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# Matching the sampling frame for FAO area 27 (Northeast Atlantic) with ICES assessments

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Abstract

#### **Matching the sampling frame for FAO area 27 (Northeast Atlantic) with ICES assessments**

This document describes the matching of the CFP indicators sampling frame for FAO area 27 (Northeast Atlantic) with ICES assessments.

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## **Abstract**

In this document the FMZs in the CFP sampling frame for FAO area 27 (Northeast Atlantic) are matched to the corresponding ICES stock assessment. The matching is performed through the ICES rectangles that make up the FMZs and stock assessment areas. Some TACs are matched to multiple assessments and some TACs are not matched to any assessments. The matching is performed by the R code that is embedded in the document.

## **1. Introduction**

The CFP indicators sampling frame for FAO area 27 has already been generated (Scott et al., 2017). In this document the FMZs in the sampling frame are matched to the corresponding ICES stock assessment. To perform the match, the ICES areas that make up the FMZs and the ICES stock assessments are expanded to their constituent ICES rectangles. The TACs and the ICES assessments are then matched by the constituent ICES rectangles and species.

This approach requires the FMZs and the ICES assessments to be mapped to ICES areas. For the FMZs, the mapping to ICES areas is not perfect and an ICES area may feature in more than one FMZ.

## 2. ICES areas and rectangles

Each ICES area is made up of ICES rectangles. These rectangles are used to merge the sampling frame and ICES assessment data sets. In this section the data set that describes the rectangles that make up each area is loaded and cleaned.

```
library(rgdal)
# Load the ICES rectangles data
rectangles <- readOGR("../data/ICES_Areas", layer=
  "ICES_StatRec_map_Areas_Full_20170124")

## OGR data source with driver: ESRI Shapefile
## Source: "../data/ICES_Areas", layer: "ICES_StatRec_map_Areas_Full_20170124"
## with 11074 features
## It has 17 fields

# Pull out the data element
rectangles <- rectangles@data
# The rectangles column is called ICESNAME
# We change it to something more helpful
colnames(rectangles)[colnames(rectangles)=="ICESNAME"] <- "Rectangle"
# And force it to be a character
rectangles$Rectangle <- as.character(rectangles$Rectangle)
rectangles$Area_27 <- as.character(rectangles$Area_27)
rectangles$AreasList <- as.character(rectangles$AreasList)
#rectangles$Max_Area <- as.character(rectangles$Max_Area)
#rectangles$Area_List <- as.character(rectangles$Area_List)
# Rename columns
colnames(rectangles)[colnames(rectangles) %in% c("Area_27", "AreasList")] <-
  c("Max_Area", "Area_List")
# Keep only columns of interest
rectangles <- rectangles[,c("Max_Area", "Area_List", "Rectangle")]
```

Due to the way ICES areas are defined, the rectangles may exist in more than one area, for example if the rectangles are on the borders of multiple areas. The analysis here is based on each rectangle being allocated to a single ICES area. The allocated area is the area that contains the majority of the rectangle. This information is stored in the column *Max\_Area*. This column needs some cleaning to make it compatible with the other data sets.

```
# There are some NAs in the max_area column.
# These have no areas so remove them - they interfere with merging
rectangles <- subset(rectangles, !is.na(Max_Area))
# A new column is added based on Max_Area so that it is comparable
# across the other data sets
rectangles$Area <- paste("27.", toupper(as.character(rectangles$Max_Area)), sep="")
```

We expect each rectangle to only feature in a single area, i.e. the rectangle is unique in the ICES rectangles data set.

```
# Check that each rectangle is unique and only appears once in the data
# i.e. each rectangle is uniquely assigned to one area
length(unique(rectangles$Rectangle)) == nrow(rectangles)

## [1] TRUE
```

As an example, we show the rectangles that make up the ICES area 27.7.D area. The *Rectangle* column stores the ICES rectangles, the *Area* column stores the ICES area that contains the majority of that rectangle and the *Area\_List* column stores all of the ICES areas that feature that rectangle. Note that several rectangles actually feature in two areas (e.g. 27E8 has 7.d and 7.e in the *Area\_List* column). However, as mentioned above, each rectangle is allocated to a single area (the *Area* column) that contains the largest part of the rectangle.

```
subset(rectangles, Area=="27.7.D")[,c("Rectangle","Area","Area_List")]
```

##	Rectangle	Area	Area_List
## 3319	28E8	27.7.D	7.d, 7.e
## 3320	29E8	27.7.D	7.d, 7.e
## 3321	30E8	27.7.D	7.d, 7.e
## 3386	27E9	27.7.D	7.d
## 3387	28E9	27.7.D	7.d
## 3388	29E9	27.7.D	7.d
## 3389	30E9	27.7.D	7.d
## 3453	27F0	27.7.D	7.d
## 3454	28F0	27.7.D	7.d
## 3455	29F0	27.7.D	7.d
## 3456	30F0	27.7.D	7.d
## 3524	28F1	27.7.D	7.d
## 3525	29F1	27.7.D	7.d
## 3526	30F1	27.7.D	7.d
## 3595	30F2	27.7.D	7.d

### 3. ICES assessment data

#### 3.1 Compilation of the ICES dataset

Stock assessment data for all ICES stocks assessed in years 2013, 2014, 2015 and 2016 were extracted from <http://standardgraphs.ices.dk/stockList.aspx>. For stocks assessed in more than one of these years, only the most recent assessment was retained. In addition, the following stocks were removed:

- bss-47 assessed in 2014, because it was also assessed in 2016 as Bss-47.
- had-34 and had-scow assessed in 2013, because they were merged in 2016 (had-346a).
- her-irlw and her-vian assessed in 2014, because they were merged in 2016 (her-67bc).
- Nop-34-june assessed in 2014, because it was also assessed in 2016 as nop-34-oct.
- her-31 assessed in 2015, because it was also assessed in 2016 as Her-31.

Stock Category and EcoRegion were not included in the ICES dataset, so these were added manually after consulting ICES. Only stocks of Category 1-3 were relevant to the analysis, hence stocks of Categories 4-6 were identified and removed.

```
#file containing stock assessment data
stks<-read.csv('../data/ices/2017/ICES_stks_fromGraphs_17.02.csv', header=TRUE)
#remove stocks of category 4+
stks<-stks[!stks$FishStock%in% c("alf-comb","bli-oth","hom-nsea",
"nep-10","nep-34","rjh-7afg","bss-8c9a","bss-wosi","Nep-32","nep-33","nep-5",
"nep-oth-6a","nep-oth-7", "ory-comb","pan-flad","ple-7b-c","ple-89a","pol-89a",
"pol-nsea","raj-89a","raj-celt","rhg-nea","rjb-34","rjb-89a","rjc-echw",
"rje-ech","rjf-celt","rjh-4aVI","rjh-4c7d","rjh-7e","rji-celt","rng-1012",
"rng-kask","rng-oth","san-ns5","san-ns6","san-ns7","sbr-678","sbr-x",
"sol-7b-c","spr-celt","usk-mar","usk-rock","whg-89a"),]
stks$FishStock<-droplevels(stks$FishStock)
nlevels(stks$FishStock)#176 stocks retained

## [1] 176

#A file containing only FishStock, Category (1-3) and Ecoregion information
#was merged with the graphs dataset
stks2<-read.csv('../data/ices/2017/ICES_Cat&Eco.csv', header=TRUE)
stks3<-merge(stks,stks2,by="FishStock")
```

The polished ICES dataset contained 147 stocks assessed in 2016, 28 stocks assessed in 2015, and 1 stock assessed in 2014. 91 stocks were Category 1, 2 stocks were Category 2 and 83 stocks were Category 3.

```
stks16<-stks[stks$AssessmentYear == "2016",]
stks16$FishStock<-droplevels(stks16$FishStock)
nlevels(stks16$FishStock)

## [1] 147

stks15<-stks[stks$AssessmentYear == "2015",]
stks15$FishStock<-droplevels(stks15$FishStock)
nlevels(stks15$FishStock)

## [1] 28

stks14<-stks[stks$AssessmentYear == "2014",]
stks14$FishStock<-droplevels(stks14$FishStock)
nlevels(stks14$FishStock)
```

```

## [1] 1

stksc1<-stks3[stks3$Category == "1",]
stksc1$FishStock<-droplevels(stksc1$FishStock)
nlevels(stksc1$FishStock)

## [1] 91

stksc2<-stks3[stks3$Category == "2",]
stksc2$FishStock<-droplevels(stksc2$FishStock)
nlevels(stksc2$FishStock)

## [1] 2

stksc3<-stks3[stks3$Category == "3",]
stksc3$FishStock<-droplevels(stksc3$FishStock)
nlevels(stksc3$FishStock)

## [1] 83

#write.csv(stks3, "ICESstks_polished_v2.csv")

```

These data were compared with the respective data available at the online summary sheets to ensure consistency. Some data were found to be placed in wrong columns; i.e. some stock size, fishing pressure and reference points data were placed in custom columns, rather than their dedicated columns. These were manually added to the correct columns. Also, stock size and fishing pressure descriptions and their respective units were found to be wrong for many stocks. These were also manually corrected based on the information available at the online summary sheets.

A detailed description of the compilation process for the ICES assessment dataset, including a list of all the corrections carried out, can be found in the dedicated "Compilation of the ICES dataset" report.

## 3.2 Pre-processing of the ICES dataset

We load and tidy the assessment data.

```

library(reshape2)
ass <- read.csv("../data/ices/2017/ICESstks_polished_v2.csv",
  stringsAsFactors=FALSE)
# Check category column
cols <- c("FishStock","ICES.Areas..splited.with.character...." , "SpeciesName",
  "SGName", "Category", "EcoRegion")
ass <- ass[,cols]
colnames(ass)[colnames(ass) == "ICES.Areas..splited.with.character...."] <- "Areas"
# Drop duplicates
ass <- unique(ass)
# Remove white space and any capital letters from assessment name
ass[,"FishStock"] <- tolower(gsub("\\s", "", ass[,"FishStock"]))
# Make a species column from the assessment name
spp <- strsplit(ass[,"FishStock"], "-")
ass$Species <- toupper(unlist(lapply(spp, function(x) x[1])))
# Split ICES area by ~
areas <- strsplit(ass[,"Areas"], "~")
names(areas) <- ass[,"FishStock"]
areas <- melt(areas)
colnames(areas) <- c("Area", "FishStock")
big_ass <- merge(ass, areas)
big_ass <- big_ass[,c("FishStock","Area", "Species", "SpeciesName", "SGName",
  "Category", "EcoRegion")]
big_ass[,"Area"] <- toupper(gsub("\\s", "", big_ass[,"Area"]))

```

It should be noted that the same ICES area can feature in multiple assessments of the same species. For example, the ICES area 27.4.B appears in several different species SAN (sandeel) assessments.

```
subset(big_ass, Area == "27.4.B" & Species == "SAN")[,c("FishStock","Area")]  
  
##      FishStock Area  
## 925   san-ns1 27.4.B  
## 927   san-ns2 27.4.B  
## 931   san-ns3 27.4.B  
## 933   san-ns4 27.4.B
```

The stock assessments are attributed to an ecoregion:

```
unique(big_ass$EcoRegion)  
  
## [1] "Bay of Biscay and the Iberian Coast"  
## [2] "Iceland Sea and Greenland Sea"  
## [3] "Widely distributed"  
## [4] "Baltic Sea"  
## [5] "Greater North Sea"  
## [6] "Barents Sea and Norwegian Sea"  
## [7] "Celtic Seas"  
## [8] "Faroes"  
## [9] "Azores"
```

We need to remove stock assessments that are in areas outside of the EU:

```
big_ass <- subset(big_ass, !(EcoRegion %in% c("Iceland Sea and Greenland Sea",  
      "Barents Sea and Norwegian Sea", "Faroes")))
```

We also remove *her-noss* which is a widely distributed species:

```
big_ass <- subset(big_ass, FishStock!="her-noss")
```

We remove category 3 stocks (but make a copy first):

```
big_ass3 <- big_ass  
big_ass <- subset(big_ass, Category != 3)
```

## 4. The TAC sampling frame

We load the already created sampling frame data.

```
load("../..neaSampFrame/report/sframe.RData")
# fmz is the frame of all TACs
# For consistency
colnames(fmz)[colnames(fmz) == "area"] <- "Area"
colnames(fmz)[colnames(fmz) == "spp"] <- "Species"
colnames(fmz)[colnames(fmz) == "stock_id"] <- "TAC_id"
```

We subset the sampling frame TACs from the FMZ file

```
sframe <- subset(fmz, TAC_id %in% sframe_TAC)
```

Each FMZ area can exist over multiple ICES areas. These constituent ICES areas can be of different scales e.g. ICES division, subdivision or subunit. To merge with the ICES rectangles we want the smallest scale possible for each constituent area. This is contained in the *Area* column.

For example, the two ICES areas that make up the stock code *PLE/7DE* (plaice in the English Channel) can be seen here. The smallest scale for the areas is the ICES division.

```
subset(sframe, TAC_id=="PLE/7DE.")[, c("TAC_id","fmz_id","f_subarea","f_division",
  "f_subdivis","f_subunit","Area")]
```

##	TAC_id	fmz_id	f_subarea	f_division	f_subdivis	f_subunit	Area
##	1162	PLE/7DE.	27000489	27.7	27.7.E	<NA>	<NA> 27.7.E
##	1164	PLE/7DE.	27000489	27.7	27.7.D	<NA>	<NA> 27.7.D

Given their different spatial characteristics, the same ICES area can feature in multiple FMZ areas, even for the same species. For example, the area *27.2.A.2* features in many different FMZs including 3 MAC FMZs.

```
# Area appears in multiple TACs
unique(subset(sframe, Area=="27.2.A.2")$TAC_id)
```

##	[1]	"MAC/2A34."	"POK/2A34."	"MAC/2A4A-N"	"MAC/2CX14-"	"HER/2A47DX"
##	[6]	"D/F/2AC4-C"	"T/B/2AC4-C"	"ANF/2AC4-C"	"DGS/2AC4-C"	"SPR/2AC4-C"
##	[11]	"SOL/24-C."	"PRA/2AC4-C"	"L/W/2AC4-C"	"LEZ/2AC4-C"	"SRX/2AC4-C"
##	[16]	"NEP/2AC4-C"	"HKE/2AC4-C"	"WHG/2AC4."	"HAD/2AC4."	"WHB/24A567"
##	[21]	"COD/2A3AX4"	"PLE/2A3AX4"	"WHB/24-N."	"OTH/2A46AN"	"WHB/2A4AXF"
##	[26]	"WHB/1X14"	"GHL/2A-C46"	"GFB/1234-"	"BSF/1234-"	"BLI/24-"
##	[31]	"RTX/124-"	"SAN/2A3A4."	"NOP/2A3A4."	"ORY/1CX14"	"JAX/2A-14"

```
# And for same the species, e.g. MAC
subset(sframe, Area=="27.2.A.2" & Species=="MAC")[, c("TAC_id","fmz_id","f_subarea",
  "f_division", "f_subdivis","f_subunit","Area")]
```

##	TAC_id	fmz_id	f_subarea	f_division	f_subdivis	f_subunit	Area
##	260	MAC/2A34.	27000014	27.2	27.2.A	27.2.A.2	<NA> 27.2.A.2
##	289	MAC/2A4A-N	27000021	27.2	27.2.A	27.2.A.2	<NA> 27.2.A.2
##	321	MAC/2CX14-	27000038	27.2	27.2.A	27.2.A.2	<NA> 27.2.A.2

Each ICES area should only appear once for each FMZ stock (to prevent the appearance of duplicate rectangles when merging with the ICES rectangle data later). We check this here:

```
library(plyr)
unarea <- dapply(sframe, .(TAC_id), function(x){
  return(length(unique(x$Area))==nrow(x))
})
all(unarea)
```

##	[1]	TRUE
----	-----	------

## 5. Pre-merge checks

Before the sampling frame can be matched to the ICES assesment data it is necessary to check that the species and area codes are consistent between the data sets.

### 5.1 Checking the areas

It is necessary that the areas in the ICES assessment data, the TAC sampling frame and the ICES rectangles data set have common names. Unfortunately, this is not the case:

```
# Areas in ICES assesment but missing in rectangles
unique(big_ass$Area)[!(unique(big_ass$Area) %in% unique(rectangles$Area))]

## [1] "27.3.A" "21.1" "21.2"

# Areas in FMZ but missing in rectangles
unique(sframe$Area)[!(unique(sframe$Area) %in% unique(rectangles$Area))]

## [1] "27.3.23" "27.3.22" "27.3.A" "21.1.F" "21.3.M" "34.1.2" "34.1.13"
## [8] "34.1.11" "34.1.12" "34.2"
```

The areas *21.x* and *34.x* are from FMZs that have ICES areas in area 27 as well either area 21 and area 34. The rectangles data only includes FAO Area 27. This means that areas *21.x* and *34.x* will be dropped when merging later (just the areas, not the TACs).

#### 5.1.1 Area 27.3.A

The area *27.3.A.X* is reported differently in the data sets. The different ways the areas are reported can be seen here:

```
# In the ICES rectangles data
rect273A <- sort(unique(rectangles[grepl("27.3.A", rectangles$Area), "Area"]))
rect273A

## [1] "27.3.A.20" "27.3.A.21"

# In the ICES assesment data
ices273A <- sort(unique(big_ass[grepl("27.3.A", big_ass$Area), "Area"]))
ices273A

## [1] "27.3.A"

# In the FMZ assesment data
sf273A <- sort(unique(sframe[grepl("27.3.A", sframe$Area), "Area"]))
sf273A

## [1] "27.3.A"
```

The areas *27.3.A.20* and *27.3.A.21* are the Skagerrak and Kattegat respectively. Together they make up *27.3.A*. They each have different constituent rectangles.

```
# 27.3.A.20 has different ICES rectangles to 27.3.A.21
subset(rectangles, Area=="27.3.A.20")$Rectangle

## [1] "44F7" "45F7" "43F8" "44F8" "45F8" "46F8" "43F9" "44F9" "45F9" "46F9"
## [11] "47F9" "48F9" "44G0" "45G0" "46G0" "47G0" "48G0" "44G1" "45G1" "46G1"
## [21] "47G1" "44G2"

subset(rectangles, Area=="27.3.A.21")$Rectangle

## [1] "42G0" "43G0" "41G1" "42G1" "43G1" "41G2" "42G2" "43G2"
```

The two areas are reported as a single area, *27.3.A*, in the ICES assessment data and TAC sampling frame. This means that the two areas can be combined in the ICES rectangles data to give a single area that contains all of the rectangles. We do this by renaming them.

```
rectangles[rectangles$Area == "27.3.A.20","Area"] <- "27.3.A"
rectangles[rectangles$Area == "27.3.A.21","Area"] <- "27.3.A"
```

### 5.1.2 Area 27.3.22

The areas 27.3.C.22 and 27.3.B.23 in the ICES rectangles and assessment data sets are reported as 27.3.22 and 27.3.23 in the TAC sampling frame. This is straightforward to fix by renaming the areas in all data sets to 27.3.C and 27.3.B.

```
rectangles[rectangles$Area == "27.3.B.23","Area"] <- "27.3.B"
rectangles[rectangles$Area == "27.3.C.22","Area"] <- "27.3.C"
big_ass[big_ass$Area == "27.3.B.23","Area"] <- "27.3.B"
big_ass[big_ass$Area == "27.3.C.22","Area"] <- "27.3.C"
sframe[sframe$Area == "27.3.23","Area"] <- "27.3.B"
sframe[sframe$Area == "27.3.22","Area"] <- "27.3.C"
```

We run the area check again.

```
# Areas in ICES assessment but missing in rectangles
unique(big_ass$Area)[!(unique(big_ass$Area) %in% unique(rectangles$Area))]
## [1] "21.1" "21.2"

# Areas in FMZ but missing in rectangles
unique(sframe$Area)[!(unique(sframe$Area) %in% unique(rectangles$Area))]
## [1] "21.1.F" "21.3.M" "34.1.2" "34.1.13" "34.1.11" "34.1.12" "34.2"
```

Only areas 21 and 34 remain which is OK.

## 5.2 Checking the species codes

Later in the analysis we merge the TAC sampling frame data and the ICES assessment data by species code and ICES rectangle. It is necessary for the assessment data and the TAC sampling frame to have a common set of species codes. Where species exist on one data set but not in the other it is necessary to understand why.

### 5.2.1 ICES assessment species not found in the sampling frame

Here we check which species that feature in the assessment data that do not feature in the TAC data.

```
# Assessment species not found in SF
sp_no_tac <- sort(unique(big_ass$Species)[!(unique(big_ass$Species) %in%
  unique(sframe$Species))])
sp_no_tac
## [1] "ANB" "ANP" "BSS" "HOM" "MEG" "MGB" "MGW" "PAN" "RNG" "SAI" "SAR"
## [12] "SMN"
```

There are several reasons why a species code in the ICES assessment data is not found in the sampling frame:

- The assessed species has a TAC but has different names in the data sets;
- The assessed *species* does not have a TAC but the *genus* does have a TAC;
- The assessed species is a special condition subspecies of a parent TAC in the full TAC definitions table (special conditions have been dropped from the sampling frame);
- The assessed species does not have a TAC or has a TAC outside of the areas of interest.

In the first case, the species codes used in the data sets are different. These include boarfish, horse mackerel, Northern shrimp and saithe. This can be fixed by changing the species code in the ICES assessment data set.

```
# Horse mackerel
big_ass[big_ass$Species=="HOM", "Species"] <- "JAX"
# Northern shrimp
big_ass[big_ass$Species=="PAN", "Species"] <- "PRA"
# Saithe
big_ass[big_ass$Species=="SAI", "Species"] <- "POK"
# Update missing species
sp_no_fmz <- sort(unique(big_ass$Species)[!(unique(big_ass$Species) %in%
  unique(sframe$Species))])
sp_no_fmz

## [1] "ANB" "ANP" "BSS" "MEG" "MGB" "MGW" "RNG" "SAR" "SMN"
```

In the second case, the species codes used in the TAC sampling frame set are at the genus level, not the species level. These include anglerfish, megrim and red fish. The species codes in the assessment data set are changed to the genus code used by the sampling frame.

```
# ANB, ANP - Anglerfish - species to genus
big_ass[big_ass$Species=="ANB", "Species"] <- "ANF" # black bellied anglerfish
big_ass[big_ass$Species=="ANP", "Species"] <- "ANF" # white anglerfish
# Megrim - species and genus to genus
big_ass[big_ass$Species=="MEG", "Species"] <- "LEZ" # sp.
big_ass[big_ass$Species=="MGB", "Species"] <- "LEZ" # 4 spot
big_ass[big_ass$Species=="MGW", "Species"] <- "LEZ" # whiff.
# Golden redfish - species to genus (Sebastes Species.)
big_ass[big_ass$Species=="SMR", "Species"] <- "RED" # Sebastes norvegicus
big_ass[big_ass$Species=="SMN", "Species"] <- "RED" # Sebastes mentella
# Update missing species
sp_no_fmz <- sort(unique(big_ass$Species)[!(unique(big_ass$Species) %in%
  unique(sframe$Species))])
sp_no_fmz

## [1] "BSS" "RED" "RNG" "SAR"

#unique(subset(big_ass, Species %in% sp_no_fmz)[,c("Species", "SpeciesName")])
```

The third case, with special conditions, needs closer inspection. The species in question is roundnose grenadier, *RNG*. In the TAC definitions, *RNG* features as a main stock outside of the areas of interest (in *REG-NAFO* and *REG-NEAFC*) and as a subspecies special condition of the parent stock *RTX* in the areas of interest. The parent stock *RTX* is a combination of *RNG* and *RHG* species.

```
unique(subset(speccond, Main.Stock.Species.Code == "RTX")[,c("Species.Code")])

## [1] "RHG" "RNG"
```

This means that the *RTX* TAC is at least partially assessed through the assessment for the subspecies *RNG*. To account for this we change the name of *RNG* in the assessment data to *RTX*.

```
big_ass[big_ass$Species=="RNG", "Species"] <- "RTX"
# Update missing species
sp_no_fmz <- sort(unique(big_ass$Species)[!(unique(big_ass$Species) %in%
  unique(sframe$Species))])
sp_no_fmz

## [1] "BSS" "RED" "SAR"
```

Some species do exist in the full list of TACs but not in the areas or groups that we are interested in. Here, redfish (*RED*, the genus, not a species, that was corrected above) does not feature in the ICES areas III, IV, VI, VII, VIII and IX and so has been dropped from the sampling frame.

```
unique(subset(fmz, Species=="RED")[,c("Species","f_subarea")])

##      Species f_subarea
##  92      RED      <NA>
## 1461     RED      27.1
## 1467     RED      27.2
## 1506     RED      27.5
## 2709     RED      27.12
## 2711     RED      27.14

# NA in f_subarea means that it is not in Area 27
```

Finally, there are some assessed species that do not feature at all in the list of TAC FMZs. These include sea bass (*BSS*) and sardine (*SAR*, although the code *PIL* is used by the EC).

### 5.2.2 Sampling frame species not found in the ICES assessments

We also need to know what species we have in the sampling frame that do not feature in the assessment:

```
sp_no_ass <- sort(unique(sframe$Species)[!(unique(sframe$Species) %in%
  unique(big_ass$Species))])
sp_no_ass

## [1] "ALF" "ARU" "BOR" "BSF" "D" "DWS" "GFB" "GHL" "L" "LIN" "ORY"
## [12] "OTH" "POL" "SBR" "SOO" "SRX" "T" "USK"
```

*OTH* is other species. There is no assessment for this.

*D*, *L* and *T* are from grouped TACs (the codes come from the code manipulation performed earlier). The species code *D* is actually *D/F*, a grouped TAC of dab and flounder (for example, *DAB/2AC4-C* and *FLE/2AC4-C*). Individually, they are special conditions.

```
speccond[grepl("D/F", speccond$main_TAC_id),c("main_TAC_id","TAC_id")]

##   main_TAC_id   TAC_id
## 36 D/F/2AC4-C DAB/2AC4-C
## 37 D/F/2AC4-C FLE/2AC4-C
```

We need to include the assessments of individual stocks that make up the grouped TACs. However, here these stocks are category 3 and are not considered when matching with the stock assessment data:

```
unique(subset(big_ass3, Species=="FLE")[,c("FishStock","Species","Category")])

##   FishStock Species Category
## 350 fle-2223     FLE         3
## 352 fle-2425     FLE         3
## 354 fle-2628     FLE         3
## 356 fle-2732     FLE         3

unique(subset(big_ass3, Species=="DAB")[,c("FishStock","Species","Category")])

##   FishStock Species Category
## 269 dab-2232     DAB         3
## 281 dab-nsea     DAB         3
```

Similarly, *L* is actually, *L/W*, a grouped TAC of lemon sole and witch flounder with the individual TACs being special conditions:

```
speccond[grepl("L/W", speccond$main_TAC_id),c("main_TAC_id","TAC_id")]
##      main_TAC_id      TAC_id
## 88   L/W/2AC4-C LEM/2AC4-C
## 278  L/W/2AC4-C WIT/2AC4-C
```

Again, these stocks are category 3:

```
unique(subset(big_ass3, Species=="LEM"),c("FishStock","Species","Category"))
##      FishStock Species Category
## 583  lem-nsea     LEM          3

unique(subset(big_ass3, Species=="WIT"),c("FishStock","Species","Category"))
##      FishStock Species Category
## 1282 wit-nsea     WIT          3
```

Finally, *T* is turbot which has a joint TAC with brill.

```
speccond[grepl("T/B", speccond$main_TAC_id),c("main_TAC_id","TAC_id")]
##      main_TAC_id      TAC_id
## 11   T/B/2AC4-C BLL/2AC4-C
## 268  T/B/2AC4-C TUR/2AC4-C
```

These stocks are also category 3:

```
unique(subset(big_ass3, Species=="TUR"),c("FishStock","Species","Category"))
##      FishStock Species Category
## 1143  tur-2232     TUR          3
## 1155  tur-kask     TUR          3
## 1156  tur-nsea     TUR          3

unique(subset(big_ass3, Species=="BLL"),c("FishStock","Species","Category"))
##      FishStock Species Category
## 108   bll-2232     BLL          3
## 120   bll-nsea     BLL          3
```

Of the other species, *BOR* (boarfish, *BOC* in the assessment data), *ARU* (Greater silver smelt, *ARG* in the assessment data), *BSF* (black scabbard fish), *USK* (tusk), *LIN* (tusk), and *GFB* (greater forkbeard) are category 3 stocks and are therefore not considered when matching the data.

Some of the other species are stocks that are less than category 3 and so do not feature in the assessment data that was read in above: *ALF* (Alfonsinus nei) is category 5, *ORY* (orange roughy) is category 6, *POL* (pollack) has categories 4 and 5, depending on the stock, and *SBR* (Blackspot(=red) seabream) has categories 3 and 6, depending on the stock (all categories are according to advice sheets on the ICES website).

```
unique(subset(big_ass3, Species %in% c("ARG","BOC", "BSF", "GFB", "LIN", "SBR",
  "USK")),c("FishStock","Species","Category"))
##      FishStock Species Category
## 50   arg-rest     ARG          3
## 126   boc-nea     BOC          3
## 148   bsf-nea     BSF          3
## 361   gfb-comb    GFB          3
## 599   lin-oth     LIN          3
## 936   sbr-ix      SBR          3
## 1170  usk-oth     USK          3
```

```
unique(subset(big_ass3, Species %in% c("ALF", "ORY", "POL", "SBR"))[,c("FishStock",
  "Species", "Category")])

##      FishStock Species Category
## 936      sbr-ix      SBR         3
```

*GHL* (Greenland halibut) is covered by two assessments (*ghl-grn* and *ghl-arct*). However, both of these assessments have been dropped through the Ecoregion subsetting above. This means that there is no assessment for *GHL*.

```
subset(ass, Species=="GHL")[,c("Species", "FishStock", "EcoRegion")]

##      Species FishStock          EcoRegion
## 1785      GHL  ghl-arct Barents Sea and Norwegian Sea
## 1808      GHL  ghl-grn Iceland Sea and Greenland Sea
```

*DWS* is a grouped TAC of deep-water sharks. There is no assessment of these species. There are also no subspecies special conditions of this TAC.

```
subset(stockdef, Species.Code == "DWS")[,c("Species.Code", "TAC_id", "Species.Name")]

##      Species.Code      TAC_id      Species.Name
## 117              DWS  DWS/10- Deep-water sharks nei
## 118              DWS  DWS/12INT- Deep-water sharks nei
## 119              DWS  DWS/56789- Deep-water sharks nei
```

*SRX* is a grouped TAC of skates and rays (*Rajiformes*). It is a parent TAC of several special condition subspecies TACs. The individual species are: *RJC* (thornback ray), *RJE* (small-eyed ray), *RJF* (shagreen ray), *RJH* (blonde ray), *RJI* (sandy ray), *RJM* (spotted ray), *RJN* (cuckoo ray) and *RJU* (undulate ray).

```
srxsp <- unique(speccond[grep("SRX", speccond$main_TAC_id)], $Species.Code)
srxsp

## [1] "RJC" "RJE" "RJF" "RJH" "RJI" "RJM" "RJN" "RJU"
```

Of these, stocks of *RJC*, *RJE*, *RJH*, *RJM*, *RJN*, *RJU* are category 3. *RJF* and *RJI* are category 5, according to the ICES advice sheets.

```
unique(subset(big_ass3, Species %in% srxsp)[,c("FishStock", "Species", "Category")])

##      FishStock Species Category
## 805      rjc-347d      RJC         3
## 810      rjc-7afg      RJC         3
## 813      rjc-bisc      RJC         3
## 820      rjc-pore      RJC         3
## 821      rjc-vi        RJC         3
## 824      rje-7fg       RJE         3
## 826      rjh-pore      RJH         3
## 827      rjm-347d      RJM         3
## 832      rjm-67bj      RJM         3
## 838      rjm-7aeh      RJM         3
## 843      rjm-bisc      RJM         3
## 850      rjm-pore      RJM         3
## 851      rjn-34        RJN         3
## 855      rjn-678abd    RJN         3
## 875      rjn-8c        RJN         3
## 876      rjn-pore      RJN         3
## 885      rju-ech       RJU         3
```

*SOO* is *Solea spp.* This only features in one TAC:

```
subset(stockdef, Species.Code=="S00")[,c("Species.Code","TAC_id","Species.Name")] # Solea spp
##      Species.Code      TAC_id Species.Name
## 586          S00 S00/8CDE34      Solea spp
```

We have assessments for *solea solea* (*SOL*) which may contribute to this TAC. Therefore we change the species code in the sampling frame (not the TAC id code) to *SOL* to ensure we match correctly. We cannot change the name in the assessment data to *S00* (as we did above) as there are TACs with that are specifically *SOL*.

```
sframe[sframe$Species=="S00","Species"] <- "SOL"
```

In summary, we have confirmed that the species codes (grouped TACs etc) in the sampling frame that appear to have no assessments, do not have assessments.

## 6. Merging

### 6.1 Merging the ICES assessment with the ICES rectangles

We merge the assessment data with the ICES rectangles data. Each area in the assessment data is exploded into its constituent rectangles.

```
ass_rect <- merge(big_ass, rectangles[,c("Area", "Rectangle")], by="Area")
```

Do we have all the assessments?

```
all(sort(unique(big_ass$FishStock)) == sort(unique(ass_rect$FishStock)))  
## [1] TRUE
```

As some assessments overlap in area, it is possible for a species and rectangle to have multiple assessments:

```
any(duplicated(ass_rect[,c("Species", "Rectangle")]))  
## [1] TRUE
```

### 6.2 Merging the sampling frame with the ICES rectangles

We do the same for the TAC FMZ sampling frame:

```
sf_rect <- merge(sframe, rectangles[,c("Area", "Rectangle")], by="Area")
```

Do we have all the TACs?

```
all(sort(unique(sframe$TAC_id)) == sort(unique(sf_rect$TAC_id)))  
## [1] TRUE
```

### 6.3 Merging the sampling frame with the assessment data

Here we bring the assessment data into the sampling frame. We merge by species and rectangle. We want to keep the species the TAC FMZ sampling frame that do not have an assessment. A species and rectangle in the TAC FMZ sampling frame may have more than 1 assessment.

We also perform a second merge which keeps all of the ICES assessments, as well as the TACs.

```
# Keep all TACs  
sf_ass <- merge(sf_rect, ass_rect[,c("Species", "Rectangle", "FishStock", "Category")],  
  by=c("Species", "Rectangle"), all.x = TRUE)  
# Keep all assessments and TACs  
all_sf_ass <- merge(sf_rect, ass_rect[,c("Species", "Rectangle", "FishStock",  
  "Category")], by=c("Species", "Rectangle"), all = TRUE)
```

Do we have all the TACs and assessments?

```
all(sort(unique(sframe$TAC_id)) == sort(unique(sf_ass$TAC_id)))  
## [1] TRUE  
  
all(sort(unique(big_ass$FishStock)) == sort(unique(all_sf_ass$FishStock)))  
## [1] TRUE
```

We know that in the TAC data, anglerfish is referred to by genus (*ANF*) whereas in the assessment data it is referred to by two species (*ANB* and *ANP*). Here we check that both assessments have been included: We can see that in some areas (27.8.C and 27.9.A) both assessments for anglerfish have been matched to the anglerfish TAC and that in some areas there is no corresponding assessment.

```
anf <- subset(all_sf_ass, TAC_id=="ANF/8C3411")
# What assessments
unique(anf$FishStock)

## [1] NA          "anb-8c9a" "anp-8c9a"

# Assessments by area
table(anf$FishStock, anf$f_division)

##
##          27.10.A 27.10.B 27.8.C 27.9.A 27.9.B
##  anb-8c9a      0      0     26    49     0
##  anp-8c9a      0      0     26    49     0
```

Some assessments do not match any TACs. For example, the assessment of sea bass:

```
unique(subset(all_sf_ass, Species=="BSS")[,c("Species", "TAC_id", "FishStock")])

##      Species TAC_id FishStock
## 16990     BSS  <NA>     bss-47
```

## 7. Analysis

Here we investigate which TACs have at least one constituent ICES rectangle that features in an ICES assessment.

```

dat <- ddply(sf_ass, .(TAC_id), function(x) {
  ass <- any(!is.na(x$FishStock))
  if (ass){
    asses <- unique(x[!is.na(x$FishStock),"FishStock"])
    nass <- length(asses)
    ass_names <- paste(asses, collapse = ", ")
  }
  else {
    ass <- FALSE
    nass <- 0
    ass_names <- NA
  }
  out <- data.frame(TAC_id = unique(x$TAC_id),
                    ass = ass,
                    nass = nass,
                    ass_names = ass_names,
                    stringsAsFactors=FALSE)
  return(out)
})

# Check all TACs are present
all(unique(sf_ass$TAC_id) %in% unique(dat$TAC_id))

## [1] TRUE

# No of TACs
dim(dat)[1]

## [1] 156

# No of TACs with assessment
sum(dat$ass)

## [1] 85

# No if TACs with no assessment
sum(!dat$ass)

## [1] 71

# Proportion assessed
sum(dat$ass) / dim(dat)[1]

## [1] 0.5448718

```

	TAC	Assessed	No. assess.	ICES assessments
1	ALF/3X14-	FALSE	0	
2	ANE/08.	TRUE	1	ane-bisc
3	ANE/9/3411	FALSE	0	
4	ANF/07.	FALSE	0	
5	ANF/2AC4-C	FALSE	0	
6	ANF/56-14	FALSE	0	
7	ANF/8ABDE.	FALSE	0	
8	ANF/8C3411	TRUE	2	anb-8c9a, anp-8c9a
9	ARU/34-C	FALSE	0	
10	ARU/567.	FALSE	0	
11	BLI/03-	FALSE	0	

12	BLI/24-	FALSE	0	
13	BLI/5B67-	TRUE	1	bli-5b67
14	BOR/678-	FALSE	0	
15	BSF/1234-	FALSE	0	
16	BSF/56712-	FALSE	0	
17	BSF/8910-	FALSE	0	
18	COD/03AN.	TRUE	1	cod-347d
19	COD/03AS.	TRUE	1	cod-347d
20	COD/07A.	TRUE	1	cod-iris
21	COD/07D.	TRUE	1	cod-347d
22	COD/2A3AX4	TRUE	1	cod-347d
23	COD/3BC+24	TRUE	1	cod-2224
24	COD/3DX32.	FALSE	0	
25	COD/5BE6A	TRUE	1	cod-scow
26	COD/5W6-14	FALSE	0	
27	COD/7XAD34	TRUE	2	cod-7e-k, cod-347d
28	D/F/2AC4-C	FALSE	0	
29	DGS/03A-C.	TRUE	1	dgs-nea
30	DGS/15X14	TRUE	1	dgs-nea
31	DGS/2AC4-C	TRUE	1	dgs-nea
32	DWS/56789-	FALSE	0	
33	GFB/1234-	FALSE	0	
34	GFB/567-	FALSE	0	
35	GFB/89-	FALSE	0	
36	GHL/2A-C46	FALSE	0	
37	HAD/07A.	FALSE	0	
38	HAD/2AC4.	TRUE	1	had-346a
39	HAD/3A/BCD	TRUE	1	had-346a
40	HAD/5BC6A.	TRUE	1	had-346a
41	HAD/6B1214	TRUE	1	had-rock
42	HAD/7X7A34	TRUE	1	had-7b-k
43	HER/03A.	TRUE	2	her-3a22, her-47d3
44	HER/03A-BC	TRUE	2	her-3a22, her-47d3
45	HER/03D.RG	TRUE	1	her-riga
46	HER/06ACL.	TRUE	1	her-67bc
47	HER/07A/MM	TRUE	2	her-irls, her-nirs
48	HER/2A47DX	TRUE	1	her-47d3
49	HER/30/31.	TRUE	1	her-30
50	HER/3BC+24	TRUE	1	her-3a22
51	HER/3D-R30	TRUE	1	her-2532-gor
52	HER/4AB.	TRUE	1	her-47d3
53	HER/4CXB7D	TRUE	1	her-47d3
54	HER/5B6ANB	TRUE	1	her-67bc
55	HER/6AS7BC	TRUE	1	her-67bc
56	HER/7EF.	FALSE	0	
57	HER/7G-K.	TRUE	2	her-irls, her-nirs
58	HKE/2AC4-C	TRUE	1	hke-nrtn
59	HKE/3A/BCD	TRUE	1	hke-nrtn
60	HKE/571214	TRUE	1	hke-nrtn
61	HKE/8ABDE.	TRUE	1	hke-nrtn
62	HKE/8C3411	TRUE	1	hke-soth
63	JAX/08C.	TRUE	1	hom-west
64	JAX/09.	TRUE	1	hom-soth
65	JAX/2A-14	TRUE	1	hom-west
66	JAX/4BC7D	FALSE	0	
67	LEZ/07.	TRUE	1	mgw-78
68	LEZ/2AC4-C	TRUE	1	meg-4a6a
69	LEZ/56-14	TRUE	1	meg-4a6a
70	LEZ/8ABDE.	TRUE	1	mgw-78
71	LEZ/8C3411	TRUE	2	mgb-8c9a, mgw-8c9a
72	LIN/04-C.	FALSE	0	

73	LIN/3A/BCD	FALSE	0	
74	LIN/6X14.	FALSE	0	
75	L/W/2AC4-C	FALSE	0	
76	MAC/2A34.	TRUE	1	mac-nea
77	MAC/2A4A-N	TRUE	1	mac-nea
78	MAC/2CX14-	TRUE	1	mac-nea
79	MAC/8C3411	TRUE	1	mac-nea
80	NEP/07.	TRUE	7	nep-16, nep-19, nep-2021, nep-22, nep-14, nep-15, nep-
81	NEP/08C.	FALSE	0	
82	NEP/2AC4-C	TRUE	4	nep-8, nep-6, nep-7, nep-9
83	NEP/3A/BCD	TRUE	1	nep-3-4
84	NEP/5BC6.	TRUE	3	nep-12, nep-13, nep-11
85	NEP/8ABDE.	TRUE	1	nep-2324
86	NEP/9/3411	FALSE	0	
87	NOP/2A3A4.	TRUE	1	nop-34-oct
88	ORY/06-	FALSE	0	
89	ORY/07-	FALSE	0	
90	ORY/1CX14	FALSE	0	
91	OTH/2A46AN	FALSE	0	
92	OTH/5B67-C	FALSE	0	
93	PLE/03AN.	TRUE	2	ple-nsea, ple-2123
94	PLE/03AS.	TRUE	1	ple-2123
95	PLE/07A.	FALSE	0	
96	PLE/2A3AX4	TRUE	2	ple-nsea, ple-2123
97	PLE/3BCD-C	TRUE	1	ple-2123
98	PLE/56-14	FALSE	0	
99	PLE/7BC.	FALSE	0	
100	PLE/7DE.	TRUE	1	ple-eche
101	PLE/7FG.	FALSE	0	
102	PLE/7HJK.	FALSE	0	
103	PLE/8/3411	FALSE	0	
104	POK/2A34.	TRUE	1	sai-3a46
105	POK/56-14	TRUE	1	sai-3a46
106	POK/7/3411	FALSE	0	
107	POL/07.	FALSE	0	
108	POL/08C.	FALSE	0	
109	POL/56-14	FALSE	0	
110	POL/8ABDE.	FALSE	0	
111	POL/9/3411	FALSE	0	
112	PRA/03A.	TRUE	1	pan-sknd
113	PRA/2AC4-C	TRUE	1	pan-sknd
114	RTX/03-	FALSE	0	
115	RTX/124-	FALSE	0	
116	RTX/5B67-	TRUE	1	rng-5b67
117	RTX/8X14-	TRUE	1	rng-5b67
118	SAN/2A3A4.	TRUE	3	san-ns2, san-ns1, san-ns3
119	SBR/09-	FALSE	0	
120	SBR/678-	FALSE	0	
121	SOL/07A.	TRUE	1	sol-iris
122	SOL/07D.	TRUE	1	sol-eche
123	SOL/07E.	TRUE	1	sol-echw
124	SOL/24-C.	TRUE	1	sol-nsea
125	SOL/3A/BCD	TRUE	1	sol-kask
126	SOL/56-14	FALSE	0	
127	SOL/7BC.	FALSE	0	
128	SOL/7FG.	TRUE	1	sol-celt
129	SOL/7HJK.	FALSE	0	
130	SOL/8AB.	TRUE	1	sol-bisc
131	SOO/8CDE34	FALSE	0	
132	SPR/03A.	FALSE	0	
133	SPR/2AC4-C	TRUE	1	spr-nsea

134	SPR/3BCD-C	TRUE	1	spr-2232
135	SPR/7DE.	FALSE	0	
136	SRX/03A-C.	FALSE	0	
137	SRX/07D.	FALSE	0	
138	SRX/2AC4-C	FALSE	0	
139	SRX/67AKXD	FALSE	0	
140	SRX/89-C.	FALSE	0	
141	T/B/2AC4-C	FALSE	0	
142	USK/04-C.	FALSE	0	
143	USK/3A/BCD	FALSE	0	
144	USK/567EI.	FALSE	0	
145	WHB/1X14	TRUE	1	whb-comb
146	WHB/24A567	TRUE	1	whb-comb
147	WHB/24-N.	TRUE	1	whb-comb
148	WHB/2A4AXF	TRUE	1	whb-comb
149	WHB/8C3411	TRUE	1	whb-comb
150	WHG/03A.	FALSE	0	
151	WHG/07A.	FALSE	0	
152	WHG/08.	FALSE	0	
153	WHG/2AC4.	TRUE	1	whg-47d
154	WHG/56-14	TRUE	1	whg-scow
155	WHG/7X7A-C	TRUE	2	whg-7e-k, whg-47d
156	WHG/9/3411	FALSE	0	

**Table 1:** TACs and the associated ICES assessments

## 8. Differences in stocks with last years analysis

Several stocks are included in this analysis that were not included in the 2016 analysis. *dgs-nea*, *mgw-78*, *nep-2021* and *nep-2324* only became category 1 or 2 in 2016 and so were excluded from the analysis last year. *rng-5b67* was not considered last year as the TACs it is linked to are subspecies special conditions of RTX/5B67 and RTX/8X14. *ane-bisc*, *whg-47d* and *whg-scow* did not have reference points in 2015.

Only one stocks was included in 2016 that is not included in 2017: Herring in Division VIa North, *her-vian*. This stock has now been combined with Division VIa South and VII.b-c.

## **9. Conclusions**

In this document the CFP indicators sampling frame for FAO area 27 (Northeast Atlantic) was matched to the corresponding ICES assessments. The matching was performed through the ICES rectangles that make up the FMZs and stock assessment areas.

## References

Scott, F., Gibin, M. and Jardim, E., 'Generating the CFP indicators sampling frame for fao area 27 (northeast atlantic', Tech. Rep. JRCxxxxxx, Joint Research Centre, Via Enrico Fermi 2749, Ispra, VA, Italy, 2017.

## **List of abbreviations and definitions**

**CFP** Common Fisheries Policy

**FAO** Food and Agriculture Organisation of the United Nations

**FMZ** Fisheries Management Zones

**ICES** International Council for the Exploration of the Sea

**TAC** Total Allowable Catch

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