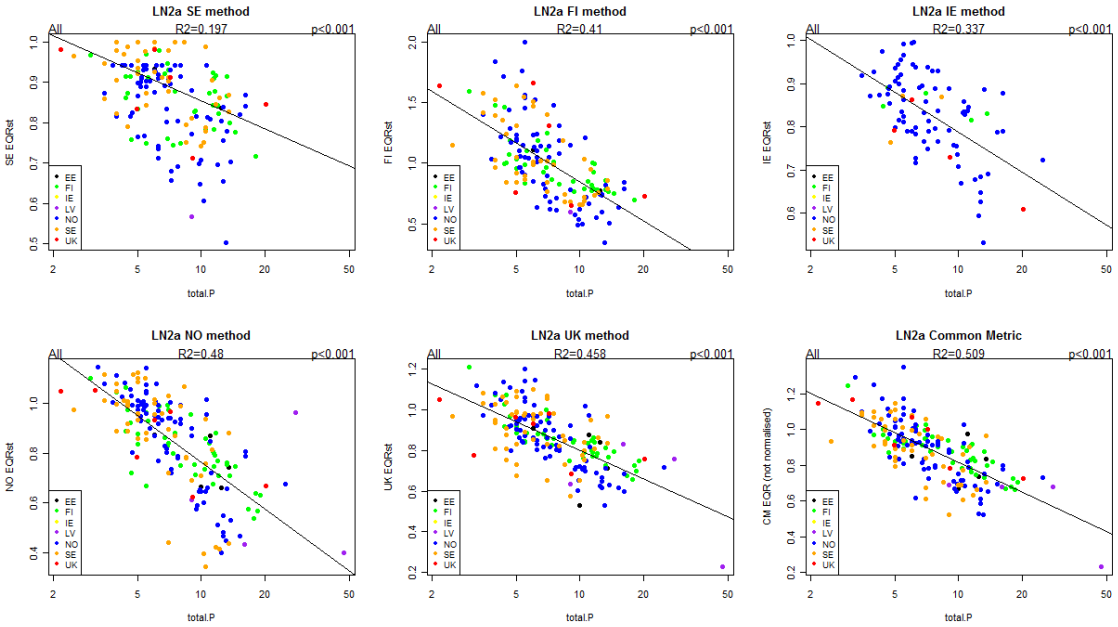


Figure G.11 *Relationship between n ational final EQRs (standardised to remove country effects) and total P. a) SE, b) FI, c) NO, d) UK, e) IE for LN2a lake type, f) Common Metric*

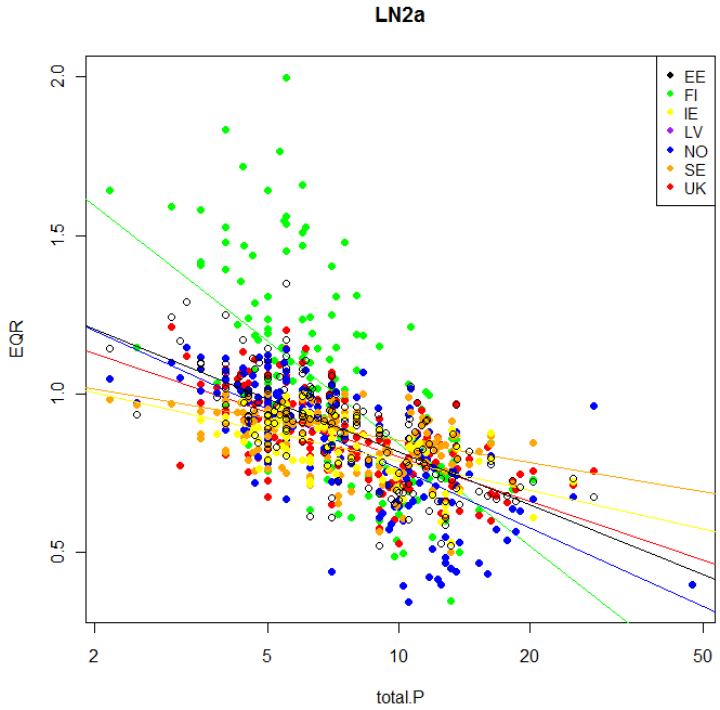


Figure G.12 *Relationship between national final EQRs (standardised to remove country effects) and total P. Points coloured by national method (applied to all countries data), open black circles are for common metric*

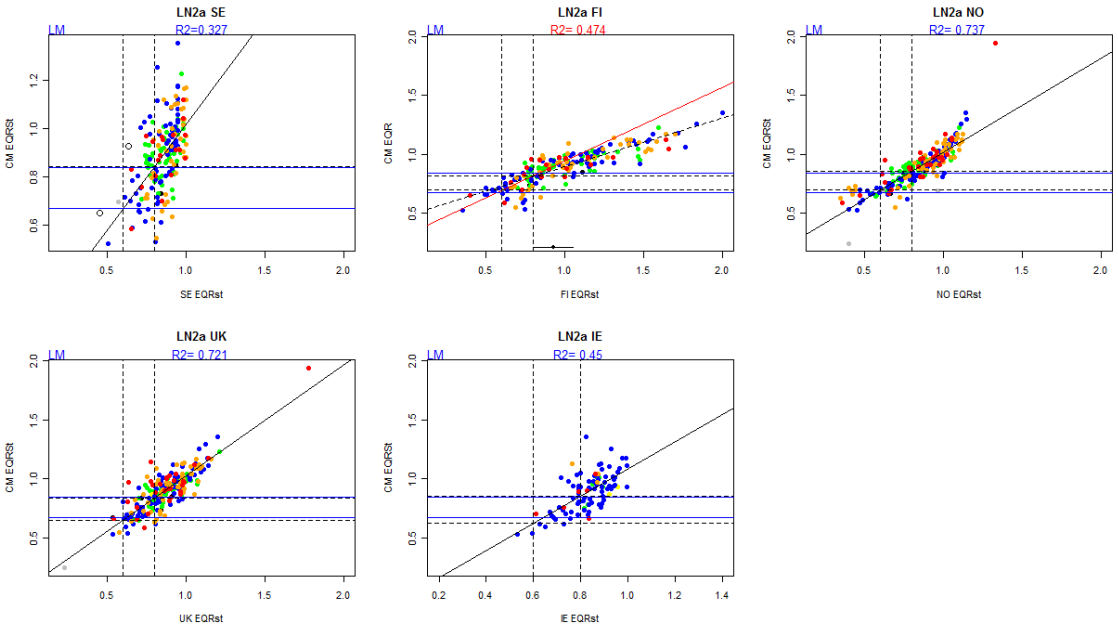


Figure G.13 *Relationship between national standardised EQR and common metric EQR. a) SE, b) FI, c) NO, d) UK, e) IE for LN2a lake type. Vertical lines mark boundaries on standardised national scale, horizontal blue line average (target) boundaries. Segmented linear regression fitted to FI (red line) as data indicate non-linearity, boundaries taken from regression for FI EQRst < 0.93 (marked by point and horizontal bar in (c)*

Regression parameters for above relationships

Table G.7 Regression parameters for relationship between final EQRs (standardised to remove country effects) and total P, based on TP range of 2-50 ug/l

	(Intercept)	log10(total.P)	adj R2	p
SE	1.086	-0.231	0.192	<0.001
FI	1.917	-1.073	0.407	<0.001
IE	1.097	-0.308	0.330	<0.001
NO	1.387	-0.623	0.477	<0.001
UK	1.267	-0.467	0.456	<0.001

Relationship with Common Metric

Table G.8 Regression parameters for relationship between national and common metric

Common Metric	UK	NO	IE	SE	FI
Intercept	0.081	0.216	-0.070	0.142	0.320
slope	0.940	0.800	1.154	0.876	0.622
Pearson's r	0.849	0.859	0.671	0.572	0.688
WARNING! Min R^2< 1/2 * Max R^2	0.721	0.737	0.455	0.328	0.474

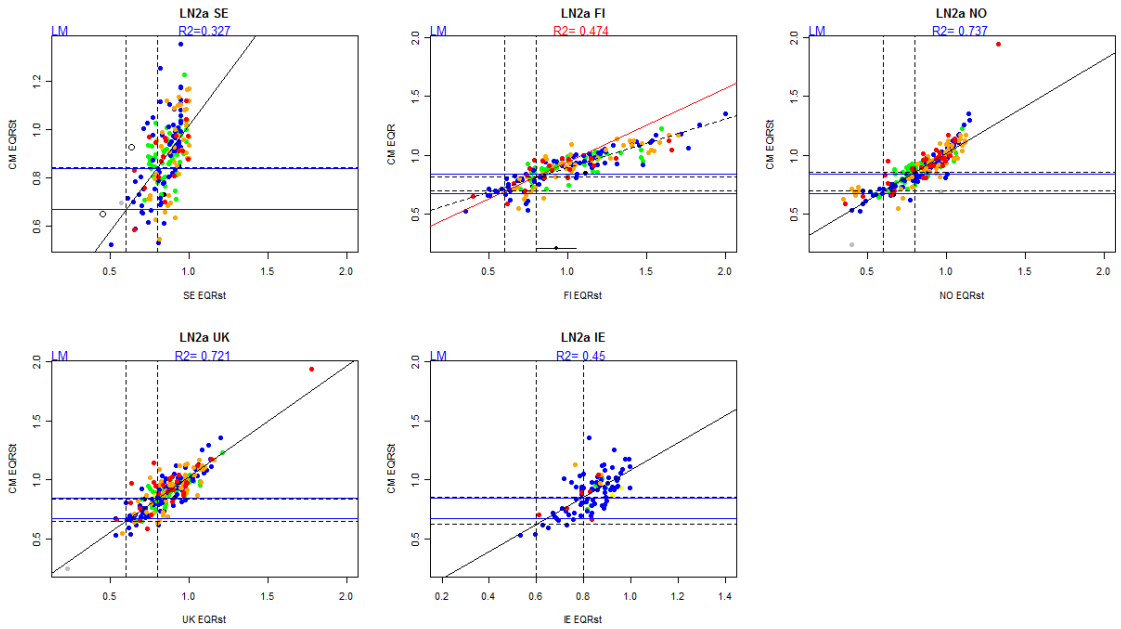


Figure G.14 *Relationship between national standardised EQR and common metric EQR. a) SE, b) FI, c) NO, d) UK, e) IE for LN2a lake type. Vertical lines mark boundaries on standardised national scale, horizontal blue line average (target) boundaries. Segmented linear regression fitted to FI (red line) as data indicate non-linearity, boundaries taken from regression for FI EQRst < 0.93 (marked by point and horizontal bar in (c)*

Distribution of pressure and biological metrics by common metric class

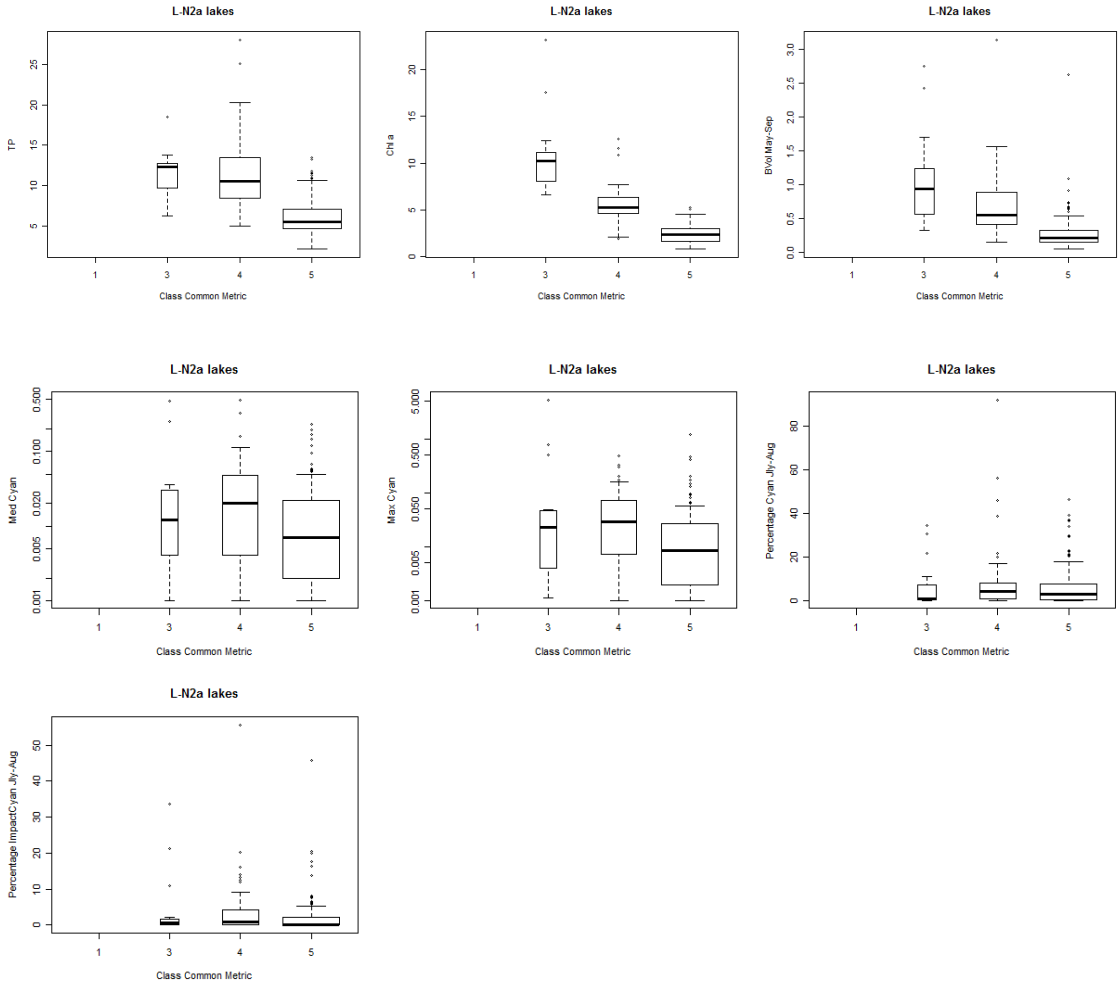


Figure G.15 distribution of a)mean (growing season) TP, b) mean (growing season)Chlorophyll a ,c) mean May-Sept Biovolume, d) median cyanobacteria biovolume, e) max summer (July-Sep) cyanobacteria biovolume, f) percentage of summer (July/Aug) cyanobacteria, g) percentage of impact cyanobacteria for LN2a lakes classified by common metric boundaries

G.3 LN2b lakes

Summary

Final version has following changes:

1. UK PTI boundary EQRs changed to match LN2a;
2. Minor changes to FI and NO boundary values caused by rounding errors;
3. Standardisation of common metric following validation workshop.

All countries have a significant relationship with pressure and achieve required relationship with common metric. All countries within or above (NO) harmonisation band

Reference Conditions

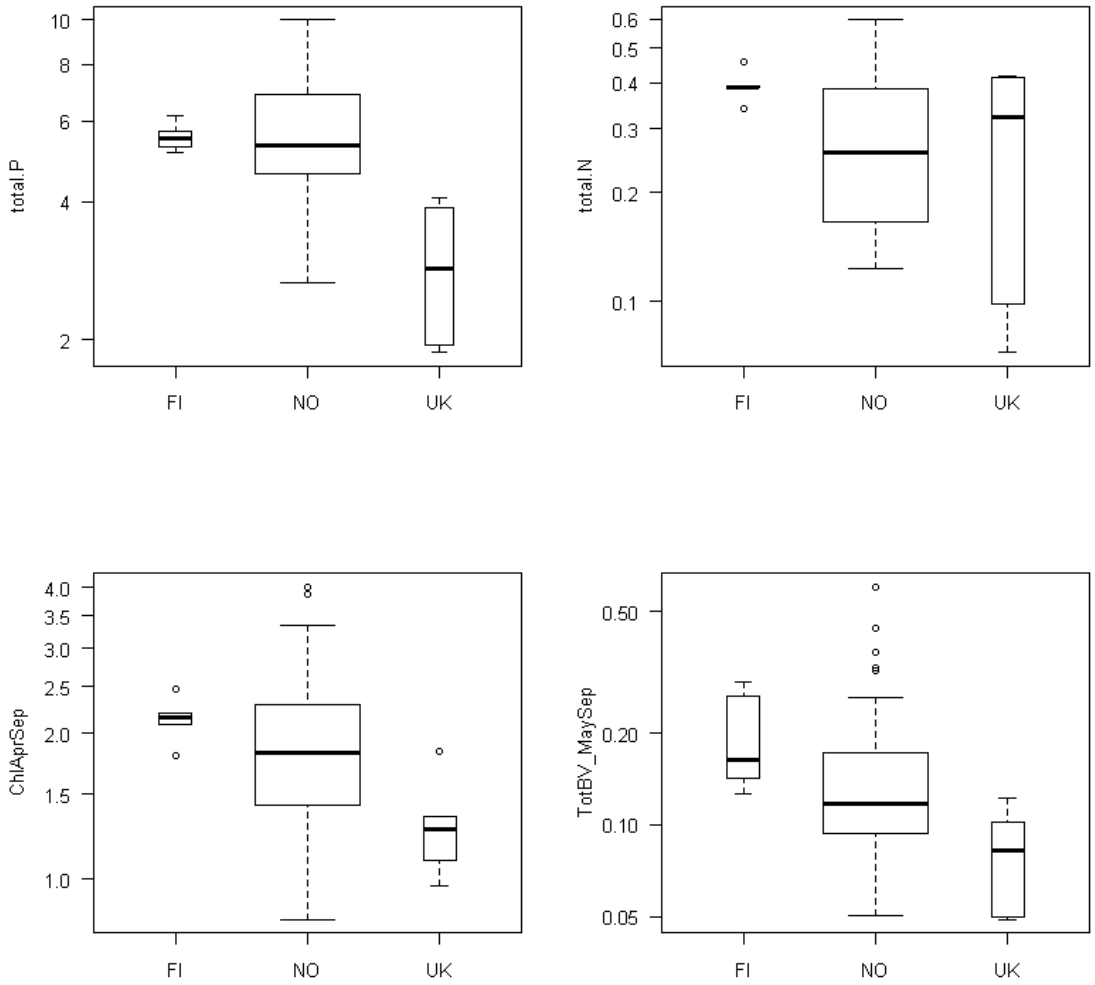


Figure G.16 Distributions of a) TP ug/l, b) TN mg/l, c) Chlorophyll a (Apr –Sept), d) total biovolume mg/l May-Sep in LN1 reference lakes for each country

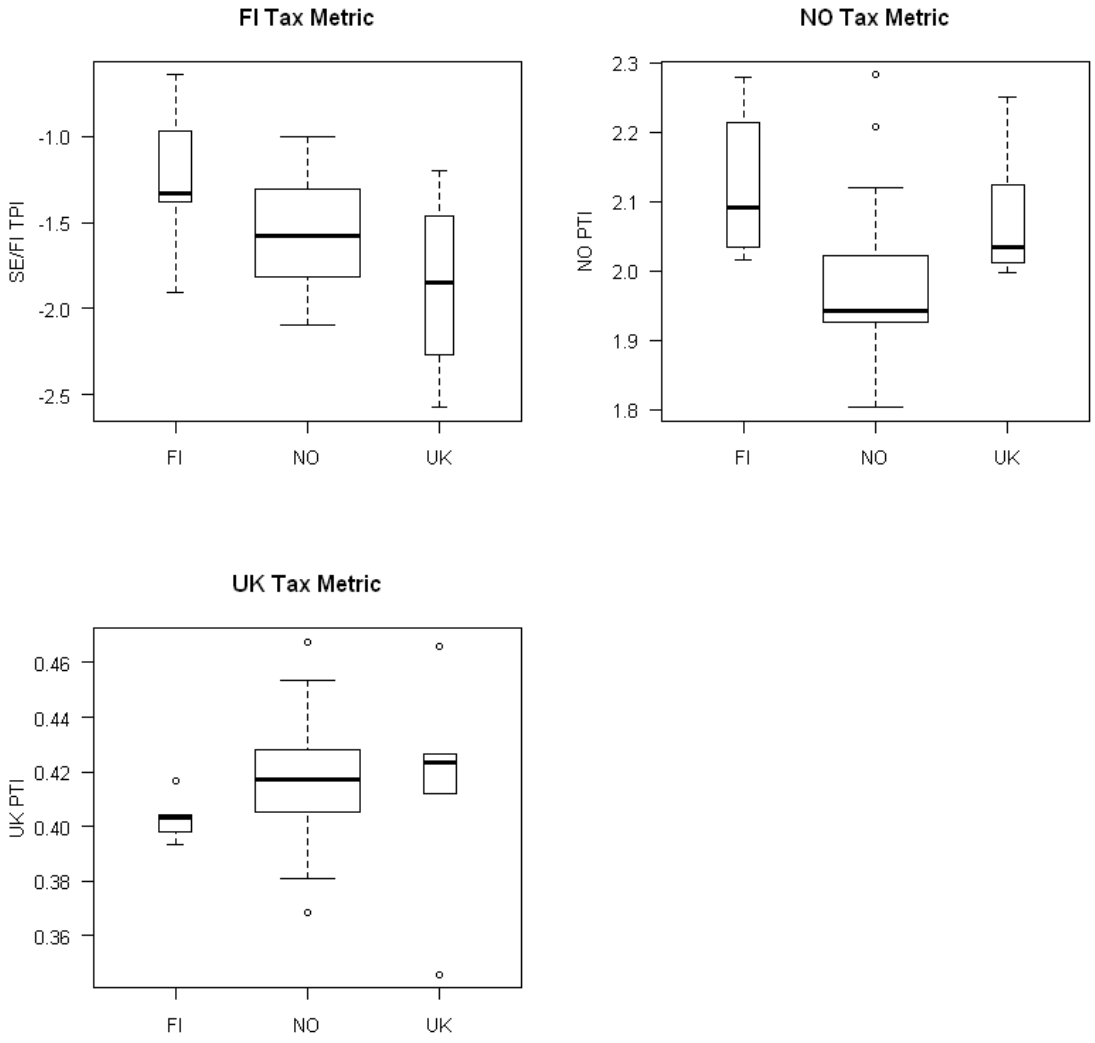


Figure G.17 Distributions of taxonomic metrics a) Finland TPI b) Norwegian PTI index, c) UK PTI index in LN1 reference lakes for each country

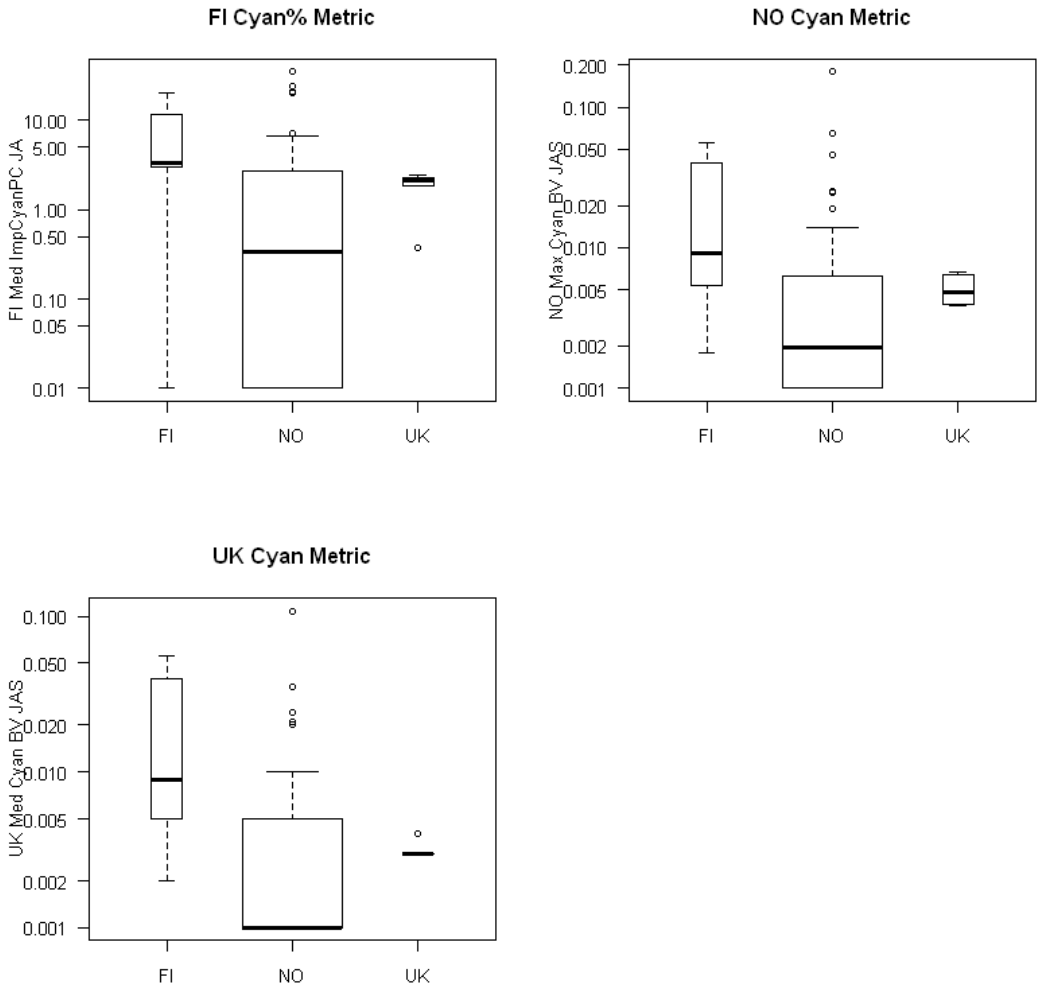


Figure G.18 Distributions of cyanobacteria metrics a) Finland % impact cyanobacteria (July & Aug), b) Norway max cyanobacteria biovolume (mg/l) July-Sept, c) UK median cyanobacteria biovolume (mg/l) July - Sept in LN1 reference lakes for each country

Table G.9 Distributions of metrics for LN2b Reference Lakes

Metric	Country	50%	90%	95%	100%	N
TP	FI	5.5	6.0	6.1	6.2	5
TP	NO	5.3	7.6	8.2	10.0	53
TP	UK	2.9	4.0	4.0	4.1	5
TP	All	5.3	7.5	8.2	10.0	
		50%	90%	95%	100%	N
Chl	FI	2.2	2.4	2.4	2.5	5
Chl	NO	1.8	2.7	3.3	4.0	53
Chl	UK	1.3	1.6	1.7	1.8	5
	All	1.8	2.6	3.2	4.0	
		50%	90%	95%	100%	N

Metric	Country	50%	90%	95%	100%	N
BVol	FI	0.163	0.282	0.288	0.294	5
BVol	NO	0.117	0.258	0.342	0.603	53
BVol	UK	0.082	0.115	0.119	0.123	5
BVol	All	0.122	0.264	0.326	0.603	
		50%	90%	95%	100%	N
SE TPI	FI	-1.333	-0.771	-0.706	-0.642	5
SE TPI	NO	-1.581	-1.148	-1.106	-0.999	53
SE TPI	UK	-1.847	-1.356	-1.277	-1.198	5
SE TPI	All	-1.578	-1.137	-1.052	-0.642	
		50%	90%	95%	100%	N
NO PTI	FI	2.090	2.252	2.265	2.279	5
NO PTI	NO	1.941	2.095	2.118	2.282	53
NO PTI	UK	2.033	2.199	2.224	2.249	5
NO PTI	All	1.969	2.119	2.212	2.282	
		50%	90%	95%	100%	N
UK PTI	FI	0.403	0.412	0.414	0.417	5
UK PTI	NO	0.417	0.438	0.446	0.468	53
UK PTI	UK	0.423	0.450	0.458	0.466	5
UK PTI	All	0.414	0.438	0.449	0.468	
UK PTI	UK Mod Ref min	0.388				
UK PTI	UK Mpd Ref max	0.442				
		50%	90%	95%	100%	N
FI ImpCyanPC	FI	3.3	16.6	18.3	20.0	5
FI ImpCyanPC	NO	0.3	6.6	20.7	35.0	53
FI ImpCyanPC	UK	2.1	2.4	2.4	2.4	5
FI ImpCyanPC	All	0.4	7.0	20.5	35.0	
		50%	90%	95%	100%	N
NO Max CyanBV	FI	0.008	0.049	0.052	0.055	5
NO Max CyanBV	NO	0.001	0.017	0.033	0.178	53
NO Max CyanBV	UK	0.004	0.006	0.006	0.006	5
NO Max CyanBV	All	0.002	0.022	0.045	0.178	
		50%	90%	95%	100%	N
UK Med CyanBV	FI	0.008	0.049	0.052	0.055	5

Metric	Country	50%	90%	95%	100%	N
UK Med CyanBV	NO	0.000	0.009	0.021	0.107	53
UK Med CyanBV	UK	0.002	0.003	0.003	0.003	5
UK Med CyanBV	All	0.001	0.017	0.033	0.107	

Based on above results the ratio of the median chlorophyll to 90th percentile chlorophyll for reference lakes is shown in Table G.9.

Table G.10 ratio of median chlorophyll a to 90th percentile chlorophyll a for reference sites. A potential HG EQR boundary.

FI	0.91
NO	0.68
UK	0.77
All	0.69

Relationship with Pressure

Regression parameters for above relationships

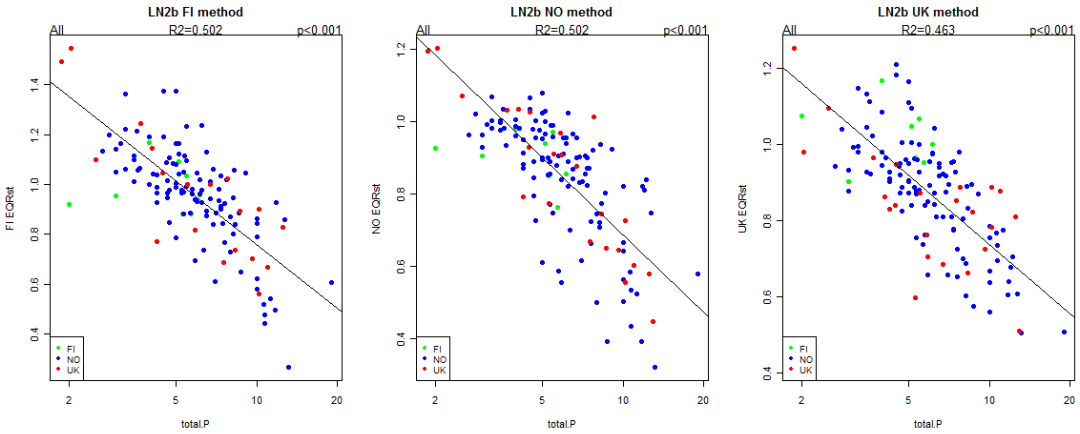


Figure G.19 Relationship between national final EQRs (standardised to remove country effects) and total P. a) FI, b) NO, c) UK for LN2b lake type

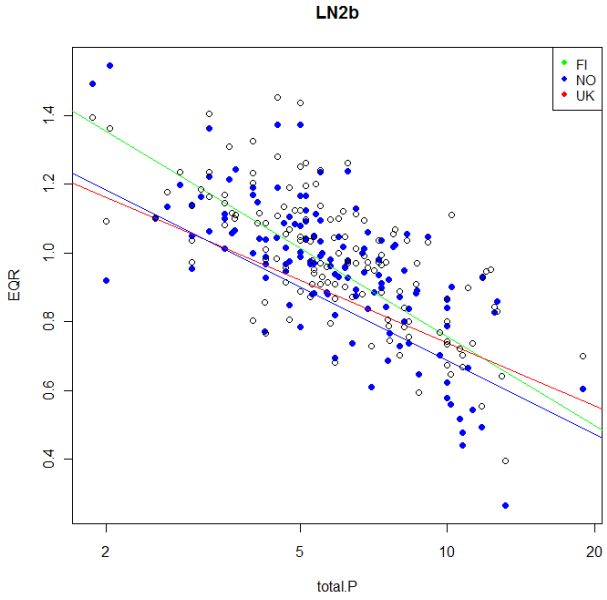


Figure G.20 Relationship between national final EQRs (standardised to remove country effects) and total P. Points coloured by national method (applied to all countries data), open black circles are for common metric

Table G.11 Regression parameters for relationship between final EQRs (standardised to remove country effects) and total P, based on TP range of 3-20 ug/l

	Intercept	log10(total.P)	adj R2	p
FI	1.613	-0.856	0.498	<0.001
NO	1.401	-0.714	0.498	<0.001
UK	1.344	-0.606	0.459	<0.001

Relationship with Common Metric

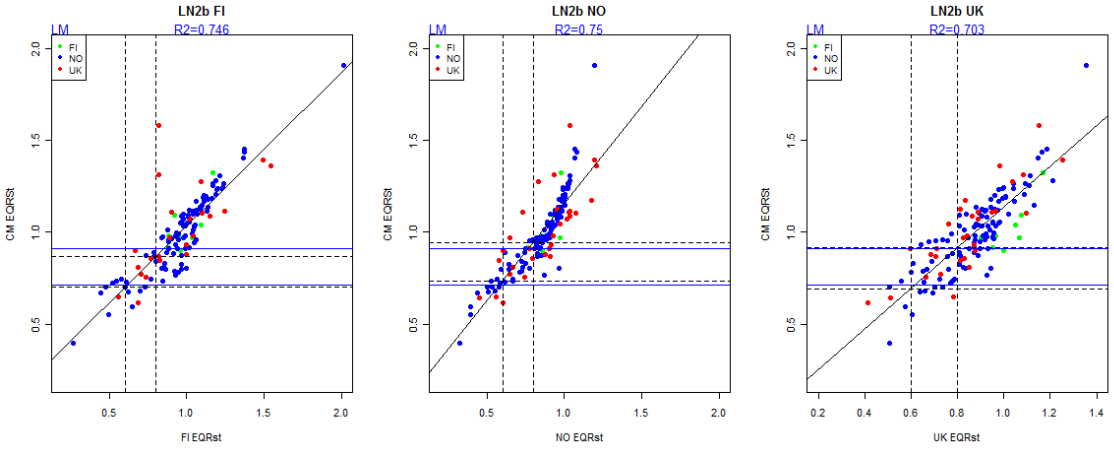


Figure G.21 Relationship between national standardised EQR and common metric EQR. a) FI, c) NO, d) UK for LN2b lake type. Vertical lines mark boundaries on standardised national scale.

Table G.12 Regression parameters for relationship between national and common metric

	UK	NO	FI
Intercept	0.028	0.097	0.198
slope	1.108	1.059	0.835
Pearson's r	0.84	0.87	0.86
R^2	0.70	0.75	0.75

Description of community at High, Good, Moderate status

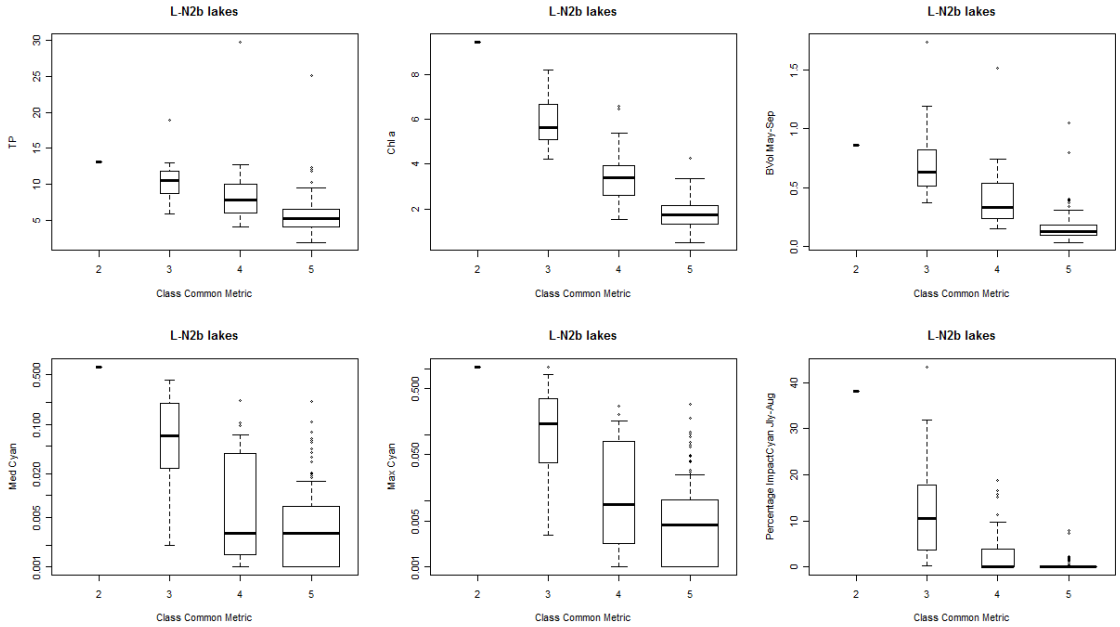


Figure G.22 Distribution of mean (growing season) TP, mean (growing season) Chlorophyll-a, mean May-Sep Biovolume, median summer (July-Sep) cyanobacteria biovolume, max summer (July-Sep) cyanobacteria biovolume, percentage of summer (July/Aug) impact cyanobacteria for lakes classified by common metric boundaries (average of NO and UK).

G.4 LN3a lakes

Summary

Final version has following changes:

1. FI Biovolume boundaries changed at Pallanza meeting;
2. SE Biovolume boundaries changed following email discussion with Anneli Harlen after ECOSTAT;
3. NO and UK combination rule changed so that cyanobacteria only averaged if worse than average of other EQRs;
4. Use standardised common metric following validation workshop;
5. Modify NO Ref Chl and GM EQR.

All countries have a significant relationship with pressure and achieve the required relationship with the common metric. All countries are in or above the harmonisation band, (IE above band).

Reference Conditions

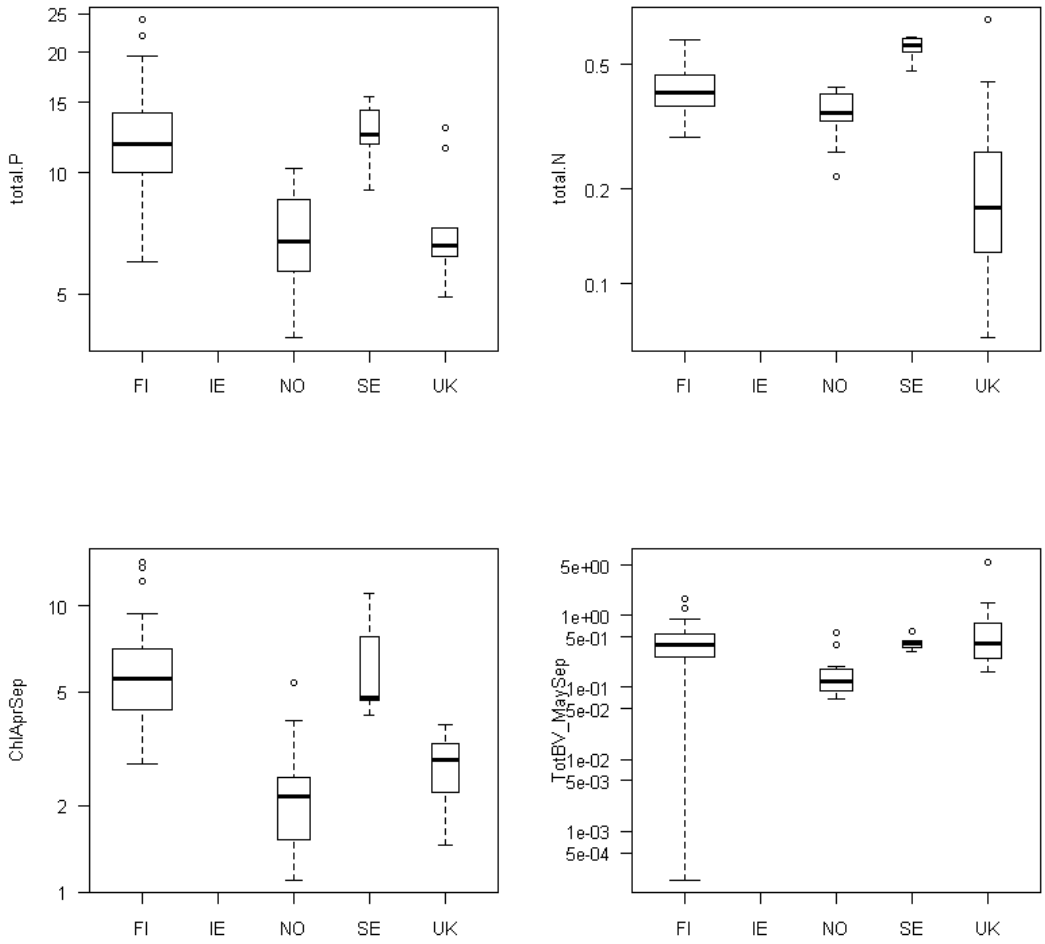


Figure G.23 Distributions of a) TP ug/l, b) TN mg/l, c) Chlorophyll a (Apr –Sept), d) total biovolume mg/l May-Sep in LN3A reference lakes for each country

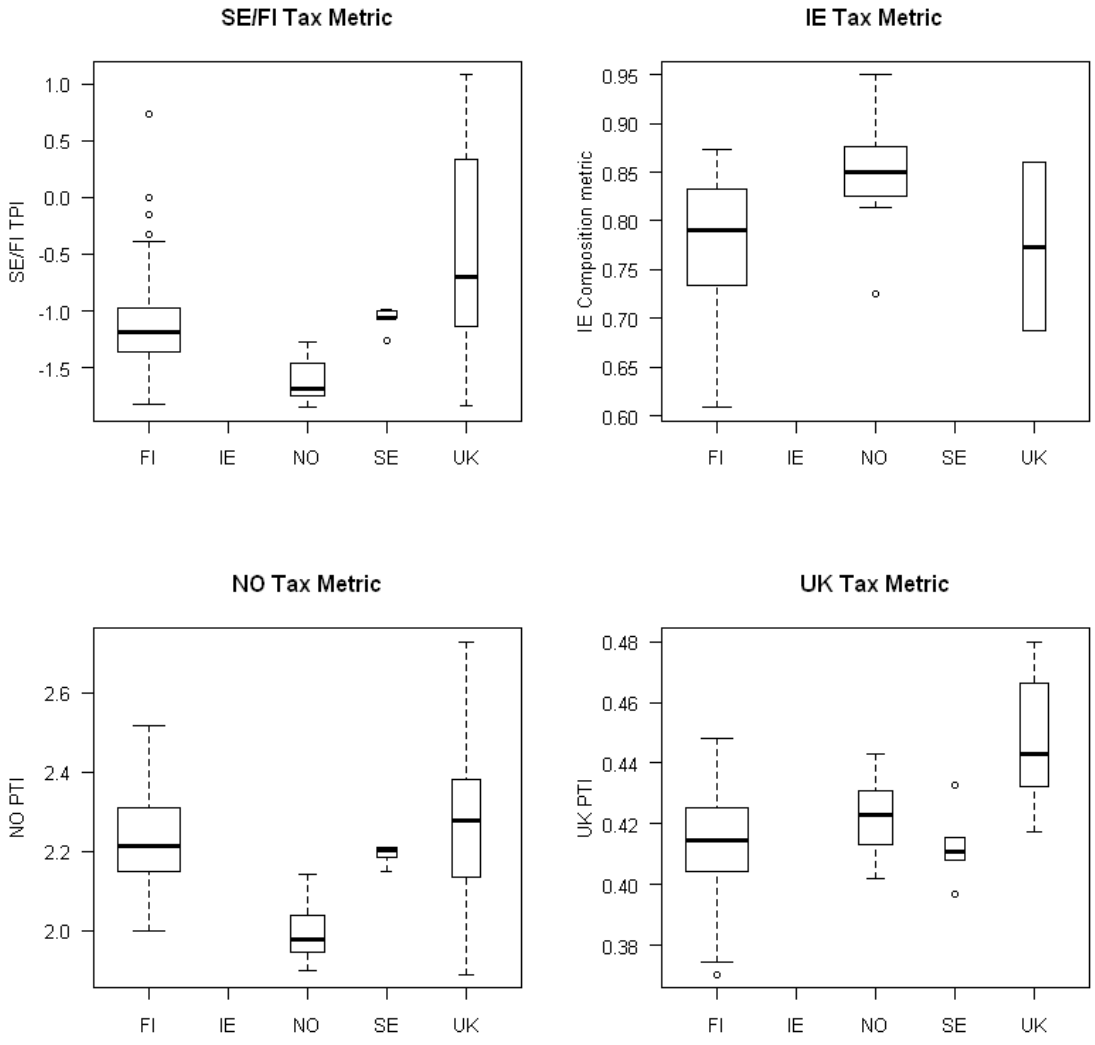


Figure G.24 Distributions of taxonomic metrics a) Finland TPI b) Norwegian PTI index, c) UK PTI index in LN3A reference lakes for each country

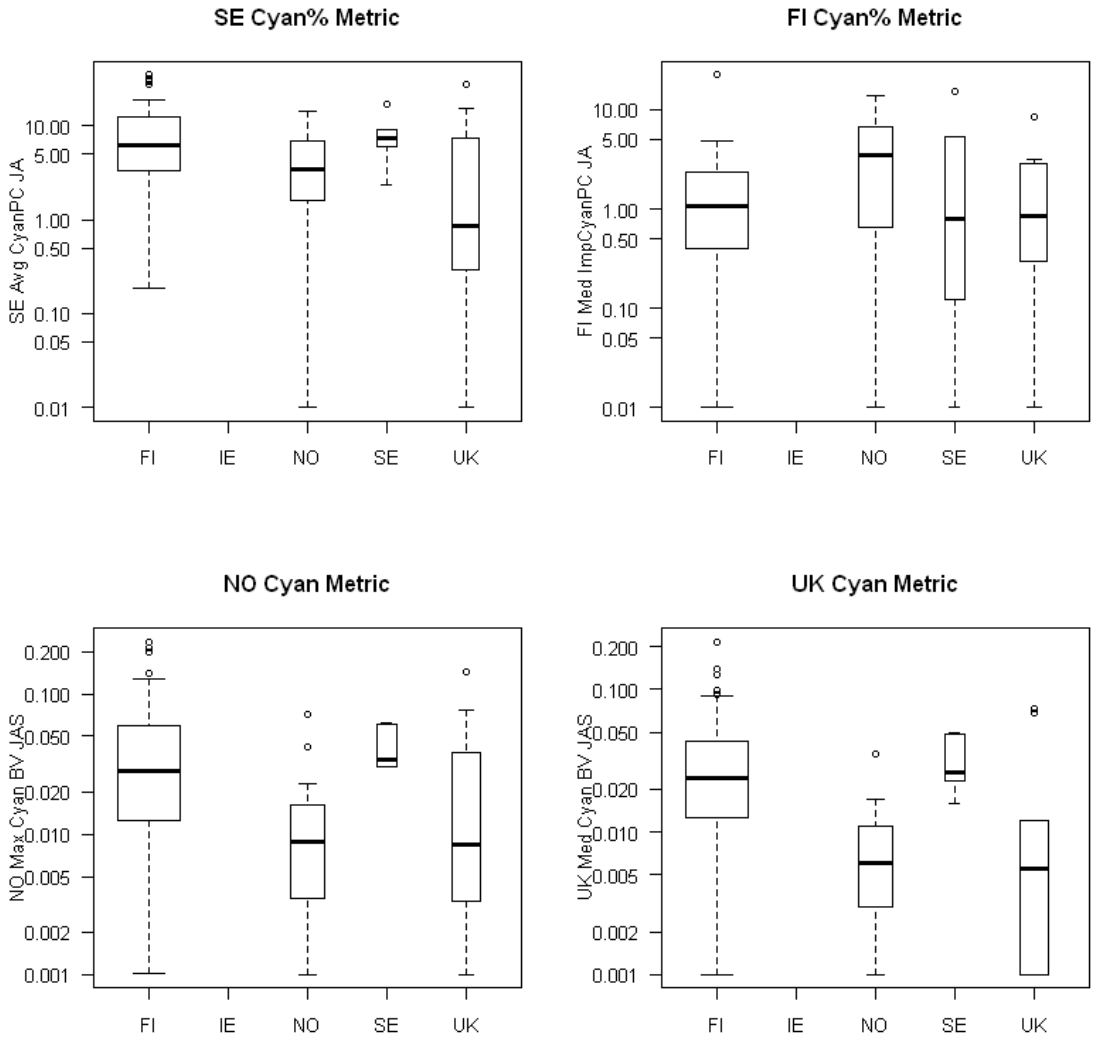


Figure G.25 Distributions of cyanobacteria metrics a) Finland % impact cyanobacteria (July & Aug), b) Norway max cyanobacteria biovolume (mg/l) July-Sept, c) UK median cyanobacteria biovolume (mg/l) July - Sept in LN3A reference lakes for each country.

Table G.13 Distributions of metrics for LN3a Reference Lakes

Metric	Country	50%	90%	95%	100%	N
TP	FI	12	16	19	24	51
TP	NO	7	10	10	10	15
TP	SE	13	15	15	16	5
TP	UK	7	12	12	13	10
TP		10	16	17	24	
		50%	90%	95%	100%	N
Chl	FI	5.6	9.1	10.8	14.3	51
Chl	NO	2.2	3.7	4.4	5.4	15
Chl	SE	4.8	9.8	10.4	11.1	5
Chl	UK	2.9	3.8	3.8	3.8	10
Chl		4.7	8.4	9.4	14.3	
		50%	90%	95%	100%	N
BVol	FI	0.39	0.80	1.10	1.70	51
BVol	NO	0.12	0.31	0.45	0.59	15
BVol	SE	0.41	0.55	0.58	0.61	5
BVol	UK	0.41	1.92	3.77	5.61	10
BVol		0.34	0.78	1.29	5.61	
		50%	90%	95%	100%	N
SE TPI	FI	-1.193	-0.469	-0.239	0.732	51
SE TPI	NO	-1.689	-1.426	-1.377	-1.271	15
SE TPI	SE	-1.058	-0.994	-0.991	-0.988	5
SE TPI	UK	-0.704	0.709	0.895	1.080	10
		-1.254	-0.511	-0.118	1.080	
		50%	90%	95%	100%	N
IE Taxonomic Score	FI	0.79	0.86	0.87	0.87	51
IE Taxonomic Score	NO	0.85	0.93	0.95	0.95	15
IE Taxonomic Score	SE					
IE Taxonomic Score	UK	0.77	0.84	0.85	0.86	10
IE Taxonomic Score		0.83	0.89	0.93	0.95	
		50%	90%	95%	100%	N
NO PTI	FI	2.214	2.392	2.451	2.518	51
NO PTI	NO	1.980	2.073	2.107	2.141	15
NO PTI	SE	2.203	2.209	2.209	2.209	5

Metric	Country	50%	90%	95%	100%	N
NO PTI	UK	2.277	2.519	2.624	2.729	10
NO PTI		2.189	2.387	2.474	2.729	
		50%	90%	95%	100%	N
UK PTI	FI	0.414	0.438	0.442	0.448	51
UK PTI	NO	0.423	0.439	0.441	0.443	15
UK PTI	SE	0.411	0.426	0.429	0.433	5
UK PTI	UK	0.443	0.471	0.476	0.480	10
UK PTI		0.420	0.443	0.450	0.480	
		50%	90%	95%	100%	N
FI ImpCyanPC	FI	1.1	3.6	4.5	22.4	51
FI ImpCyanPC	NO	3.4	11.3	12.9	13.7	15
FI ImpCyanPC	SE	0.8	11.2	13.1	15.1	5
FI ImpCyanPC	UK	0.8	4.2	6.4	8.5	10
		1.1	5.8	9.5	22.4	
	>					
		50%	90%	95%	100%	N
SE Cyan PC	FI	6.3	18.6	30.2	34.8	51
SE Cyan PC	NO	3.4	13.2	13.7	14.0	15
SE Cyan PC	SE	7.4	13.9	15.5	17.1	5
SE Cyan PC	UK	0.8	17.7	22.6	27.4	10
SE Cyan PC		5.6	17.1	27.5	34.8	
	>					
		50%	90%	95%	100%	N
	FI	0.027	0.122	0.168	0.235	51
NO Max CyanBV	NO	0.008	0.033	0.050	0.071	15
NO Max CyanBV	SE	0.033	0.061	0.061	0.061	5
NO Max CyanBV	UK	0.007	0.083	0.112	0.141	10
NO Max CyanBV		0.022	0.088	0.139	0.235	
		50%	90%	95%	100%	N
	FI	0.023	0.089	0.112	0.215	51
UK Med CyanBV	NO	0.005	0.014	0.021	0.034	15
UK Med CyanBV	SE	0.025	0.049	0.049	0.049	5
UK Med CyanBV	UK	0.005	0.068	0.070	0.072	10
UK Med CyanBV		0.016	0.072	0.092	0.215	

Based on above results the ratio of the median chlorophyll to 90th percentile chlorophyll for reference lakes is shown in Table G.13.

Table G.14 ratio of median chlorophyll a to 90th percentile chlorophyll a for reference sites. A potential HG EQR boundary.

FI	0.62
NO	0.58
SE	0.49
UK	0.76
All	0.55

Relationship with Pressure

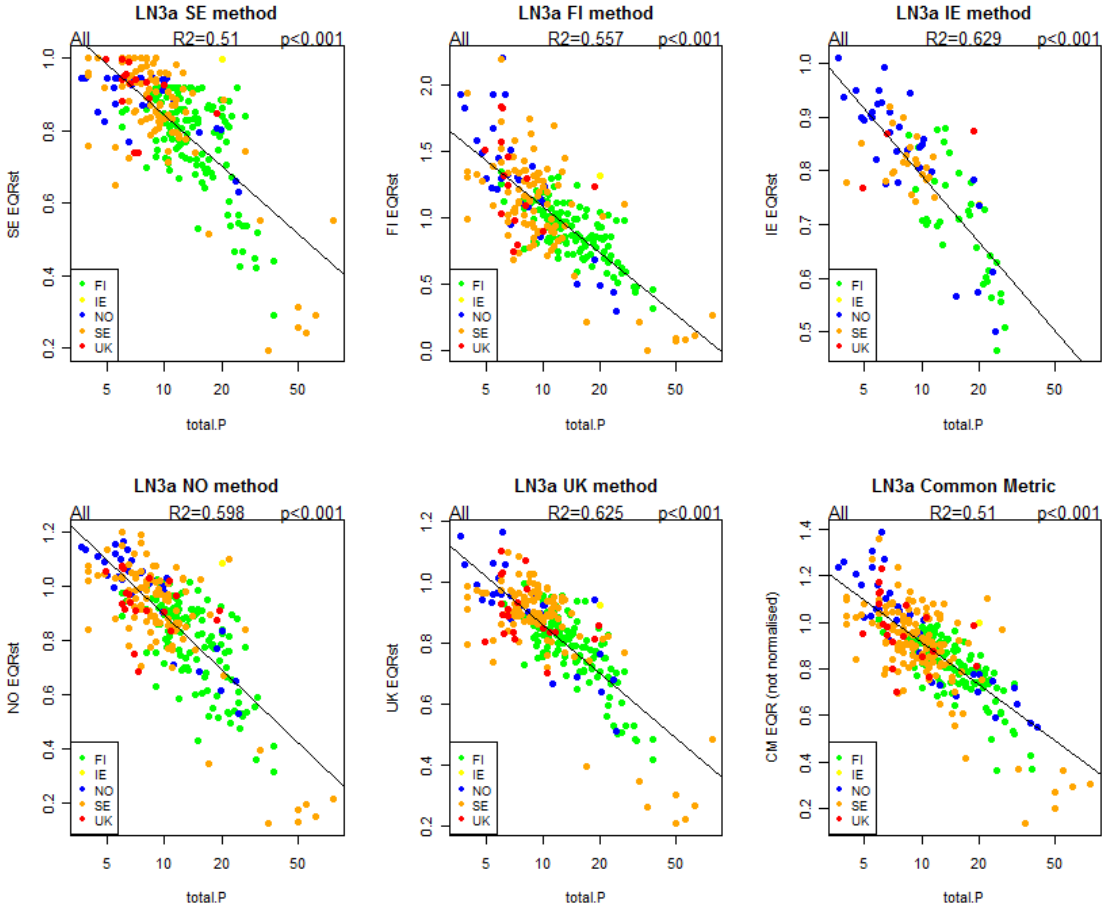


Figure G.26 Relationship between national final EQRs (standardised to remove country effects) and total P. a) SE, b) FI, c) NO, d) UK, e) IE, f) common metric for LN3A lake type

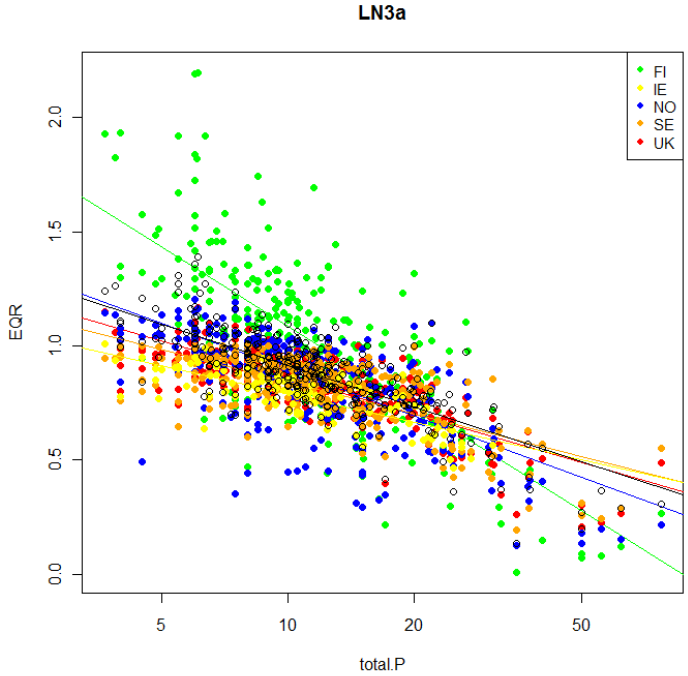


Figure G.27 Relationship between national EQRs (standardised to remove country effects) and total P. Points coloured by national method (applied to all countries data), open black circles are for common metric.)

Regression parameters for above relationships D:\RegressionsWithTP.xls

Table G.15 Regression parameters for relationship between final EQRs (standardised to remove country effects) and total P

	(Intercept)	log10(total.P)	adj R2	p
SE	1.311	-0.468	0.509	<0.001
FI	2.242	-1.158	0.579	<0.001
IE	1.204	-0.414	0.614	<0.001
NO	1.568	-0.674	0.589	<0.001
UK	1.395	-0.532	0.630	<0.001

Relationship with Common Metric

Table G.16 Parameters for relationship between national and common metrics

	UK	NO	IE	SE	FI		FI GM FI EQR <0.715	FI HG FI EQR >0.715
Intercept	-0.006	0.243	-0.129	0.086	0.412		0.253	0.504
slope	1.059	0.760	1.338	0.957	0.460		0.717	0.382
Pearson's r	0.844	0.913	0.870	0.756	0.889		0.813	0.832
R^2	0.713	0.749	0.757	0.572	0.790		0.661	0.693

For Finland segmented regression demonstrated different linear relationships above and below a break point of FI EQR = 0.715 (see point and bar in fig 5b). The regression parameter for the upper segment have been used to determine the FI HG boundary on the common metric scale and the lower segment has been used for the GM boundary.

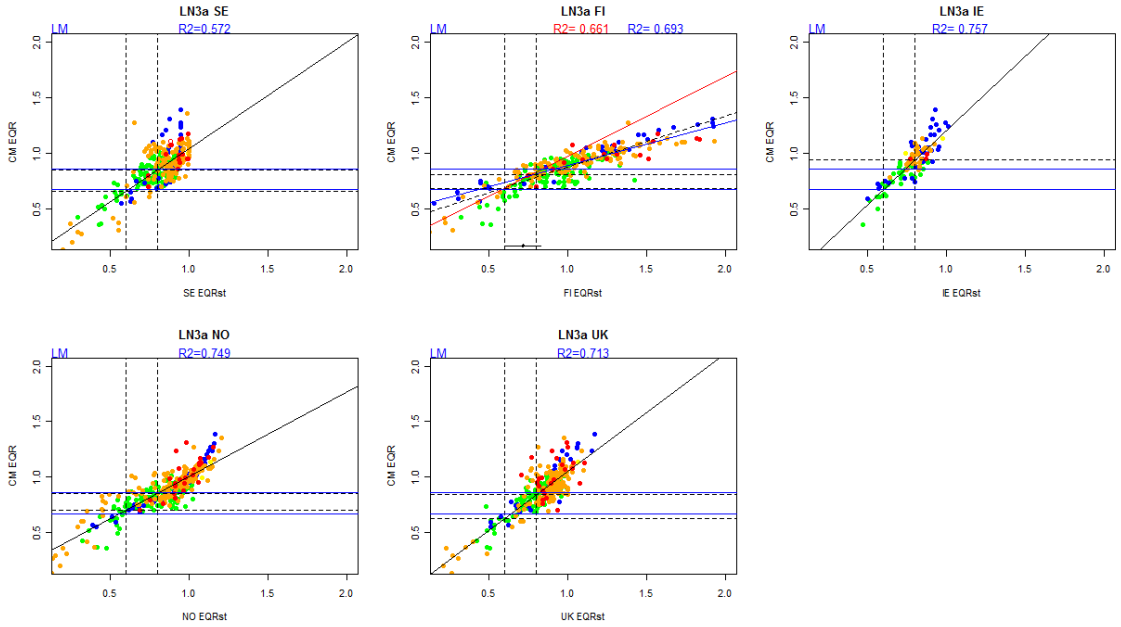


Figure G.28 *Relationship between national standardised EQR and common metric EQR. a) SE, b) FI, c) IE, d) NO, e) UK. Vertical lines mark boundaries on standardised national scale, horizontal blue line average(target) boundaries. Segmented linear regression fitted to FI as data indicate non-linearity, boundaries taken from regression for FI EQRst < 0.72 (red line) for GM and > 0.72 (blue line) for HG*

Descriptions of community at High, Good, Moderate, Poor status

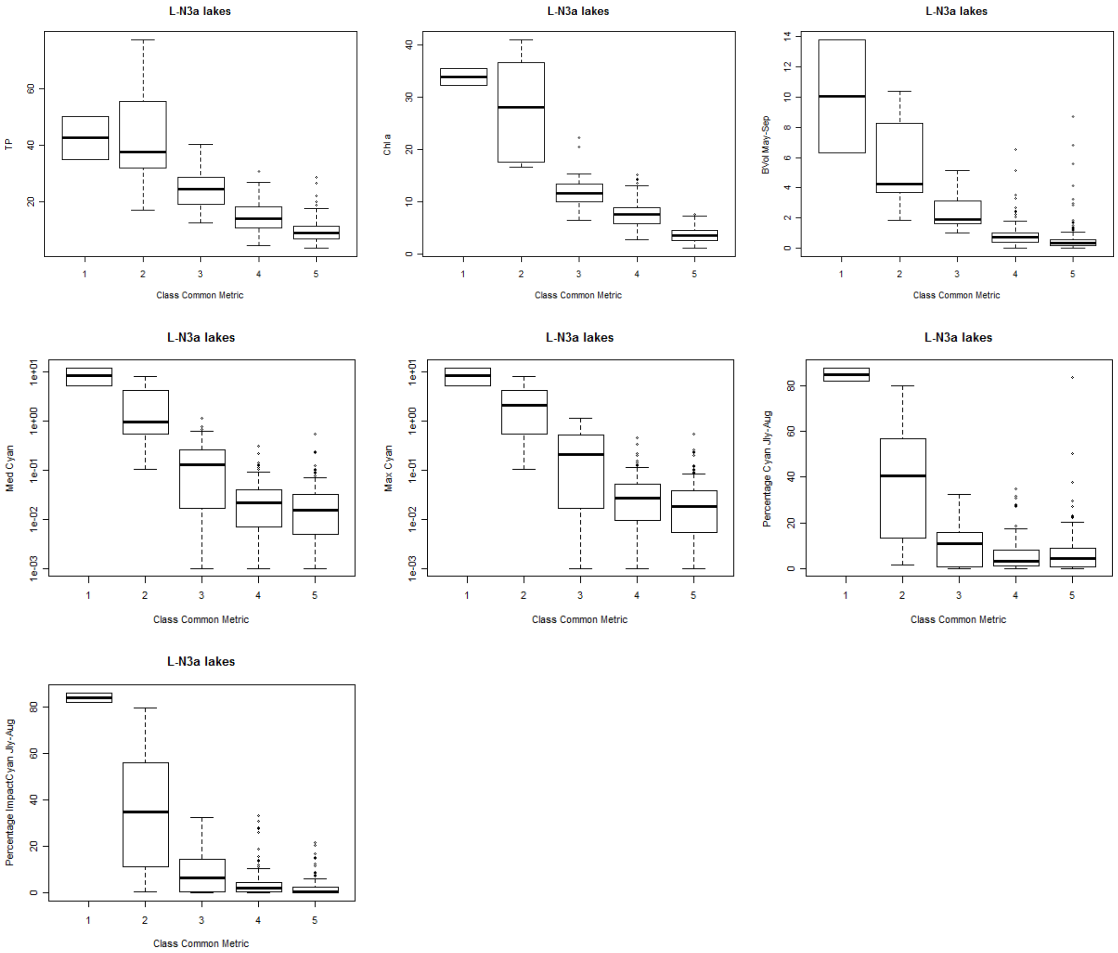


Figure G.29 distribution of a)mean (growing season) TP, b) mean (growing season)Chlorophyll a ,c) mean May-Sept Biovolume, d) median cyanobacteria biovolume, e) max summer (July-Sep) cyanobacteria biovolume, f) percentage of summer (July/Aug) cyanobacteria, g percentage of impact cyanobacteria for LN3a lakes classified by common metric boundaries

G.5 LN5 lakes

Summary

Final version has the following changes:

1. Common metric standardized;
2. NO Ref Chl changed;
3. SE Ref , HG, MP and PB boundaries for BVol changed to match GIG regressions with Chlorophyll.

All countries have significant relationship with pressure and achieve the required relationship with the common metric. All countries in the harmonisation band

Reference Conditions

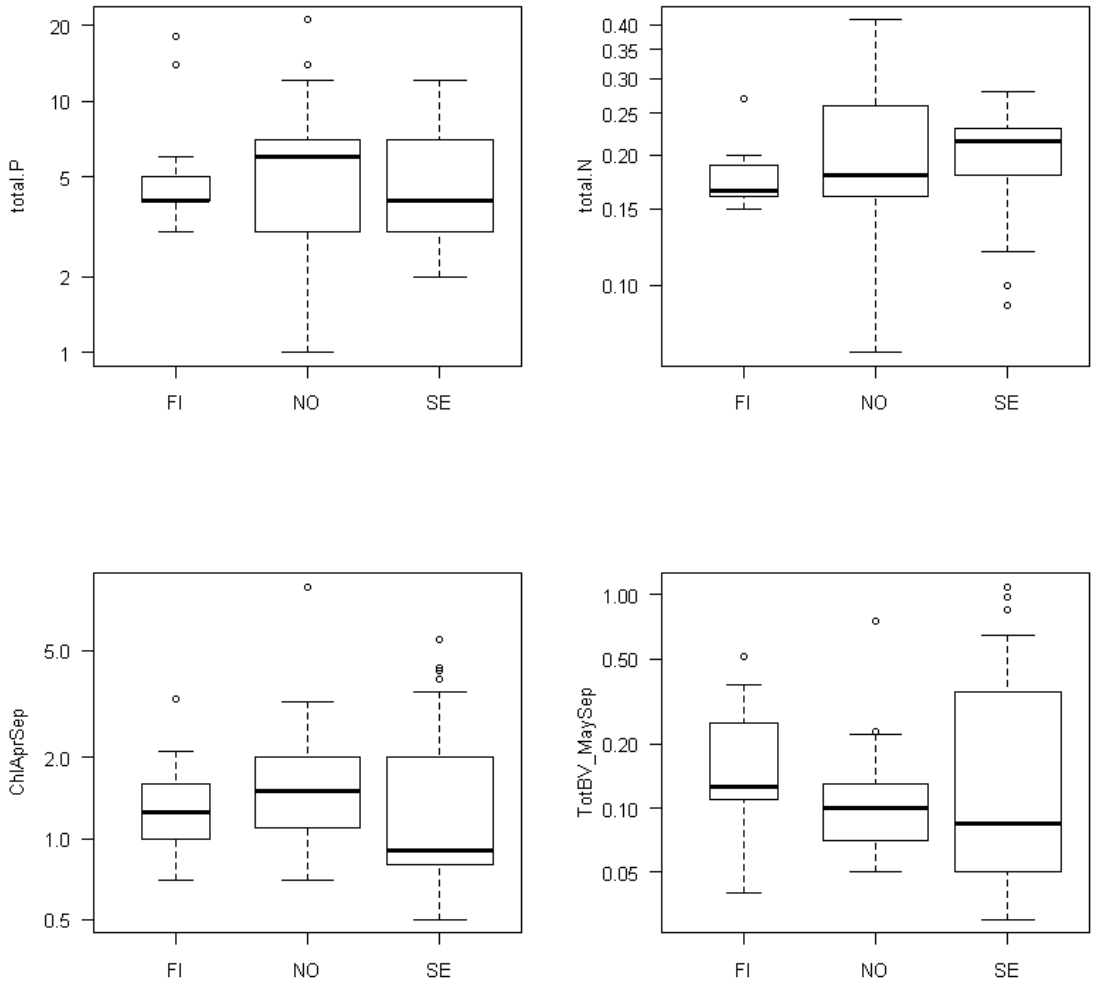


Figure G.30 Distributions of a) TP ug/l, b) TN mg/l, c) Chlorophyll a (Apr –Sept), d) Total biovolume mg/l May-Sep in LN5 reference lakes for each country

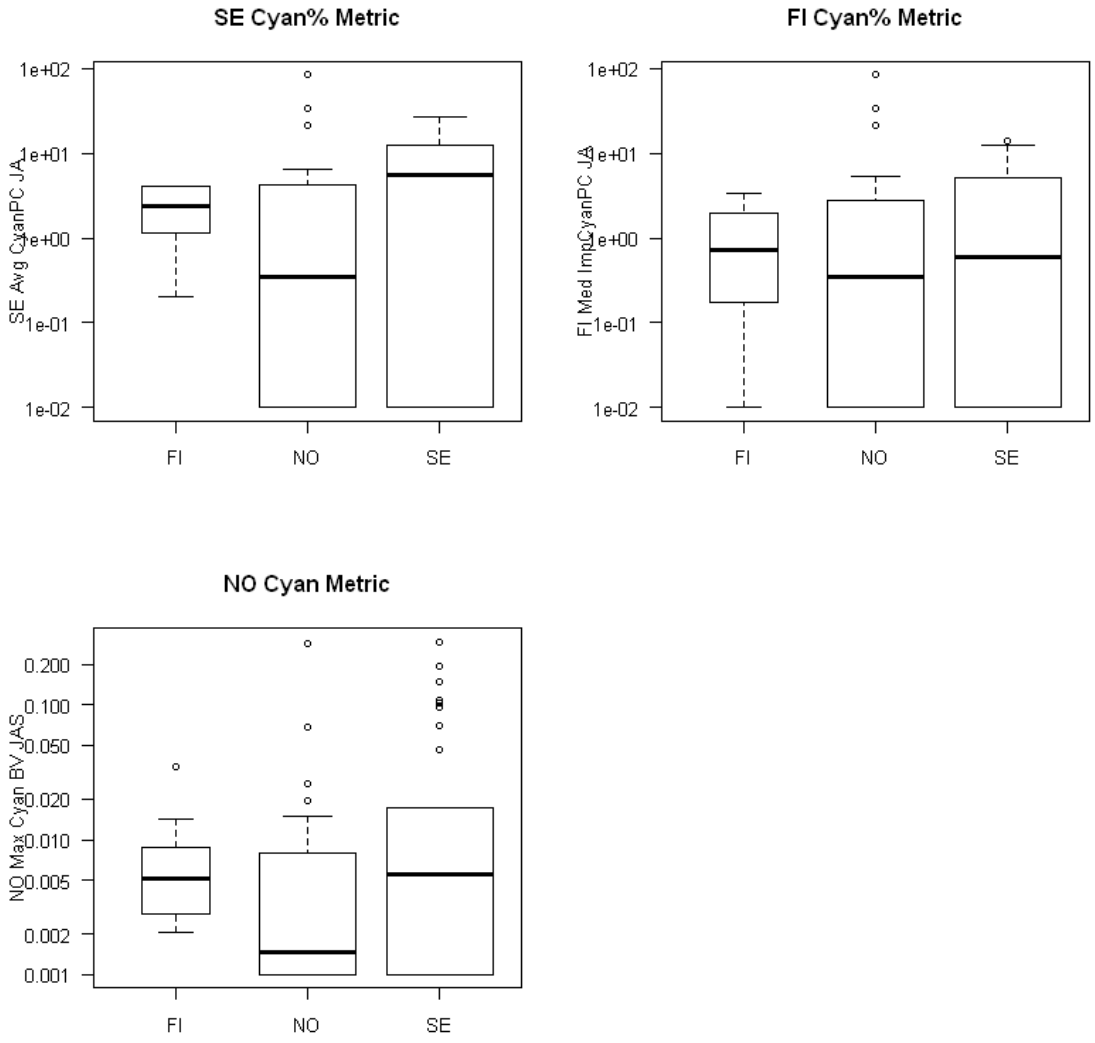


Figure G.31 Distributions of cyanobacteria metrics a) Sweden % cyanobacteria (July & Aug), b) Finland % impact cyanobacteria (July & Aug), c) Norway max cyanobacteria biovolume (mg/l) July-Sept in LN5 reference lakes for each country

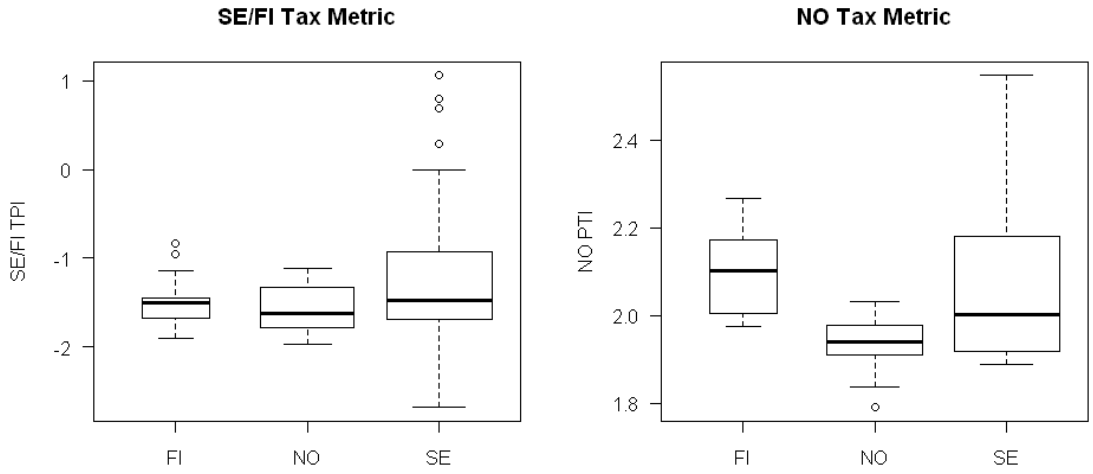


Figure G.32 Distributions of taxonomic metrics a) Swedish TPI index, b) Norwegian PTI index, index in LN5 reference lakes for each country

Table G.17 Distributions of metrics for LN1 Reference Lakes

		50%	90%	95%	100%	N
TP	FI	4	12	15	18	14
TP	NO	5	7	7	8	28
TP	SE	4	10	12	12	34
TP		5	9	12	18	
Chl		50%	90%	95%	100%	N
Chl	FI	1.2	2.0	2.5	3.3	14
Chl	NO	1.5	2.3	2.4	2.5	28
Chl	SE	0.9	3.7	4.2	5.5	34
		1.3	3.0	3.6	5.5	
		50%	90%	95%	100%	N
BVol	FI	0.13	0.36	0.42	0.51	14
BVol	NO	0.09	0.19	0.22	0.23	28
BVol	SE	0.09	0.64	0.89	1.09	34
BVol		0.10	0.42	0.62	1.09	
		50%	90%	95%	100%	N
SE TPI	FI	-1.506	-1.012	-0.912	-0.832	14
SE TPI	NO	-1.618	-1.192	-1.150	-1.116	28
SE TPI	SE	-1.479	0.197	0.725	1.059	34
SE TPI		-1.536	-0.774	0.080	1.059	

		50%	90%	95%	100%	N
		50%	90%	95%	100%	N
NO PTI	FI	2.101	2.182	2.214	2.266	14
NO PTI	NO	1.940	2.000	2.013	2.030	28
NO PTI	SE	2.003	2.276	2.343	2.546	34
NO PTI		1.989	2.188	2.271	2.546	
		50%	90%	95%	100%	N
FI ImpCyanPC	FI	0.7	2.8	3.1	3.4	14
FI ImpCyanPC	NO	0.3	10.2	29.4	84.0	28
FI ImpCyanPC	SE	0.6	11.0	11.9	14.1	34
FI ImpCyanPC		0.4	8.7	13.0	84.0	
		50%	90%	95%	100%	N
SE CyanPC	FI	2.4	4.1	4.1	4.1	14
SE CyanPC	NO	0.3	11.1	29.4	84.0	28
SE CyanPC	SE	5.5	21.9	23.2	26.8	34
SE CyanPC		2.2	17.8	23.1	84.0	
		50%	90%	95%	100%	N
NO Max CyanBV	FI	0.004	0.013	0.020	0.034	14
NO Max CyanBV	NO	0.000	0.020	0.052	0.283	28
NO Max CyanBV	SE	0.004	0.105	0.162	0.292	34
NO Max CyanBV		0.003	0.068	0.116	0.292	

Based on above results the ratio of the median chlorophyll to 90th percentile chlorophyll for reference lakes is shown in Table G.17.

Table G.18 Ratio of median chlorophyll a to 90th percentile chlorophyll a for reference sites. A potential HG EQR boundary.

FI	0.62
NO	0.66
SE	0.24
All	0.43

Relationship with Pressure

Table G.19 Regression parameters for relationships D:\RegressionsWithTP.xls between national final EQRs (standardised to remove country effects) and total P for LN5 Lakes

	(Intercept)	log10(total.P)	adj R2	p
SE	1.302	-0.508	0.410	<0.001
FI	1.818	-1.018	0.438	<0.001
NO	1.499	-0.827	0.588	<0.001

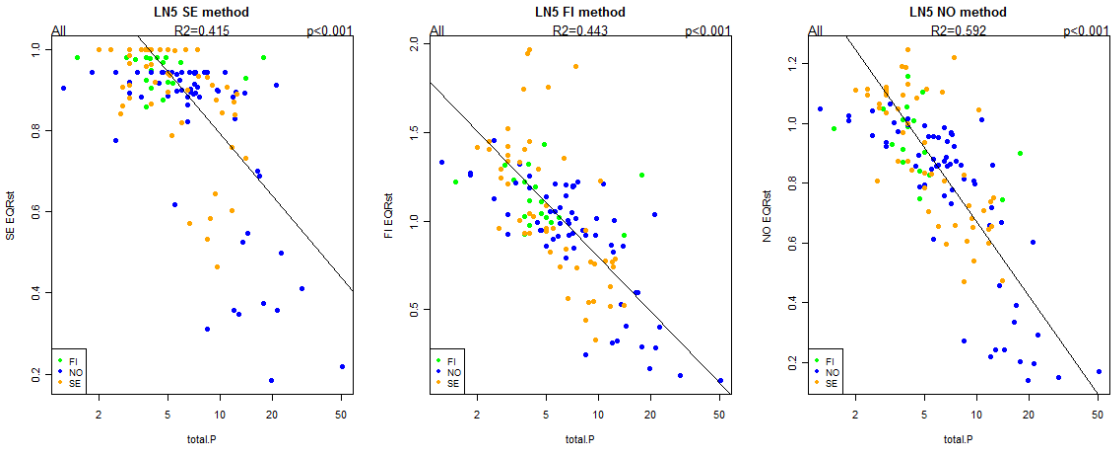


Figure G.33 Relationship between national final EQRs (standardised to remove country effects) and total P. a) SE, b) FI, c) NO for LN5 lake type.

Relationship with Common Metric

Table G.20 Relationship between national standardised EQR and common metric EQR.

	NO	SE	FI
Intercept	0.19	0.02	0.33
slope	0.96	1.13	0.65
Pearson's r	0.96	0.81	0.94
R^2	0.928	0.658	0.892

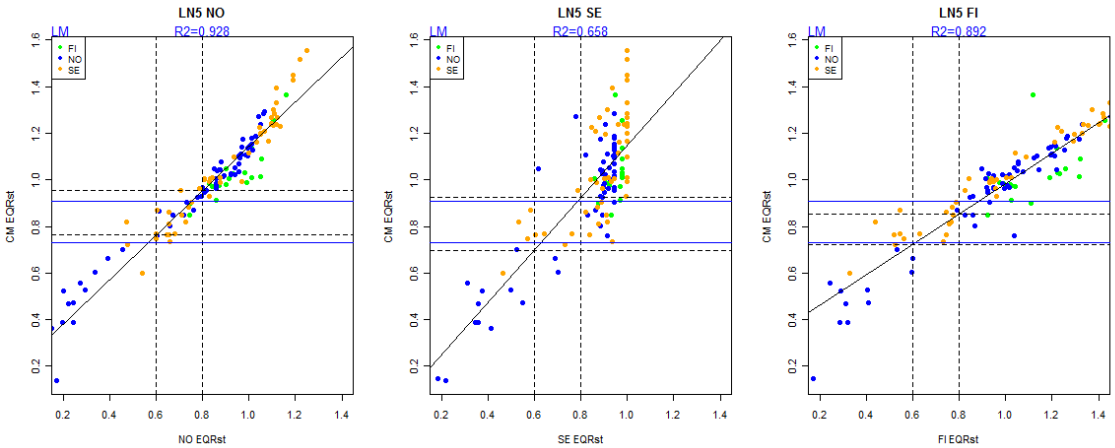


Figure G.34 Relationship between national standardised EQR and common metric EQR. a) NO, b) SE, c) FI for LN5 lake type. Vertical lines mark boundaries on standardised national scale.

Description of community at High, Good, Moderate status

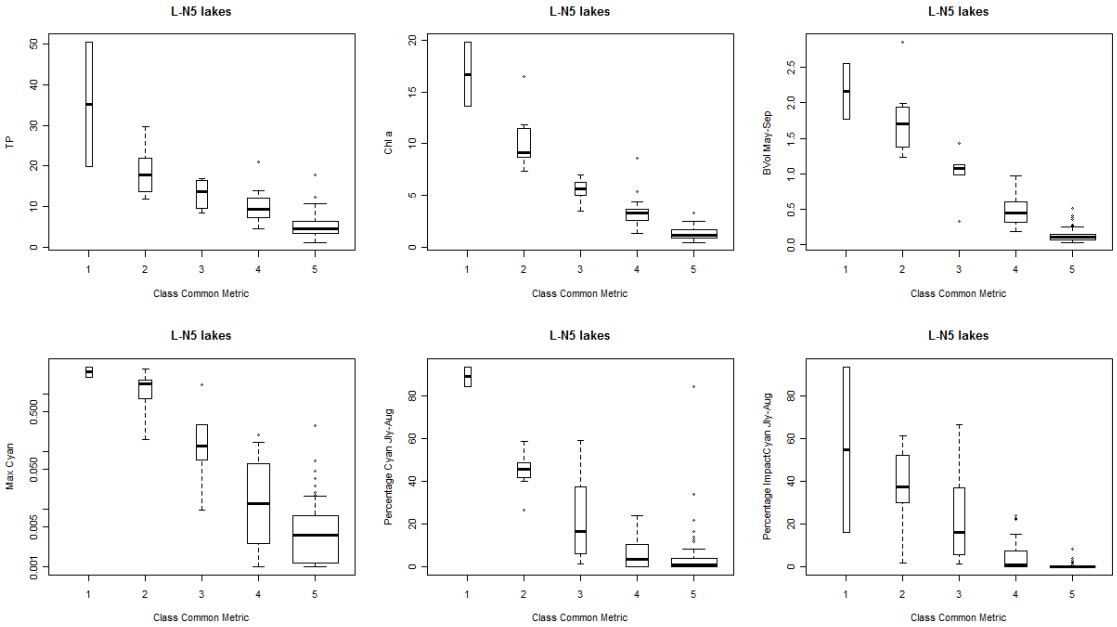


Figure G.35 distribution of mean (growing season) TP, mean (growing season)Chlorophyll-a, mean May-Sep Biovolume, max summer (July-Sep) cyanobacteria biovolume, percentage of summer (July/Aug) impact cyanobacteria for lakes classified by common metric boundaries

G.6 LN6a lakes

Summary

Final version has following changes: Use of standardised common metric and national chlorophyll boundary values following validation workshop

All countries have significant relationship with pressure and achieve the required relationship with common metric. All countries are within the harmonisation band.

Reference Conditions

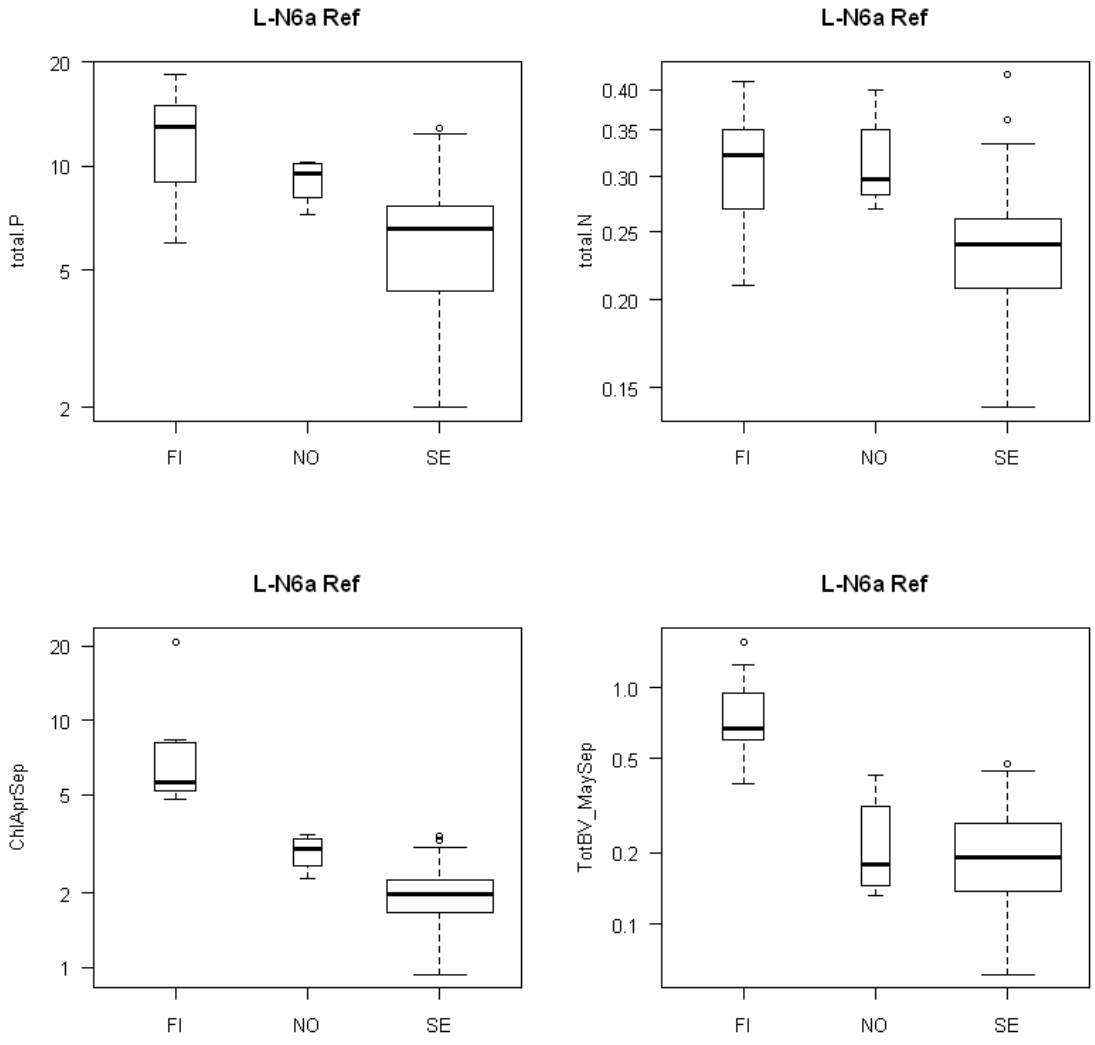


Figure G.36 Distributions of a) TP ug/l, b) TN mg/l, c) Chlorophyll-a (Apr -Sept), d) Total biovolume mg/l May-Sep in LN6a reference lakes for each country

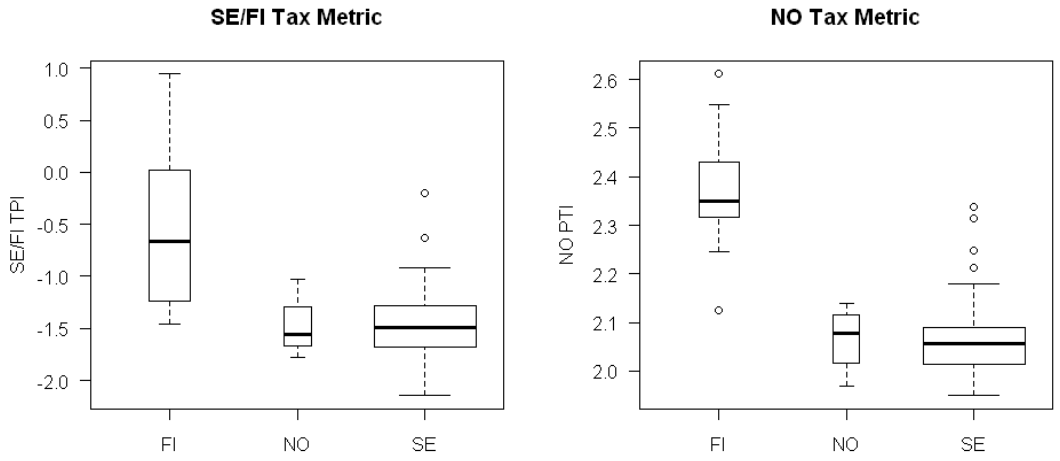


Figure G.37 Distributions of taxonomic metrics a) Finland TPI, b) Norwegian PTI index in LN6a reference lakes for each country

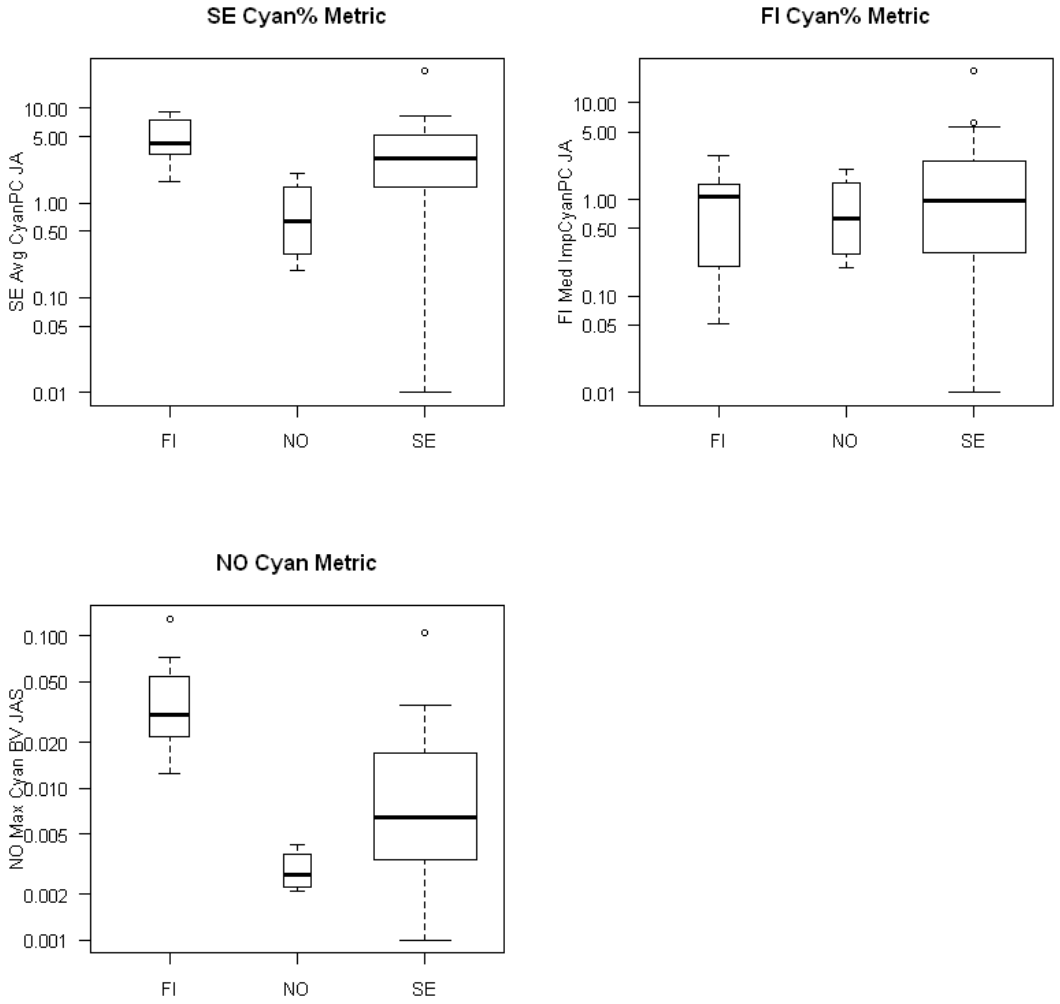


Figure G.38 Distributions of cyanobacteria metrics a) Finland % impact cyanobacteria (July & Aug), b) Norway max cyanobacteria biovolume (mg/l) July-Sept in LN6a reference lakes for each country

Table G.21 Distributions of metrics for LN6a Reference Lakes

Metric	Country	50%	90%	95%	100%	N
TP	FI	13	18	18	18	9
TP	NO	10	10	10	10	4
TP	SE	7	9	12	13	58
TP		7	12	13	18	71
		50%	90%	95%	100%	N
Chl	FI	5.6	10.8	15.8	20.8	9
Chl	NO	3.0	3.4	3.4	3.5	4
Chl	SE	2.0	2.6	2.8	3.4	58
Chl	All	2.1	5.1	6.5	20.8	71
		50%	90%	95%	100%	N
BVol	FI	0.67	1.31	1.44	1.56	9
BVol	NO	0.18	0.36	0.39	0.43	4
BVol	SE	0.19	0.32	0.35	0.47	58
BVol		0.20	0.59	0.79	1.56	
		50%	90%	95%	100%	N
SE TPI	FI	-0.668	0.817	0.881	0.944	9
SE TPI	NO	-1.554	-1.182	-1.103	-1.023	4
SE TPI	SE	-1.489	-1.135	-0.951	-0.194	58
SE TPI		-1.424	-0.870	-0.330	0.944	
		50%	90%	95%	100%	N
NO PTI	FI	2.349	2.560	2.586	2.611	9
NO PTI	NO	2.077	2.125	2.132	2.140	4
NO PTI	SE	2.056	2.172	2.217	2.338	58
NO PTI		2.069	2.317	2.360	2.611	
		50%	90%	95%	100%	N
FI ImpCyanPC	FI	1.0	1.8	2.3	2.9	9
FI ImpCyanPC	NO	0.6	1.7	1.9	2.0	4
FI ImpCyanPC	SE	1.0	3.9	5.4	21.2	58
FI ImpCyanPC		0.9	3.3	5.3	21.2	
		50%	90%	95%	100%	N
SE Cyan PC	FI	4.2	7.9	8.5	9.0	9
SE Cyan PC	NO	0.6	1.7	1.9	2.0	4
SE Cyan PC	SE	2.9	6.5	7.4	24.4	58
SE Cyan PC		3.0	7.4	7.6	24.4	
		50%	90%	95%	100%	N
NO Max CyanBV	FI	0.029	0.083	0.106	0.128	9
NO Max CyanBV	NO	0.002	0.003	0.003	0.003	4
NO Max CyanBV	SE	0.005	0.022	0.026	0.103	58

Metric	Country	50%	90%	95%	100%	N
NO Max CyanBV		0.008	0.029	0.052	0.128	

Based on above results the ratio of the median chlorophyll to 90th percentile chlorophyll for reference lakes is shown in Table G.22

Table G.22 Ratio of median chlorophyll a to 90th percentile chlorophyll a for reference sites. A potential HG EQR boundary.

FI	0.52
NO	0.90
SE	0.77
All	0.41

Relationship with Pressure

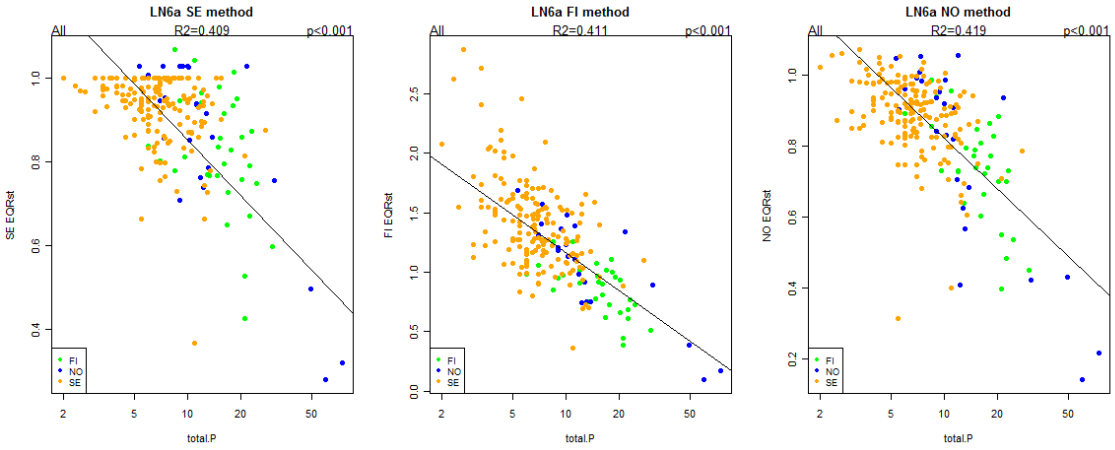


Figure G.39 Relationship between national final EQRs (standardised to remove country effects) and total P. a) SE, b) FI, c) NO for LN6a lake type, lines show regression fit for TP in range 5-100 ug/l.

Table G.23 Regression parameters for relationship between final EQRs (standardised to remove country effects) and total P, based on TP range of 5-100 ug/l

	(Intercept)	log10(total.P)	adj R2	p
SE	1.300	-0.446	0.405	<0.001
FI	2.231	-1.065	0.408	<0.001
NO	1.301	-0.477	0.416	<0.001

Relationship with Common Metric

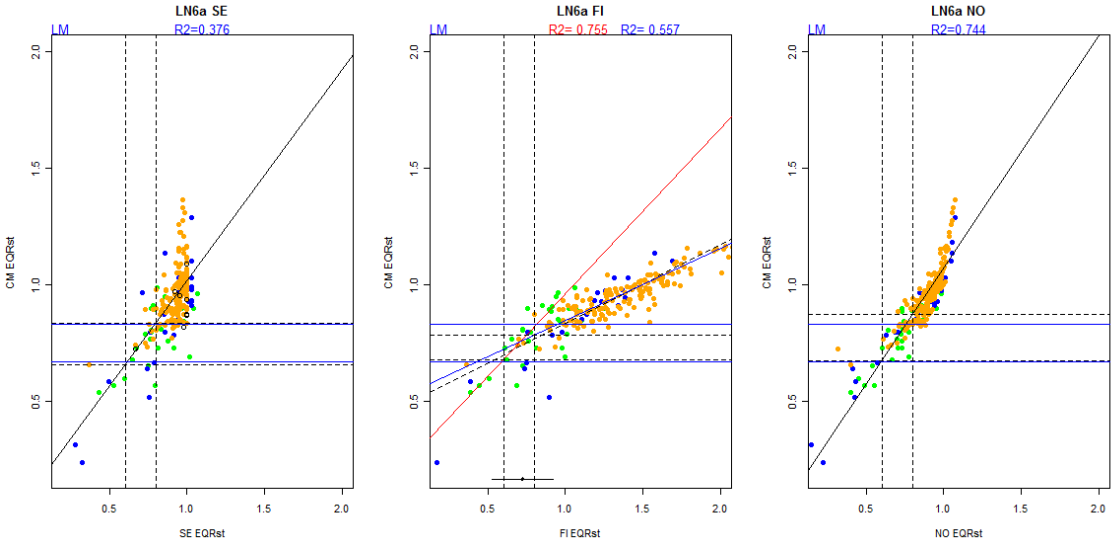


Figure G.40 *Relationship between national standardised EQR and standardised common metric EQR. a) SE, b) FI, c) NO for LN6a lake type. Vertical lines mark boundaries on standardised national scale, horizontal blue line average (target) boundaries.*

Table G.24 *Relationship between national standardised EQR and standardised common metric EQR*

	NO	SE	FI	FI_GM FI EQR <0.72	FI_HG FI EQR >0.72
Intercept	0.075	0.112	0.495	0.252	0.537
slope	0.998	0.906	0.338	0.710	0.309
Pearson's r	0.86	0.61	0.80	0.87	0.75
R^2	0.74	0.38	0.69	0.76	0.557

Description of community at High, Good, Moderate status

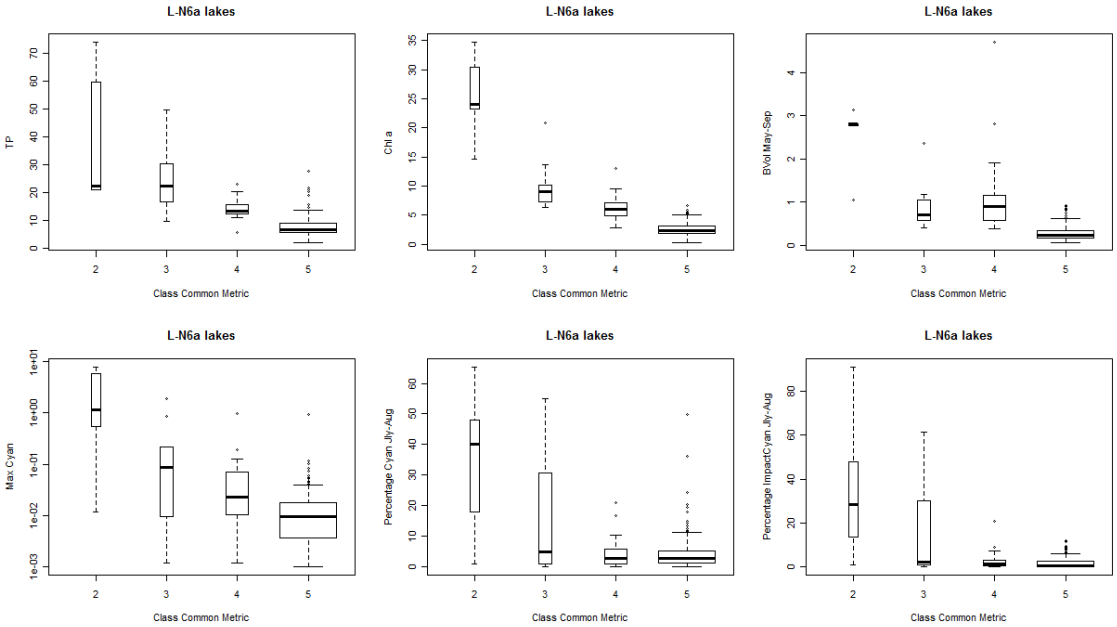


Figure G.41 distribution of mean (growing season) TP, mean (growing season) Chlorophyll-a, mean May-Sept Biovolume, cyanobacteria biovolume, max summer (July-Sep) cyanobacteria biovolume, percentage of summer (July/Aug) impact cyanobacteria for lakes classified by common metric boundaries

G.7 LN8a lakes

Summary

Final version has following changes:

1. At final GIG meeting it was agreed to change the FI Biovolume boundaries to Ref 0.7, HG 0.9, GM 1.7,MP 3.4, PB 6.8;
3. SE Biovolume boundaries changed following email discussion with Anneli Harlen after ECOSTAT;
4. NO and UK combination rule changed so that cyanobacteria only averaged if worse than average of other EQRs;
5. Standardisation of common metric following validation workshop;
6. NO ref Chl changed. NO PTI changed, IE reference Chl changed, standardization checked.

All countries have a significant relationship with pressure and achieve the required relationship with the common metric.All countries are in or above the harmonisation band (IE above band)

Reference Conditions

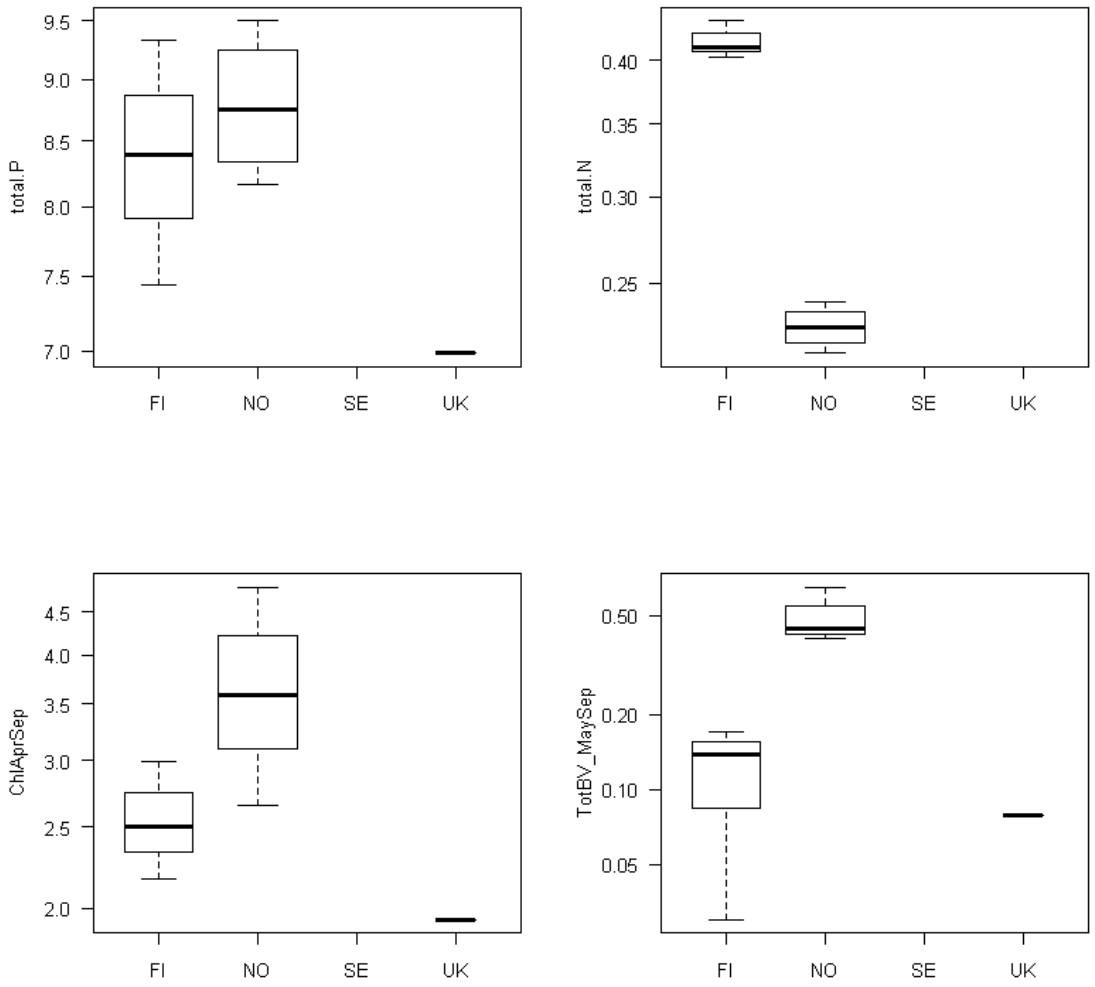


Figure G.42 Distributions of a) TP ug/l, b) TN mg/l, c) Chlorophyll a (Apr –Sept), d) Total biovolume mg/l May-Sep in LN8A reference lakes for each country

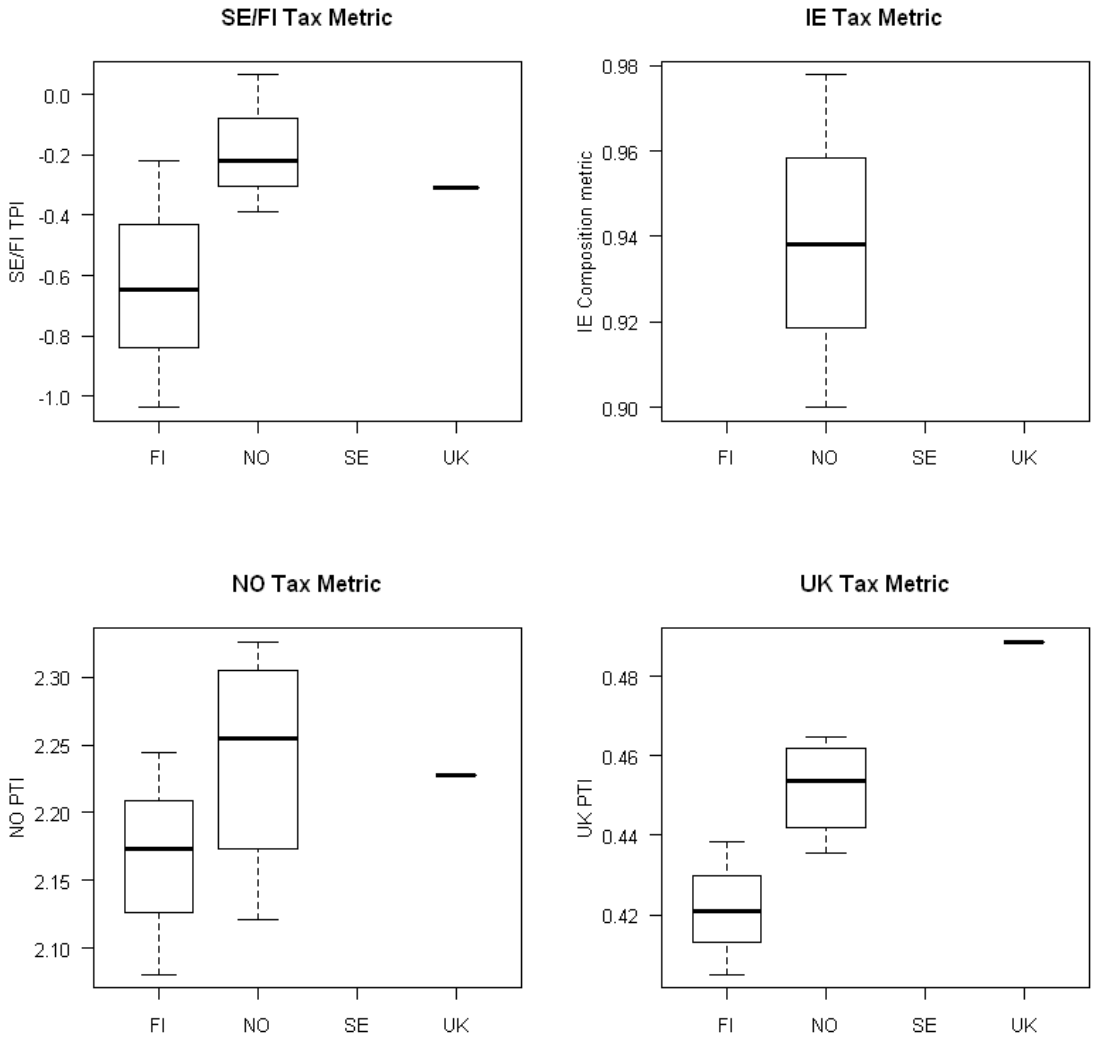


Figure G.43 Distributions of taxonomic metrics a) Finland TPI b) Norwegian PTI index, c) UK PTI index in LN8A reference lakes for each country

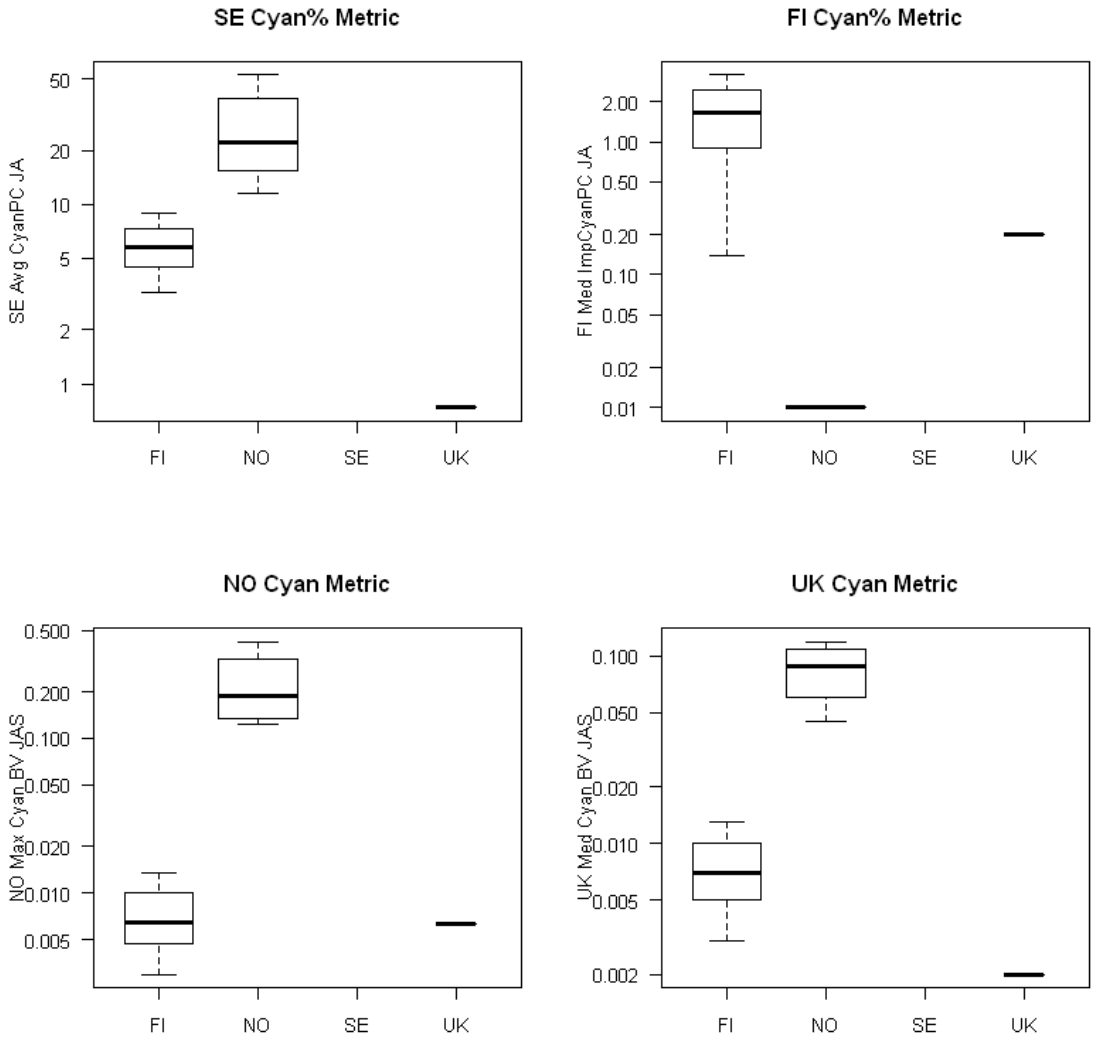


Figure G.44 Distributions of cyanobacteria metrics a) Finland % impact cyanobacteria (July & Aug), b) Norway max cyanobacteria biovolume (mg/l) July-Sept, c) UK median cyanobacteria biovolume (mg/l) July - Sept in LN8A reference lakes for each country

Table G.25 Distributions of metrics for LN8a Reference Lakes

		50%	90%	95%	100%	N
TP	FI	8	9	9	9	3
TP	NO	9	9	9	10	4
TP	UK	7	7	7	7	1
TP		8	9	9	10	
		50%	90%	95%	100%	N
Chl	FI	2.5	2.9	2.9	3.0	3
Chl	NO	3.6	4.5	4.6	4.8	4
Chl	UK	1.9	1.9	1.9	1.9	1
Chl		2.8	4.0	4.4	4.8	
		50%	90%	95%	100%	N
BVol	FI	0.14	0.17	0.17	0.17	3
BVol	NO	0.44	0.59	0.62	0.65	4
BVol	UK	0.08	0.08	0.08	0.08	1
BVol		0.29	0.51	0.58	0.65	
		50%	90%	95%	100%	N
SE TPI	FI	-0.644	-0.306	-0.264	-0.221	3
SE TPI	NO	-0.222	0.007	0.036	0.064	4
SE TPI	UK	-0.309	-0.309	-0.309	-0.309	1
SE TPI		-0.309	-0.107	-0.021	0.064	
		50%	90%	95%	100%	N
IE Taxonomic Score	FI	NA	NA	NA	NA	3
IE Taxonomic Score	NO	0.938	0.966	0.972	0.978	4
IE Taxonomic Score	UK	NA	NA	NA	NA	1
IE Taxonomic Score		0.938	0.966	0.972	0.978	
		50%	90%	95%	100%	N
NO PTI	FI	2.173	2.230	2.237	2.245	3
NO PTI	NO	2.255	2.314	2.320	2.326	4
NO PTI	UK	2.227	2.227	2.227	2.227	1
NO PTI		2.226	2.296	2.311	2.326	
		50%	90%	95%	100%	N
UK PTI	FI	0.421	0.435	0.437	0.438	3
UK PTI	NO	0.454	0.463	0.464	0.465	4
UK PTI	UK	0.489	0.489	0.489	0.489	1
UK PTI		0.443	0.472	0.480	0.489	
		50%	90%	95%	100%	N
FI ImpCyanPC	FI	1.7	2.9	3.0	3.2	3
FI ImpCyanPC	NO	0.0	0.0	0.0	0.0	4
FI ImpCyanPC	UK	0.2	0.2	0.2	0.2	1

		50%	90%	95%	100%	N
FI ImpCyanPC		0.1	2.1	2.7	3.2	
		>				
		50%	90%	95%	100%	N
SE Cyan PC	FI	5.7	8.3	8.6	8.9	3
SE Cyan PC	NO	22.0	44.3	48.5	52.6	4
SE Cyan PC	UK	0.7	0.7	0.7	0.7	1
SE Cyan PC		10.3	33.2	42.9	52.6	
		50%	90%	95%	100%	N
NO Max CyanBV	FI	0.006	0.011	0.012	0.012	3
NO Max CyanBV	NO	0.186	0.363	0.391	0.420	4
NO Max CyanBV	UK	0.005	0.005	0.005	0.005	1
NO Max CyanBV		0.068	0.287	0.354	0.420	
		50%	90%	95%	100%	N
UK Med CyanBV	FI	0.006	0.011	0.011	0.012	3
UK Med CyanBV	NO	0.087	0.112	0.115	0.118	4
UK Med CyanBV	UK	0.001	0.001	0.001	0.001	1
UK Med CyanBV		0.028	0.104	0.111	0.118	

Based on above results the ratio of the median chlorophyll to 90th percentile chlorophyll for reference lakes is shown in Table G.25

Table G.26 Ratio of median chlorophyll a to 90th percentile chlorophyll a for reference sites. A potential HG EQR boundary.

HG	0.86
FI	0.80
NO	1.00
UK	0.71

Relationship with Pressure

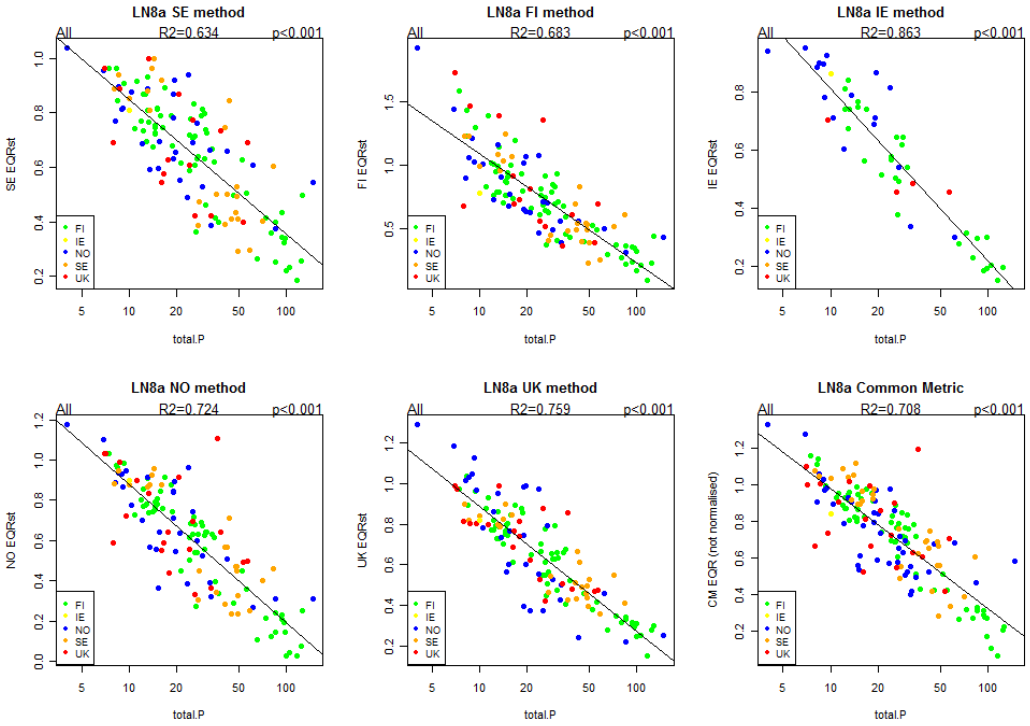


Figure G.45 Relationship between national final EQRs (standardised to remove country effects) and total P. a) SE, b) FI, c) NO, d) UK, e) IE, f) Common Metric for LN8A lake type

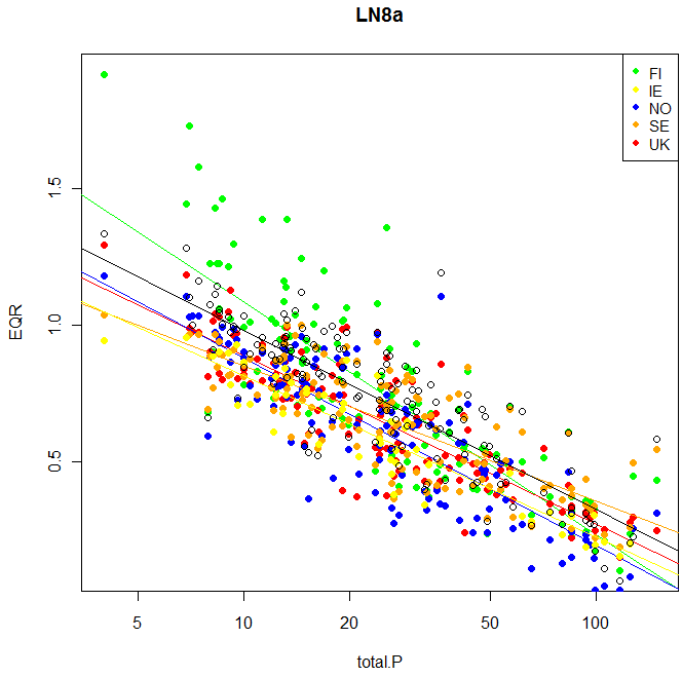


Figure G.46 *Relationship between national EQRs (standardised to remove country effects) and total P. Points coloured by national method (applied to all countries data), open black circles are for common metric.)*

Table G.27 *Regression parameters for relationship between final EQRs (standardised to remove country effects) and total P.*

	(Intercept)	log10(total.P)	adj R2	p
SE	1.347	-0.496	0.631	<0.001
FI	1.936	-0.852	0.680	<0.001
IE	1.406	-0.592	0.860	<0.001
NO	1.564	-0.685	0.722	<0.001
UK	1.503	-0.617	0.757	<0.001

Relationship with Common Metric

Table G.28 *Parameters for relationship between national and common metrics*

	UK	NO	IE	SE	FI	FI GM FI EQR <0.75	FI HG FI EQR >0.75
Intercept	0.124	0.189	0.028	0.020	0.238	0.045	0.520
slope	0.928	0.895	1.164	1.071	0.651	1.026	0.391
Pearson's r	0.868	0.928	0.929	0.886	0.892	0.855	0.734
R^2	0.754	0.861	0.863	0.786	0.795	0.731	0.539

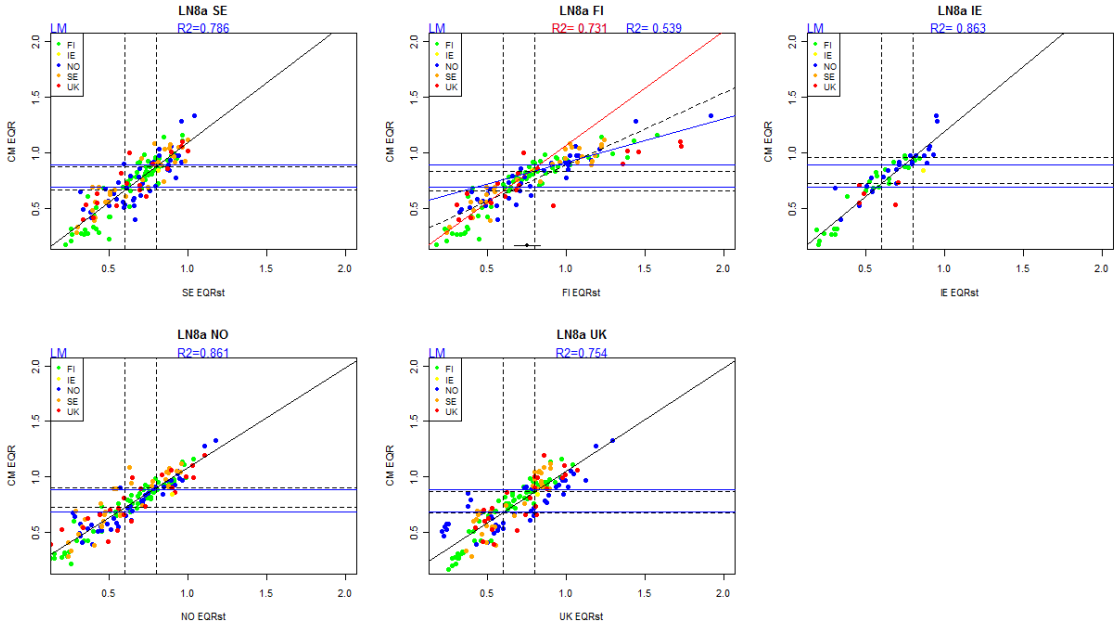


Figure G.47 *Relationship between national standardised EQR and common metric EQR. a) SE, b) FI, c) IE, d) NO, e) UK for LN8a lake type. Vertical lines mark boundaries on standardised national scale, horizontal blue line*

average(target) boundaries. Segmented linear regression fitted to FI as data indicate non-linearity, HG boundary taken from regression for FI EQRst > 0.75, GM from segment FIEQR <0.75.

Segmented regression shows split for FI at FIEQR>0.75, value above are for regression where FIEQR <0.75 (red line in fig 5) and >0.75 (blue line in fig 5). Parameters for segmented regression used for both HG and GM boundaries. (Parameters for FI global regression show for information)

Distribution of pressure and biological metrics by common metric class

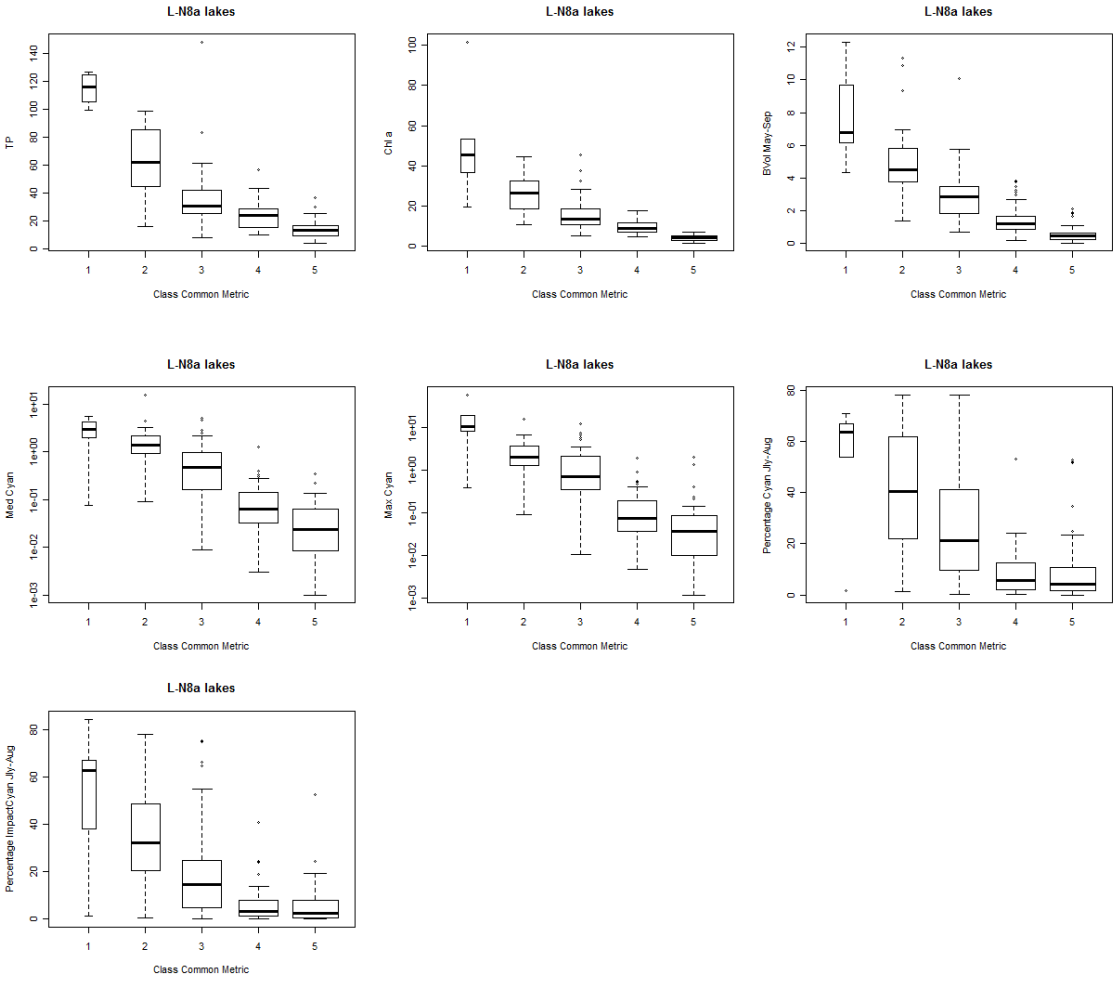


Figure G.48 Distribution of mean (growing season) TP, mean (growing season) Chlorophyll-a , mean May-Sep Biovolume, median summer (July-Sep) cyanobacteria biovolume, max summer (July-Sep) cyanobacteria biovolume, percentage of summer (July/Aug) impact cyanobacteria for lakes classified by common metric boundaries

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Abstract

One of the key actions identified by the Water Framework Directive (WFD; 2000/60/EC) is to develop ecological assessment tools and carry out a European intercalibration (IC) exercise. The aim of the Intercalibration is to ensure that the values assigned by each Member State to the good ecological class boundaries are consistent with the Directive's generic description of these boundaries and comparable to the boundaries proposed by other MS.
In total, 83 lake assessment methods were submitted for the 2nd phase of the WFD intercalibration (2008-2012) and 62 intercalibrated and included in the EC Decision on Intercalibration (EC 2013). The intercalibration was carried out in the 13 Lake Geographical Intercalibration Groups according to the ecoregion and biological quality element. In this report we describe how the intercalibration exercise has been carried out in the Northern Lake Phytoplankton group.

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