

Annex II - STREAM: Auxiliary scripts for the conversion from DG MARE Med&BS format to GFCM/DCRF format

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Tools

R, Rstudio and packages.

```
#R general option:

#chunk option
knitr::opts_chunk$set(cache=TRUE,echo=TRUE, warning=FALSE,
  message=FALSE, fig.height=6,progress=FALSE,verbose=FALSE,
  include=TRUE,dev='png',autodep=FALSE)

#Load packages
library(reshape2)
library(reshape)
library(dplyr)
library(knitr)
library(pander)

#pander options
panderOptions('table.split.table', 60)
panderOptions('table.style', 'grid')
panderOptions('table.split.cells', 10)
panderOptions('table.alignment.default', 'left')
panderOptions('table.alignment.rownames', 'right')
panderOptions('decimal.mark', ',')
panderOptions('graph.fontsize', '10')
```

script 01: Table II.2

This script allow to convert the DG MARE Med&BS A_Catch table into the GFCM/DCRF Table II.2 (Catch data per species) using the communication table between fleet segments as defined in GFCM DCRF and metier-LOA as defined within DCF

Settings

```
# set the working directory
myWD <- paste("C:\\Users\\Bitetto Isabella\\OneDrive - Coispa Tecnologia & Ricerca
S.C.A.R.L\\MARE22\\STREAM\\FINAL REVISION OF DELIVERABLES\\DG_MARE_MedBS_to_GFCM",
sep="")
```

```
setwd(myWD)
```

```
ACatch=read.table("A_Catch_medbs_example.csv", sep=";", header=T)  
CT=read.table("Communication_table.csv", sep=";", header=T)  
species=read.table("Species TableII.2.csv", sep=";", header=F)
```

```
AREA=99
```

Input Data

1) DG MARE Med&BS A_Catch

Table continues below

ID	COUNTRY	YEAR
COUNTRY199991VL1218OTB50D100DEMSPSA 99	COUNTRY1	9999
COUNTRY199992VL1218OTB50D100DEMSPSA 99	COUNTRY1	9999
COUNTRY19999-1-10TB50D100DWSPSA 99	COUNTRY1	9999
COUNTRY199991-10TB50D100MDDWSPSA 99	COUNTRY1	9999
COUNTRY199992-10TB50D100MDDWSPSA 99	COUNTRY1	9999
COUNTRY199991-1GNS16D20DEMFS A 99	COUNTRY1	9999

Table continues below

QUARTER	VESSEL_LENGTH	GEAR	MESH_SIZE_RANGE
1	VL1218	OTB	50D100
2	VL1218	OTB	50D100
-1	-1	OTB	50D100
1	-1	OTB	50D100
2	-1	OTB	50D100
1	-1	GNS	16D20

Table continues below

FISHERY	AREA	SPECON	SPECIES	LANDINGS
DEMSP	SA 99	-1	HKE	51,56
DEMSP	SA 99	-1	HKE	23,48
DWSP	SA 99	-1	HKE	1,442
MDDWSP	SA 99	-1	HKE	13,47

MDDWSP	SA 99	-1	HKE	15,26
DEMF	SA 99	DIS-DEROG	HKE	111,1

Table continues below

DISCARDS	NO_SAMPLES_LANDINGS
1,977	0
0,9396	2
0,01478	2
0,2537	1
0	1
-1	11

Table continues below

NO_LENGTH_MEASUREMENTS_LANDINGS
109
101
51
573
162
79

Table continues below

NO_AGE_MEASUREMENTS_LANDINGS	NO_SAMPLES_DISCARDS
55	3
46	2
45	4
105	2
55	1
58	3

Table continues below

NO_LENGTH_MEASUREMENTS_DISCARDS
219
104
35

109

14

-1

Table continues below

NO_AGE_MEASUREMENTS_DISCARDS	NO_SAMPLES_CATCH
39	3
38	4
35	6
17	3
10	2
-1	14

Table continues below

NO_LENGTH_MEASUREMENTS_CATCH	NO_AGE_MEASUREMENTS_CATCH
328	94
205	84
86	80
682	122
176	65
79	58

Table continues below

MIN_AGE	MAX_AGE	AGE_0	AGE_0_NO_LANDED
0	5	0	0
0	3	0	2,709
0	6	0	1,05
0	4	0	172,7
0	7	0	5,465
1	10	0	0

Table continues below

AGE_0_MEAN_WEIGHT_LANDED	AGE_0_MEAN_LENGTH_LANDED
0	0

0,025	15,7
0,019	14,3
0,013	13
0,021	15,1
0	0

Table continues below

AGE_0_NO_DISCARD	AGE_0_MEAN_WEIGHT_DISCARD
237,2	0,009
111,5	0,009
3,022	0,005
37,54	0,007
0	0
-1	-1

Table continues below

AGE_0_MEAN_LENGTH_DISCARD	AGE_20_PLUS
11,7	20
11	20
9,3	20
10,7	20
0	20
-1	20

Table continues below

AGE_20_PLUS_NO_LANDED	AGE_20_PLUS_MEAN_WEIGHT_LANDED
0	0
0	0
0	0
0	0
0	0

0 0

Table continues below

AGE_20_PLUS_MEAN_LENGTH_LANDED	AGE_20_PLUS_NO_DISCARD
0	0
0	0
0	0
0	0
0	0
0	-1

Table continues below

AGE_20_PLUS_MEAN_WEIGHT_DISCARD
0
0
0
0
0
-1
AGE_20_PLUS_MEAN_LENGTH_DISCARD
0
0
0
0
0
-1

2) Communication table between GFCM/DCRF fleet segments and DCF metier-LOA

Table continues below

AREA	Fleet_segment	METIER	LOA
10	Longliners 12-24	LLS_DEF_0_0_0	VL1218
10	Trawlers 6- >24	OTB_DEF_>=40_0_0	VL1218
GEAR_ACatch	MESH_SIZE_RANGE_ACatch	FISHERY_ACatch	
LLS	-1	DEMF	
OTB	50D100	DEMSP	

3) List of species

V1

MUT

HKE

Processing tables

Using some data in the DG MARE Med&BS format :

```
# Association of GFCM fleet segment to Bland and ACatch tables

# selection of the species
ACatch=ACatch[as.character(ACatch$SPECIES) %in% as.character(species[,1]),]
ACatch=ACatch[,c(2:9,11:13)]
ACatch_L=aggregate(ACatch$LANDINGS,by=list(ACatch$COUNTRY, ACatch$YEAR,
      ACatch$VESSEL_LENGTH, ACatch$GEAR,ACatch$MESH_SIZE_RANGE,
      ACatch$FISHERY, ACatch$AREA, ACatch$SPECIES),FUN
="sum")
ACatch_D=aggregate(ACatch$DISCARDS,by=list(ACatch$COUNTRY, ACatch$YEAR, ACatch$VESSEL_LENGTH,
      ACatch$GEAR,ACatch$MESH_SIZE_RANGE, ACatch$FISHERY,
      ACatch$AREA, ACatch$SPECIES),FUN="sum")

Merge=merge(ACatch_L,ACatch_D,by=c("Group.1","Group.2","Group.3","Group.4","Group.5",
      "Group.6","Group.7","Group.8"))
colnames(Merge) =c("COUNTRY", "YEAR", "VESSEL_LENGTH","GEAR", "MESH_SIZE_RANGE","FISHERY",
      "AREA", "SPECIES", "LANDINGS", "DISCARDS")
Merge$DISCARDS[Merge$DISCARDS<0]=NA
Merge$GFCM_fleetsegment=as.character(Merge$GEAR)
Merge$GFCM_fleetsegment=""

for (i in 1:nrow(Merge)){
  if (nrow(CT[as.character(CT$LOA)== as.character(Merge$VESSEL_LENGTH[i]) &
    as.character(CT$GEAR_ACatch)== as.character(Merge$GEAR[i]) &
    as.character(CT$MESH_SIZE_RANGE_ACatch) ==
    as.character(Merge$MESH_SIZE_RANGE[i]) &
    as.character(CT$FISHERY_ACatch)== as.character(Merge$FISHERY[i]),])>0)
  {
    Merge$GFCM_fleetsegment[i]= as.character(CT[as.character(CT$LOA)==
    as.character(Merge$VESSEL_LENGTH[i]) &
    as.character(CT$GEAR_ACatch)== as.character(Merge$GEAR[i]) &
    as.character(CT$MESH_SIZE_RANGE_ACatch)==
    as.character(Merge$MESH_SIZE_RANGE[i]) &
    as.character(CT$FISHERY_ACatch)==
```

```

    as.character(Merge$FISHERY[i]) ,]$Fleet_segment)
} else {
Merge$GFCM_fleetsegment[i]=""}
}

Merge_noempty=Merge[Merge$GFCM_fleetsegment!="",]

Merge_noempty_L=aggregate(Merge_noempty$LANDINGS,by=list(Merge_noempty$COUNTRY,
    Merge_noempty$YEAR, Merge_noempty$GFCM_fleetsegment,
    Merge_noempty$SPECIES),FUN="sum")
Merge_noempty_D=aggregate(Merge_noempty$DISCARDS,by=list(Merge_noempty$COUNTRY,
    Merge_noempty$YEAR, Merge_noempty$GFCM_fleetsegment,
    Merge_noempty$SPECIES),FUN="sum")

Merge=merge(Merge_noempty_L,Merge_noempty_D,by=c("Group.1","Group.2","Group.3",
    "Group.4"))

Merge$GSA=AREA
Merge=Merge[,c(1,2,7,3,4,5,6)]
Merge$Catch= rowSums(data.frame(col1=Merge[,6],col2=Merge[,7]),na.rm=T)
colnames(Merge) =c("Country","Reference_year","GSA","Fleet_segment","Species",
    "Total_landing_per_species_(tons)","Total_discards_per_species_(tons)",
    "Total_catch_per_species")

```

Output

GFCM/DCRF TableII.2

Table continues below

Country	Reference_year	GSA	Fleet_segment
COUNTRY1	9999	99	Longliners 12-24
COUNTRY1	9999	99	Trawlers 6- >24

Table continues below

Species	Total_landing_per_species_(tons)
HKE	100,1
HKE	75,04

Table continues below

Total_discards_per_species_(tons)
NA
2,916
Total_catch_per_species
100,1

script 02: Table VII.2

This script allow to convert the DG MARE Med&BS B_Landings table into the GFCM/DCRF Table VII.2 (Biological information: Length data) using the communication table between fleet segments as defined in GFCM DCRF and metier-LOA as defined within DCF and the primary data in SDEF format

Settings

```
# set the working directory
myWD <- paste("C:\\Users\\Bitetto Isabella\\OneDrive - Coispa Tecnologia & Ricerca
S.C.A.R.L\\MARE22\\STREAM\\FINAL REVISION OF DELIVERABLES\\DG_MARE_MedBS_to_GFCM",
sep="")
setwd(myWD)

Bland=read.table("B_Landings_medbs_example.csv", sep=";", header=T)
CA=read.table("CA_example.csv", sep=";", header=T)
TR=read.table("TR_example.csv", sep=";", header=T)
CT=read.table("Communication_table.csv", sep=";", header=T)
alpha=read.table("Scientific name to FAO 3alphacode.csv", sep=";", header=T)
species=read.table("Species TableVII.2.csv", sep=";", header=F)

AREA=99
```

Input Data

1) DG MARE Med&BS B_Landings

Table continues below

ID	COUNTRY	YEAR
COUNTRY199991-1GNS16D20DEMFS A 99	COUNTRY1	9999
COUNTRY199992-1GNS16D20DEMFS A 99	COUNTRY1	9999
COUNTRY199991-1GNS16D20SLPFSA 99	COUNTRY1	9999
COUNTRY199992-1GNS16D20SLPFSA 99	COUNTRY1	9999
COUNTRY199991-1GTR16D20DEMSPSA 99	COUNTRY1	9999
COUNTRY199992-1GTR16D20DEMSPSA 99	COUNTRY1	9999

Table continues below

QUARTER	VESSEL_LENGTH	GEAR	MESH_SIZE_RANGE
1	-1	GNS	16D20

2	-1	GNS	16D20
1	-1	GNS	16D20
2	-1	GNS	16D20
1	-1	GTR	16D20
2	-1	GTR	16D20

Table continues below

FISHERY	AREA	SPECON	SPECIES	LANDINGS	UNIT
DEMF	SA 99	-1	HKE	101	cm
DEMF	SA 99	-1	HKE	113,1	cm
SLPF	SA 99	-1	HKE	5,723	cm
SLPF	SA 99	-1	HKE	3,585	cm
DEMSP	SA 99	-1	HKE	40,98	cm
DEMSP	SA 99	-1	HKE	51,83	cm

Table continues below

LENGTHCLASS0	LENGTHCLASS1	LENGTHCLASS2
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0

LENGTHCLASS100_PLUS

0
0
0
0
0
0

2) Communication table between GFCM/DCRF fleet segments and DCF metier-LOA

Table continues below

AREA	Fleet_segment	METIER	LOA
99	Longliners 12-24	LLS_DEF_0_0_0	VL1218
99	Trawlers 6- >24	OTB_DEF_>=40_0_0	VL1218
GEAR_ACatch	MESH_SIZE_RANGE_ACatch	FISHERY_ACatch	
LLS	-1	DEMF	
OTB	50D100	DEMSP	

3) List of species

V1

MUT

HKE

4) *Scientific name to FAO 3alphacode*

Scientific	X3ALPHACODE
<i>Chamaelea gallina</i>	SVE
<i>Centrophorus granulosus</i>	GUP
<i>Chimaera monstrosa</i>	CMO
<i>Dalatias licha</i>	SCK
<i>Dasyatis pastinaca</i>	JDP
<i>Etmopterus spinax</i>	ETX

5) SDEF CA table

Table continues below

[illegible]

Table continues below

month	proj	trpCode	staNum	area	rect
5	PROJECT	46_10_2017	999	99	NA
5	PROJECT	46_10_2017	999	99	NA
5	PROJECT	46_10_2017	999	99	NA
5	PROJECT	46_10_2017	999	99	NA
5	PROJECT	46_10_2017	999	99	NA
5	PROJECT	46_10_2017	999	99	NA

Table continues below

subRect	foCatEu6	stock	spp
NA	OTB_DEF_>=40_0_0	NA	Scyliorhinus canicula
NA	OTB_DEF_>=40_0_0	NA	Lophius budegassa
NA	OTB_DEF_>=40_0_0	NA	Lophius budegassa
NA	OTB_DEF_>=40_0_0	NA	Lophius budegassa
NA	OTB_DEF_>=40_0_0	NA	Citharus linguatula
NA	OTB_DEF_>=40_0_0	NA	Citharus linguatula

Table continues below

catchCat	landCat	commCatScl	commCat	sex
DIS	NA	NA	S	F
DIS	NA	NA	S	N
DIS	NA	NA	S	N
DIS	NA	NA	S	N
DIS	NA	NA	S	N
DIS	NA	NA	S	N

Table continues below

lenCls	age	fishId	lenCode	ageMeth	plusGrp
175	NA	4856914	scm	NA	NA
90	NA	4851033	scm	NA	NA
90	NA	4851034	scm	NA	NA

75	NA	4851035	scm	NA	NA
155	NA	4844380	scm	NA	NA
135	NA	4844381	scm	NA	NA
otoWt	otoSide	indWt	matMeth	matScale	matStage
NA	NA	14,9	NA	NA	1
NA	NA	10,5	NA	NA	0
NA	NA	8,9	NA	NA	0
NA	NA	6,2	NA	NA	0
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA

6) SDEF TR table

Table continues below

sampType	landCtry	vslFlgCtry	year	proj
S	COUNTRY1	COUNTRY1	9999	PROJECT
S	COUNTRY1	COUNTRY1	9999	PROJECT
S	COUNTRY1	COUNTRY1	9999	PROJECT
S	COUNTRY1	COUNTRY1	9999	PROJECT
S	COUNTRY1	COUNTRY1	9999	PROJECT
S	COUNTRY1	COUNTRY1	9999	PROJECT

Table continues below

trpCode	vslLen	vslPwr	vslSize	vslType
59_10_2017	VL0612	NA	NA	NA
63_10_2017	VL0612	NA	NA	NA
58_10_2017	VL0612	NA	NA	NA
57_10_2017	VL0612	NA	NA	NA
84_10_2017	VL0612	NA	NA	NA
60_10_2017	VL0612	NA	NA	NA

Table continues below

harbour	foNum	daysAtSea	vslId	sampCtry
Port	NA	NA	1	COUNTRY1
Port	NA	NA	1	COUNTRY1
Port	NA	NA	2	COUNTRY1
Port	NA	NA	3	COUNTRY1
Port	NA	NA	3	COUNTRY1
Port	NA	NA	3	COUNTRY1
sampMeth	asvslSize	asdaysAtSea		
SelfSampling	NA	NA		
SelfSampling	NA	NA		
SelfSampling	NA	NA		
SelfSampling	NA	NA		
SelfSampling	NA	NA		
SelfSampling	NA	NA		

Processing tables

Using some data in the DG MARE Med&BS format :

selection of the species

```
Bland=Bland[as.character(Bland$SPECIES) %in% as.character(species[,1]),]
```

Transformation of BLanding

```
B_melt <- melt(Bland, id=c( "ID" , "COUNTRY", "YEAR" , "QUARTER" ,
                           "VESSEL_LENGTH" , "GEAR" , "MESH_SIZE_RANGE" , "FISHER
Y" ,
                           "AREA" , "SPECON" , "SPECIES" , "LANDINGS" , "UNIT"
))
```

```
B_melt$variable <- apply(B_melt, 1, function(x) substring(x[14], 12, nchar(x[14]
)) )
```

```
B_melt <- B_melt[B_melt$variable != "", ]
```

```
B_melt$variable[B_melt$variable == "100_PLUS"] <- 100
```

```
B_melt$variable <- as.numeric(as.character(B_melt$variable))
```

```
B_melt$value <- as.numeric(as.character(B_melt$value))
```

#Association of GFCM fleet segment to B Landings

```
B_melt$GFCM_fleetsegment=as.character(B_melt$GEAR)
B_melt$GFCM_fleetsegment=""
```

```
for (i in 1:nrow(B_melt)){
  if (nrow(CT[as.character(CT$LOA)== as.character(B_melt$VESSEL_LENGTH[i]) &
as.character(CT$GEAR_ACatch)== as.character(B_melt$GEAR[i]) &
as.character(CT$MESH_SIZE_RANGE_ACatch)== as.character(B_melt$MESH_SIZE_RANGE[i])
&
as.character(CT$FISHERY_ACatch)== as.character(B_melt$FISHERY[i]),])>0) {

B_melt$GFCM_fleetsegment[i]=
  as.character(CT[as.character(CT$LOA)== as.character(B_melt$VESSEL_LENGTH[i]) &
as.character(CT$GEAR_ACatch)== as.character(B_melt$GEAR[i]) &
as.character(CT$MESH_SIZE_RANGE_ACatch)== as.character(B_melt$MESH_SIZE_RANGE[i])
&
as.character(CT$FISHERY_ACatch)== as.character(B_melt$FISHERY[i]) ,]$Fleet_segment
)

} else {
  B_melt$GFCM_fleetsegment[i]=""}
}
```

```
B_melt=B_melt[as.character(B_melt$GFCM_fleetsegment)!="",]
```

```
B_land1=aggregate(B_melt$value,by=list(B_melt$COUNTRY,
B_melt$YEAR,B_melt$AREA,B_melt$GFCM_fleetsegment,
B_melt$SPECIES,B_melt$UNIT,B_melt$variable),FUN="sum")
```

```
B_land1[,3]=AREA
```

```
B_land1$Source_of_data="BS"
```

```
B_land1$Name_of_the_scientific_survey = ""
```

```
B_land1=B_land1[,c(1,2,3,9,10,4,5,6,7,8)]
```

```
colnames(B_land1)=c("Country", "YEAR", "GSA", "Source_of_data",
"Name_of_the_scientific_survey",
"GFCM_fleetsegment", "SPECIES", "Length_unit", "Length",
"Number_of_individuals_expanded_per_length_classes")
```

only Landing should be taken into account, according to the specifications

```
CA=CA[CA$catchCat=="LAN",]
```

Association of 3alpha code to primary data

```
CA2 = merge(CA,alpha,by.x="spp",by.y="Scientific")
```

```
colnames(CA2)[ncol(CA2)]= "spp2"
```

```
CA2$spp= CA2$spp2
```

```
CA <- CA2[,c(2:15, 1, 16:32)]
```

```
length_unit <- unique(data.frame(species = Bland$SPECIES, unit = Bland$UNIT) )
```

```

for (nr in 1:nrow(length_unit) ) {
  if (nrow(CA[as.character(CA$spp) == as.character(length_unit$species[nr]), ]) > 0) {
    if (length_unit$unit[nr] == "cm") {
      CA$lenCls[as.character(CA$spp) == as.character(length_unit$species[nr])] <-
      CA$lenCls[as.character(CA$spp) == as.character(length_unit$species[nr])]/10
    }
  }
}

# association of GFCM fleet segment to primary data

TR_CA=merge(TR,CA,by=c("year", "trpCode", "sampType", "landCtry",
                      "vslFlgCtry", "proj"),all=F)
TR_CA$GFCM_fleetsegment=TR_CA$landCtry
TR_CA$GFCM_fleetsegment=""

TR_CA=TR_CA[,c(1,15,7,25,27,32,33,41,44,45)]

TR_CA$lenCls=round(TR_CA$lenCls,0)

for (i in 1:nrow(TR_CA)){
  if (nrow(CT[as.character(CT$LOA)== as.character(TR_CA$vslLen[i]) &
               as.character(CT$METIER)== as.character(TR_CA$foCatEu6[i]) ,])>0) {
    TR_CA$GFCM_fleetsegment[i]=
      as.character(CT[as.character(CT$LOA)== as.character(TR_CA$vslLen[i]) &
                      as.character(CT$METIER)== as.character(TR_CA$foCatEu6[i]) ,]$Fleet_segment)
  } else {
    TR_CA$GFCM_fleetsegment[i]=" "
  }
}

TR_CA=TR_CA[as.character(TR_CA$GFCM_fleetsegment)!="",]

TR_CA <- TR_CA[as.character(TR_CA$spp) %in% as.character(length_unit$species),]

write.table(TR_CA, "TR_CA.csv", sep=";", row.names=F)

agg=aggregate(TR_CA$spp, by=list(TR_CA$year, TR_CA$spp,
                                TR_CA$GFCM_fleetsegment, TR_CA$lenCls), FUN="length"
)
colnames(agg)=c("YEAR", "SPECIES", "GFCM_fleetsegment", "Length",
                "Number_of_individuals_sampled")

agg_w=aggregate(TR_CA$indWt, by=list(TR_CA$year, TR_CA$spp,
                                      TR_CA$GFCM_fleetsegment, TR_CA$lenCls), FUN="mean", na.rm=T)
colnames(agg_w)=c("YEAR", "SPECIES", "GFCM_fleetsegment", "Length",
                  "Weight_of_individuals_sampled")

```



```

Merg=merge(B_land1,agg,by=c("YEAR","SPECIES","GFCM_fleetsegment","Length"),all.x=T
)

Merg2=merge(Merg,agg_w,by=c("YEAR","SPECIES","GFCM_fleetsegment","Length"),all.x=T
)

# conversion in kg

Merg2$Weight_of_individuals_sampled=Merg2$Weight_of_individuals_sampled/1000

Final=merge(B_land1,Merg2,by=c("YEAR","SPECIES","GFCM_fleetsegment","Length"))
Final=Final[,c(5,1,6,7,8,3,2,9,4,17,18,16)]

colnames(Final)=c("Country","Reference_year","GSA","Source_of_data",
                  "Name_of_the_scientific_survey","Fleet_segment","Species",
                  "Length_unit","Length",
                  "Number_of_individuals_sampled_per_length_classes",
                  "Weight_of_individuals_sampled_per_length_classes",
                  "Number_of_individuals_expanded_per_length_classes")

# Final[Final[, 10] == 0, 10] = NA
Final[,ncol(Final)]=round(Final[,ncol(Final)]*1000,0)

```

Output

GFCM/DCRF Table VII.2

Table continues below

	Country	Reference_year	GSA
24	COUNTRY1	9999	99
27	COUNTRY1	9999	99
28	COUNTRY1	9999	99
29	COUNTRY1	9999	99
30	COUNTRY1	9999	99
31	COUNTRY1	9999	99

Table continues below

	Source_of_data	Name_of_the_scientific_survey
24	BS	
27	BS	
28	BS	

29 BS

30 BS

31 BS

Table continues below

	Fleet_segment	Species	Length_unit
24	Longliners 12-24	HKE	cm
27	Longliners 12-24	HKE	cm
28	Longliners 12-24	HKE	cm
29	Longliners 12-24	HKE	cm
30	Longliners 12-24	HKE	cm
31	Longliners 12-24	HKE	cm

Table continues below

	Length
24	29
27	31
28	32
29	33
30	34
31	35

Table continues below

	Number_of_individuals_sampled_per_length_classes
24	NA
27	NA
28	NA
29	NA
30	NA
31	NA

Table continues below

	Weight_of_individuals_sampled_per_length_classes
--	--

24 NA
 27 NA
 28 NA
 29 NA
 30 NA
 31 NA

	Number_of_individuals_expanded_per_length_classes
24	1150
27	766
28	383
29	766
30	1832
31	2598

script 03: *Table VII.3.1*

This script allow to convert the DG MARE Med&BS ML table into the GFCM/DCRF Table VII.3.1 (Biological information: Size at first maturity)

Settings

```
# set the working directory
myWD <- paste("C:\\Users\\Bitetto Isabella\\OneDrive - Coispa Tecnologia & Ricerca
S.C.A.R.L\\MARE22\\STREAM\\FINAL REVISION OF DELIVERABLES\\DG_MARE_MedBS_to_GFCM",
sep="")
setwd(myWD)

ML_tab=read.table("ML_table.csv",sep=";",header=T)
species=read.table("Species TableVII.3.1.csv",sep=";",header=F)

AREA=99
YEAR=9999
```

Input Data

1) DG MARE Med&BS ML (Maturity at length)

Table continues below

COUNTRY	AREA	START_YEAR	END_YEAR	SPECIES	
COUNTRY1	99	9999	9999	HKE	
COUNTRY1	99	9999	9999	HKE	
COUNTRY1	99	9999	9999	HKE	
COUNTRY1	99	9999	9999	HKE	
COUNTRY1	99	9999	9999	HKE	
COUNTRY1	99	9999	9999	HKE	
SEX	LENGTHCLASS	UNIT	SAMPLE_SIZE	PRM	COMMENTS
F	14	cm	55	0	NA
F	15	cm	35	0	NA
F	16	cm	33	0	NA
F	17	cm	43	0	NA
F	18	cm	36	0	NA
F	19	cm	43	0	NA

2) List of species

V1

MUT

HKE

Processing tables

Using some data in the DG MARE Med&BS format :

selection of the species

```
ML_tab=ML_tab[as.character(ML_tab$SPECIES) %in% as.character(species[,1]),]
ML_tab_50=ML_tab[ML_tab$PRM<0.60 & ML_tab$PRM>0.4,]
```

```
L50=aggregate(ML_tab_50$LENGTHCLASS,
               by=list(ML_tab_50$COUNTRY,ML_tab_50$START_YEAR,ML_tab_50$END_YEAR,
                       ML_tab_50$SPECIES,ML_tab_50$SEX),FUN="mean")
```

```
L50=L50[L50$Group.2<=YEAR & L50$Group.3>=YEAR,]    # selection on the year
L50$AREA=AREA
L50$YEAR=YEAR
L50$Reference = ""
```

```
Final=L50[,c(1,8,7,4,5,6,9)]
colnames(Final)=c("Country", "Reference_year", "GSA", "Species", "Sex", "L50", "Reference")
```

Output

GFCM/DCRF Table VII.2

Table continues below

Country	Reference_year	GSA	Species	Sex
COUNTRY1	9999	99	HKE	F
COUNTRY1	9999	99	MUT	F

L50 Reference

33

11

script 04: Table VII.3.2

This script allow to create the GFCM/DCRF Table VII.3.2 (Biological information: Maturity data) using the GFCM/DCRF Table VII.2 (Biological information: Length data) and the primary data in SDEF format (CA merged with TR)

Settings

```
# set the working directory
myWD <- paste("C:\\Users\\Bitetto Isabella\\OneDrive - Coispa Tecnologia & Ricerca
S.C.A.R.L\\MARE22\\STREAM\\FINAL REVISION OF DELIVERABLES\\DG_MARE_MedBS_to_GFCM",
sep="")
setwd(myWD)
```

```
TR_CA=read.table("TR_CA.csv", sep=";", header=T)
T_VII2=read.table("TableVII.2.csv", sep=";", header=T)
```

```
species=read.table("Species TableVII.2.csv", sep=";", header=F)
```

```
AREA=10
```

Input Data

1) Primary data SDEF format (CA merged with TR)

Table continues below

year	sampCtry	vslLen	foCatEu6	spp
------	----------	--------	----------	-----

9999	COUNTRY1	VL1218	OTB_DEF_>=40_0_0	MUT
9999	COUNTRY1	VL1218	OTB_DEF_>=40_0_0	HKE
9999	COUNTRY1	VL1218	OTB_DEF_>=40_0_0	HKE
9999	COUNTRY1	VL1218	OTB_DEF_>=40_0_0	MUT
9999	COUNTRY1	VL1218	OTB_DEF_>=40_0_0	MUT
9999	COUNTRY1	VL1218	OTB_DEF_>=40_0_0	MUT

sex	lenCls	indWt	matStage	GFCM_fleetsegment
M	12	NA	2c	Trawlers 6- >24
M	22	70,4	2c	Trawlers 6- >24
F	22	72,54	1	Trawlers 6- >24
M	12	15	2c	Trawlers 6- >24
M	12	NA	2c	Trawlers 6- >24
F	20	97,1	2b	Trawlers 6- >24

2) GFCM/DCRF Table VII.2

Table continues below

Country	Reference_year	GSA	Source_of_data
COUNTRY1	9999	99	BS
COUNTRY1	9999	99	BS
COUNTRY1	9999	99	BS
COUNTRY1	9999	99	BS
COUNTRY1	9999	99	BS
COUNTRY1	9999	99	BS

Table continues below

Name_of_the_scientific_survey	Fleet_segment	Species
NA	Longliners 12-24	HKE
NA	Longliners 12-24	HKE
NA	Longliners 12-24	HKE
NA	Longliners 12-24	HKE

NA	Longliners 12-24	HKE
----	------------------	-----

NA	Longliners 12-24	HKE
----	------------------	-----

Table continues below

Length_unit	Length
cm	29
cm	31
cm	32
cm	33
cm	34
cm	35

Table continues below

Number_of_individuals_sampled_per_length_classes
--

NA
NA
NA
NA
NA
NA

Table continues below

Weight_of_individuals_sampled_per_length_classes
--

NA
NA
NA
NA
NA
NA

Number_of_individuals_expanded_per_length_classes

1150
766
383
766
1832
2598

Processing tables

Using some data in the DG MARE Med&BS format :

selection of the species

```
TR_CA=TR_CA[as.character(TR_CA$spp) %in% as.character(species[,1]),]

agg=aggregate(TR_CA$spp,by=list(TR_CA$year,TR_CA$spp,
    TR_CA$GFCM_fleetsegment,TR_CA$lenCls,TR_CA$sex,TR_CA$matStage),
    FUN="length")
colnames(agg)=c("YEAR","SPECIES","GFCM_fleetsegment","Length","Sex",
    "Maturity","Number_of_individuals_sampled")

agg_w=aggregate(TR_CA$indWt,by=list(TR_CA$year,TR_CA$spp,
    TR_CA$GFCM_fleetsegment,TR_CA$lenCls,TR_CA$sex,TR_CA$matStage),
    FUN="mean",na.rm=T)
colnames(agg_w)=c("YEAR","SPECIES","GFCM_fleetsegment","Length","Sex",
    "Maturity","Weight_of_individuals_sampled")

agg_tot=aggregate(TR_CA$spp,by=list(TR_CA$year,TR_CA$spp,
    TR_CA$GFCM_fleetsegment,TR_CA$lenCls,TR_CA$sex),FUN="length")
colnames(agg_tot)=c("YEAR","SPECIES","GFCM_fleetsegment","Length",
    "Sex","Number_of_individuals_sampled")

AGG=merge(agg,agg_tot,by=c("YEAR","SPECIES","GFCM_fleetsegment","Length","Sex"))
colnames(AGG)[c(7,8)]=c("Numbers_by_sex_stage","Numbers_by_sex")

AGG$Perc_of_stage_in_sex= AGG$Numbers_by_sex_stage/AGG$Numbers_by_sex

Mer=merge(T_VII2, AGG,by.y=c("YEAR","SPECIES","GFCM_fleetsegment","Length"),
    by.x=c("Reference_year","Species","Fleet_segment","Length"))

Mer$Percentage_of_sex= Mer$Numbers_by_sex/ Mer$Number_of_individuals_sampled_per_
length_classes

Mer$Number_of_individuals_expanded=
    Mer$Number_of_individuals_expanded_per_length_classes*Mer$Percentage_of_sex*Mer$
Perc_of_stage_in_sex

mer2=merge(Mer,agg_w,by.y=c("YEAR","SPECIES","GFCM_fleetsegment","Length","Sex",
    "Maturity"),
    by.x=c("Reference_year","Species","Fleet_segment","Length","Sex",
    "Maturity"))

Final=mer2[,c(7,1,8,9,10,3,2,11,4,5,6,15,20,19)]
Final$Weight_of_individuals_sampled=Final$Weight_of_individuals_sampled/1000
Final[,ncol(Final)]=round(Final[,ncol(Final)],0)
```



```
colnames(Final)=c("Country","Reference_year","GSA","Source_of_data",
                  "Name_of_the_scientific_survey","Fleet_segment",
                  "Species","Length_unit","Length","Sex","Maturity",
                  "Number_of_individuals_sampled_(per_length_class_sex_and_maturity_stage)",
                  "Weight_of_individuals_sampled_(per_length_class_sex_and_maturity_stage)",
                  "Number_of_individuals_expanded_(per_length_class_sex_and_maturity_stage)")
```

Output

GFCM/DCRF Table VII.3.2

Table continues below

Country	Reference_year	GSA	Source_of_data
COUNTRY1	9999	99	BS
COUNTRY1	9999	99	BS
COUNTRY1	9999	99	BS
COUNTRY1	9999	99	BS
COUNTRY1	9999	99	BS
COUNTRY1	9999	99	BS

Table continues below

Name_of_the_scientific_survey	Fleet_segment	Species
NA	Trawlers 6- >24	HKE
NA	Trawlers 6- >24	HKE
NA	Trawlers 6- >24	HKE
NA	Trawlers 6- >24	HKE
NA	Trawlers 6- >24	HKE
NA	Trawlers 6- >24	HKE

Table continues below

Length_unit	Length	Sex	Maturity
cm	16	F	1
cm	16	M	2b
cm	16	M	2c
cm	17	F	1
cm	17	M	2b

cm	18	F	1
----	----	---	---

Table continues below

Number_of_individuals_sampled_(per_length_class_sex_and_maturity_stage)

1

1

1

1

1

5

Table continues below

Weight_of_individuals_sampled_(per_length_class_sex_and_maturity_stage)

0,02693

0,02664

0,03109

0,03414

0,03209

0,04054

Number_of_individuals_expanded_(per_length_class_sex_and_maturity_stage)
--

2795

2795

2795

21123

21123

41994