

Metabarcoding the tuna stomach

Babett Günther, including scripts from Deagle et al. 2019, and Günther et al. 2015

18/05/2021

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#####EXPLANATION GUIDE ##### PROCESSING IN 5 STEPS ##### 1. Read and process datasets ##### 2. calculating values RRA,POO,wPOO,FOO for 18S, ##### 3. calculating values RRA,POO,wPOO,FOO for COI ##### 4. RRA PER YEAR TO COMPARE TO MOPHOLOGICAL RA, relative abundance data ##### 5.Statistical distribution tests with euclidean distance/Sorensen dissimilarity, based on OTU level, finding driving factors ##### 6.GIMs and predictive models and their Drawings

```
##### 1. Read and process datasets
#reading in all data
data_1 <-read.csv ("18S_Metazoa.csv", sep=";", dec=",", header=TRUE, check.names=TRUE)
str(data_1)
```

1. Read and process datasets

```
## 'data.frame': 74 obs. of 51 variables:
## $ ClusterID: Factor w/ 74 levels "OTU_10","OTU_106",...: 36 10 11 15 23 17 33 18 42 32 ...
## $ Phylum : Factor w/ 7 levels "Annelida","Arthropoda",...: 1 1 1 1 2 2 2 2 2 ...
## $ Species : Factor w/ 47 levels "Acartia clausii",...: 5 4 4 4 1 3 8 10 11 17 ...
## $ M275 : int 0 0 0 0 0 0 0 0 0 0 ...
## $ J290 : int 0 0 0 0 0 0 0 0 0 0 ...
## $ J269 : int 0 0 0 0 0 0 0 0 0 0 ...
## $ M281 : int 0 0 0 0 0 0 0 0 0 0 ...
## $ M261 : int 0 0 0 0 0 0 0 0 0 2 ...
## $ M198 : int 0 0 7 0 679 0 0 0 0 0 ...
## $ M273 : int 0 0 0 0 0 0 0 8 0 0 ...
## $ J233 : int 0 0 0 0 0 0 0 0 0 0 ...
## $ J201 : int 0 0 0 0 0 0 0 0 0 0 ...
## $ M280 : int 0 0 0 10 0 0 0 0 0 0 ...
## $ J222 : int 0 0 0 0 0 0 0 0 0 0 ...
## $ M118 : int 0 0 0 0 0 0 0 0 0 0 ...
## $ M277 : int 0 0 0 0 0 0 0 0 0 0 ...
```

```

## $ J221      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M262      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M279      : int  0 0 0 0 0 0 2 0 0 0 0 ...
## $ J226      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J53       : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J215      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M117      : int  0 0 0 0 0 0 0 0 229 0 ...
## $ M33       : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J47       : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J276      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M59       : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J52       : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M29       : int  0 0 4 0 0 0 0 0 0 0 0 ...
## $ J138      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J125      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J121      : int  0 0 0 0 50 0 0 0 0 0 0 ...
## $ M49       : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J144      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J134      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J150      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J227      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J93       : int  1 0 0 0 0 0 0 0 0 0 0 ...
## $ J57       : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M30       : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J46       : int  0 0 0 0 0 0 0 3 0 0 0 ...
## $ J145      : int  0 0 0 0 0 9 0 0 0 0 0 ...
## $ J96       : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J164      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M123      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J128      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M253      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J229      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J217      : int  0 14 0 0 0 0 0 0 0 0 0 ...
## $ J205      : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J170      : int  0 0 0 0 0 0 0 0 0 0 0 ...

```

```

d1_1<-data_1
data_2 <-read.csv ("COI.csv", sep=";", dec=".", header=TRUE, check.names=TRUE)
str(data_2)

```

```

## 'data.frame':  91 obs. of  51 variables:
## $ ClusterID: Factor w/ 91 levels "OTU_1","OTU_101",...: 22 30 35 34 23 24 27 21 19 18 ...
## $ Taxon    : Factor w/ 9 levels "Arthropoda","Chaetognatha",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ Species  : Factor w/ 84 levels "Acartia_clausii",...: 4 33 46 49 52 58 79 11 26 82 ...
## $ Best    : Factor w/ 15 levels "anchovy","Arthropoda",...: 2 2 2 2 2 2 2 2 2 ...
## $ M275    : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J290    : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J269    : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M281    : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M261    : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M198    : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ M273    : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J233    : int  0 0 0 0 0 0 0 0 0 0 0 ...
## $ J201    : int  0 0 0 0 0 0 0 0 0 0 0 ...

```

```

## $ M280      : int  0 0 0 0 3 0 0 0 0 0 ...
## $ J222      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ M118      : int  0 2 0 0 0 3 0 0 0 0 ...
## $ M277      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J221      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ M262      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ M279      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J226      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J53       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J215      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ M117      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ M33       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J47       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J276      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ M59       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J52       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ M29       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J138      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J125      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J121      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ M49       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J144      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J134      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J150      : int  0 0 0 0 0 0 3 0 0 0 ...
## $ J227      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J57       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ M30       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J46       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J145      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J96       : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J164      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ M123      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J128      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ M253      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J229      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J217      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ J205      : int  0 0 2 2 0 0 0 4 4 4 ...
## $ J170      : int  0 0 0 0 0 0 0 0 0 0 ...

```

```

#reading metatdata
dm <-read.csv ("metaCOI.csv", sep=";", dec=",", header=TRUE,check.names=TRUE,row.names = 1)
dm2 <-read.csv ("meta18S.csv", sep=";", dec=",", header=TRUE,check.names=TRUE,row.names = 1)
#reading data from Morpho study
morp <-read.csv ("morpho_year_best.csv", sep=";", dec=".", header=TRUE,check.names=TRUE,row.names = 1)
#18S
d1_1$ClusterID <- NULL
d1_1$Species <- NULL
#sum up identic species ##### this process is on Phylum level not on OTU level
d1_2 <- ddply(d1_1,"Phylum",numcolwise(sum))
#first row speices name
df1_3 <- data.frame(d1_2[,-1], row.names= d1_2[,1])
#delete fish without any prey, and undetected prey after processing
i <- (colSums(df1_3) != 0)
df1_4 <- df1_3[, i]

```

```

df1_5 <- subset(df1_4, select = -J93)  #( none in COI, to better comparison deleted here)
df1_6<- df1_5 [rowSums(df1_5) != 0, ]
#same for COI
#count are most important species, based on previous tests, rest count together on phyla
d2_1 <- data_2
d2_1$ClusterID <- NULL
d2_1$Species <- NULL
d2_1$Taxon <- NULL
#sum up identic species ##### this process is on species level not on OTU level
d2_2 <- ddply(d2_1,"Best",numcolwise(sum))
#first row speices name
df2_3 <- data.frame(d2_2[,-1], row.names= d2_2[,1])
#delete fish without any prey, and undetected prey after processing
i <- (colSums(df2_3) != 0)
df2_4 <- df2_3[, i]
df2_5<- df2_4[rowSums(df2_4) != 0, ]
write.csv (df2_5,'COI_clean.csv')

##### Now the same, but on OTU level for statistical analyses
d3_1<-data_1 #18S but now working on OTU level
d4_1<-data_2 #COI on OTu level
d3_1$Phylum <- NULL
d3_1$Species <- NULL
#sum up identic species ##### this process is on species level not on OTU level
d3_2 <- ddply(d3_1,"ClusterID",numcolwise(sum))
df3_3 <- data.frame(d3_2[,-1], row.names= d3_2[,1])
i <- (colSums(df3_3) != 0)
df3_4 <- df3_3[, i]
df3_5 <- subset(df3_4, select = -J93)  #(ONLY 2 SEQUENCES IN 18S, none in COI, to better comparsion dele
df3_6<- df3_5 [rowSums(df3_5) != 0, ]
df3_7<-t(df3_6)
df3_8pa<-decostand(df3_7, method="total")
df3_8<-decostand(df3_7, method="pa")
df3_8<-data.frame(df3_8)
df3_8pa<-data.frame(df3_8pa)
##forCOI
d4_1$Best <- NULL
d4_1$Species <- NULL
d4_1$Taxon <- NULL
#sum up identic species ##### this process is on species level not on OTU level
d4_2 <- ddply(d4_1,"ClusterID",numcolwise(sum))
#first row speices name
df4_3 <- data.frame(d4_2[,-1], row.names= d4_2[,1])
#delete fish without any prey, and undetected prey after processing
i <- (colSums(df4_3) != 0)
df4_4 <- df4_3[, i]
df4_5<- df4_4[rowSums(df4_4) != 0, ]
df4_6<-t(df4_5)
df4_7<-decostand(df4_6, method="total")
df4_7pa<-decostand(df4_6, method="pa")
df4_8<-data.frame(df4_7)
df4_8pa<-data.frame(df4_7)

```

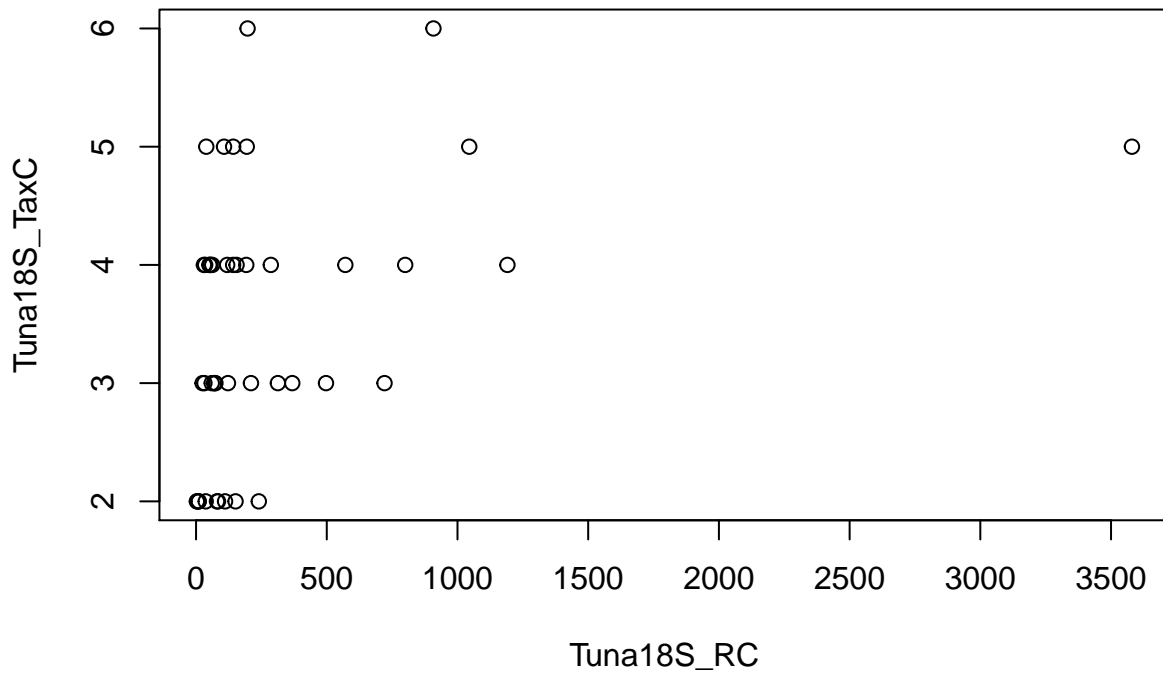
```
##### 2. calculating values RRA,POO,wPOO,FOO for 18S
Tuna18S_D=as.matrix(df1_6)
# How many seq per stomach?
Tuna18S_RC=apply(Tuna18S_D,2,sum);Tuna18S_RC;mean(Tuna18S_RC)
```

2. calculating values RRA,POO,wPOO,FOO for 18S

```
## M275 J290 J269 M281 M261 M198 M273 J233 J201 M280 J222 M118 M277 J221 M262 M279
## 5 37 10 84 25 908 286 80 60 1045 151 107 10 111 210 800
## J226 J53 J215 M117 M33 J47 J276 J52 M29 J138 J125 J121 M49 J144 J134 J150
## 3 51 32 497 240 721 39 194 35 142 122 1191 197 74 192 155
## J227 J57 M30 J46 J145 J96 J164 M123 M253 J229 J217 J205
## 53 119 71 571 62 30 3580 313 142 368 55 69

## [1] 301.0682
```

```
write.csv(Tuna18S_RC,'Tuna18S_reads_per_stomach.csv')
# number of taxa against read depth
Tuna18S_TaxC=apply(Tuna18S_D,2,function(x) length(unique(x)))
plot(Tuna18S_RC,Tuna18S_TaxC)
```



```
write.csv(Tuna18S_TaxC,'Tuna18S_taxa_per_stomach.csv')
#Turn into proportions, proportional dataset
Tuna18S_Dprop=prop.table(Tuna18S_D,2)
dim(Tuna18S_Dprop)
```

```
## [1] 7 44
```

```
apply(Tuna18S_Dprop,2,sum)
```

```
## M275 J290 J269 M281 M261 M198 M273 J233 J201 M280 J222 M118 M277 J221 M262 M279
## 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## J226 J53 J215 M117 M33 J47 J276 J52 M29 J138 J125 J121 M49 J144 J134 J150
## 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## J227 J57 M30 J46 J145 J96 J164 M123 M253 J229 J217 J205
## 1 1 1 1 1 1 1 1 1 1 1 1
```

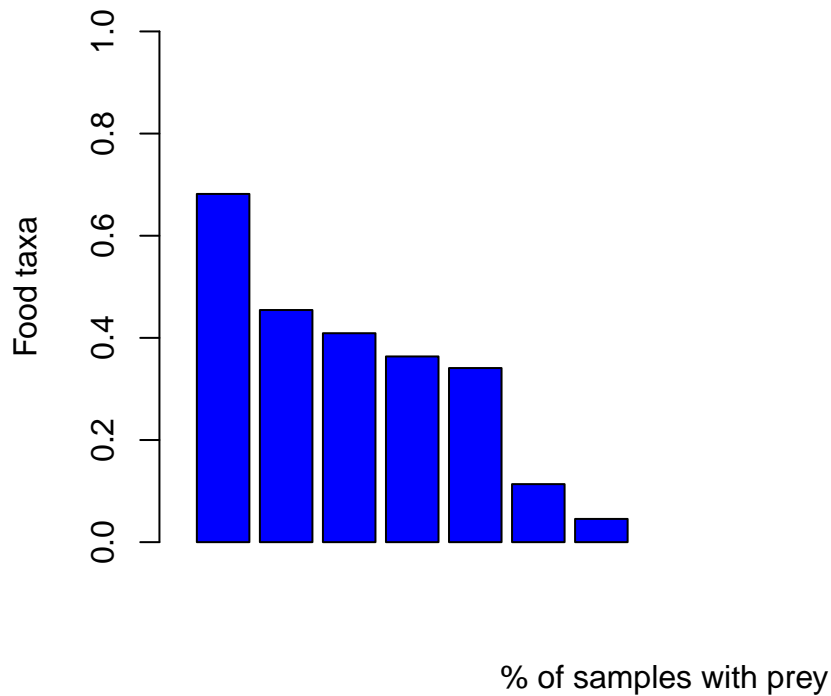
```
write.csv(Tuna18S_Dprop,'Tuna18S_proportions.csv')
# Make Presence absence (PA) dataset,
PA_Tuna18S_D= Tuna18S_Dprop
PA_Tuna18S_D[PA_Tuna18S_D>.0099999999]=1 ## here we fix the threshold for presence absence transformation
PA_Tuna18S_D[PA_Tuna18S_D<.01]=0 ## else 0
write.csv(Tuna18S_D,'Tuna18S_pres_abs.csv')
FOO_All_Tuna18S_=apply(PA_Tuna18S_D,1,sum)/length(PA_Tuna18S_D[1,])
Ord_Tuna18S_=order(-FOO_All_Tuna18S_)
write.csv(Ord_Tuna18S_,'Tuna18S_Foo.csv', row.names = TRUE)#
P_FOO_Tuna18S_= apply(PA_Tuna18S_D,1,sum)/sum(apply(PA_Tuna18S_D,1,sum))
P_FOO_Tuna18S_
```

```
## Annelida Arthropoda Cnidaria Ctenophora Platyhelminthes
## 0.01886792 0.14150943 0.18867925 0.15094340 0.04716981
## Tunicata Vertebrata
## 0.16981132 0.28301887
```

```
sum(P_FOO_Tuna18S_)
```

```
## [1] 1
```

```
df_FOO_Tuna18S <- data.frame(P_FOO_Tuna18S_)
write.csv(df_FOO_Tuna18S,'Tuna18S_Poo.csv', row.names = TRUE)
barplot(FOO_All_Tuna18S_[Ord_Tuna18S_][1:15],ylim=c(0,1),col="blue",xaxt='n', xlab="% of samples with")
```



```
P_wFOO_Tuna18S_ = apply(prop.table(PA_Tuna18S_D, 2), 1, mean, na.rm=T)
P_wFOO_Tuna18S_
```

```
##      Annelida      Arthropoda      Cnidaria      Ctenophora Platyhelminthes
##      0.01515152  0.12840909  0.17083333  0.15492424  0.03560606
##      Tunicata      Vertebrata
##      0.16136364  0.33371212
```

```
sum(P_wFOO_Tuna18S_)
```

```
## [1] 1
```

```
df_wFOO_Tuna18S <- data.frame(P_wFOO_Tuna18S_)
write.csv(df_wFOO_Tuna18S, 'Tuna18S_wPoo.csv', row.names = TRUE)
```

```
P_RRA_Tuna18S_ = apply(prop.table(as.matrix(Tuna18S_D), 2), 1, mean)
P_RRA_Tuna18S_
```

```
##      Annelida      Arthropoda      Cnidaria      Ctenophora Platyhelminthes
##      0.008775223  0.103940195  0.160764761  0.178458873  0.029076247
##      Tunicata      Vertebrata
##      0.151849864  0.367134838
```

```
sum(P_RRA_Tuna18S_)
```

```
## [1] 1
```

```
df_RRA_Tuna18S <- data.frame(P_RRA_Tuna18S_)
```

```
write.csv(df_RRA_Tuna18S,'Tuna18S_RRA.csv', row.names = TRUE)
```

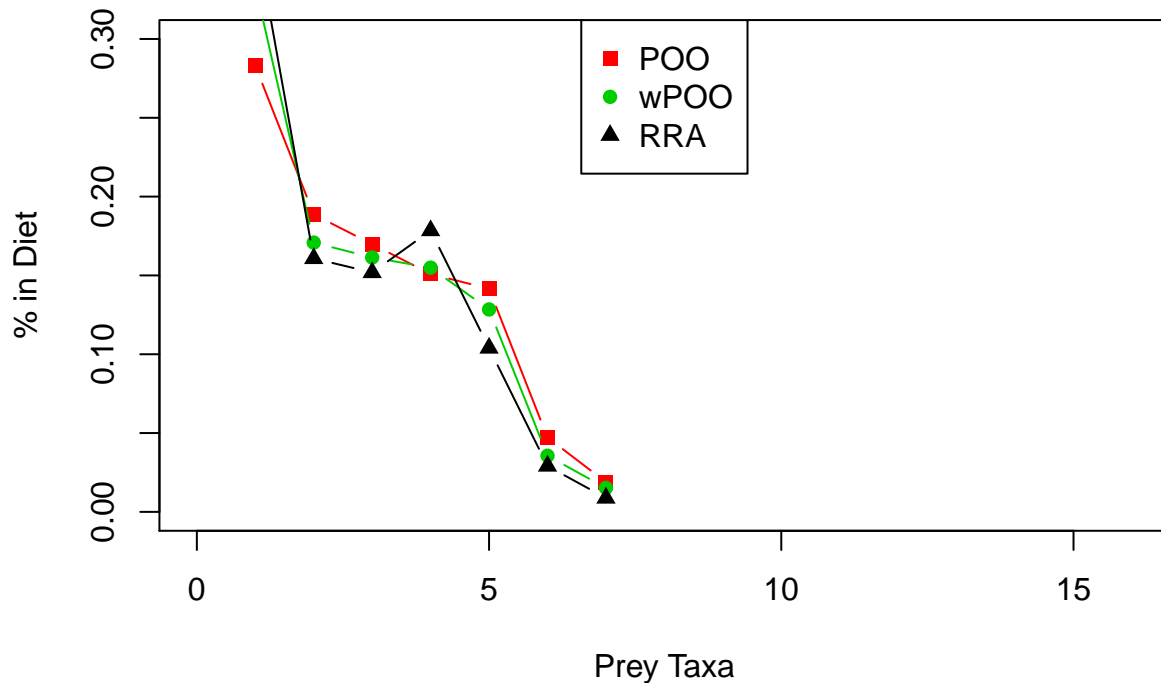
```
plot(P_FOO_Tuna18S_[Ord_Tuna18S_][1:15],pch=15,col=2,type="b",ylim= c(0,0.3),ylab="% in Diet", xlab="Prey Taxa",  
points(16, sum(P_FOO_Tuna18S_[Ord_Tuna18S_][16:length(P_FOO_Tuna18S_)]),pch=15,col=2,cex=1.2 )  
points(P_wFOO_Tuna18S_[Ord_Tuna18S_][1:15],pch=16,col=3,type="b")  
points(16, sum(P_wFOO_Tuna18S_[Ord_Tuna18S_][16:length(P_wFOO_Tuna18S_)]),pch=16,col=3,cex=1.2 )  
sum(P_wFOO_Tuna18S_[Ord_Tuna18S_][1:15])
```

```
## [1] NA
```

```
points(P_RRA_Tuna18S_[Ord_Tuna18S_][1:15],pch=17,type="b")
```

```
points(16, sum(P_RRA_Tuna18S_[Ord_Tuna18S_][16:length(P_RRA_Tuna18S_)]),pch=17,cex=1.2 )
```

```
legend('top',c('POO', 'wPOO', 'RRA'),pch=c(15,16,17),col=c(2,3,1))
```



```
#dev.new()
```

```
#####3. calculating values RRA,POO,wPOO,FOO for COI
```

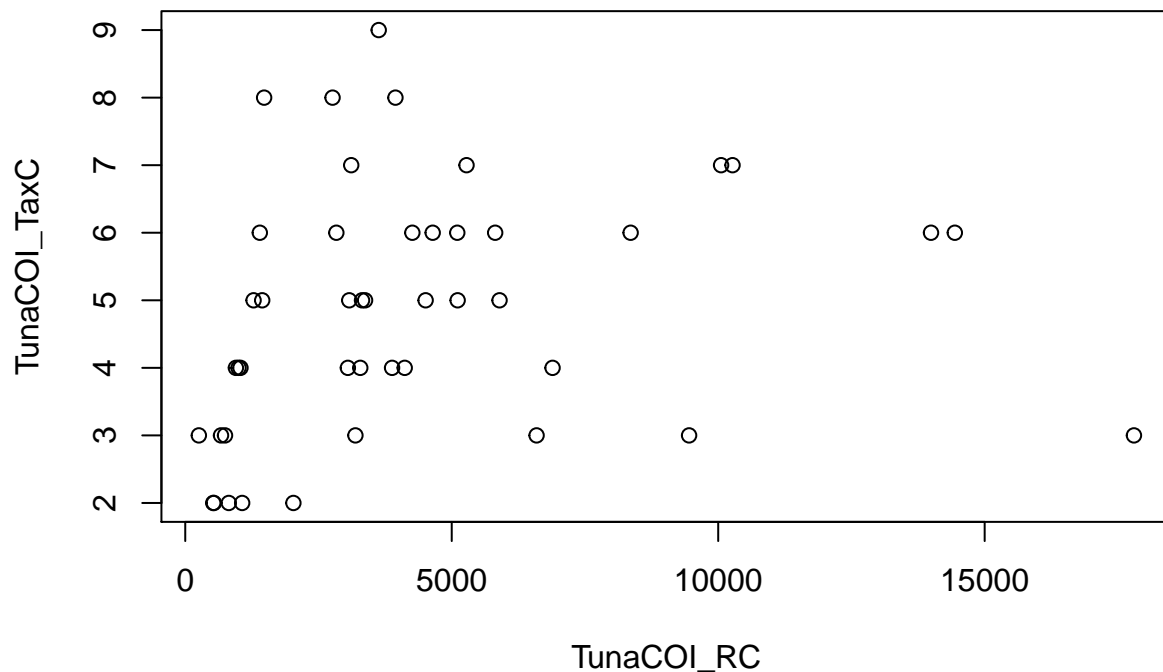


```
#####3. calculating values RRA,POO,wPOO,FOO for COI
TunaCOI_D=as.matrix(df2_5)
# How many seq per stomach?
TunaCOI_RC=apply(TunaCOI_D,2,sum);TunaCOI_RC;mean(TunaCOI_RC)
```

```
## M275 J290 J269 M281 M261 M198 M273 J233 J201 M280 J222 M118 M277
## 2029 537 1480 1444 671 3630 6892 3051 3077 2764 13993 1399 8357
## J221 M262 M279 J226 J53 J215 M117 M33 J47 J276 J52 M29 J138
## 17801 3374 1282 1068 4118 2835 10054 1036 5815 3284 4510 950 4643
## J125 J121 M49 J144 J134 J150 J227 J57 M30 J46 J145 J96 J164
## 525 817 255 5104 3881 10269 5278 999 746 3317 5111 9454 3193
## M123 M253 J229 J217 J205 J170
## 4261 3114 6592 3944 14440 5897
```

```
## [1] 4384.244
```

```
write.csv(TunaCOI_RC,'TunaCOI_reads_per_stomach.csv')
# number of taxa against read depth
TunaCOI_TaxC=apply(TunaCOI_D,2,function(x) length(unique(x)))
plot(TunaCOI_RC,TunaCOI_TaxC)
```



```
write.csv(TunaCOI_TaxC,'TunaCOI_taxa_per_stomach.csv')
#Turn into proportions, proportional dataset
TunaCOI_D
```

##	M275	J290	J269	M281	M261	M198	M273	J233	J201	M280	J222	M118	
## anchovy	0	537	406	882	569	1238	4740	311	0	2170	3859	0	
## Arthropoda	0	0	6	17	102	100	0	0	361	167	0	51	
## cephaloda	0	0	0	0	0	0	0	0	0	0	0	0	
## Cepolaepola	0	0	0	0	0	0	0	0	0	0	0	0	
## Chaetognatha	0	0	0	0	0	17	0	0	0	0	0	0	
## Cnidaria	0	0	12	0	0	81	2	0	0	30	6	6	
## Echinodermata	0	0	0	0	0	0	0	0	0	0	0	0	
## mackerel	0	0	251	0	0	0	0	0	0	0	0	224	
## Mollusca	0	0	23	0	0	26	0	0	0	16	0	0	
## sardine	2029	0	0	0	0	2153	2150	1034	1556	351	8178	1103	
## sprat	0	0	756	328	0	0	0	1706	1081	0	1863	0	
## Tunicata	0	0	0	0	0	0	0	0	0	9	0	0	
## Vertebrata	0	0	26	217	0	13	0	0	79	21	87	15	
## Xenacoelomorpha	0	0	0	0	0	2	0	0	0	0	0	0	
##	M277	J221	M262	M279	J226	J53	J215	M117	M33	J47	J276	J52	M29
## anchovy	8030	11410	1799	800	1068	3088	2699	4161	0	4223	2498	2180	433
## Arthropoda	181	0	34	0	0	0	110	3	0	6	0	0	0
## cephaloda	0	0	0	0	0	0	0	0	0	0	0	0	0
## Cepolaepola	0	0	0	0	0	0	0	0	0	0	0	0	0
## Chaetognatha	0	0	0	0	0	0	0	0	0	0	0	0	0
## Cnidaria	39	0	0	2	0	0	5	0	0	0	0	0	0
## Echinodermata	0	0	0	0	0	0	9	0	0	17	0	0	0
## mackerel	0	0	0	0	0	1027	0	0	0	1474	0	0	0
## Mollusca	57	0	29	0	0	0	12	24	9	89	0	13	0
## sardine	0	0	0	383	0	0	0	5223	992	0	705	1634	424
## sprat	0	6391	0	0	0	0	0	564	0	0	81	683	93
## Tunicata	0	0	0	0	0	3	0	0	0	0	0	0	0
## Vertebrata	50	0	1512	97	0	0	0	79	35	6	0	0	0
## Xenacoelomorpha	0	0	0	0	0	0	0	0	0	0	0	0	0
##	J138	J125	J121	M49	J144	J134	J150	J227	J57	M30	J46	J145	J96
## anchovy	0	0	0	242	3281	2833	2756	3063	677	723	1995	1847	8991
## Arthropoda	118	0	0	0	0	0	37	5	0	0	0	20	0
## cephaloda	2745	0	0	0	0	0	0	0	0	0	0	0	0
## Cepolaepola	0	525	817	0	0	0	0	0	0	0	0	0	0
## Chaetognatha	0	0	0	0	0	0	0	4	0	0	0	0	0
## Cnidaria	0	0	0	0	3	0	8	9	0	0	3	3	0
## Echinodermata	0	0	0	0	0	0	0	0	0	0	0	0	0
## mackerel	460	0	0	13	603	1045	3579	345	311	0	1027	0	463
## Mollusca	0	0	0	0	0	0	0	0	0	0	0	0	0
## sardine	1312	0	0	0	983	0	3161	0	0	0	0	3241	0
## sprat	0	0	0	0	234	0	728	1852	0	23	292	0	0
## Tunicata	0	0	0	0	0	0	0	0	0	0	0	0	0
## Vertebrata	8	0	0	0	0	3	0	0	11	0	0	0	0
## Xenacoelomorpha	0	0	0	0	0	0	0	0	0	0	0	0	0
##	J164	M123	M253	J229	J217	J205	J170						
## anchovy	784	1599	0	2983	449	5173	2722						
## Arthropoda	0	0	1006	0	269	75	0						
## cephaloda	0	0	0	0	0	0	0						
## Cepolaepola	0	0	0	0	0	0	0						
## Chaetognatha	0	0	6	0	0	0	0						
## Cnidaria	0	0	0	0	6	13	0						
## Echinodermata	0	0	0	0	0	0	0						
## mackerel	0	728	0	0	0	0	0						

```
## Mollusca      0  0  4  0  0  0  16
## sardine      2409 1812 1733 3609 2496 8098  0
## sprat        0  115  360  0  680 1068 3123
## Tunicata     0  0  0  0  0  0  0
## Vertebrata   0  7  5  0  24  13  36
## Xenacoelomorpha 0  0  0  0  20  0  0
```

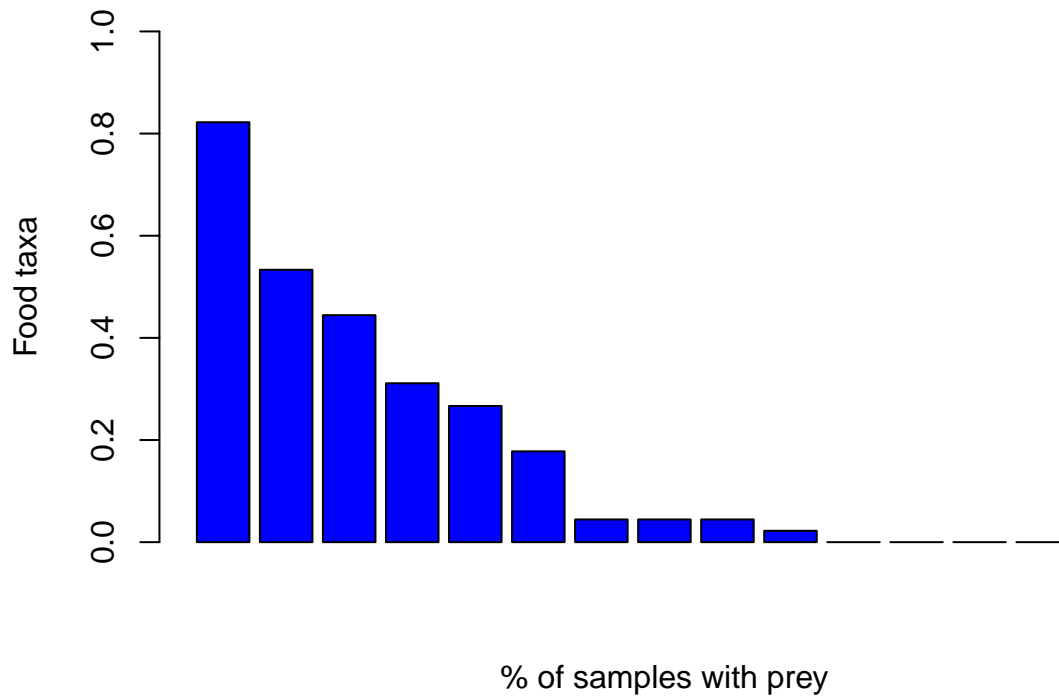
```
TunaCOI_Dprop=prop.table(TunaCOI_D,2)
dim(TunaCOI_Dprop)
```

```
## [1] 14 45
```

```
apply(TunaCOI_Dprop,2,sum)
```

```
## M275 J290 J269 M281 M261 M198 M273 J233 J201 M280 J222 M118 M277 J221 M262 M279
##      1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1
## J226 J53 J215 M117 M33 J47 J276 J52 M29 J138 J125 J121 M49 J144 J134 J150
##      1  1  1  1  1  1  1  1  1  1  1  1  1  1  1  1
## J227 J57 M30 J46 J145 J96 J164 M123 M253 J229 J217 J205 J170
##      1  1  1  1  1  1  1  1  1  1  1  1  1  1
```

```
write.csv(TunaCOI_Dprop, 'TunaCOI_proportions.csv')
# Make Presence absence (PA) dataset,
PA_TunaCOI_D= TunaCOI_Dprop
PA_TunaCOI_D[PA_TunaCOI_D>.0099999999]=1 ## here we fix the threshold for presence absence transformati
PA_TunaCOI_D[PA_TunaCOI_D<.01]=0 ## else 0
write.csv(TunaCOI_D, 'TunaCOI_pres_abs.csv')
FOO_All_TunaCOI_=apply(PA_TunaCOI_D,1,sum)/length(PA_TunaCOI_D[1,])
Ord_TunaCOI_=order(-FOO_All_TunaCOI_)
write.csv(Ord_TunaCOI_, 'TunaCOI_Foo.csv', row.names = TRUE)
barplot(FOO_All_TunaCOI_[Ord_TunaCOI_ ][1:15],ylim=c(0,1),col="blue",xaxt='n', xlab="% of samples with p
```



```
P_FOO_TunaCOI_ = apply(PA_TunaCOI_D,1,sum)/sum(apply(PA_TunaCOI_D,1,sum))
P_FOO_TunaCOI_
```

```
##      anchovy      Arthropoda      cephaloda      Cepolaepola      Chaetognatha
## 0.303278689 0.098360656 0.008196721 0.016393443 0.000000000
##      Cnidaria      Echinodermata      mackerel      Mollusca      sardine
## 0.016393443 0.000000000 0.114754098 0.016393443 0.196721311
##      sprat      Tunicata      Vertebrata      Xenacoelomorpha
## 0.163934426 0.000000000 0.065573770 0.000000000
```

```
sum(P_FOO_TunaCOI_)
```

```
## [1] 1
```

```
df_FOO_TunaCOI <- data.frame(P_FOO_TunaCOI_)
write.csv(df_FOO_TunaCOI,'TunaCOI_Poo.csv', row.names = TRUE)
```

```
P_wFOO_TunaCOI_=apply(prop.table(PA_TunaCOI_D,2),1,mean,na.rm=T)
P_wFOO_TunaCOI_
```

```
##      anchovy      Arthropoda      cephaloda      Cepolaepola      Chaetognatha
## 0.339629630 0.087037037 0.005555556 0.044444444 0.000000000
##      Cnidaria      Echinodermata      mackerel      Mollusca      sardine
## 0.011111111 0.000000000 0.106296296 0.011851852 0.194444444
```

```
##          sprat          Tunicata          Vertebrata Xenacoelomorpha
## 0.145185185 0.000000000 0.054444444 0.000000000
```

```
sum(P_wFOO_TunaCOI_)
```

```
## [1] 1
```

```
df_wFOO_TunaCOI <- data.frame(P_wFOO_TunaCOI_)
write.csv(df_wFOO_TunaCOI, 'TunaCOI_wPoo.csv', row.names = TRUE)
```

```
P_RRA_TunaCOI_ = apply(prop.table(as.matrix(TunaCOI_D), 2), 1, mean)
P_RRA_TunaCOI_
```

```
##          anchovy          Arthropoda          cephaloda          Cepolaepola          Chaetognatha
## 4.880851e-01 2.026187e-02 1.313806e-02 4.444444e-02 1.637298e-04
##          Cnidaria          Echinodermata          mackerel          Mollusca          sardine
## 1.361316e-03 1.355128e-04 5.832636e-02 1.808894e-03 2.654016e-01
##          sprat          Tunicata          Vertebrata Xenacoelomorpha
## 8.835000e-02 8.854799e-05 1.830967e-02 1.249324e-04
```

```
sum(P_RRA_TunaCOI_)
```

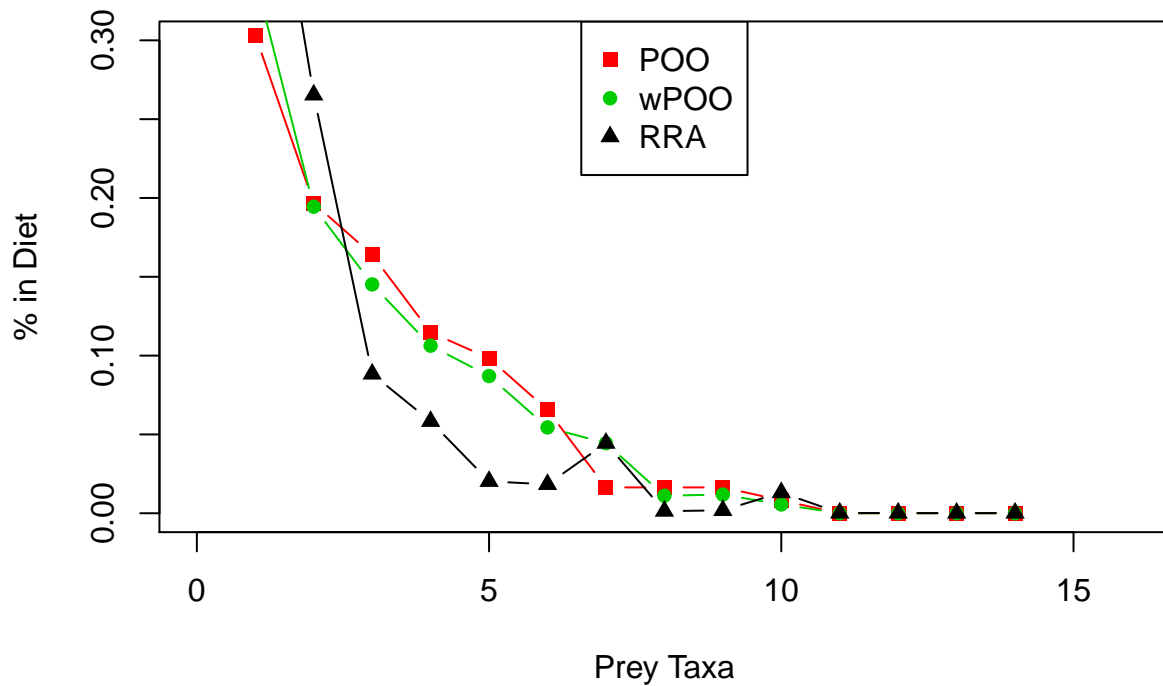
```
## [1] 1
```

```
df_RRA_TunaCOI <- data.frame(P_RRA_TunaCOI_)
write.csv(df_RRA_TunaCOI, 'TunaCOI_RRA.csv', row.names = TRUE)
```

```
plot(P_FOO_TunaCOI_[Ord_TunaCOI_][1:15], pch=15, col=2, type="b", ylim= c(0,0.3), ylab="% in Diet", xlab="Pr
points(16, sum(P_FOO_TunaCOI_[Ord_TunaCOI_][16:length(P_FOO_TunaCOI_)]), pch=15, col=2, cex=1.2 )
points(P_wFOO_TunaCOI_[Ord_TunaCOI_][1:15], pch=16, col=3, type="b")
points(16, sum(P_wFOO_TunaCOI_[Ord_TunaCOI_][16:length(P_wFOO_TunaCOI_)]), pch=16, col=3, cex=1.2 )
sum(P_wFOO_TunaCOI_[Ord_TunaCOI_][1:15])
```

```
## [1] NA
```

```
points(P_RRA_TunaCOI_[Ord_TunaCOI_][1:15], pch=17, type="b")
points(16, sum(P_RRA_TunaCOI_[Ord_TunaCOI_][16:length(P_RRA_TunaCOI_)]), pch=17, cex=1.2 )
legend('top', c('P00', 'wP00', 'RRA'), pch=c(15,16,17), col=c(2,3,1))
```



4. RRA PER YEAR TO COMPARE TO MOPHOLOGICAL RA, relative abundance data

```
df1_7<-t(df1_6)
```

```
df2_6<-t(df2_5)
```

```
S182011 <- subset(df1_7,dm2$Year == 2011)
```

```
S18_2011<-t(S182011)
```

```
S182012 <- subset(df1_7,dm2$Year == 2012)
```

```
S18_2012<-t(S182012)
```

```
S182013 <- subset(df1_7,dm2$Year == 2013)
```

```
S18_2013<-t(S182013)
```

```
S182014 <- subset(df1_7,dm2$Year == 2014)
```

```
S18_2014<-t(S182014)
```

```
COI2011 <- subset(df2_6,dm$Year == 2011)
```

```
COI_2011<-t(COI2011)
```

```
COI2012 <- subset(df2_6,dm$Year == 2012)
```

```
COI_2012<-t(COI2012)
```

```
COI2013 <- subset(df2_6,dm$Year == 2013)
```

```
COI_2013<-t(COI2013)
```

```
COI2014 <- subset(df2_6,dm$Year == 2014)
```

```
COI_2014<-t(COI2014)
```

```
RRA_2011_18S=apply(prop.table(as.matrix(S18_2011),2),1,mean)
```

```
RRA_2012_18S=apply(prop.table(as.matrix(S18_2012),2),1,mean)
```

```
RRA_2013_18S=apply(prop.table(as.matrix(S18_2013),2),1,mean)
```

```

RRA_2014_18S=apply(prop.table(as.matrix(S18_2014),2),1,mean)
RRA_2011_COI=apply(prop.table(as.matrix(COI_2011),2),1,mean)
RRA_2012_COI=apply(prop.table(as.matrix(COI_2012),2),1,mean)
RRA_2013_COI=apply(prop.table(as.matrix(COI_2013),2),1,mean)
RRA_2014_COI=apply(prop.table(as.matrix(COI_2014),2),1,mean)
RRA_18S_year <- cbind (RRA_2011_18S, RRA_2012_18S, RRA_2013_18S, RRA_2014_18S)
colnames(RRA_18S_year) <- c("RRA_2011","RRA_2012","RRA_2013","RRA_2014")
write.csv(RRA_18S_year,'RRA_Year_18S.csv', row.names = TRUE)
RRA_COI_year.all <- cbind (RRA_2011_COI, RRA_2012_COI, RRA_2013_COI, RRA_2014_COI)
colnames(RRA_COI_year.all) <- c("RRA_2011","RRA_2012","RRA_2013","RRA_2014")
RRA_COI_year<- data.frame(RRA_COI_year.all)
write.csv(RRA_COI_year.all,'RRA_Year_COI.csv', row.names = TRUE)

#include morphological data
RRA_COI_year<- cbind (RRA_2011_COI, RRA_2012_COI, RRA_2013_COI)
colnames(RRA_COI_year) <- c("RRA_2011","RRA_2012","RRA_2013")
colnames(morp) <- c("RA_2011","RA_2012","RA_2013")
morp<- data.frame(morp)
RRA_COI_year<- data.frame(RRA_COI_year)
Metazoa_verg<-merge(RRA_COI_year,morp,by="row.names",all.x=TRUE)

###T test,
t.test(Metazoa_verg$RRA_2011,Metazoa_verg$RA_2011)

```

4. RRA PER YEAR TO COMPARE TO MOPHOLOGICAL RA, relative abundance data

```

##
## Welch Two Sample t-test
##
## data: Metazoa_verg$RRA_2011 and Metazoa_verg$RA_2011
## t = -0.92498, df = 3.2972, p-value = 0.4176
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.7093934 0.3772505
## sample estimates:
## mean of x mean of y
## 0.07142857 0.23750000

```

```
t.test(Metazoa_verg$RRA_2012,Metazoa_verg$RA_2012)
```

```

##
## Welch Two Sample t-test
##
## data: Metazoa_verg$RRA_2012 and Metazoa_verg$RA_2012
## t = -1.3235, df = 3.5262, p-value = 0.2649
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.5417421 0.2045993
## sample estimates:
## mean of x mean of y
## 0.07142857 0.24000000

```

```
t.test(Metazoa_verg$RRA_2013, Metazoa_verg$RA_2013)
```

```
##  
## Welch Two Sample t-test  
##  
## data: Metazoa_verg$RRA_2013 and Metazoa_verg$RA_2013  
## t = -1.5372, df = 4.45, p-value = 0.1919  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -0.4612733 0.1241304  
## sample estimates:  
## mean of x mean of y  
## 0.07142857 0.24000000
```

```
t.test(RRA_COI_year, morp)
```

```
##  
## Welch Two Sample t-test  
##  
## data: RRA_COI_year and morp  
## t = -1.6405, df = 23.627, p-value = 0.1142  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -0.21390384 0.02453876  
## sample estimates:  
## mean of x mean of y  
## 0.07142857 0.16611111
```

```
Metazoa_verg.all<-merge(RRA_COI_year.all, morp, by="row.names", all.x=TRUE)  
write.csv(Metazoa_verg.all, 'RRA_RA_compPerYear.csv', row.names = TRUE)
```

```
##
```

```
##### 5. Statistical distribution tests with euclidean distance/Sorensen dissimilarity, based on OTU lev
```

```
#Euclidian 18S
```

```
euc.18S =vegdist(df3_8, binary=TRUE)  
anosim(euc.18S, dm2$Weight)
```

```
##  
## Call:  
## anosim(x = euc.18S, grouping = dm2$Weight)  
## Dissimilarity: binary bray  
##  
## ANOSIM statistic R: 0.332  
## Significance: 0.037  
##  
## Permutation: free  
## Number of permutations: 999
```



```
anosim(euc.18S, dm2$code.port)
```

```
##  
## Call:  
## anosim(x = euc.18S, grouping = dm2$code.port)  
## Dissimilarity: binary bray  
##  
## ANOSIM statistic R: -0.0007829  
##      Significance: 0.486  
##  
## Permutation: free  
## Number of permutations: 999
```

```
anosim(euc.18S, dm2$Longueur_Bouche)
```

```
##  
## Call:  
## anosim(x = euc.18S, grouping = dm2$Longueur_Bouche)  
## Dissimilarity: binary bray  
##  
## ANOSIM statistic R: -0.1191  
##      Significance: 0.84  
##  
## Permutation: free  
## Number of permutations: 999
```

```
anosim(euc.18S, dm2$Sexe)
```

```
##  
## Call:  
## anosim(x = euc.18S, grouping = dm2$Sexe)  
## Dissimilarity: binary bray  
##  
## ANOSIM statistic R: -0.01499  
##      Significance: 0.621  
##  
## Permutation: free  
## Number of permutations: 999
```

```
anosim(euc.18S, dm2$Reproductive.Stage)
```

```
##  
## Call:  
## anosim(x = euc.18S, grouping = dm2$Reproductive.Stage)  
## Dissimilarity: binary bray  
##  
## ANOSIM statistic R: -0.02501  
##      Significance: 0.649  
##  
## Permutation: free  
## Number of permutations: 999
```

```
anosim(euc.18S, dm2$SIZE_CLASS)
```

```
##  
## Call:  
## anosim(x = euc.18S, grouping = dm2$SIZE_CLASS)  
## Dissimilarity: binary bray  
##  
## ANOSIM statistic R: -0.06999  
##      Significance: 0.991  
##  
## Permutation: free  
## Number of permutations: 999
```

```
anosim(euc.18S, dm2$Year)
```

```
##  
## Call:  
## anosim(x = euc.18S, grouping = dm2$Year)  
## Dissimilarity: binary bray  
##  
## ANOSIM statistic R: 0.01035  
##      Significance: 0.371  
##  
## Permutation: free  
## Number of permutations: 999
```

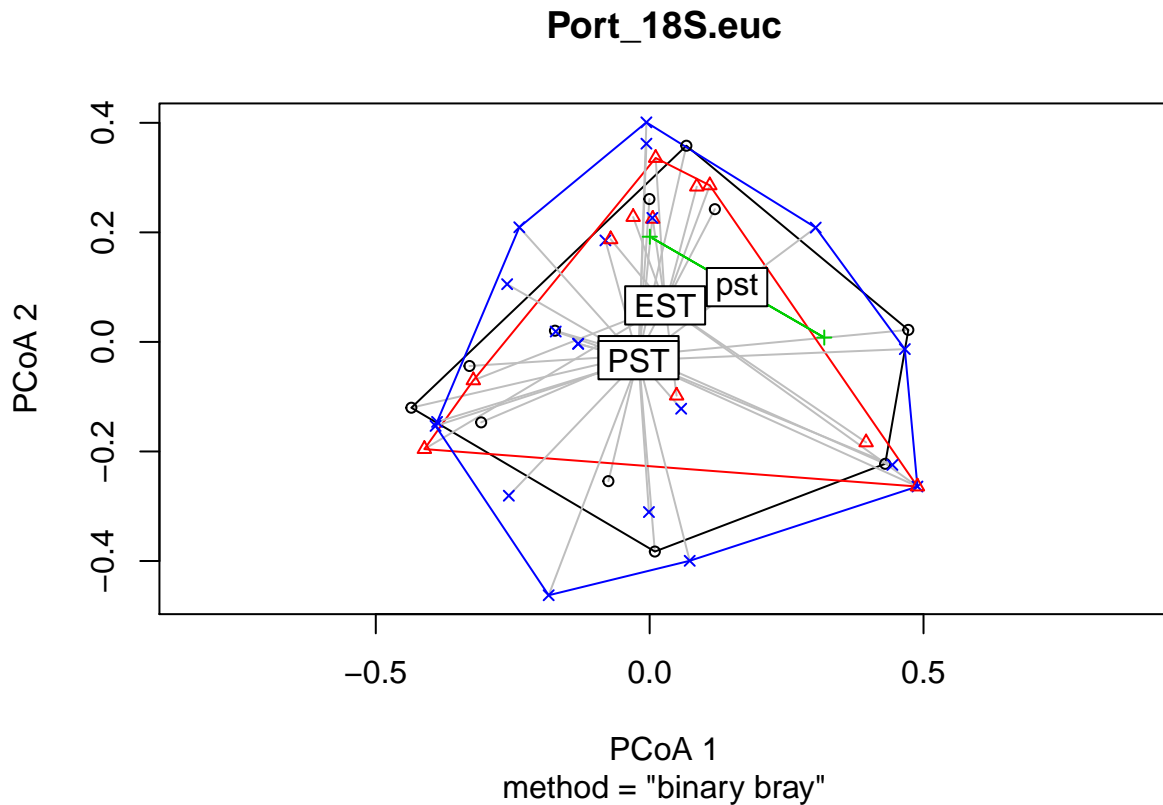
```
Weight_18S.euc<- betadisper(euc.18S, dm2$Weight, type = c("centroid"))  
Port_18S.euc<- betadisper(euc.18S, dm2$code.port, type = c("centroid"))  
mouth.Lengt_18S.euc<- betadisper(euc.18S, dm2$Longueur_Bouche, type = c("centroid"))  
Sex_18S.euc<- betadisper(euc.18S, dm2$Sexe, type = c("centroid"))  
rep.stage_18S.euc<- betadisper(euc.18S, dm2$Reproductive.Stage, type = c("centroid"))  
size.class_18S.euc<- betadisper(euc.18S, dm2$SIZE_CLASS, type = c("centroid"))  
Year_18S.euc<- betadisper(euc.18S, dm2$Year, type = c("centroid"))  
anova(Weight_18S.euc)
```

```
## Analysis of Variance Table  
##  
## Response: Distances  
##           Df Sum Sq Mean Sq F value Pr(>F)  
## Groups    36 1.64314 0.045643  15.714 0.00046 ***  
## Residuals  7 0.02033 0.002905  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot (Weight_18S.euc)
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non  
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '31' de pch non  
## implémentée
```

```
anova(mouth.Lengt_18S.euc)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df Sum Sq Mean Sq F value    Pr(>F)
## Groups  29  2.86170  0.098679   74.153 4.178e-11 ***
## Residuals 14  0.01863  0.001331
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(mouth.Lengt_18S.euc)
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '29' de pch non
## implémentée
```

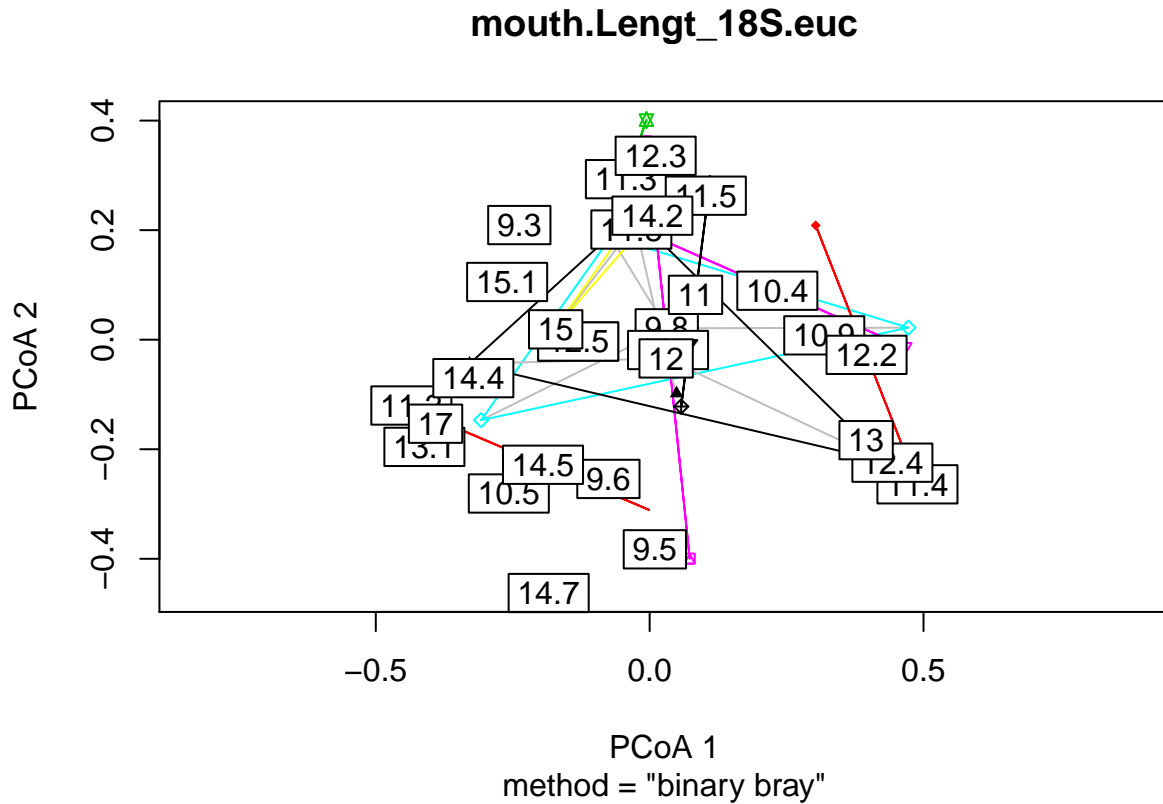
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '30' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '28' de pch non
## implémentée
```

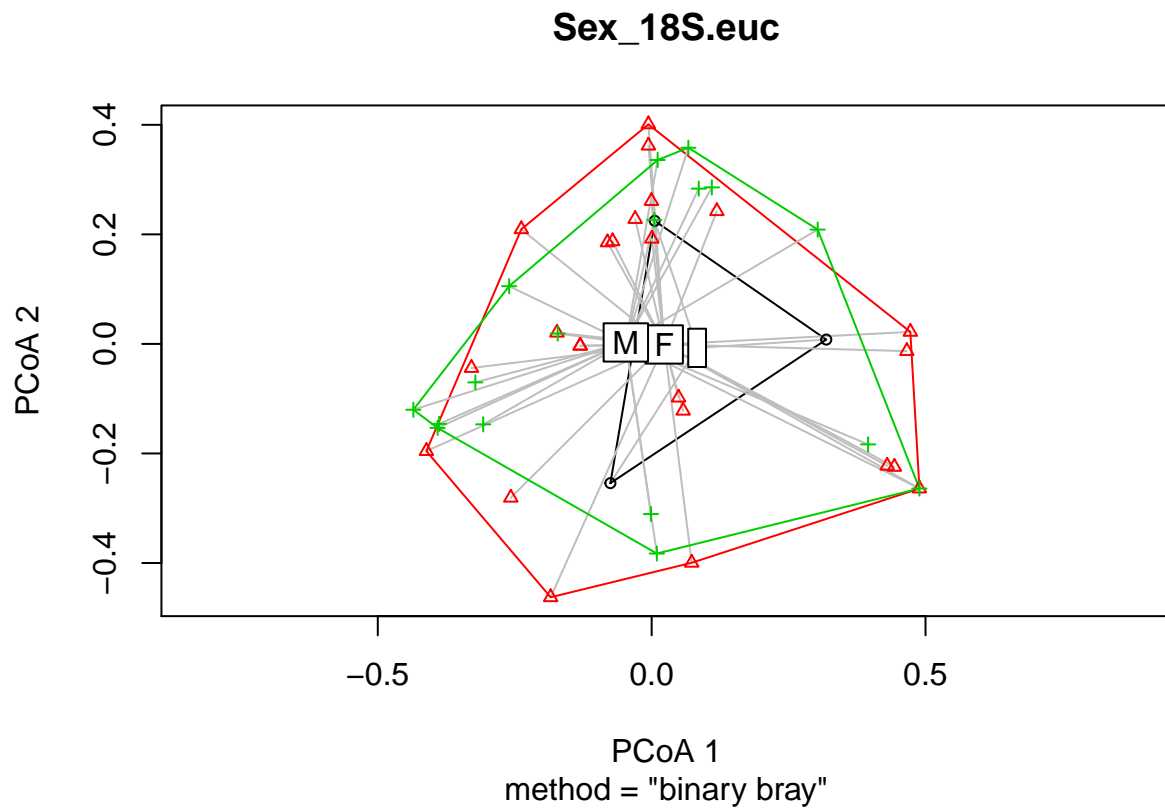
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '27' de pch non
## implémentée
```



```
anova(Sex_18S.euc)
```

```
## Analysis of Variance Table
##
## Response: Distances
##          Df  Sum Sq  Mean Sq F value Pr(>F)
## Groups    2 0.038222 0.0191109  3.3269 0.04582 *
## Residuals 41 0.235520 0.0057444
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(Sex_18S.euc)
```

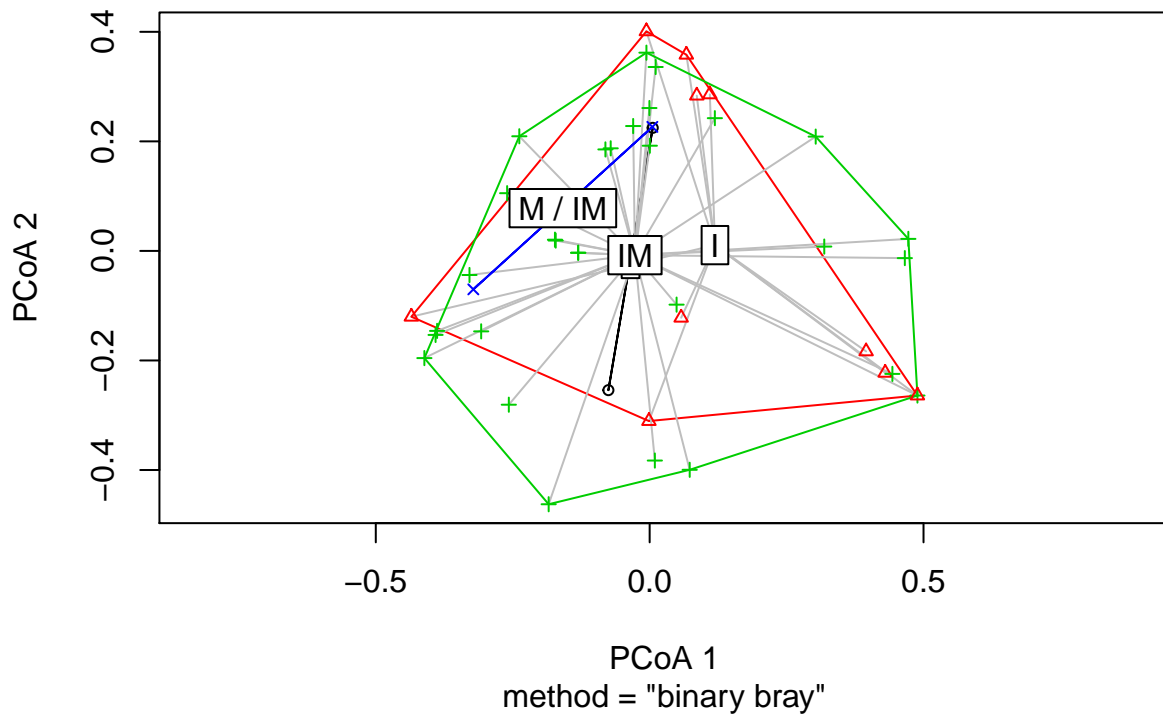


```
anova(rep.stage_18S.euc)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df  Sum Sq  Mean Sq F value Pr(>F)
## Groups   3 0.058879 0.0196264  3.6315 0.0208 *
## Residuals 40 0.216182 0.0054046
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(rep.stage_18S.euc)
```

rep.stage_18S.euc

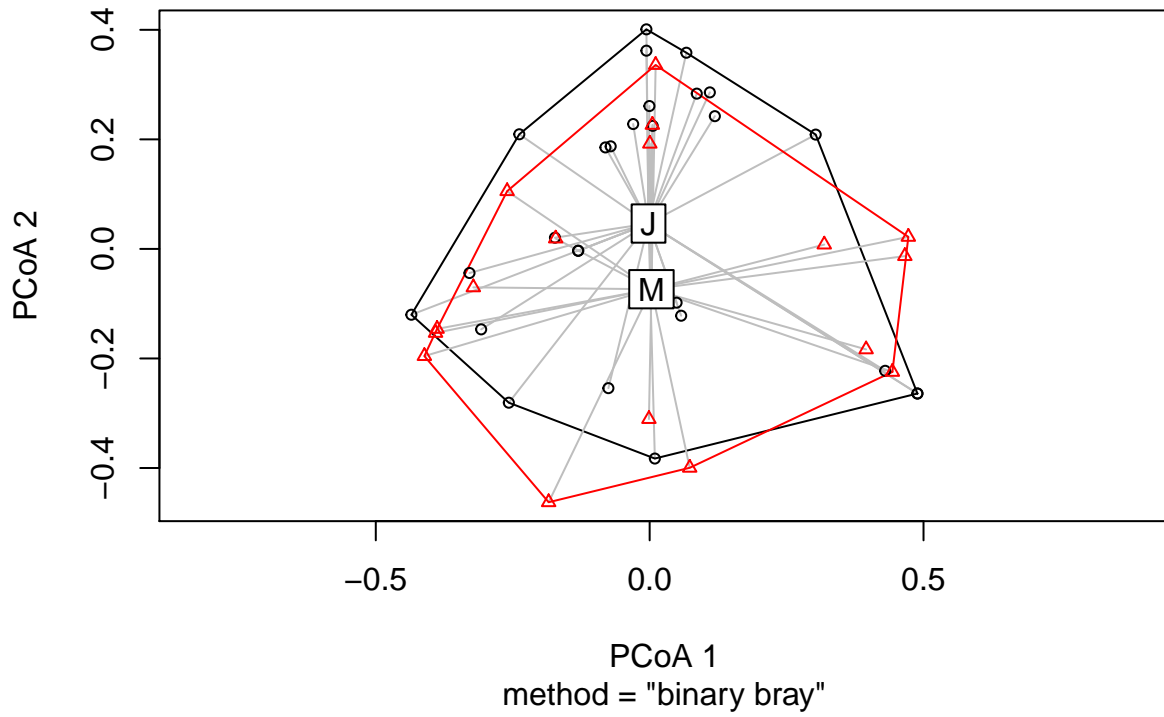


```
anova(size.class_18S.euc)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df  Sum Sq Mean Sq F value Pr(>F)
## Groups    1 0.038615 0.038615  6.3065 0.01596 *
## Residuals 42 0.257169 0.006123
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(size.class_18S.euc)
```

size.class_18S.euc

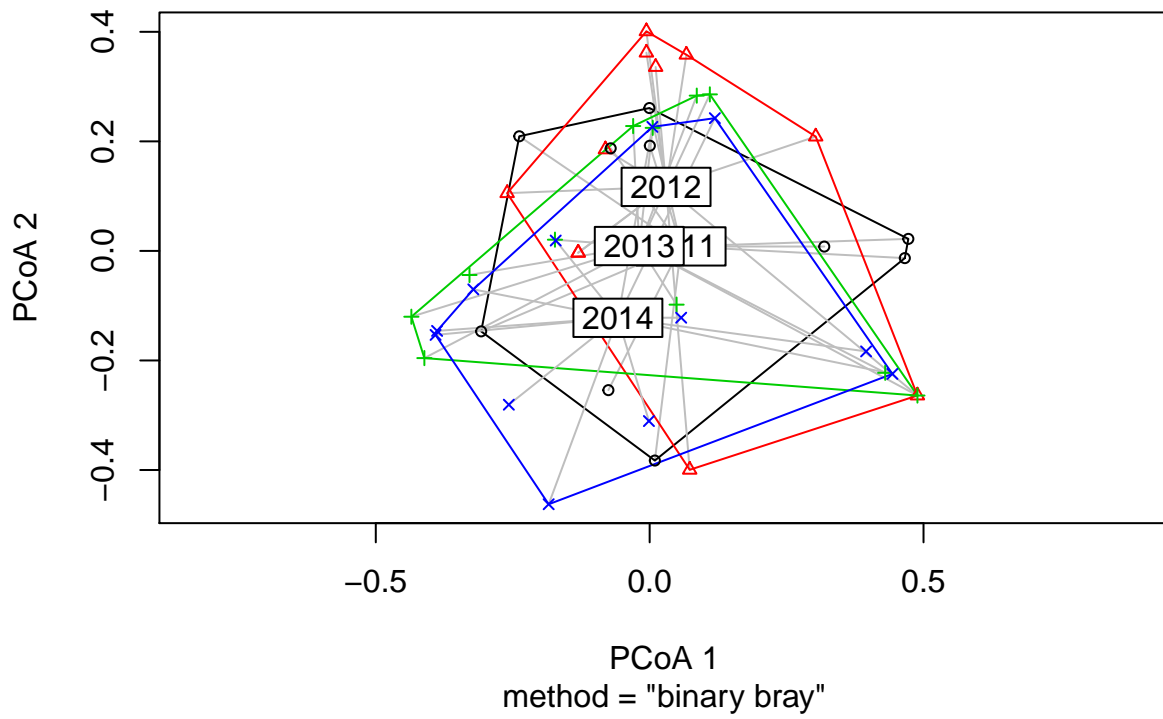


```
anova(Year_18S.euc)
```

```
## Analysis of Variance Table  
##  
## Response: Distances  
##      Df  Sum Sq  Mean Sq F value Pr(>F)  
## Groups   3 0.023615 0.0078718  1.1881 0.3265  
## Residuals 40 0.265013 0.0066253
```

```
plot(Year_18S.euc)
```


Year_18S.euc



```
#####Sorensen 18S
```

```
sor.18S =vegdist(df3_8pa,binary=TRUE)  
anosim(sor.18S, dm2$Weight)
```

```
##  
## Call:  
## anosim(x = sor.18S, grouping = dm2$Weight)  
## Dissimilarity: binary bray  
##  
## ANOSIM statistic R: 0.332  
##      Significance: 0.057  
##  
## Permutation: free  
## Number of permutations: 999
```

```
anosim(sor.18S, dm2$code.port)
```

```
##  
## Call:  
## anosim(x = sor.18S, grouping = dm2$code.port)  
## Dissimilarity: binary bray  
##  
## ANOSIM statistic R: -0.0007829  
##      Significance: 0.47  
##
```

```
## Permutation: free
## Number of permutations: 999
```

```
anosim(sor.18S, dm2$Longueur_Bouche)
```

```
##
## Call:
## anosim(x = sor.18S, grouping = dm2$Longueur_Bouche)
## Dissimilarity: binary bray
##
## ANOSIM statistic R: -0.1191
##      Significance: 0.852
##
## Permutation: free
## Number of permutations: 999
```

```
anosim(sor.18S, dm2$Sexe)
```

```
##
## Call:
## anosim(x = sor.18S, grouping = dm2$Sexe)
## Dissimilarity: binary bray
##
## ANOSIM statistic R: -0.01499
##      Significance: 0.646
##
## Permutation: free
## Number of permutations: 999
```

```
anosim(sor.18S, dm2$Reproductive.Stage)
```

```
##
## Call:
## anosim(x = sor.18S, grouping = dm2$Reproductive.Stage)
## Dissimilarity: binary bray
##
## ANOSIM statistic R: -0.02501
##      Significance: 0.63
##
## Permutation: free
## Number of permutations: 999
```

```
anosim(sor.18S, dm2$SIZE_CLASS)
```

```
##
## Call:
## anosim(x = sor.18S, grouping = dm2$SIZE_CLASS)
## Dissimilarity: binary bray
##
## ANOSIM statistic R: -0.06999
##      Significance: 0.993
```

```
##  
## Permutation: free  
## Number of permutations: 999
```

```
anosim(sor.18S, dm2$Year)
```

```
##  
## Call:  
## anosim(x = sor.18S, grouping = dm2$Year)  
## Dissimilarity: binary bray  
##  
## ANOSIM statistic R: 0.01035  
##      Significance: 0.369  
##  
## Permutation: free  
## Number of permutations: 999
```

```
Weight_18S.sor<- betadisper(sor.18S, dm2$Weight, type = c("centroid"))  
Port_18S.sor<- betadisper(sor.18S, dm2$code.port, type = c("centroid"))  
mouth.Lengt_18S.sor<- betadisper(sor.18S, dm2$Longueur_Bouche, type = c("centroid"))  
Sex_18S.sor<- betadisper(sor.18S, dm2$Sexe, type = c("centroid"))  
rep.stage_18S.sor<- betadisper(sor.18S, dm2$Reproductive.Stage, type = c("centroid"))  
size.class_18S.sor<- betadisper(sor.18S, dm2$SIZE_CLASS, type = c("centroid"))  
Year_18S.sor<- betadisper(sor.18S, dm2$Year, type = c("centroid"))  
anova(Weight_18S.sor)
```

```
## Analysis of Variance Table  
##  
## Response: Distances  
##           Df Sum Sq Mean Sq F value Pr(>F)  
## Groups    36 1.64314  0.045643  15.714 0.00046 ***  
## Residuals  7 0.02033  0.002905  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot (Weight_18S.sor)
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non  
## implémentée
```

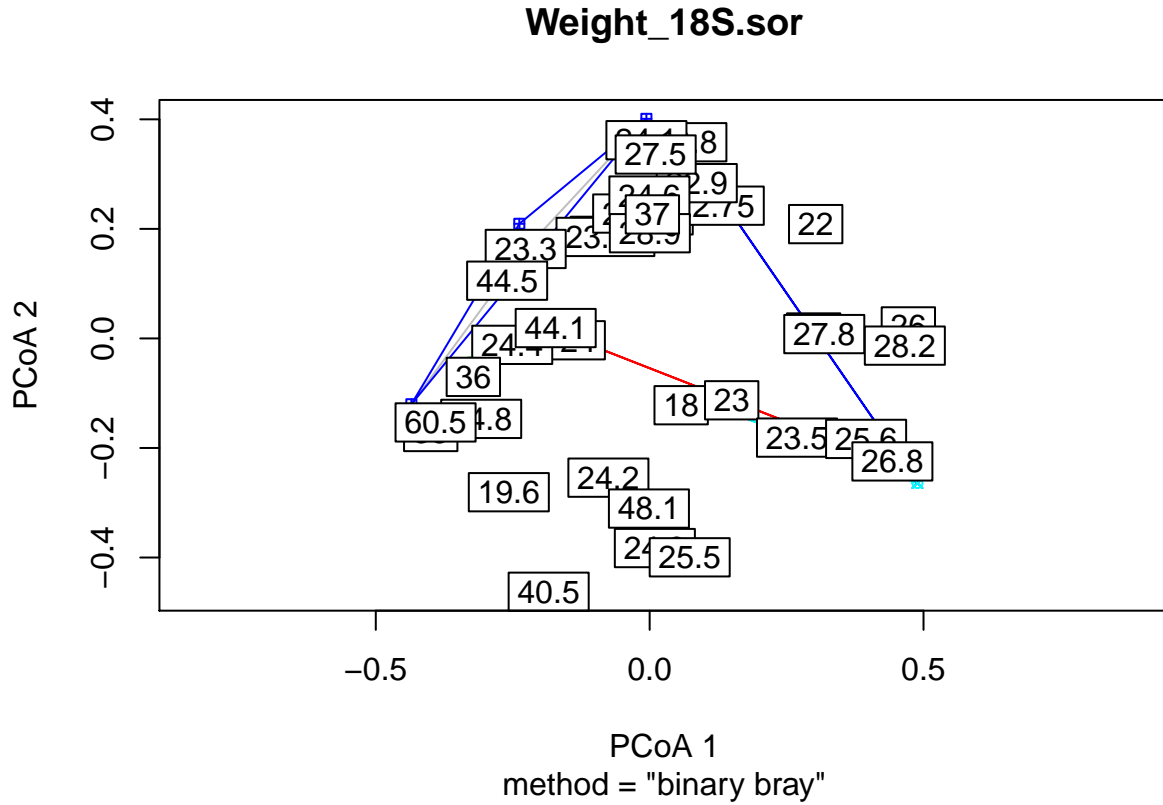
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '31' de pch non  
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '30' de pch non  
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '27' de pch non  
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '29' de pch non  
## implémentée
```

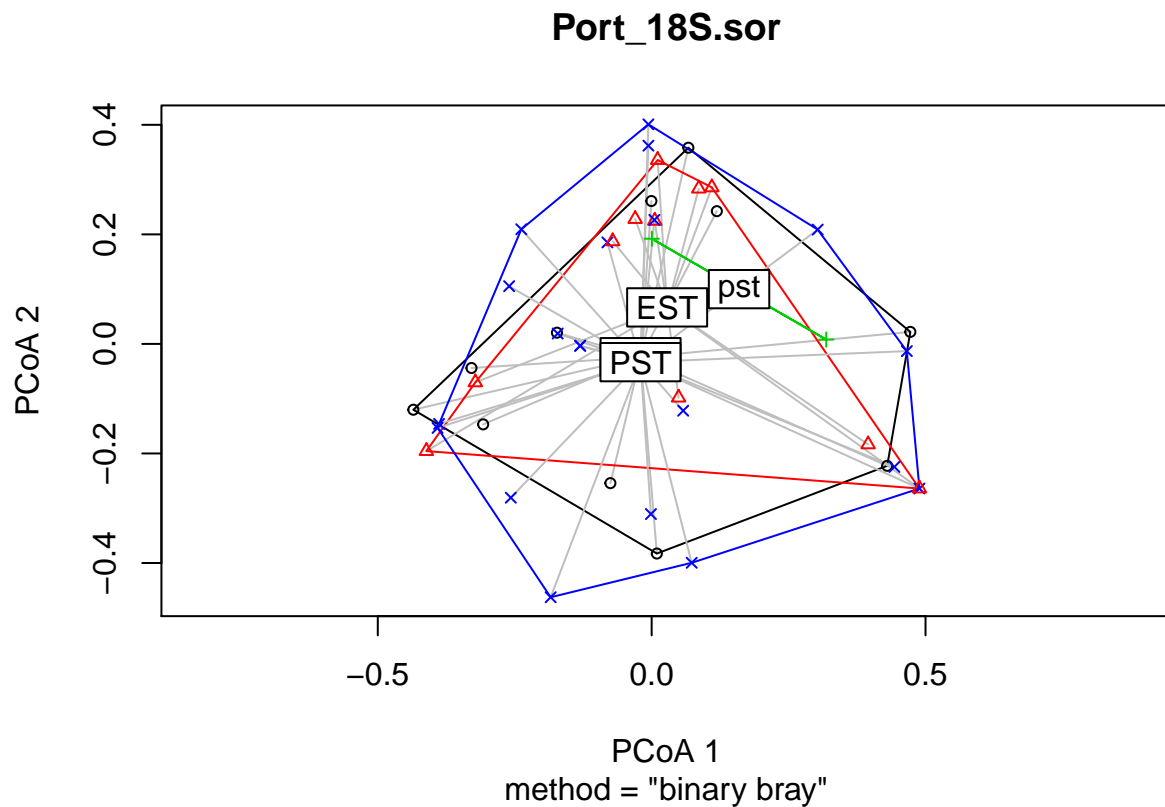
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '28' de pch non
## implémentée
```



```
anova(Port_18S.sor)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df  Sum Sq  Mean Sq F value Pr(>F)
## Groups     3 0.029892 0.0099641  1.8234 0.1584
## Residuals 40 0.218589 0.0054647
```

```
plot(Port_18S.sor)
```



```
anova(mouth.Lengt_18S.sor)
```

```
## Analysis of Variance Table
##
## Response: Distances
##          Df Sum Sq Mean Sq F value    Pr(>F)
## Groups   29 2.86170 0.098679  74.153 4.178e-11 ***
## Residuals 14 0.01863 0.001331
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(mouth.Lengt_18S.sor)
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '29' de pch non
## implémentée
```

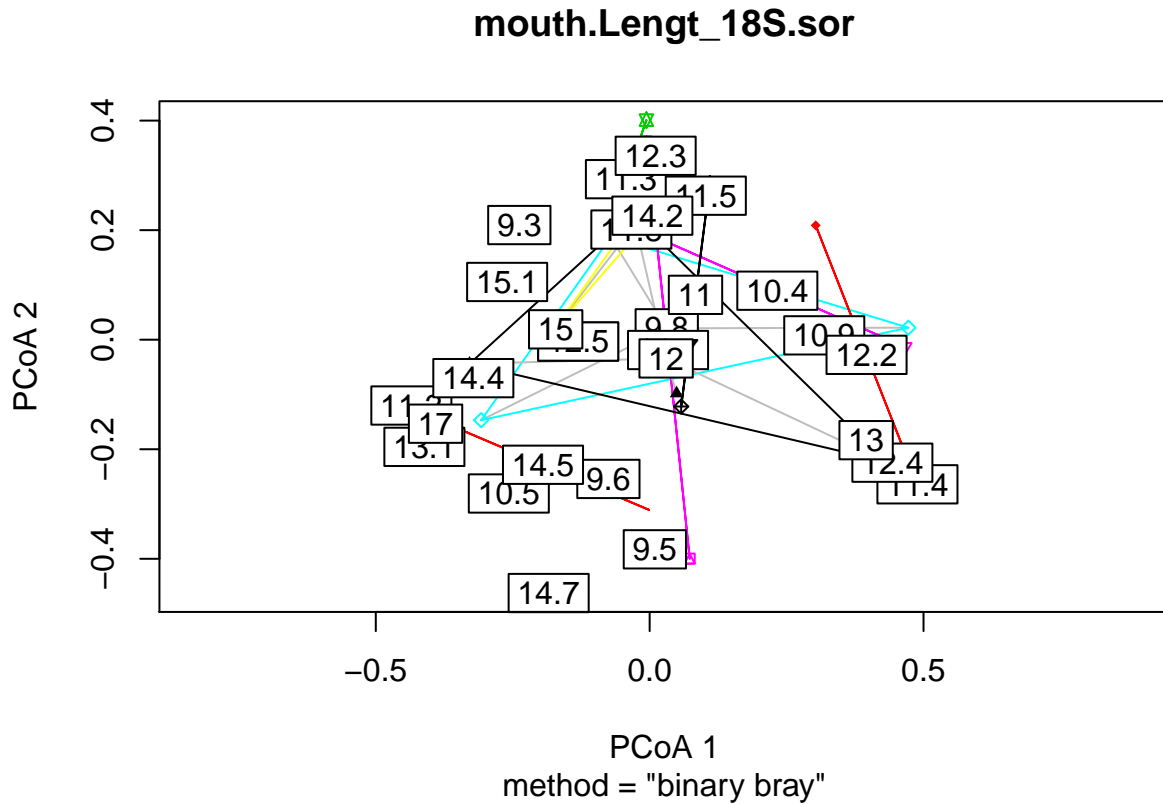
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '30' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '28' de pch non
## implémentée
```

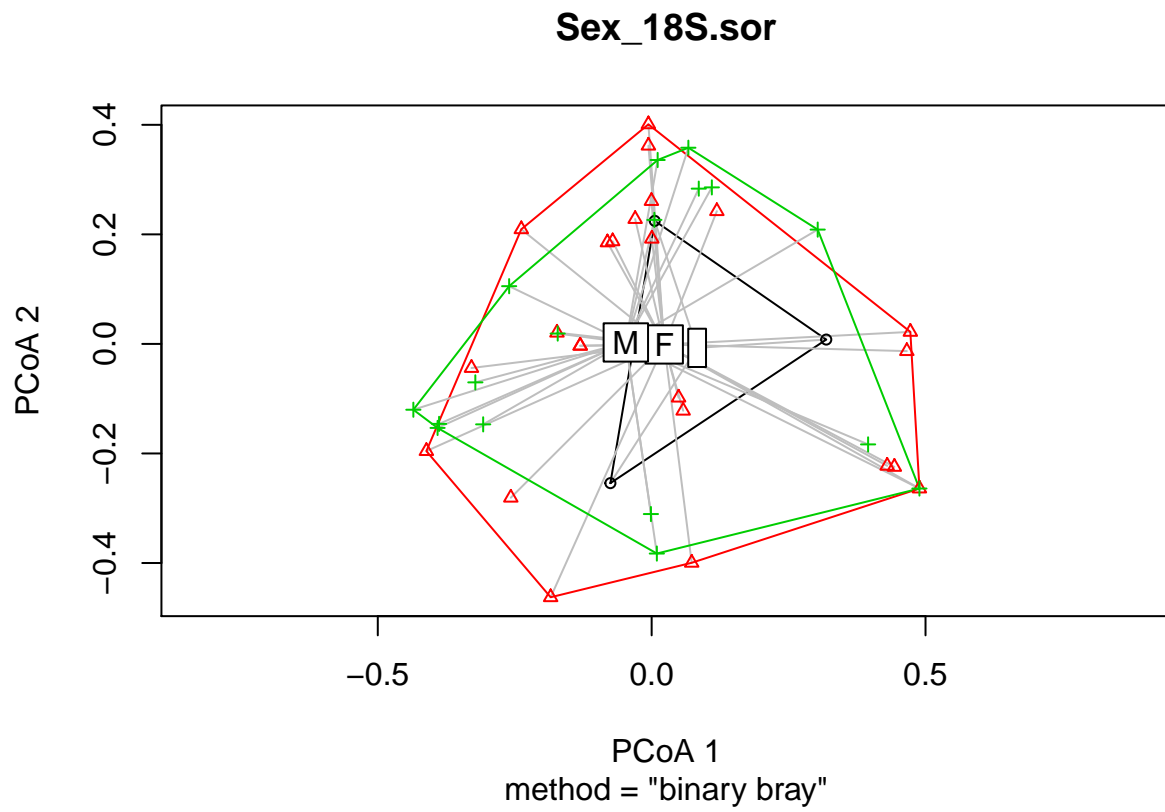
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '27' de pch non
## implémentée
```



```
anova(Sex_18S.sor)
```

```
## Analysis of Variance Table
##
## Response: Distances
##          Df  Sum Sq  Mean Sq F value Pr(>F)
## Groups    2  0.038222  0.0191109   3.3269 0.04582 *
## Residuals 41  0.235520  0.0057444
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(Sex_18S.sor)
```

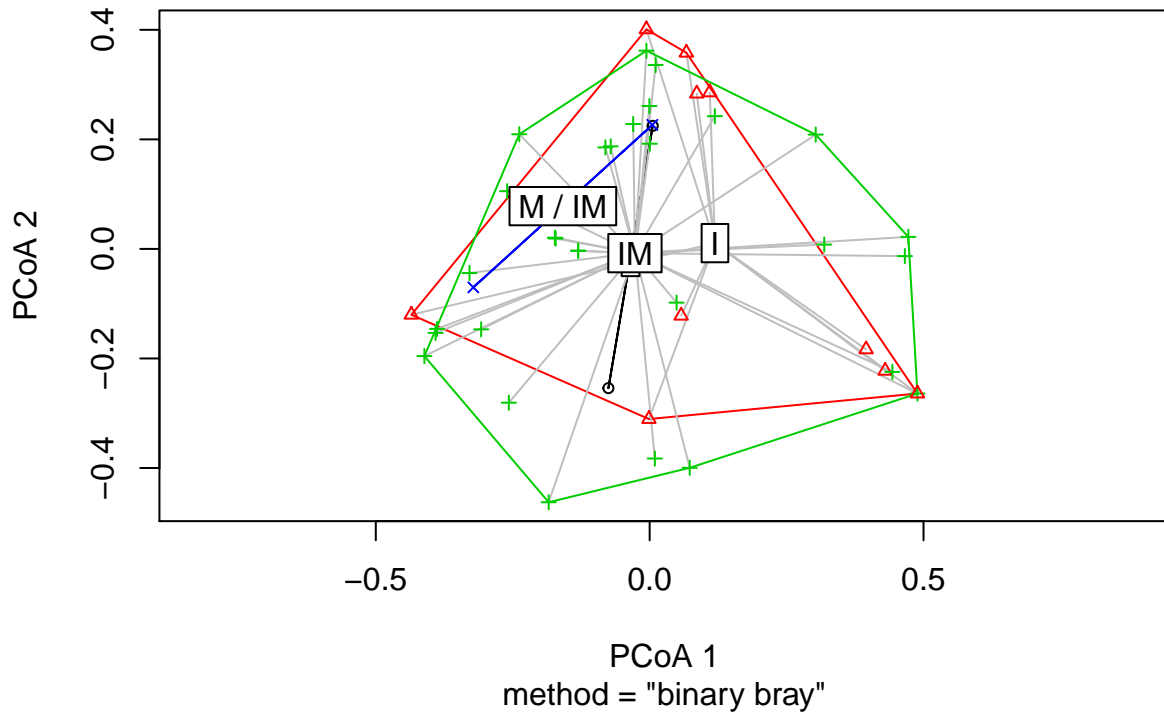


```
anova(rep.stage_18S.sor)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df  Sum Sq  Mean Sq F value Pr(>F)
## Groups   3 0.058879 0.0196264  3.6315 0.0208 *
## Residuals 40 0.216182 0.0054046
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(rep.stage_18S.sor)
```

rep.stage_18S.sor

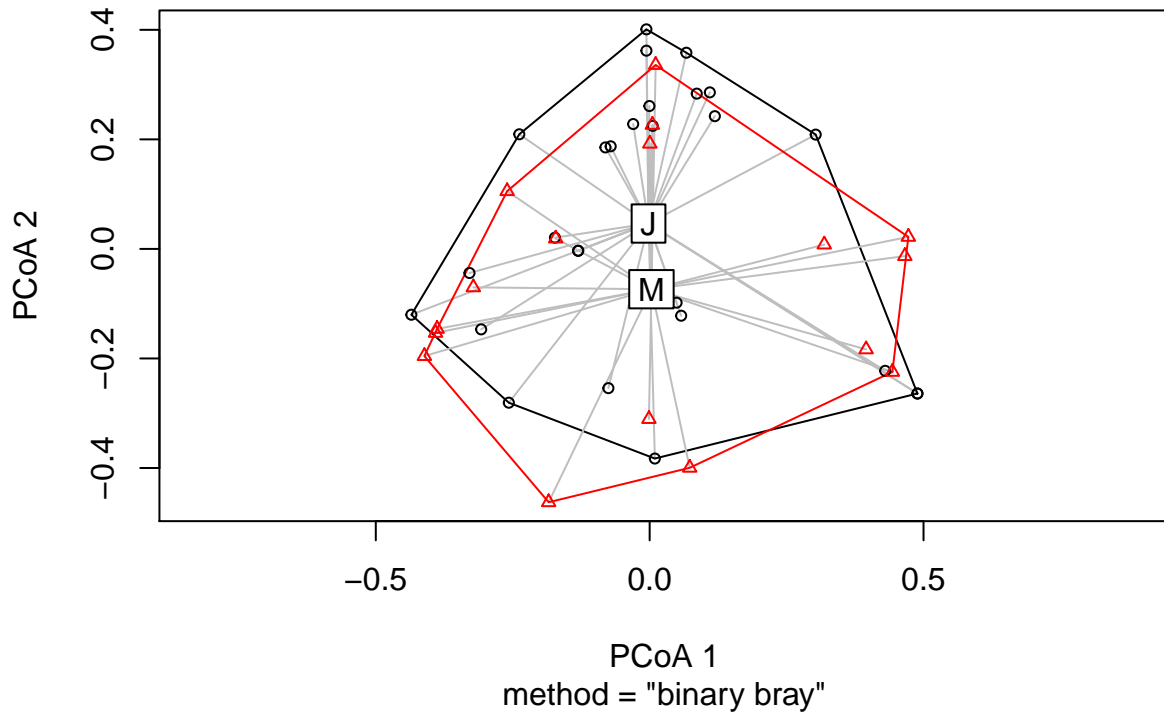


```
anova(size.class_18S.sor)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df  Sum Sq Mean Sq F value Pr(>F)
## Groups   1 0.038615 0.038615  6.3065 0.01596 *
## Residuals 42 0.257169 0.006123
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(size.class_18S.sor)
```


size.class_18S.sor

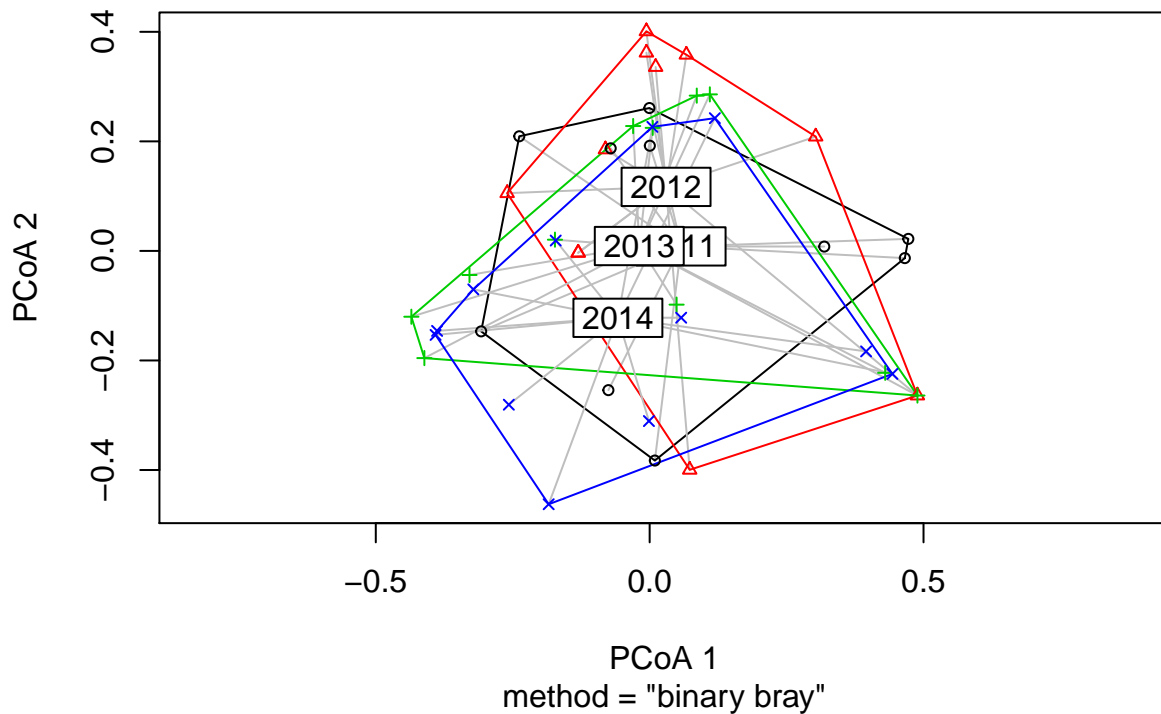


```
anova(Year_18S.sor)
```

```
## Analysis of Variance Table  
##  
## Response: Distances  
##      Df  Sum Sq  Mean Sq F value Pr(>F)  
## Groups    3 0.023615 0.0078718  1.1881 0.3265  
## Residuals 40 0.265013 0.0066253
```

```
plot(Year_18S.sor)
```

Year_18S.sor



```
#####Euclidian COI
```

```
euc.COI =vegdist(df4_8,method="euclidean")  
anosim(euc.COI, dm$Weight)
```

```
##  
## Call:  
## anosim(x = euc.COI, grouping = dm$Weight)  
## Dissimilarity: euclidean  
##  
## ANOSIM statistic R: 0.2279  
##      Significance: 0.113  
##  
## Permutation: free  
## Number of permutations: 999
```

```
anosim(euc.COI, dm$code.port)
```

```
##  
## Call:  
## anosim(x = euc.COI, grouping = dm$code.port)  
## Dissimilarity: euclidean  
##  
## ANOSIM statistic R: 0.04341  
##      Significance: 0.205  
##
```

```
## Permutation: free
## Number of permutations: 999
```

```
anosim(euc.COI, dm$Longueur_Bouche)
```

```
##
## Call:
## anosim(x = euc.COI, grouping = dm$Longueur_Bouche)
## Dissimilarity: euclidean
##
## ANOSIM statistic R: 0.2149
##      Significance: 0.05
##
## Permutation: free
## Number of permutations: 999
```

```
anosim(euc.COI, dm$Sexe)
```

```
##
## Call:
## anosim(x = euc.COI, grouping = dm$Sexe)
## Dissimilarity: euclidean
##
## ANOSIM statistic R: 0.0436
##      Significance: 0.158
##
## Permutation: free
## Number of permutations: 999
```

```
anosim(euc.COI, dm$Reproductive.Stage)
```

```
##
## Call:
## anosim(x = euc.COI, grouping = dm$Reproductive.Stage)
## Dissimilarity: euclidean
##
## ANOSIM statistic R: -0.07427
##      Significance: 0.81
##
## Permutation: free
## Number of permutations: 999
```

```
anosim(euc.COI, dm$SIZE_CLASS)
```

```
##
## Call:
## anosim(x = euc.COI, grouping = dm$SIZE_CLASS)
## Dissimilarity: euclidean
##
## ANOSIM statistic R: -0.01529
##      Significance: 0.558
```

```
##  
## Permutation: free  
## Number of permutations: 999
```

```
anosim(euc.COI, dm$Year)
```

```
##  
## Call:  
## anosim(x = euc.COI, grouping = dm$Year)  
## Dissimilarity: euclidean  
##  
## ANOSIM statistic R: 0.05183  
##      Significance: 0.085  
##  
## Permutation: free  
## Number of permutations: 999
```

```
Weight_COI.euc<- betadisper(euc.COI, dm$Weight, type = c("centroid"))  
Port_COI.euc<- betadisper(euc.COI, dm$code.port, type = c("centroid"))  
mouth.Length_COI.euc<- betadisper(euc.COI, dm$Longueur_Bouche, type = c("centroid"))  
Sex_COI.euc<- betadisper(euc.COI, dm$Sexe, type = c("centroid"))  
rep.stage_COI.euc<- betadisper(euc.COI, dm$Reproductive.Stage, type = c("centroid"))  
size.class_COI.euc<- betadisper(euc.COI, dm$SIZE_CLASS, type = c("centroid"))  
Year_COI.euc<- betadisper(euc.COI, dm$Year, type = c("centroid"))
```

```
anova(Weight_COI.euc)
```

```
## Analysis of Variance Table  
##  
## Response: Distances  
##          Df Sum Sq Mean Sq F value Pr(>F)  
## Groups    37  1.41857  0.038340  10.764 0.001569 **  
## Residuals   7  0.02493  0.003562  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot (Weight_COI.euc)
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '28' de pch non  
## implémentée
```

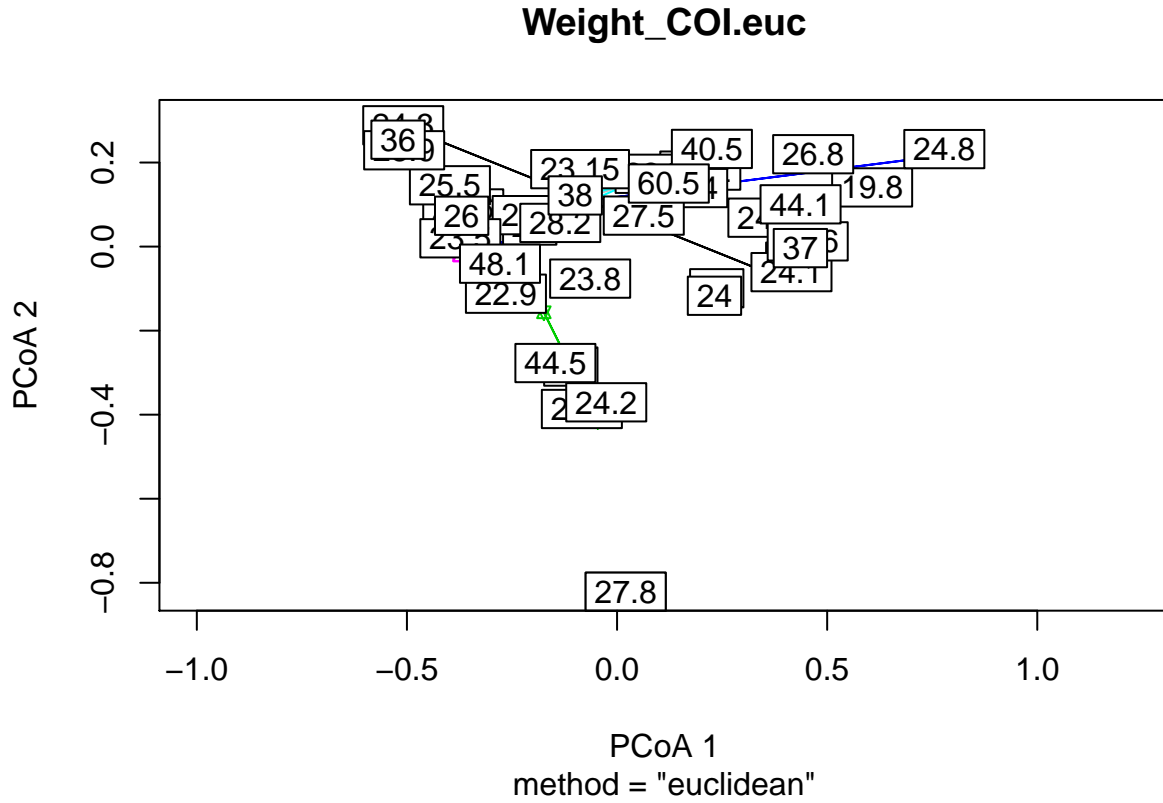
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '30' de pch non  
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '29' de pch non  
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '27' de pch non  
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '31' de pch non  
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non
## implémentée
```

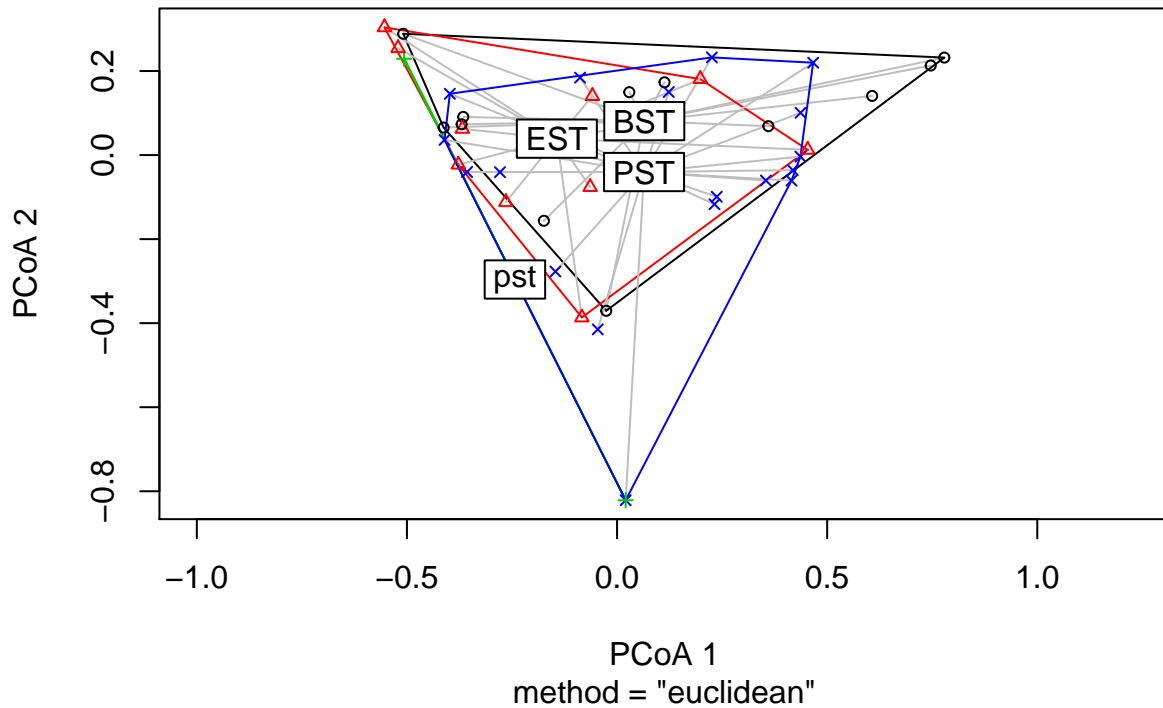


```
anova(Port_COI.euc)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df Sum Sq Mean Sq F value Pr(>F)
## Groups     3  0.10027  0.033424   1.0942  0.3624
## Residuals  41  1.25246  0.030548
```

```
plot(Port_COI.euc)
```

Port_COI.euc



```
anova(mouth.Length_COI.euc)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Groups     29  1.70356  0.058743  19.258 1.559e-07 ***
## Residuals  15  0.04575  0.003050
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(mouth.Length_COI.euc)
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '29' de pch non
## implémentée
```

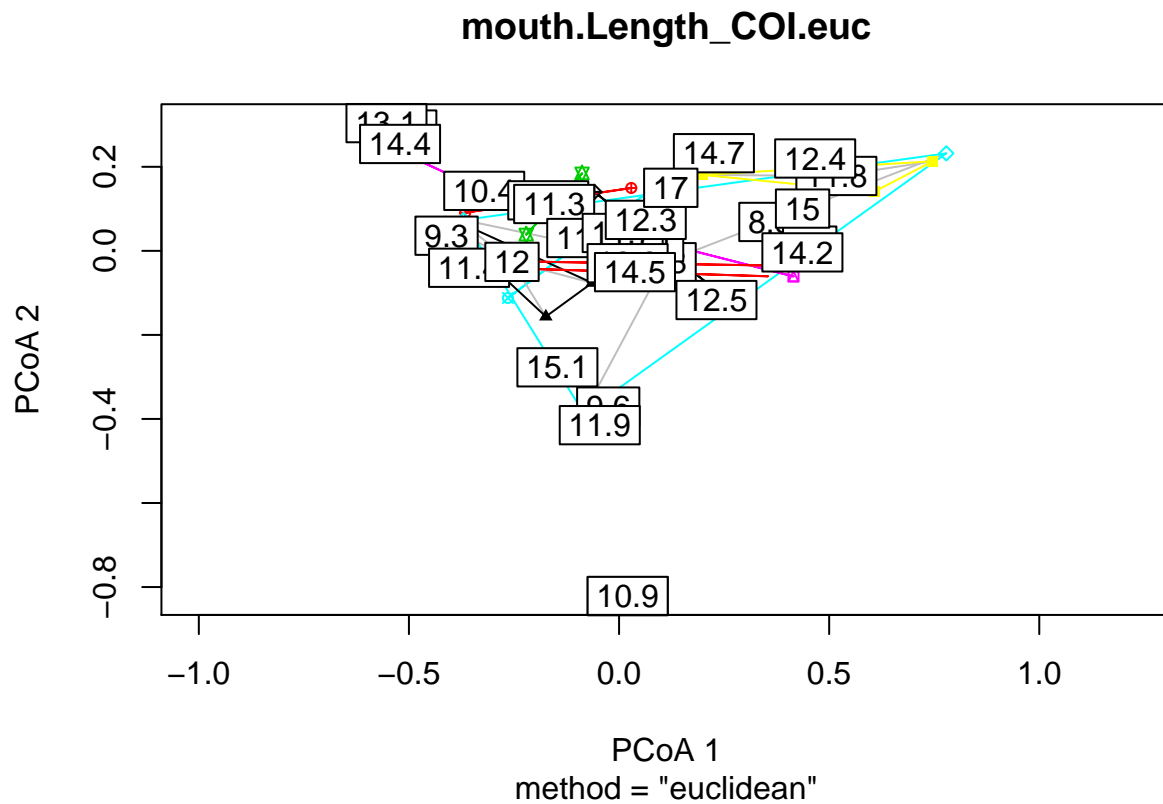
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '30' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '28' de pch non
## implémentée
```

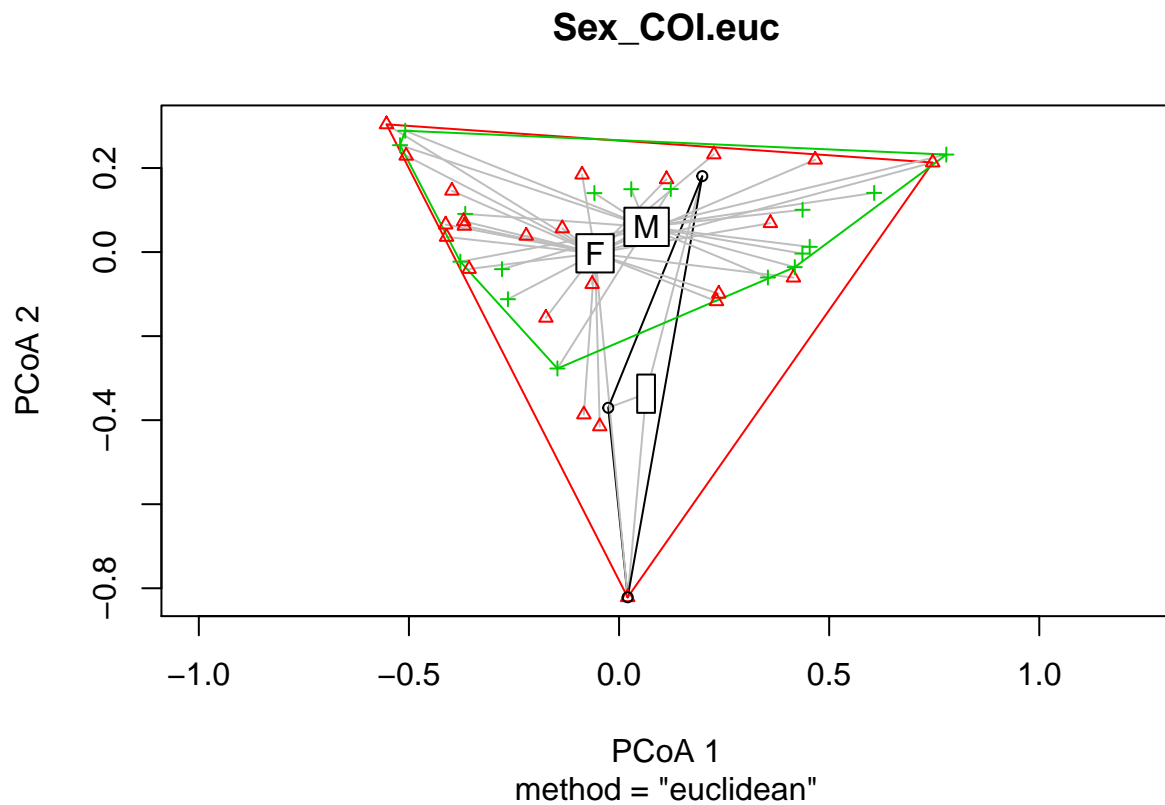
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '27' de pch non
## implémentée
```



```
anova(Sex_COI.euc)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df Sum Sq Mean Sq F value Pr(>F)
## Groups  2  0.05264  0.026318  0.7447  0.4811
## Residuals 42  1.48437  0.035342
```

```
plot(Sex_COI.euc)
```

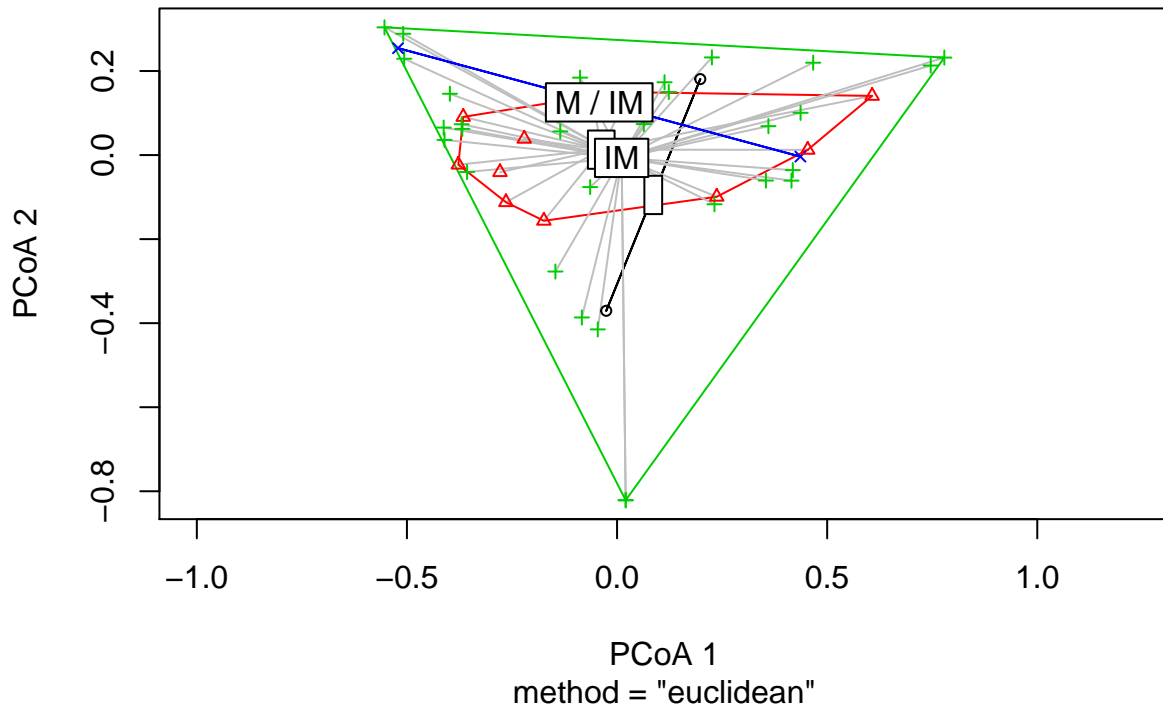


```
anova(rep.stage_COI.euc)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df Sum Sq Mean Sq F value Pr(>F)
## Groups    3 0.08514 0.028381  0.7531 0.5269
## Residuals 41 1.54500 0.037683
```

```
plot(rep.stage_COI.euc)
```


rep.stage_COI.euc

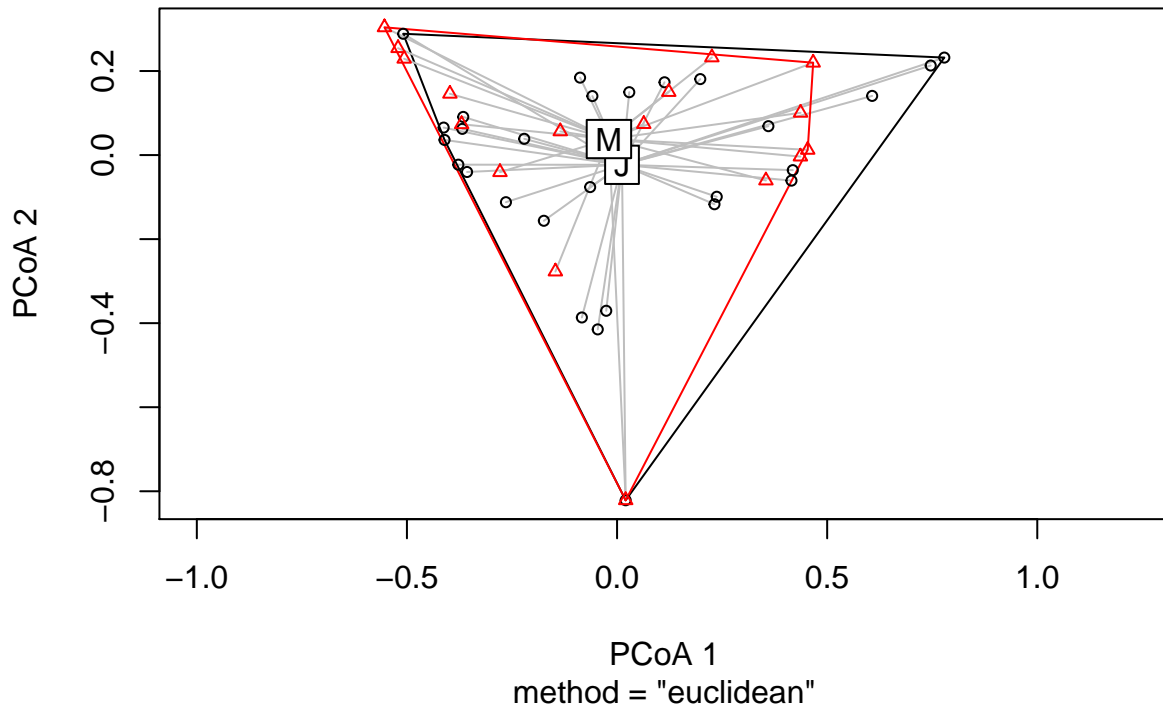


```
anova(size.class_COI.euc)
```

```
## Analysis of Variance Table  
##  
## Response: Distances  
##           Df Sum Sq Mean Sq F value Pr(>F)  
## Groups      1 0.00114 0.001141  0.0287 0.8662  
## Residuals  43 1.70816 0.039725
```

```
plot(size.class_COI.euc)
```

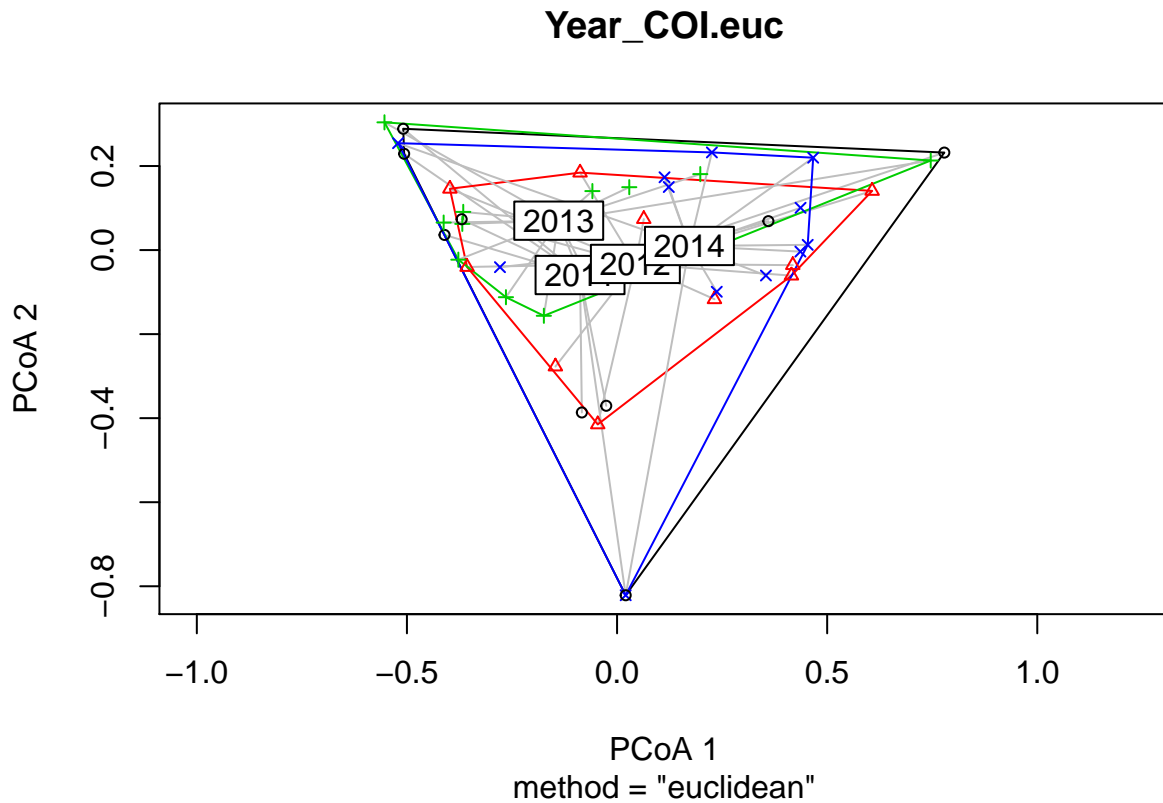
size.class_COI.euc



```
anova(Year_COI.euc)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df Sum Sq Mean Sq F value Pr(>F)
## Groups    3  0.15961  0.053204    1.283  0.293
## Residuals 41  1.70026  0.041470
```

```
plot(Year_COI.euc)
```



```
#####sorensen COI
sor.COI=vegdist(df4_8,binary=TRUE)
anosim(sor.COI, dm$Weight)
```

```
##
## Call:
## anosim(x = sor.COI, grouping = dm$Weight)
## Dissimilarity: binary bray
##
## ANOSIM statistic R: 0.08936
##      Significance: 0.318
##
## Permutation: free
## Number of permutations: 999
```

```
anosim(sor.COI, dm$code.port)
```

```
##
## Call:
## anosim(x = sor.COI, grouping = dm$code.port)
## Dissimilarity: binary bray
##
## ANOSIM statistic R: 0.0196
##      Significance: 0.335
##
```

```
## Permutation: free
## Number of permutations: 999
```

```
anosim(sor.COI, dm$Longueur_Bouche)
```

```
##
## Call:
## anosim(x = sor.COI, grouping = dm$Longueur_Bouche)
## Dissimilarity: binary bray
##
## ANOSIM statistic R: -0.1258
##      Significance: 0.834
##
## Permutation: free
## Number of permutations: 999
```

```
anosim(sor.COI, dm$Sexe)
```

```
##
## Call:
## anosim(x = sor.COI, grouping = dm$Sexe)
## Dissimilarity: binary bray
##
## ANOSIM statistic R: 0.02986
##      Significance: 0.253
##
## Permutation: free
## Number of permutations: 999
```

```
anosim(sor.COI, dm$Reproductive.Stage)
```

```
##
## Call:
## anosim(x = sor.COI, grouping = dm$Reproductive.Stage)
## Dissimilarity: binary bray
##
## ANOSIM statistic R: 0.01397
##      Significance: 0.417
##
## Permutation: free
## Number of permutations: 999
```

```
anosim(sor.COI, dm$SIZE_CLASS)
```

```
##
## Call:
## anosim(x = sor.COI, grouping = dm$SIZE_CLASS)
## Dissimilarity: binary bray
##
## ANOSIM statistic R: -0.07794
##      Significance: 0.958
```

```
##  
## Permutation: free  
## Number of permutations: 999
```

```
anosim(sor.COI, dm$Year)
```

```
##  
## Call:  
## anosim(x = sor.COI, grouping = dm$Year)  
## Dissimilarity: binary bray  
##  
## ANOSIM statistic R: -0.00137  
##      Significance: 0.463  
##  
## Permutation: free  
## Number of permutations: 999
```

```
Weight_COI.sor<- betadisper(sor.COI, dm$Weight, type = c("centroid"))  
Port_COI.sor<- betadisper(sor.COI, dm$code.port, type = c("centroid"))  
mouth.Length_COI.sor<- betadisper(sor.COI, dm$Longueur_Bouche, type = c("centroid"))  
Sex_COI.sor<- betadisper(sor.COI, dm$Sexe, type = c("centroid"))  
rep.stage_COI.sor<- betadisper(sor.COI, dm$Reproductive.Stage, type = c("centroid"))  
size.class_COI.sor<- betadisper(sor.COI, dm$SIZE_CLASS, type = c("centroid"))  
Year_COI.sor<- betadisper(sor.COI, dm$Year, type = c("centroid"))
```

```
anova(Weight_COI.sor)
```

```
## Analysis of Variance Table  
##  
## Response: Distances  
##           Df Sum Sq Mean Sq F value    Pr(>F)  
## Groups     37  1.2730  0.034405  13.603 0.0007349 ***  
## Residuals   7  0.0177  0.002529  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot (Weight_COI.sor)
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '28' de pch non  
## implémentée
```

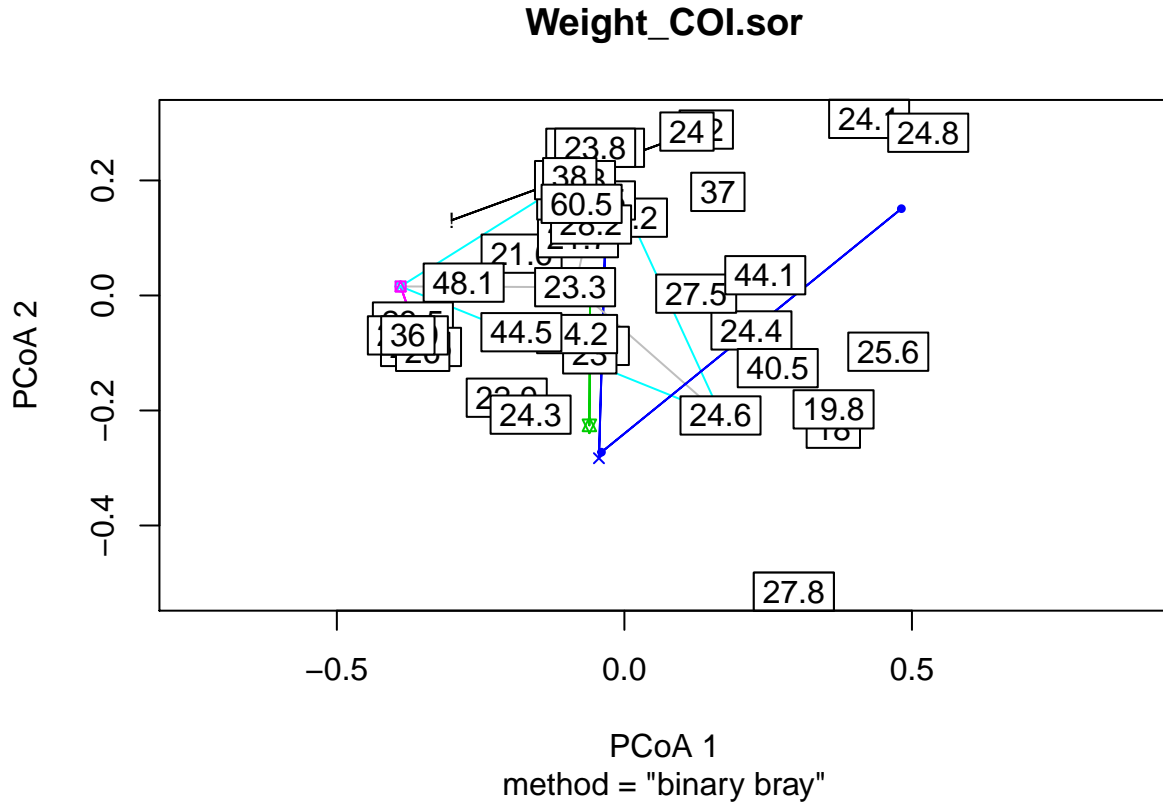
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '30' de pch non  
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '29' de pch non  
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '27' de pch non  
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '31' de pch non  
## implémentée
```

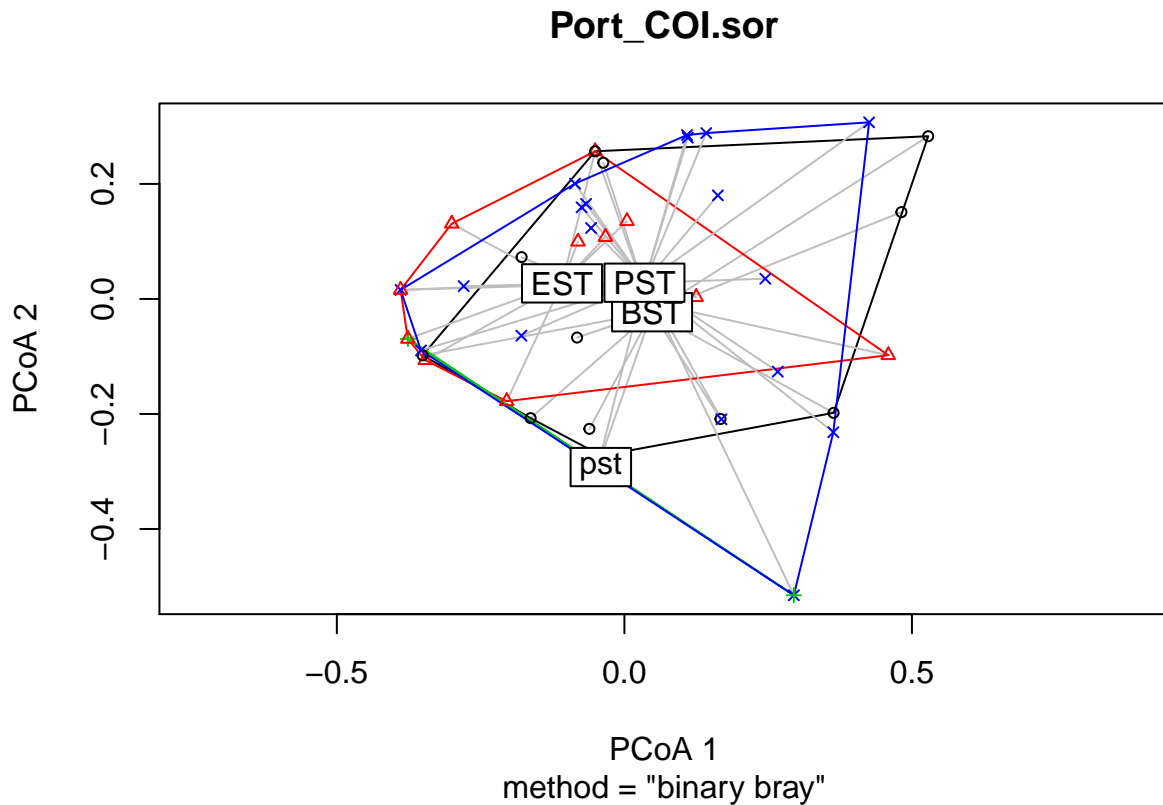
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non
## implémentée
```



```
anova(Port_COI.sor)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df Sum Sq Mean Sq F value Pr(>F)
## Groups    3 0.09739 0.032464  1.5571 0.2144
## Residuals 41 0.85483 0.020849
```

```
plot(Port_COI.sor)
```



```
anova(mouth.Length_COI.sor)
```

```
## Analysis of Variance Table
##
## Response: Distances
##          Df Sum Sq Mean Sq F value    Pr(>F)
## Groups   29  1.99564  0.068815  33.653 2.946e-09 ***
## Residuals 15  0.03067  0.002045
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
plot(mouth.Length_COI.sor)
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '29' de pch non
## implémentée
```

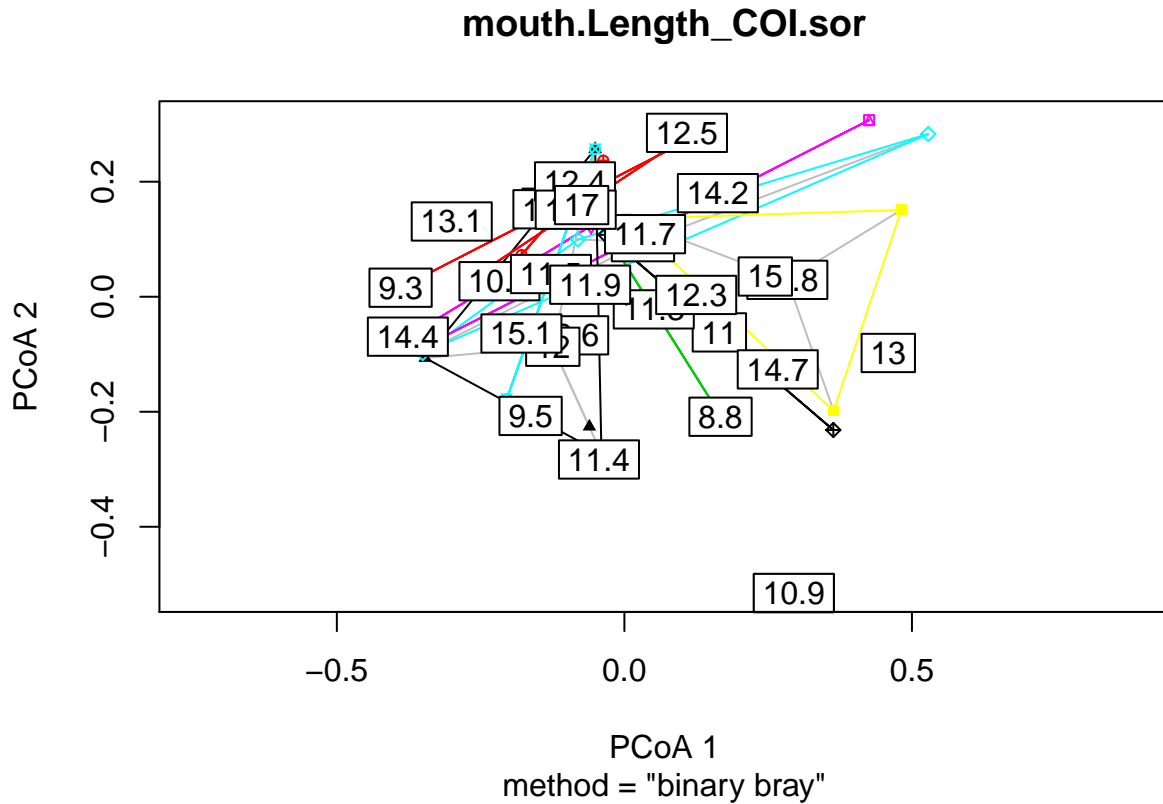
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '30' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '26' de pch non
## implémentée
```

```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '28' de pch non
## implémentée
```

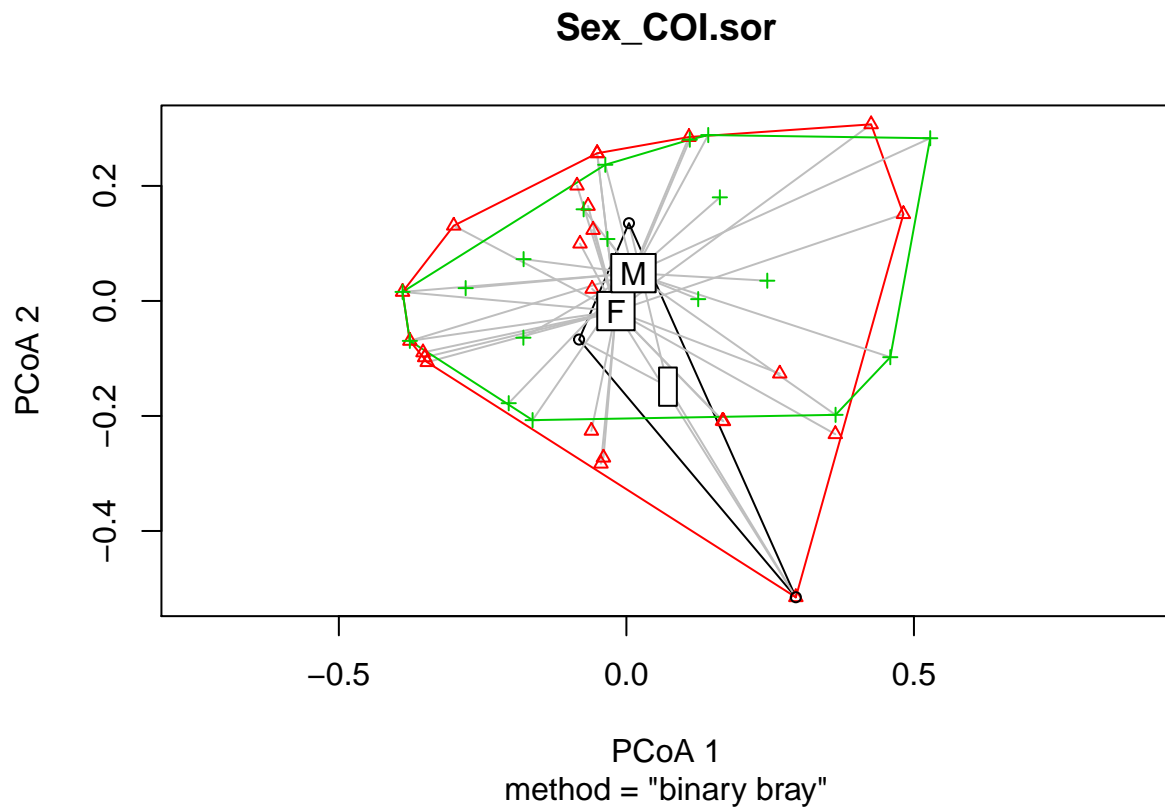
```
## Warning in plot.xy(xy.coords(x, y), type = type, ...): valeur '27' de pch non
## implémentée
```



```
anova(Sex_COI.sor)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df Sum Sq Mean Sq F value Pr(>F)
## Groups  2  0.01099  0.0054928  0.2413  0.7867
## Residuals 42  0.95619  0.0227665
```

```
plot(Sex_COI.sor)
```

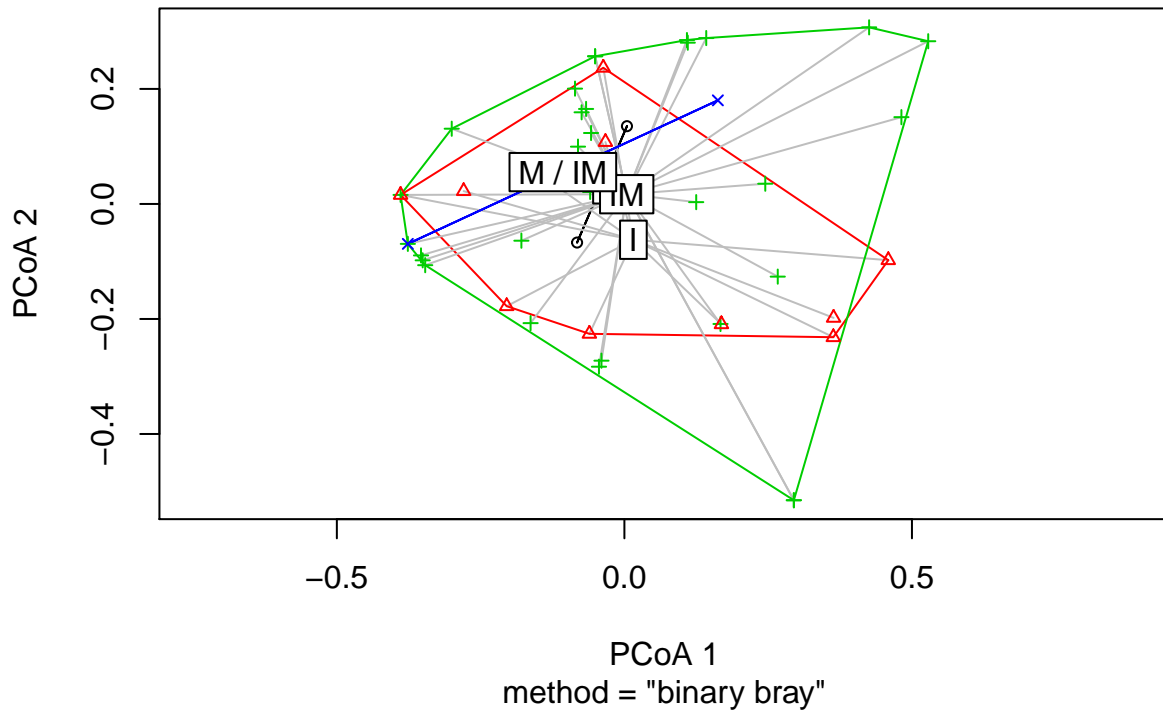



```
anova(rep.stage_COI.sor)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df Sum Sq Mean Sq F value Pr(>F)
## Groups    3  0.05859  0.019531  0.7842  0.5097
## Residuals 41  1.02120  0.024907
```

```
plot(rep.stage_COI.sor)
```

rep.stage_COI.sor

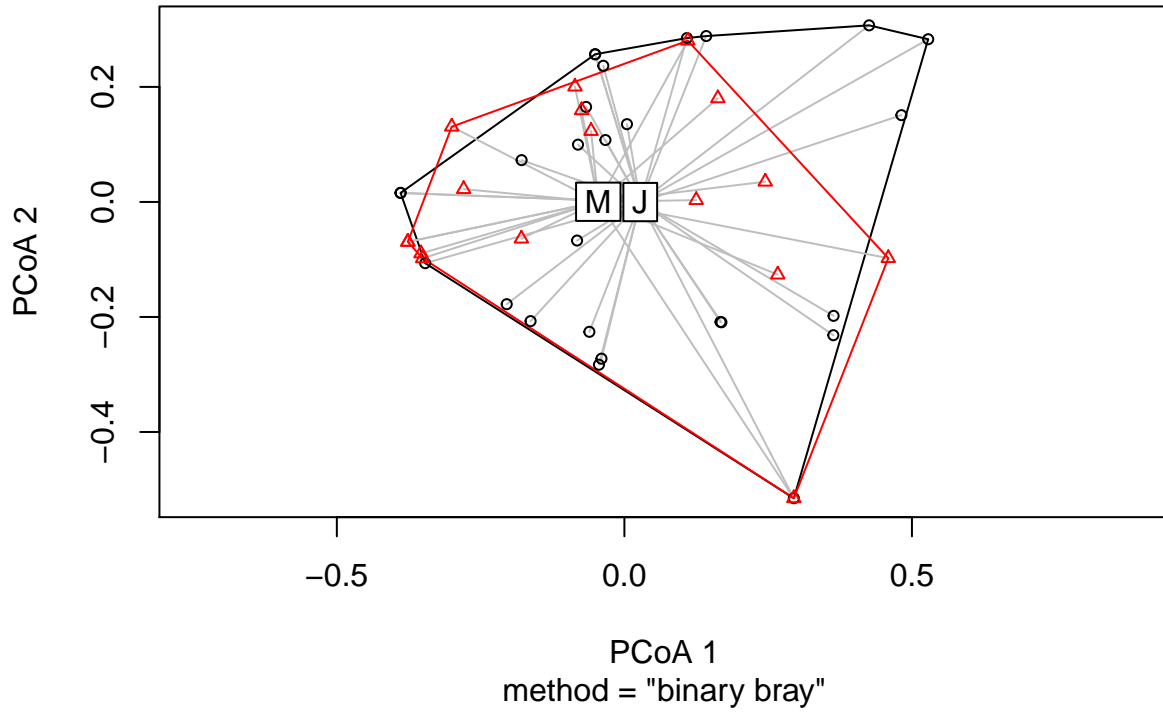


```
anova(size.class_COI.sor)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df Sum Sq Mean Sq F value Pr(>F)
## Groups  1 0.07354 0.073541   2.807 0.1011
## Residuals 43 1.12656 0.026199
```

```
plot(size.class_COI.sor)
```

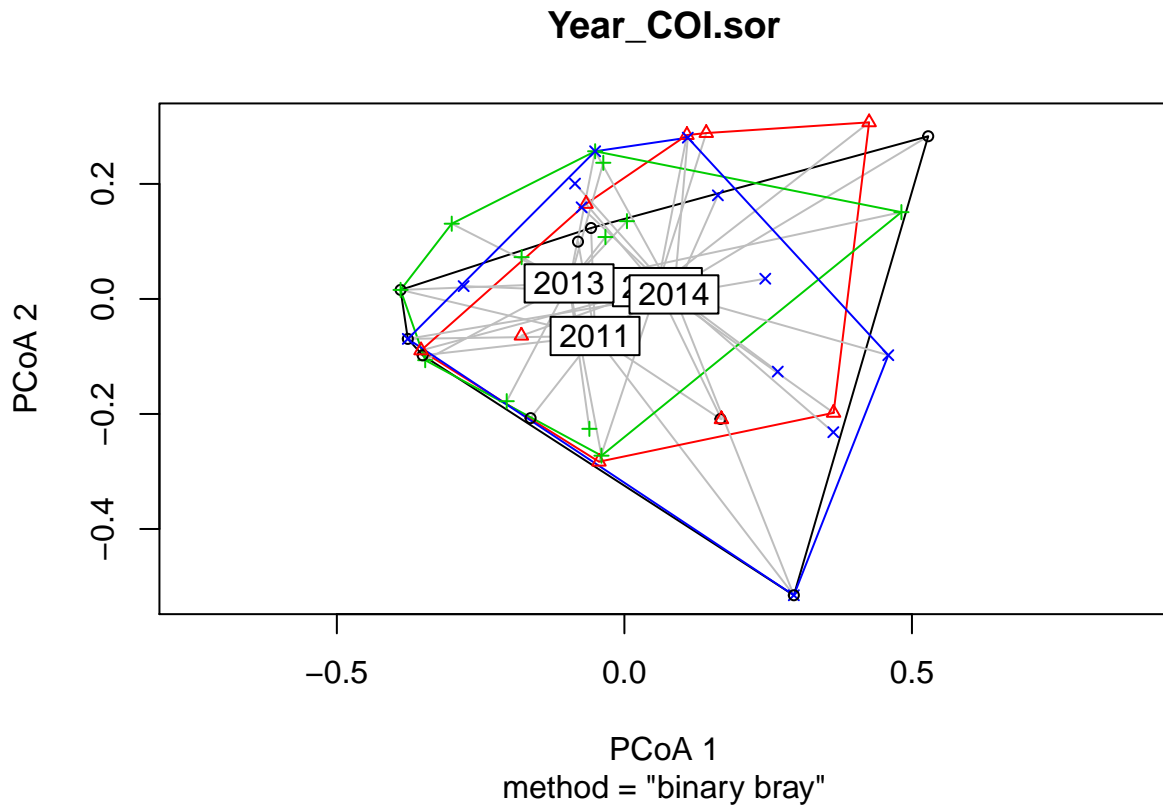
size.class_COI.sor



```
anova(Year_COI.sor)
```

```
## Analysis of Variance Table
##
## Response: Distances
##      Df Sum Sq Mean Sq F value Pr(>F)
## Groups    3  0.05604  0.018681  0.8481 0.4757
## Residuals 41  0.90314  0.022028
```

```
plot(Year_COI.sor)
```



6.GIM and predictive models and their Drawings

#PREP DATASETS

```
tPA_Tuna18S_D<-t(PA_Tuna18S_D)
tPA_TunaCOI_D<-t(PA_TunaCOI_D)
df5 <- cbind(dm2,tPA_Tuna18S_D)
df6 <- cbind(dm,tPA_TunaCOI_D)
PA_TunaCOI_D
```

##	M275	J290	J269	M281	M261	M198	M273	J233	J201	M280	J222	M118	
## anchovy	0	1	1	1	1	1	1	1	0	1	1	0	
## Arthropoda	0	0	0	1	1	1	0	0	1	1	0	1	
## cephaloda	0	0	0	0	0	0	0	0	0	0	0	0	
## Cepolaepola	0	0	0	0	0	0	0	0	0	0	0	0	
## Chaetognatha	0	0	0	0	0	0	0	0	0	0	0	0	
## Cnidaria	0	0	0	0	0	1	0	0	0	1	0	0	
## Echinodermata	0	0	0	0	0	0	0	0	0	0	0	0	
## mackerel	0	0	1	0	0	0	0	0	0	0	0	1	
## Mollusca	0	0	1	0	0	0	0	0	0	0	0	0	
## sardine	1	0	0	0	0	1	1	1	1	1	1	1	
## sprat	0	0	1	1	0	0	0	1	1	0	1	0	
## Tunicata	0	0	0	0	0	0	0	0	0	0	0	0	
## Vertebrata	0	0	1	1	0	0	0	0	1	0	0	1	
## Xenacoelomorpha	0	0	0	0	0	0	0	0	0	0	0	0	
##	M277	J221	M262	M279	J226	J53	J215	M117	M33	J47	J276	J52	M29
## anchovy	1	1	1	1	1	1	1	1	0	1	1	1	1
## Arthropoda	1	0	1	0	0	0	1	0	0	0	0	0	0

## cephaloda	0	0	0	0	0	0	0	0	0	0	0	0	0
## Cepolaepola	0	0	0	0	0	0	0	0	0	0	0	0	0
## Chaetognatha	0	0	0	0	0	0	0	0	0	0	0	0	0
## Cnidaria	0	0	0	0	0	0	0	0	0	0	0	0	0
## Echinodermata	0	0	0	0	0	0	0	0	0	0	0	0	0
## mackerel	0	0	0	0	0	1	0	0	0	1	0	0	0
## Mollusca	0	0	0	0	0	0	0	0	0	1	0	0	0
## sardine	0	0	0	1	0	0	0	1	1	0	1	1	1
## sprat	0	1	0	0	0	0	0	1	0	0	1	1	1
## Tunicata	0	0	0	0	0	0	0	0	0	0	0	0	0
## Vertebrata	0	0	1	1	0	0	0	0	1	0	0	0	0
## Xenacoelomorpha	0	0	0	0	0	0	0	0	0	0	0	0	0
##	J138	J125	J121	M49	J144	J134	J150	J227	J57	M30	J46	J145	J96
## anchovy	0	0	0	1	1	1	1	1	1	1	1	1	1
## Arthropoda	1	0	0	0	0	0	0	0	0	0	0	0	0
## cephaloda	1	0	0	0	0	0	0	0	0	0	0	0	0
## Cepolaepola	0	1	1	0	0	0	0	0	0	0	0	0	0
## Chaetognatha	0	0	0	0	0	0	0	0	0	0	0	0	0
## Cnidaria	0	0	0	0	0	0	0	0	0	0	0	0	0
## Echinodermata	0	0	0	0	0	0	0	0	0	0	0	0	0
## mackerel	1	0	0	1	1	1	1	1	1	0	1	0	1
## Mollusca	0	0	0	0	0	0	0	0	0	0	0	0	0
## sardine	1	0	0	0	1	0	1	0	0	0	0	1	0
## sprat	0	0	0	0	1	0	1	1	0	1	1	0	0
## Tunicata	0	0	0	0	0	0	0	0	0	0	0	0	0
## Vertebrata	0	0	0	0	0	0	0	0	1	0	0	0	0
## Xenacoelomorpha	0	0	0	0	0	0	0	0	0	0	0	0	0
##	J164	M123	M253	J229	J217	J205	J170						
## anchovy	1	1	0	1	1	1	1						
## Arthropoda	0	0	1	0	1	0	0						
## cephaloda	0	0	0	0	0	0	0						
## Cepolaepola	0	0	0	0	0	0	0						
## Chaetognatha	0	0	0	0	0	0	0						
## Cnidaria	0	0	0	0	0	0	0						
## Echinodermata	0	0	0	0	0	0	0						
## mackerel	0	1	0	0	0	0	0						
## Mollusca	0	0	0	0	0	0	0						
## sardine	1	1	1	1	1	1	0						
## sprat	0	1	1	0	1	1	1						
## Tunicata	0	0	0	0	0	0	0						
## Vertebrata	0	0	0	0	0	0	0						
## Xenacoelomorpha	0	0	0	0	0	0	0						

PA_Tuna18S_D

##	M275	J290	J269	M281	M261	M198	M273	J233	J201	M280	J222	M118	
## Annelida	0	0	0	0	0	0	0	0	0	0	0	0	0
## Arthropoda	0	0	0	0	1	1	1	0	1	0	0	0	1
## Cnidaria	0	0	0	1	1	1	1	0	0	1	0	0	1
## Ctenophora	0	0	0	0	0	0	0	0	0	0	0	0	1
## Platyhelminthes	0	0	0	0	0	0	0	0	0	0	0	0	0
## Tunicata	1	0	0	0	0	1	1	0	0	1	0	0	1
## Vertebrata	0	1	1	0	0	1	0	1	1	0	1	0	1
##	M277	J221	M262	M279	J226	J53	J215	M117	M33	J47	J276	J52	M29

```

## Annelida      0  0  0  0  0  0  0  0  0  0  0  0  1
## Arthropoda    0  0  1  0  0  0  0  1  0  0  1  0  0
## Cnidaria      0  0  0  1  0  0  1  0  0  0  1  1  0
## Ctenophora    0  0  0  0  1  1  0  0  1  1  1  1  0
## Platyhelminthes 0  0  0  0  0  0  0  0  0  0  0  1  1
## Tunicata      0  0  0  1  0  1  1  0  0  1  0  1  1
## Vertebrata    1  1  1  0  0  1  0  1  0  0  1  1  0
##              J138 J125 J121 M49 J144 J134 J150 J227 J57 M30 J46 J145 J96
## Annelida      0  0  0  0  0  0  0  0  0  0  0  0  0
## Arthropoda    0  0  1  1  0  0  0  0  0  1  1  1  0
## Cnidaria      0  1  0  1  0  1  1  1  1  0  0  1  1
## Ctenophora    1  0  0  0  1  1  1  0  1  0  1  0  1
## Platyhelminthes 0  0  0  1  0  0  0  1  0  0  0  0  0
## Tunicata      1  0  1  1  0  0  0  0  0  0  0  0  0
## Vertebrata    1  1  0  1  1  1  1  1  1  1  1  1  1
##              J164 M123 M253 J229 J217 J205
## Annelida      0  0  0  0  1  0
## Arthropoda    0  0  1  1  0  0
## Cnidaria      1  0  1  0  0  0
## Ctenophora    1  1  0  0  0  0
## Platyhelminthes 0  0  0  1  0  0
## Tunicata      1  0  1  0  1  1
## Vertebrata    0  1  1  0  1  1

```

```

tPA_Tuna18S_D<-t(PA_Tuna18S_D)
tPA_TunaCOI_D<-t(PA_TunaCOI_D)
df5 <- cbind(dm2,tPA_Tuna18S_D)
df5$Year<-as.factor(df5$Year)
df6 <- cbind(dm,tPA_TunaCOI_D)
df6$Year<-as.factor(df6$Year)
df5$log.body.mass <- log10(df5$Weight)
df5$log.Length <- log10(df5$Longueur_Bouche)
df6$log.body.mass <- log10(df6$Weight)
df6$log.Length <- log10(df6$Longueur_Bouche)

#18S
modelCNI <- glm(Cnidaria ~ (Year+log.body.mass+log.Length), family = binomial, data = df5)
modelCNI02 <- step(modelCNI, direction = "both")

```

```

## Start: AIC=70.06
## Cnidaria ~ (Year + log.body.mass + log.Length)
##
##              Df Deviance   AIC
## - Year          3   58.540 64.540
## - log.Length     1   58.194 68.194
## - log.body.mass  1   58.658 68.658
## <none>           58.061 70.061
##
## Step: AIC=64.54
## Cnidaria ~ log.body.mass + log.Length
##
##              Df Deviance   AIC
## - log.Length     1   58.555 62.555
## - log.body.mass  1   59.327 63.327

```

```
## <none>          58.540 64.540
## + Year          3  58.061 70.061
##
## Step: AIC=62.56
## Cnidaria ~ log.body.mass
##
##           Df Deviance   AIC
## <none>          58.555 62.555
## - log.body.mass 1  60.633 62.633
## + log.Length    1  58.540 64.540
## + Year          3  58.194 68.194
```

```
modelCNI03 <- glm(Cnidaria~ 1,family = binomial, data = df5)
modelCNI04 <- step(modelCNI03
, direction = "both", scope = list(lower = ~1,upper = ~(Year+log.body.mass+log.Length))
```

```
## Start: AIC=62.63
## Cnidaria ~ 1
##
##           Df Deviance   AIC
## + log.body.mass 1  58.555 62.555
## <none>          60.633 62.633
## + log.Length    1  59.327 63.327
## + Year          3  59.340 67.340
##
## Step: AIC=62.56
## Cnidaria ~ log.body.mass
##
##           Df Deviance   AIC
## <none>          58.555 62.555
## - log.body.mass 1  60.633 62.633
## + log.Length    1  58.540 64.540
## + Year          3  58.194 68.194
```

```
AIC(modelCNI,modelCNI02,modelCNI03,modelCNI04)
```

```
##           df      AIC
## modelCNI    6 70.06078
## modelCNI02  2 62.55541
## modelCNI03  1 62.63281
## modelCNI04  2 62.55541
```

```
summary(modelCNI, test="Chisq")
```

```
##
## Call:
## glm(formula = Cnidaria ~ (Year + log.body.mass + log.Length),
##      family = binomial, data = df5)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.7111  -1.0310  -0.8776   1.2323   1.4846
```

```

##
## Coefficients:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.5498   10.6781  -0.145   0.885
## Year2012      0.9303    2.0428   0.455   0.649
## Year2013      0.5372    1.9628   0.274   0.784
## Year2014      1.0924    2.1330   0.512   0.609
## log.body.mass 5.8629    7.6532   0.766   0.444
## log.Length   -7.1420   19.5955  -0.364   0.716
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 60.633  on 43  degrees of freedom
## Residual deviance: 58.061  on 38  degrees of freedom
## AIC: 70.061
##
## Number of Fisher Scoring iterations: 4

modelCTE <- glm(Ctenophora ~ (Year+log.body.mass+log.Length), family = binomial, data = df5)
modelCTE02 <- step(modelCTE, direction = "both")

## Start: AIC=54.45
## Ctenophora ~ (Year + log.body.mass + log.Length)
##
##           Df Deviance   AIC
## <none>           42.446 54.446
## - Year            3  48.976 54.976
## - log.Length      1  46.303 56.303
## - log.body.mass   1  49.345 59.345

modelCTE03 <- glm(Ctenophora~ 1,family = binomial, data = df5)
modelCTE04 <- step(modelCTE03
, direction = "both", scope = list(lower = ~1,upper = ~(Year+log.body.mass+log.Length)

## Start: AIC=59.68
## Ctenophora ~ 1
##
##           Df Deviance   AIC
## + log.body.mass  1  50.517 54.517
## + Year            3  50.883 58.883
## <none>           57.682 59.682
## + log.Length      1  56.251 60.251
##
## Step: AIC=54.52
## Ctenophora ~ log.body.mass
##
##           Df Deviance   AIC
## <none>           50.517 54.517
## + log.Length      1  48.976 54.976
## + Year            3  46.303 56.303
## - log.body.mass   1  57.682 59.682

```



```
AIC(modelCTE,modelCTE02,modelCTE03,modelCTE04)
```

```
##           df      AIC
## modelCTE    6 54.44555
## modelCTE02  6 54.44555
## modelCTE03  1 59.68240
## modelCTE04  2 54.51744
```

```
summary(modelCTE, test="Chisq")
```

```
##
## Call:
## glm(formula = Ctenophora ~ (Year + log.body.mass + log.Length),
##      family = binomial, data = df5)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8862  -0.8674  -0.4349   0.8116   1.9476
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    11.703     13.489   0.868  0.3856
## Year2012         2.485       2.806   0.886  0.3758
## Year2013         4.554       2.832   1.608  0.1078
## Year2014         4.858       2.918   1.665  0.0959 .
## log.body.mass   26.947     12.503   2.155  0.0311 *
## log.Length     -50.389     28.886  -1.744  0.0811 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 57.682  on 43  degrees of freedom
## Residual deviance: 42.446  on 38  degrees of freedom
## AIC: 54.446
##
## Number of Fisher Scoring iterations: 5
```

```
modelART <- glm(Arthropoda ~ (Year+log.body.mass+log.Length), family = binomial, data = df5)
modelART02 <- step(modelART, direction = "both")
```

```
## Start:  AIC=63.15
## Arthropoda ~ (Year + log.body.mass + log.Length)
##
##           Df Deviance   AIC
## - Year      3  55.233 61.233
## <none>      0  51.153 63.153
## - log.body.mass  1  54.941 64.941
## - log.Length    1  55.540 65.540
##
## Step:  AIC=61.23
## Arthropoda ~ log.body.mass + log.Length
```

```

##
##           Df Deviance   AIC
## - log.body.mass 1  56.008 60.008
## - log.Length    1  56.459 60.459
## <none>          55.233 61.233
## + Year          3  51.153 63.153
##
## Step: AIC=60.01
## Arthropoda ~ log.Length
##
##           Df Deviance   AIC
## - log.Length    1  56.464 58.464
## <none>          56.008 60.008
## + log.body.mass 1  55.233 61.233
## + Year          3  54.941 64.941
##
## Step: AIC=58.46
## Arthropoda ~ 1
##
##           Df Deviance   AIC
## <none>          56.464 58.464
## + log.Length    1  56.008 60.008
## + log.body.mass 1  56.459 60.459
## + Year          3  55.543 63.543

modelART03 <- glm(Arthropoda~ 1,family = binomial, data = df5)
modelART04 <- step(modelART03
, direction = "both", scope = list(lower = ~1,upper = ~(Year+log.body.mass+log.Length)

## Start: AIC=58.46
## Arthropoda ~ 1
##
##           Df Deviance   AIC
## <none>          56.464 58.464
## + log.Length    1  56.008 60.008
## + log.body.mass 1  56.459 60.459
## + Year          3  55.543 63.543

AIC(modelART,modelART02,modelART03,modelART04)

##           df      AIC
## modelART      6 63.15254
## modelART02    1 58.46402
## modelART03    1 58.46402
## modelART04    1 58.46402

summary(modelART, test="Chisq")

##
## Call:
## glm(formula = Arthropoda ~ (Year + log.body.mass + log.Length),
##      family = binomial, data = df5)

```

```

##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4933  -0.9142  -0.6786   1.0691   1.8454
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -24.252    13.259  -1.829  0.0674 .
## Year2012       -3.649     2.396  -1.523  0.1278
## Year2013       -4.286     2.372  -1.806  0.0709 .
## Year2014       -4.374     2.571  -1.701  0.0890 .
## log.body.mass -16.925     9.378  -1.805  0.0711 .
## log.Length     47.387    24.626   1.924  0.0543 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 56.464  on 43  degrees of freedom
## Residual deviance: 51.153  on 38  degrees of freedom
## AIC: 63.153
##
## Number of Fisher Scoring iterations: 4

```

```

modelVER <- glm(Vertebrata ~ (Year+log.body.mass+log.Length), family = binomial, data = df5)
modelVER02 <- step(modelVER, direction = "both")

```

```

## Start: AIC=62.04
## Vertebrata ~ (Year + log.body.mass + log.Length)
##
##              Df Deviance   AIC
## - Year          3  52.020 58.020
## - log.body.mass 1  50.086 60.086
## - log.Length    1  51.120 61.120
## <none>          0  50.043 62.043
##
## Step: AIC=58.02
## Vertebrata ~ log.body.mass + log.Length
##
##              Df Deviance   AIC
## - log.Length    1  52.037 56.037
## - log.body.mass 1  53.504 57.504
## <none>          0  52.020 58.020
## + Year          3  50.043 62.043
##
## Step: AIC=56.04
## Vertebrata ~ log.body.mass
##
##              Df Deviance   AIC
## <none>          0  52.037 56.037
## - log.body.mass 1  55.043 57.043
## + log.Length    1  52.020 58.020
## + Year          3  51.120 61.120

```

```

modelVER03 <- glm(Vertebrata ~ 1, family = binomial, data = df5)
modelVER04 <- step(modelVER03
, direction = "both", scope = list(lower = ~1, upper = ~(Year+log.body.mass+log.Length)

```

```

## Start: AIC=57.04
## Vertebrata ~ 1
##
##           Df Deviance   AIC
## + log.body.mass  1  52.037 56.037
## <none>           55.043 57.043
## + log.Length    1  53.504 57.504
## + Year          3  53.762 61.762
##
## Step: AIC=56.04
## Vertebrata ~ log.body.mass
##
##           Df Deviance   AIC
## <none>           52.037 56.037
## - log.body.mass  1  55.043 57.043
## + log.Length    1  52.020 58.020
## + Year          3  51.120 61.120

```

```
AIC(modelVER,modelVER02,modelVER03,modelVER04)
```

```

##           df      AIC
## modelVER      6 62.04323
## modelVER02    2 56.03721
## modelVER03    1 57.04324
## modelVER04    2 56.03721

```

```
summary(modelVER, test="Chisq")
```

```

##
## Call:
## glm(formula = Vertebrata ~ (Year + log.body.mass + log.Length),
##      family = binomial, data = df5)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.1311  -1.0603   0.5821   0.8881   1.2635
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -18.390    12.107  -1.519   0.129
## Year2012       -2.667     2.263  -1.178   0.239
## Year2013       -1.729     2.186  -0.791   0.429
## Year2014       -2.352     2.342  -1.004   0.315
## log.body.mass  -1.757     8.467  -0.207   0.836
## log.Length     21.931    21.360   1.027   0.305
##
## (Dispersion parameter for binomial family taken to be 1)
##

```

```

## Null deviance: 55.043 on 43 degrees of freedom
## Residual deviance: 50.043 on 38 degrees of freedom
## AIC: 62.043
##
## Number of Fisher Scoring iterations: 4

modelTUN <- glm(Tunicata ~ (Year+log.body.mass+log.Length), family = binomial, data = df5)
modelTUN02 <- step(modelTUN, direction = "both")

```

```

## Start: AIC=63.92
## Tunicata ~ (Year + log.body.mass + log.Length)
##
##           Df Deviance   AIC
## - Year      3  55.933 61.933
## - log.body.mass 1  52.522 62.522
## - log.Length  1  52.603 62.603
## <none>      0  51.923 63.923
##

```

```

## Step: AIC=61.93
## Tunicata ~ log.body.mass + log.Length
##
##           Df Deviance   AIC
## - log.body.mass 1  56.186 60.186
## <none>          0  55.933 61.933
## - log.Length  1  58.661 62.661
## + Year        3  51.923 63.923
##

```

```

## Step: AIC=60.19
## Tunicata ~ log.Length
##
##           Df Deviance   AIC
## <none>          0  56.186 60.186
## - log.Length  1  59.534 61.534
## + log.body.mass 1  55.933 61.933
## + Year        3  52.522 62.522
##

```

```

modelTUN03 <- glm(Tunicata ~ 1, family = binomial, data = df5)
modelTUN04 <- step(modelTUN03
  , direction = "both", scope = list(lower = ~1, upper = ~(Year+log.body.mass+log.Length))
)

```

```

## Start: AIC=61.53
## Tunicata ~ 1
##
##           Df Deviance   AIC
## + log.Length  1  56.186 60.186
## + Year        3  52.610 60.610
## <none>        0  59.534 61.534
## + log.body.mass 1  58.661 62.661
##
## Step: AIC=60.19
## Tunicata ~ log.Length
##
##           Df Deviance   AIC

```

```
## <none>          56.186 60.186
## - log.Length    1  59.534 61.534
## + log.body.mass 1  55.933 61.933
## + Year          3  52.522 62.522
```

```
AIC(modelTUN,modelTUN02,modelTUN03,modelTUN04)
```

```
##          df      AIC
## modelTUN    6 63.92257
## modelTUN02  2 60.18589
## modelTUN03  1 61.53428
## modelTUN04  2 60.18589
```

```
summary(modelTUN, test="Chisq")
```

```
##
## Call:
## glm(formula = Tunicata ~ (Year + log.body.mass + log.Length),
##      family = binomial, data = df5)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.5941  -0.9816  -0.6203   0.9335   1.9846
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -7.588     12.068  -0.629  0.5295
## Year2012       -2.697      2.268  -1.189  0.2344
## Year2013       -2.993      2.187  -1.369  0.1711
## Year2014       -4.185      2.483  -1.686  0.0919 .
## log.body.mass -6.351      8.306  -0.765  0.4445
## log.Length    17.510     21.490   0.815  0.4152
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 59.534  on 43  degrees of freedom
## Residual deviance: 51.923  on 38  degrees of freedom
## AIC: 63.923
##
## Number of Fisher Scoring iterations: 4
```

```
# same for COI
```

```
modelan01 <- glm(anchovy~ (Year+log.body.mass+log.Length), family = binomial, data = df6)
modelan02 <- step(modelan01, direction = "both")
```

```
## Start:  AIC=43.53
## anchovy ~ (Year + log.body.mass + log.Length)
##
##          Df Deviance   AIC
```

```

## - Year          3   37.163 43.163
## <none>          31.534 43.534
## - log.Length    1   33.549 43.549
## - log.body.mass 1   37.521 47.521
##
## Step: AIC=43.16
## anchovy ~ log.body.mass + log.Length
##
##           Df Deviance   AIC
## - log.Length    1   37.203 41.203
## <none>          31.534 43.534
## + Year          3   31.534 43.534
## - log.body.mass 1   41.110 45.110
##
## Step: AIC=41.2
## anchovy ~ log.body.mass
##
##           Df Deviance   AIC
## <none>          37.203 41.203
## + log.Length    1   37.163 43.163
## + Year          3   33.549 43.549
## - log.body.mass 1   42.121 44.121

```

```

modelan03 <- glm(anchovy~ 1,family = binomial, data = df6)
modelan04 <- step(modelan03
, direction = "both", scope = list(lower = ~1,upper = ~(Year+log.body.mass+log.Length)

```

```

## Start: AIC=44.12
## anchovy ~ 1
##
##           Df Deviance   AIC
## + log.body.mass 1   37.203 41.203
## <none>          42.121 44.121
## + log.Length    1   41.110 45.110
## + Year          3   40.819 48.819
##
## Step: AIC=41.2
## anchovy ~ log.body.mass
##
##           Df Deviance   AIC
## <none>          37.203 41.203
## + log.Length    1   37.163 43.163
## + Year          3   33.549 43.549
## - log.body.mass 1   42.121 44.121

```

```

AIC(modelan01,modelan02,modelan03,modelan04)

```

```

##           df      AIC
## modelan01  6 43.53367
## modelan02  2 41.20300
## modelan03  1 44.12063
## modelan04  2 41.20300

```

```
summary(modelan01, test="Chisq")
```

```
##
## Call:
## glm(formula = anchovy ~ (Year + log.body.mass + log.Length),
##     family = binomial, data = df6)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.46190  0.07094  0.39318  0.52515  1.35065
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -1.235     16.366  -0.075  0.9399
## Year2012        4.452       3.196   1.393  0.1636
## Year2013        5.056       2.994   1.689  0.0912 .
## Year2014        2.729       2.916   0.936  0.3493
## log.body.mass  30.178     14.363   2.101  0.0356 *
## log.Length    -39.844     29.631  -1.345  0.1787
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 42.121  on 44  degrees of freedom
## Residual deviance: 31.534  on 39  degrees of freedom
## AIC: 43.534
##
## Number of Fisher Scoring iterations: 6
```

```
modelar01 <- glm(Arthropoda ~ (Year+log.body.mass+log.Length), family = binomial, data = df6)
modelar02 <- step(modelar01, direction = "both")
```

```
## Start:  AIC=58.96
## Arthropoda ~ (Year + log.body.mass + log.Length)
##
##           Df Deviance   AIC
## - Year      3  48.982 54.982
## - log.Length 1  47.104 57.104
## - log.body.mass 1  48.406 58.406
## <none>      0  46.963 58.963
##
## Step:  AIC=54.98
## Arthropoda ~ log.body.mass + log.Length
##
##           Df Deviance   AIC
## - log.Length 1  48.983 52.983
## - log.body.mass 1  50.878 54.878
## <none>      0  48.982 54.982
## + Year      3  46.963 58.963
##
## Step:  AIC=52.98
```



```

## Arthropoda ~ log.body.mass
##
##           Df Deviance   AIC
## <none>           48.983 52.983
## - log.body.mass  1   52.192 54.192
## + log.Length     1   48.982 54.982
## + Year           3   47.104 57.104

modelar03 <- glm(Arthropoda~ 1,family = binomial, data = df6)
modelar04 <- step(modelar03
, direction = "both", scope = list(lower = ~1,upper = ~(Year+log.body.mass+log.Length)

## Start: AIC=54.19
## Arthropoda ~ 1
##
##           Df Deviance   AIC
## + log.body.mass  1   48.983 52.983
## <none>           52.192 54.192
## + log.Length     1   50.878 54.878
## + Year           3   50.947 58.947
##
## Step: AIC=52.98
## Arthropoda ~ log.body.mass
##
##           Df Deviance   AIC
## <none>           48.983 52.983
## - log.body.mass  1   52.192 54.192
## + log.Length     1   48.982 54.982
## + Year           3   47.104 57.104

AIC(modelar01,modelar02,modelar03,modelar04)

##           df      AIC
## modelar01  6 58.96261
## modelar02  2 52.98265
## modelar03  1 54.19237
## modelar04  2 52.98265

summary(modelar01, test="Chisq")

##
## Call:
## glm(formula = Arthropoda ~ (Year + log.body.mass + log.Length),
##      family = binomial, data = df6)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.2187 -0.8124 -0.6083  0.9081  2.2695
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    6.3402    12.4061  0.511   0.609

```

```

## Year2012      -0.6547      2.3040  -0.284   0.776
## Year2013      -1.7461      2.2715  -0.769   0.442
## Year2014      -0.5027      2.3619  -0.213   0.831
## log.body.mass -11.0264      9.5105  -1.159   0.246
## log.Length    8.3316      22.2404  0.375   0.708
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 52.192 on 44 degrees of freedom
## Residual deviance: 46.963 on 39 degrees of freedom
## AIC: 58.963
##
## Number of Fisher Scoring iterations: 5

modelmr01 <- glm(mackerel~ (Year+log.body.mass+log.Length), family = binomial, data = df6)
modelmr02 <- step(modelmr01, direction = "both")

```

```

## Start: AIC=63
## mackerel ~ (Year + log.body.mass + log.Length)
##
##           Df Deviance   AIC
## - Year      3  52.752 58.752
## - log.Length 1  51.128 61.128
## - log.body.mass 1  51.162 61.162
## <none>      51.005 63.005
##

```

```

## Step: AIC=58.75
## mackerel ~ log.body.mass + log.Length
##
##           Df Deviance   AIC
## - log.Length 1  53.238 57.238
## <none>      52.752 58.752
## - log.body.mass 1  55.212 59.212
## + Year      3  51.005 63.005
##

```

```

## Step: AIC=57.24
## mackerel ~ log.body.mass
##
##           Df Deviance   AIC
## <none>      53.238 57.238
## - log.body.mass 1  55.799 57.799
## + log.Length 1  52.752 58.752
## + Year      3  51.128 61.128

```

```

modelmr03 <- glm(mackerel~ 1,family = binomial, data = df6)
modelmr04 <- step(modelmr03
, direction = "both", scope = list(lower = ~1,upper = ~(Year+log.body.mass+log.Length)

```

```

## Start: AIC=57.8
## mackerel ~ 1
##
##           Df Deviance   AIC
## + log.body.mass 1  53.238 57.238

```

```
## <none>          55.799 57.799
## + log.Length    1  55.212 59.212
## + Year          3  53.971 61.971
##
## Step: AIC=57.24
## mackerel ~ log.body.mass
##
##           Df Deviance   AIC
## <none>          53.238 57.238
## - log.body.mass 1  55.799 57.799
## + log.Length    1  52.752 58.752
## + Year          3  51.128 61.128
```

```
AIC(modelmr01,modelmr02,modelmr03,modelmr04)
```

```
##           df      AIC
## modelmr01  6 63.00483
## modelmr02  2 57.23836
## modelmr03  1 57.79881
## modelmr04  2 57.23836
```

```
summary(modelmr01, test="Chisq")
```

```
##
## Call:
## glm(formula = mackerel ~ (Year + log.body.mass + log.Length),
##      family = binomial, data = df6)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.2037  -0.8971  -0.6048   1.1929   2.2000
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -12.3754    12.3174  -1.005   0.315
## Year2012      -0.7957     2.1940  -0.363   0.717
## Year2013     -1.7617     2.1188  -0.831   0.406
## Year2014     -1.8070     2.4218  -0.746   0.456
## log.body.mass  3.2378     8.1481   0.397   0.691
## log.Length    7.4815    21.4473   0.349   0.727
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 55.799  on 44  degrees of freedom
## Residual deviance: 51.005  on 39  degrees of freedom
## AIC: 63.005
##
## Number of Fisher Scoring iterations: 4
```

```
modelsa01 <- glm(sardine~ (Year+log.body.mass+log.Length), family = binomial, data = df6)
modelsa02 <- step(modelsa01, direction = "both")
```

```

## Start: AIC=67.8
## sardine ~ (Year + log.body.mass + log.Length)
##
##           Df Deviance   AIC
## - Year      3   59.163 65.163
## - log.Length 1   55.803 65.803
## - log.body.mass 1   55.968 65.968
## <none>      3   55.795 67.795
##
## Step: AIC=65.16
## sardine ~ log.body.mass + log.Length
##
##           Df Deviance   AIC
## - log.body.mass 1   60.477 64.477
## <none>          3   59.163 65.163
## - log.Length   1   62.149 66.149
## + Year         3   55.795 67.795
##
## Step: AIC=64.48
## sardine ~ log.Length
##
##           Df Deviance   AIC
## - log.Length   1   62.183 64.183
## <none>         3   60.477 64.477
## + log.body.mass 1   59.163 65.163
## + Year         3   55.968 65.968
##
## Step: AIC=64.18
## sardine ~ 1
##
##           Df Deviance   AIC
## <none>       3   62.183 64.183
## + Year      3   56.435 64.435
## + log.Length 1   60.477 64.477
## + log.body.mass 1   62.149 66.149

modelsa03 <- glm(sardine~ 1,family = binomial, data = df6)
modelsa04 <- step(modelsa03
, direction = "both", scope = list(lower = ~1,upper = ~(Year+log.body.mass+log.Length)

## Start: AIC=64.18
## sardine ~ 1
##
##           Df Deviance   AIC
## <none>       3   62.183 64.183
## + Year      3   56.435 64.435
## + log.Length 1   60.477 64.477
## + log.body.mass 1   62.149 66.149

AIC(modelsa01,modelsa02,modelsa03,modelsa04)

##           df       AIC
## modelsa01  6 67.7953

```

```
## modelsa02 1 64.1831
## modelsa03 1 64.1831
## modelsa04 1 64.1831
```

```
summary(modelsa01, test="Chisq")
```

```
##
## Call:
## glm(formula = sardine ~ (Year + log.body.mass + log.Length),
##      family = binomial, data = df6)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9265  -1.0544   0.6229   0.9368   1.6033
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      2.038     11.556   0.176   0.860
## Year2012         1.217      2.157   0.564   0.573
## Year2013         0.290      2.053   0.141   0.888
## Year2014         2.114      2.317   0.912   0.362
## log.body.mass   -3.328      8.049  -0.414   0.679
## log.Length       1.797     20.827   0.086   0.931
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 62.183  on 44  degrees of freedom
## Residual deviance: 55.795  on 39  degrees of freedom
## AIC: 67.795
##
## Number of Fisher Scoring iterations: 4
```

```
modelsp01 <- glm(sprat ~ (Year+log.body.mass+log.Length), family = binomial, data = df6)
modelsp02 <- step(modelsp01, direction = "both")
```

```
## Start: AIC=67.41
## sprat ~ (Year + log.body.mass + log.Length)
##
##              Df Deviance    AIC
## - Year          3  56.828 62.828
## - log.body.mass 1  55.483 65.483
## - log.Length    1  55.918 65.918
## <none>          0  55.414 67.414
##
## Step: AIC=62.83
## sprat ~ log.body.mass + log.Length
##
##              Df Deviance    AIC
## - log.body.mass 1  57.168 61.168
## - log.Length    1  57.905 61.905
## <none>          0  56.828 62.828
## + Year          3  55.414 67.414
##
```

```
## Step: AIC=61.17
## sprat ~ log.Length
##
##           Df Deviance   AIC
## <none>           57.168 61.168
## + log.body.mass 1   56.828 62.828
## - log.Length    1   61.827 63.827
## + Year          3   55.483 65.483

modelsp03 <- glm(sprat~ 1,family = binomial, data = df6)
modelsp04 <- step(modelsp03
, direction = "both", scope = list(lower = ~1,upper = ~(Year+log.body.mass+log.Length)
```

```
## Start: AIC=63.83
## sprat ~ 1
##
##           Df Deviance   AIC
## + log.Length    1   57.168 61.168
## + log.body.mass 1   57.905 61.905
## <none>           61.827 63.827
## + Year          3   60.312 68.312
##
## Step: AIC=61.17
## sprat ~ log.Length
##
##           Df Deviance   AIC
## <none>           57.168 61.168
## + log.body.mass 1   56.828 62.828
## - log.Length    1   61.827 63.827
## + Year          3   55.483 65.483
```

```
AIC(modelsp01,modelsp02,modelsp03,modelsp04)
```

```
##           df      AIC
## modelsp01  6 67.41386
## modelsp02  2 61.16769
## modelsp03  1 63.82654
## modelsp04  2 61.16769
```

```
summary(modelsp01, test="Chisq")
```

```
##
## Call:
## glm(formula = sprat ~ (Year + log.body.mass + log.Length), family = binomial,
##      data = df6)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.4381  -1.0623  -0.6026   1.0925   1.7905
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
```

```

## (Intercept)    -18.6381    12.5318   -1.487    0.137
## Year2012       -0.1934     2.1366   -0.091    0.928
## Year2013       -0.6075     2.0433   -0.297    0.766
## Year2014       -1.4233     2.3606   -0.603    0.547
## log.body.mass  2.1234      8.0662    0.263    0.792
## log.Length    14.8976    21.2226    0.702    0.483
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 61.827  on 44  degrees of freedom
## Residual deviance: 55.414  on 39  degrees of freedom
## AIC: 67.414
##
## Number of Fisher Scoring iterations: 4

```

```
### make drawing
```

```

line.length <- 1000
df5$Year<-as.factor(df5$Year)

plot(df5$log.body.mass, df5$Ctenophora, type="n", xlab="", ylab = "")
modelan <- glm(anchovy~ (Year+log.body.mass+log.Length), family = binomial, data = df6)
x.anchovy.1 <- seq(min(df6$log.body.mass),max(df6$log.body.mass),length=line.length)
y.anchovy.1 <- predict(modelan, list(log.body.mass=x.anchovy.1, log.Length=rep(mean(df5$log.Length),1000),
                                     Year=as.factor(rep("2012",1000))), type="response")
rug(jitter(df6$log.body.mass[df6$anchovy==0]), col = "navy")
rug(jitter(df6$log.body.mass[df6$anchovy==0]), col = "navy", line=-0.06)
rug(jitter(df6$log.body.mass[df6$anchovy==1]),side=3, col="navy")
rug(jitter(df6$log.body.mass[df6$anchovy==1]),side=3, col="navy",line=-0.06)
lines(x.anchovy.1,y.anchovy.1,type="l", col="navy", lwd=2)

modelCTE <- glm(Ctenophora ~ (Year+log.body.mass+log.Length), family = binomial, data = df5)
x.Ctenophora.1 <- seq(min(df5$log.body.mass),max(df5$log.body.mass),length=line.length)
y.Ctenophora.1 <- predict(modelCTE , list(log.body.mass=x.Ctenophora.1,
                                           log.Length=rep(mean(df5$log.Length),1000),Year=as.factor(rep(
rug(jitter(df5$log.body.mass[df5$Ctenophora==0]), col = "aquamarine2",line=-0.02)
rug(jitter(df5$log.body.mass[df5$Ctenophora==1]),side=3, col="aquamarine2", line=-0.02)
lines(x.Ctenophora.1,y.Ctenophora.1,type="l", col="aquamarine2", lwd=2)

```

