Supplement 1

Maps characterizing the study area in relation to environmental and anthropic variables

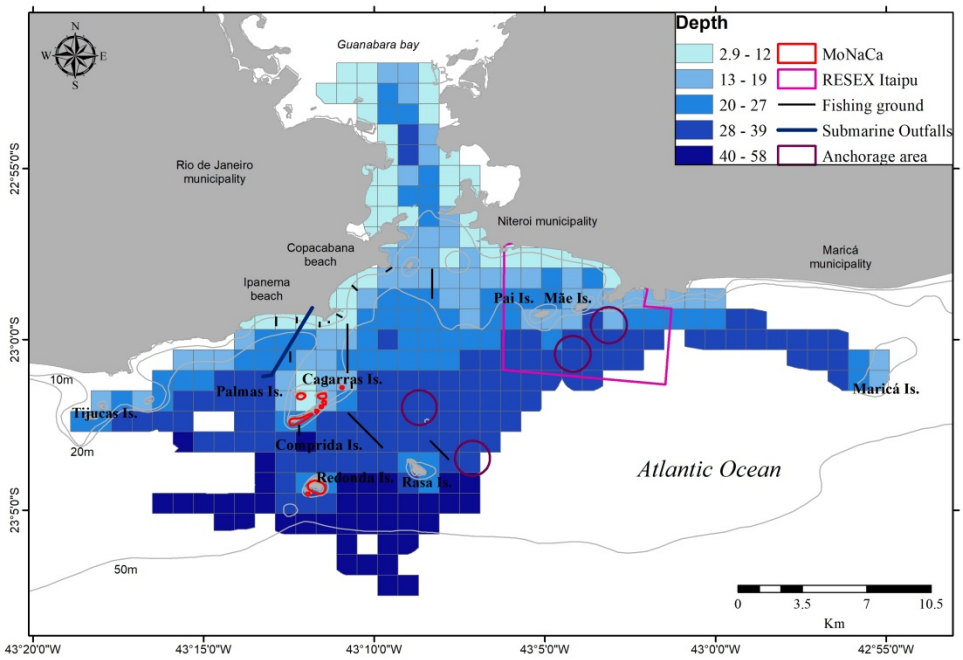


Fig. S. 1.1. Study area located off the coast of the city of Rio de Janeiro, in southeastern Brazil, showing depth values, in meters, for each 1 km^2 grid cell.

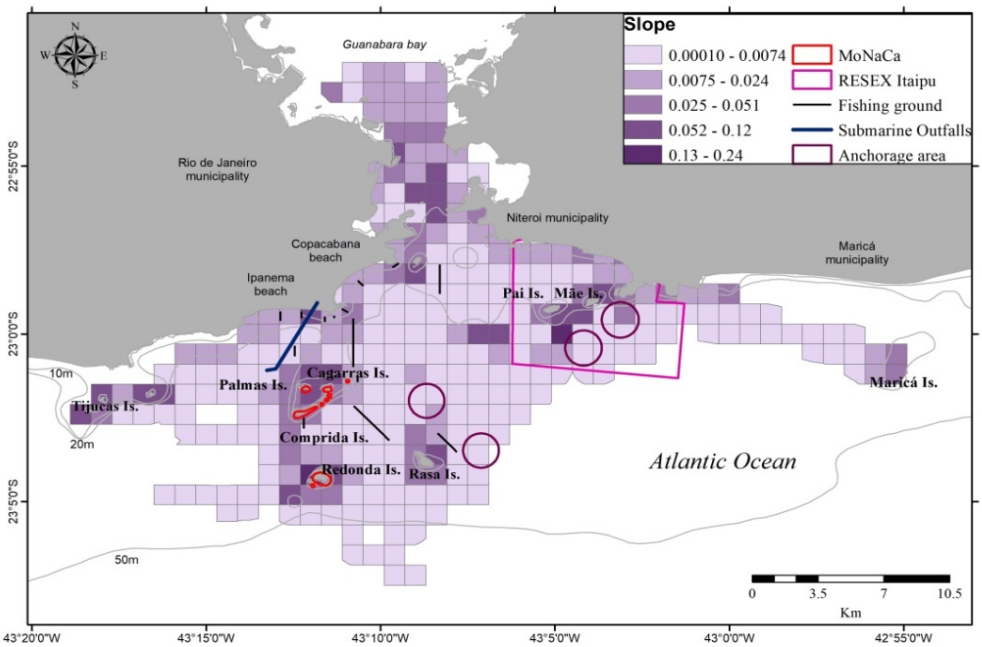


Fig. S. 1.2. Study area located off the coast of the city of Rio de Janeiro, in southeastern Brazil, showing slope values for each 1 km^2 grid cell.

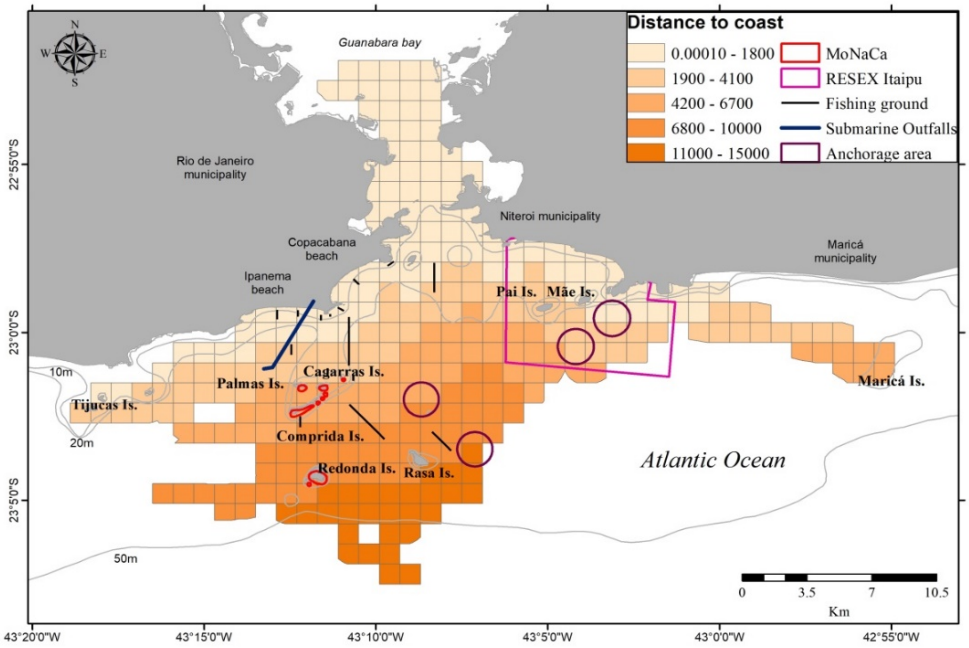


Fig. S. 1.3. Study area located off the coast of the city of Rio de Janeiro, in southeastern Brazil, showing distance to coast values, in meters, for each 1 km^2 grid cell.

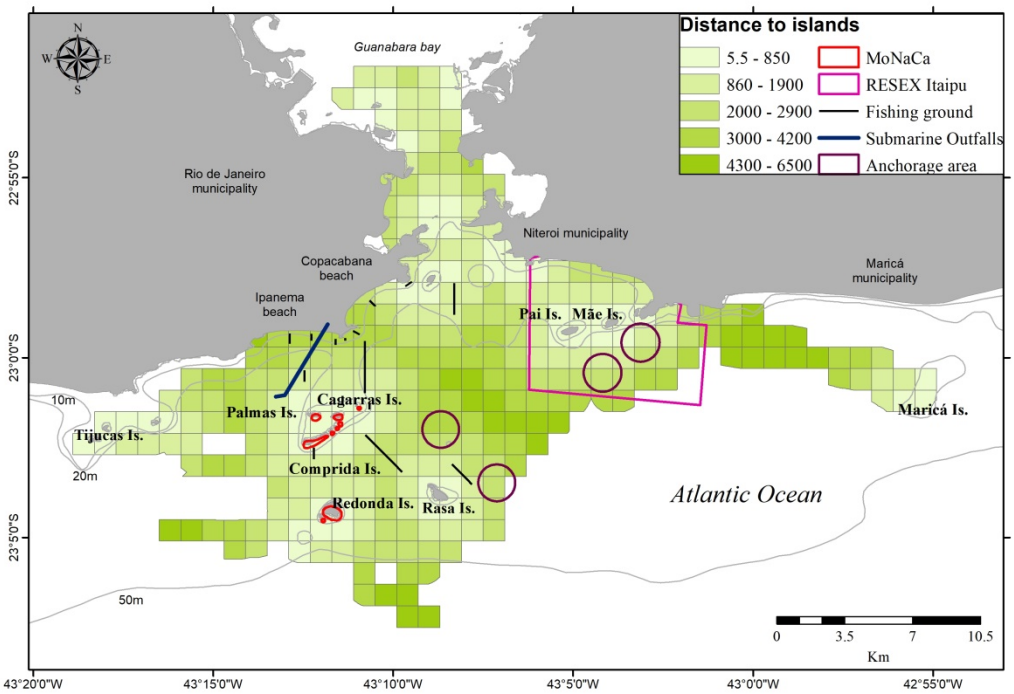


Fig. S. 1.4. Study area located off the coast of the city of Rio de Janeiro, in southeastern Brazil, showing distance to islands values, in meters, for each 1 km^2 grid cell.

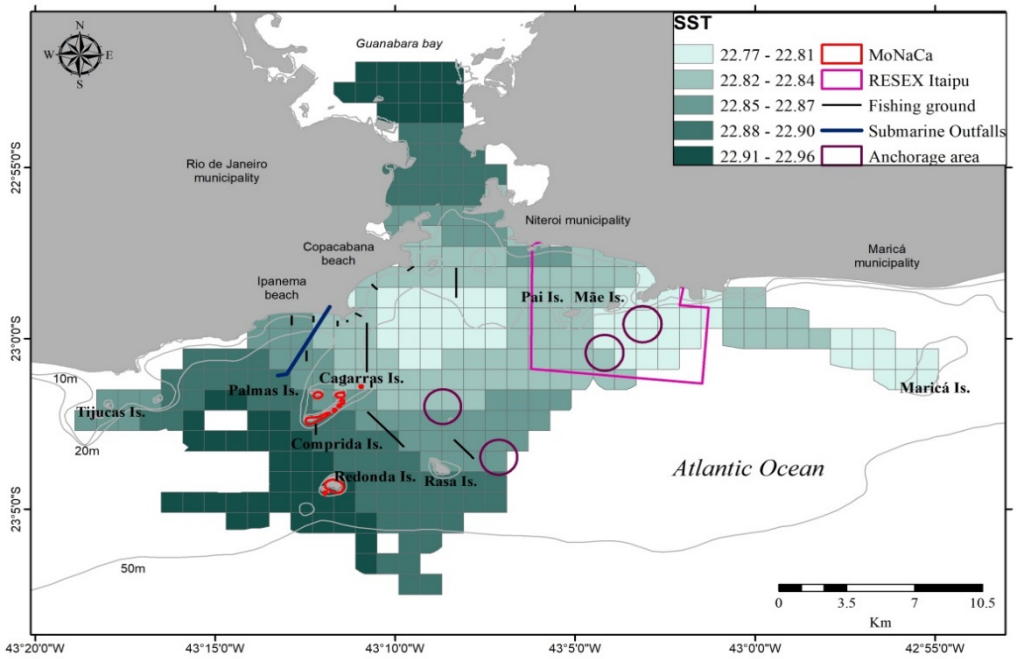


Fig. S. 1.5. Study area located off the coast of the city of Rio de Janeiro, in southeastern Brazil, showing sea surface temperature values, in ºC, for each 1 km^2 grid cell.

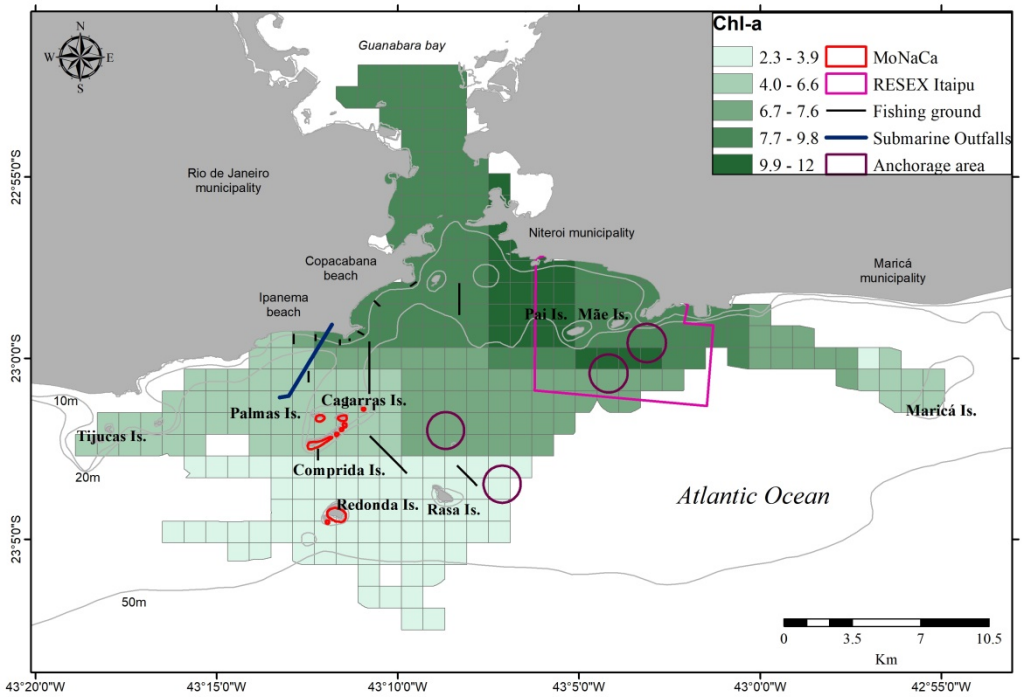


Fig. S. 1.6. Study area located off the coast of the city of Rio de Janeiro, in southeastern Brazil, showing chlorophyll-a concentration values for each 1 km^2 grid cell.

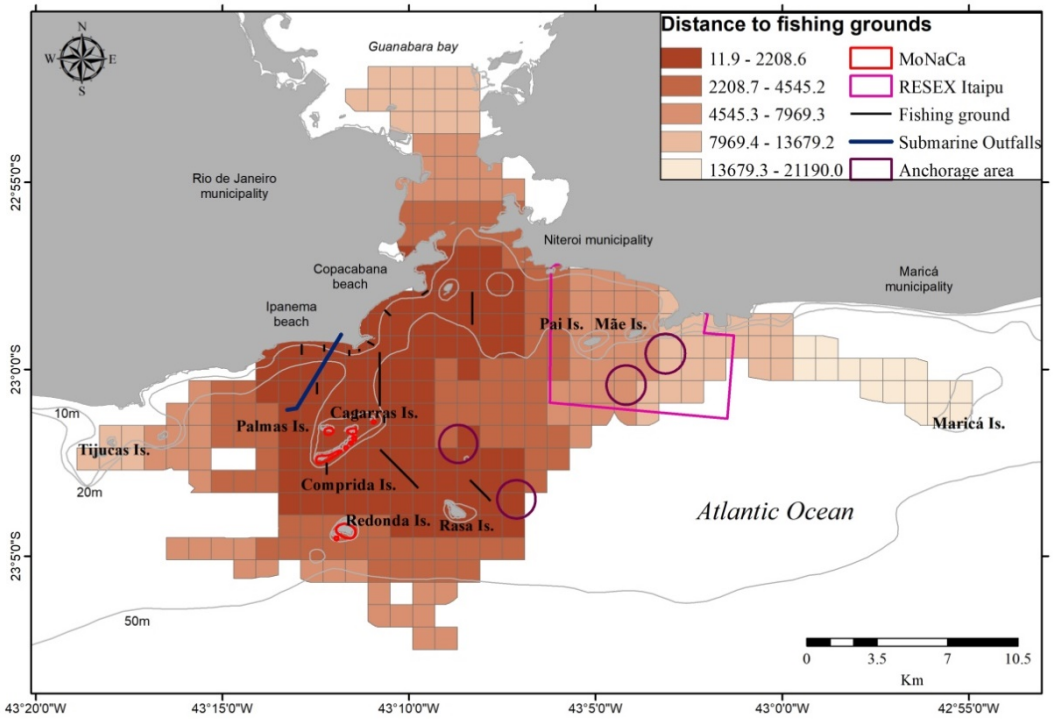


Fig. S. 1.7. Study area located off the coast of the city of Rio de Janeiro, in southeastern Brazil, showing distance to fishing grounds values, in meters, for each 1 km^2 grid cell.

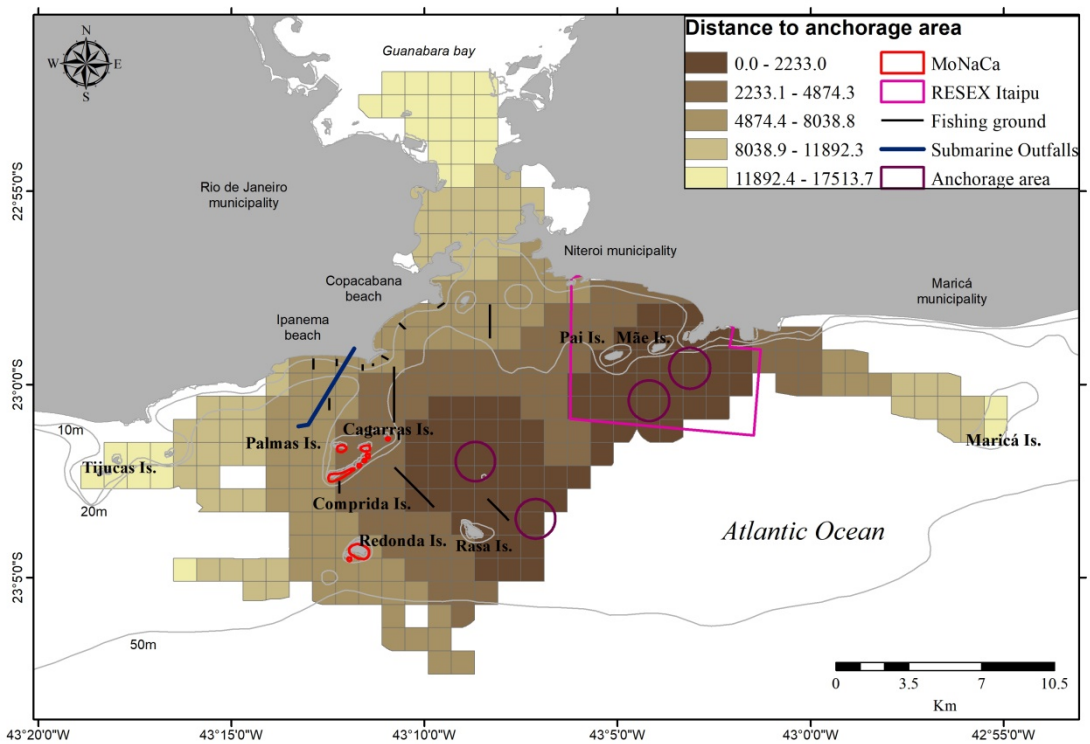


Fig. S. 1.8. Study area located off the coast of the city of Rio de Janeiro, in southeastern Brazil, showing distance to anchorage values, in meters, for each 1 km^2 grid cell.

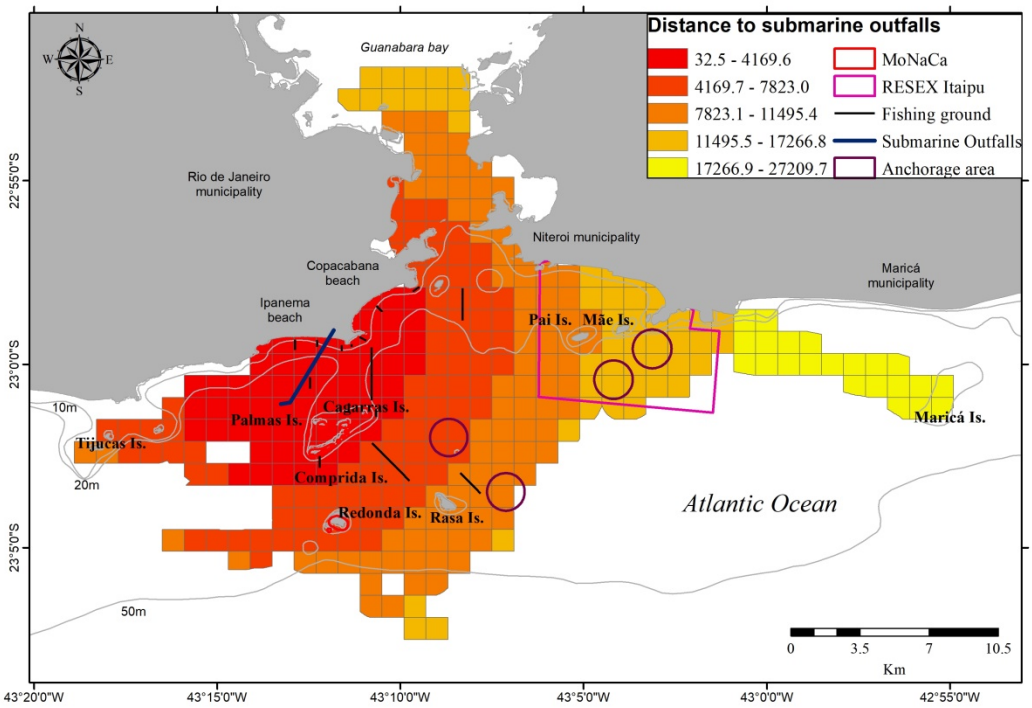


Fig. S. 1.9. Study area located off the coast of the city of Rio de Janeiro, in southeastern Brazil, showing distance to submarine outfalls values, in meters, for each 1 km^2 grid cell.

Supplement 2

R Script describing the modeling protocol

```
library(spdep)
library(ggplot2)
library(car)
library(maptools)
library(hier.part)
library(MuMIn)
library(bbmle)
library(boot)
library(AER)
library(xtable)
##########################################################################
#            1 km models                                ##
##########################################################################
#Getting data
cagarras <- readShapePoly("Fishnet9.shp")
names(cagarras)
#############################################################################
#                                                  ###
#       Bryde's whale habitat use model                          ###
#############################################################################
#################################################################
#           Data exploration                    ####
#################################################################
#Visual inspection to include or not a polynomial term
depth=cagarras$Depth
Bryde=cagarras$BRYDETOTAL
```

```
Humpback=cagarras$HUMPTOTAL
depth=cagarras$Depth
plot(depth,Bryde)
plot(depth,Humpback)
#nonlinear
slope=cagarras$Slope
plot(slope,Bryde)
plot(slope,Humpback)
#Linear
distilhas=cagarras$DISTILHAS
plot(distilhas,Bryde)
plot(distilhas,Humpback)
#Linear
distcoast=cagarras$DISTCOAST
plot(distcoast,Bryde)
#Non-linear
plot(distcoast,Humpback)
#Linear
sstfull=cagarras$SSTMEANFUL
plot(sstfull,Bryde)
#Linear
plot(sstfull,Humpback)
#Linear
chlorfull=cagarras$CHLSUM
plot(chlorfull, Bryde)
#Non-linear
plot(chlorfull, Humpback)
#Linear
fishground=cagarras$FSHGRD
```

```
plot(fishground,Bryde)
#Linear
plot(fishground,Humpback)
#Linear
anchorage=cagarras$FUND
plot(anchorage,Bryde)
#Linear
plot(anchorage,Humpback)
#Linear
sewage=cagarras$EMISSARIO
plot(sewage,Bryde)
#Linear
plot(sewage,Humpback)
#Linear
####################################
##############################################################################
##### Autocorrelation check                          #############
##############################################################################
##Neighbourhood with Queen specification
cagarras.nb.q1 <- poly2nb(cagarras, queen=TRUE)
cagarras.lw.q1  <-  nb2listw(cagarras.nb.q1,  style="W")
##Moran Test check for spatial autocorrelation
moran.test(cagarras$HUMPTOTAL,nb2listw(cagarras.nb.q1,  style="W"))
moran.test(cagarras$BRYDETOTAL,nb2listw(cagarras.nb.q1,  style="W"))
#Existence of spatial autocorrelation
#Multicollinearity check
vif(sevglmfcet)
vif=xtable(vif(sevglmfcet))write.csv(vif, file="vif.csv")
#Overdispersion check
```

```
dispersiontest(sevglmfbry)

##############################################################################
###

### Spatial Eigenvector Modelling                    ########

##############################################################################
###

## Moran Eigenvectors

#Environmental

eigebry <- ME(BRYDETOTAL ~
CHLMEANCM+I(CHLMEANCM^2)+DEPTHCM+I(DEPTHCM^2)+DISTCOASTCM+I(DIS
TCOASTCM^2) + Slope+DISTILHAS+SSTMEANFUL,

        data=cagarras, family="poisson", listw=cagarras.lw.q1,offset=log(KM_TOTAL),
alpha=0.05,

        verbose=TRUE)

#Anthropogenic

eigabry <- ME(BRYDETOTAL ~ EMISSARIO+FSHGRD+FUND,

        data=cagarras, family="poisson", offset=log(KM_TOTAL),listw=cagarras.lw.q1,
alpha=0.05,

        verbose=TRUE)

#Full

eigfbry <- ME(BRYDETOTAL ~
CHLMEANCM+I(CHLMEANCM^2)+DEPTHCM+I(DEPTHCM^2)+DISTCOASTCM+I(DIS
TCOASTCM^2) +

Slope+DISTILHAS+SSTMEANFUL+EMISSARIO+FSHGRD+FUND,

        data=cagarras, family="poisson", listw=cagarras.lw.q1,offset=log(KM_TOTAL),
alpha=0.05,

        verbose=TRUE)

##############################################################################
####

##                                                  ##

##                SEV-GLM STEPWISE BACKWARD SELECTION            ##

##############################################################################
####
```

```
#Environmental

sevglmebry  <-  step(glm(BRYDETOTAL ~
CHLMEANCM+I(CHLMEANCM^2)+DEPTHCM+I(DEPTHCM^2)
+DISTCOASTCM+I(DISTCOASTCM^2)+

Slope+SSTMEANFUL+fitted(eigebry),  data=cagarras, family="poisson",

                offset=log(KM_TOTAL)) )

#Anthropogenic

sevglmabry  <-  step(glm(BRYDETOTAL ~
EMISSARIO+FSHGRD+FUNDCM+I(FUNDCM^2)+fitted(eigabry),  data=cagarras,
family="poisson",

                offset=log(KM_TOTAL)))

#Full

sevglmfbry  <-  step(glm(BRYDETOTAL ~
CHLMEANCM+I(CHLMEANCM^2)+DEPTHCM+I(DEPTHCM^2)+DISTCOASTCM+I(DIS
TCOASTCM^2) +

Slope+DISTILHAS+SSTMEANFUL+EMISSARIO+FSHGRD+FUNDCM+I(FUNDCM^2)+fi
tted(eigfbry),  data=cagarras, family="poisson",

                offset=log(KM_TOTAL)))

sevglmbrybest= glm(BRYDETOTAL ~ CHLMEANCM + I(CHLMEANCM^2) +
I(DEPTHCM^2) + DISTILHAS +

                 SSTMEANFUL + FUNDCM + fitted(eigfbry), data=cagarras, family="poisson",

               offset=log(KM_TOTAL))

#Model Selection - full period

summary(sevglmbrybest)

tablebry=xtable(summary(sevglmbrybest))

print(tablebry)

write.csv(tablebry, file="tablebry.csv")

##Hierarchical partitioning analysis

depth2=as.data.frame(depth)

fundeio2=as.data.frame(fundeio)

chlmean2=as.data.frame(chlorfull)

sstmeanful2=as.data.frame(sstfull)
```

```
envmist<-c(depth2,sstmeanful2,distilhas2,fundeio2,chlmean2)

env1mist<-as.data.frame(envmist)

hier.part(cagarras$BRYDETOTAL, env1mist)

## test if the fitted values explain the observed value

glmMEbry <- glm(cagarras$BRYDETOTAL ~ fitted(sevglmbrybest),

            family="poisson")

anova(glmMEbry, test="Chisq")

#PSeudoR

#Full

psdr.sevglmbrybest <- lm(cagarras$BRYDETOTAL~ fitted(sevglmbrybest))

summary(psdr.sevglmbrybest)$r.square

#0.57

# Model predictions in relation to each explanatory variable selected from the best SEV-GLM

neo.pred <- predict(sevglmbrybest, type = "response", se.fit = F)

depthpredbry<-ggplot(as.data.frame(cagarras), aes(x = depth, y = neo.pred)) + theme_bw() +
theme(

  panel.grid.major = element_line(size = 0.5, colour = 'NA'),

  panel.grid.minor = element_line(colour = NA),axis.line = element_line(colour =
"black"),panel.border = element_blank(),

  panel.background = element_rect(colour = NA),

  axis.ticks = element_line(colour = NA)

)+geom_point()+

  stat_smooth(method = "loess", col="black", bg="black", family = "poisson", se = TRUE) +

  labs(x = "Depth (m)",

      y = "Bryde's whale sighting prediction")

depthpredbry

ggsave(depthpredbry, file="depthpredbry.jpg", dpi=600)

chlpredbry<-ggplot(as.data.frame(cagarras), aes(x = chlorfull, y = neo.pred)) + theme_bw() +
theme(

  panel.grid.major = element_line(size = 0.5, colour = 'NA'),
```

```
  panel.grid.minor = element_line(colour = NA),axis.line = element_line(colour =
"black"),panel.border = element_blank(),

  panel.background = element_rect(colour = NA),

  axis.ticks = element_line(colour = NA)

)+geom_point()+

  stat_smooth(method = "glm", col="black", bg="black", family = "poisson", se = TRUE) +

  labs(x = "Mean Chl-a (m mg-1)",

       y = "Bryde's whale sighting prediction")

chlpredbryggsave(chlpredbry, file="chlpredbry.jpg", dpi=600)

sstpredbry<-ggplot(as.data.frame(cagarras), aes(x = sstfull, y = neo.pred)) + theme_bw() +
theme(

  panel.grid.major = element_line(size = 0.5, colour = 'NA'),

  panel.grid.minor = element_line(colour = NA),axis.line = element_line(colour =
"black"),panel.border = element_blank(),

  panel.background = element_rect(colour = NA),

  axis.ticks = element_line(colour = NA)

)+geom_point()+

  stat_smooth(method = "glm", col="black", bg="black", family = "poisson", se = TRUE) +

  labs(x = "Mean SST (ºC)",

       y = "Bryde's whale sighting prediction")

sstpredbry

ggsave(sstpredbry, file="sstpredbry.jpg", dpi=600)

ilhaspredbry<-ggplot(as.data.frame(cagarras), aes(x = distilhas, y = neo.pred)) + theme_bw() +
theme(

  panel.grid.major = element_line(size = 0.5, colour = 'NA'),

  panel.grid.minor = element_line(colour = NA),axis.line = element_line(colour =
"black"),panel.border = element_blank(),

  panel.background = element_rect(colour = NA),

  axis.ticks = element_line(colour = NA)

)+geom_point()+

  stat_smooth(method = "glm", col="black", bg="black", family = "poisson", se = TRUE) +
```

```
  labs(x = "Distance to islands (m)",
       y = "Bryde's whale sighting prediction")
ilhaspredbry
ggsave(ilhaspredbry, file="ilhaspredbry.jpg", dpi=600)
fundpredbry<-ggplot(as.data.frame(cagarras), aes(x = fundeio, y = neo.pred)) + theme_bw() +
theme(
  panel.grid.major = element_line(size = 0.5, colour = 'NA'),
  panel.grid.minor = element_line(colour = NA),axis.line = element_line(colour =
"black"),panel.border = element_blank(),
  panel.background = element_rect(colour = NA),
  axis.ticks = element_line(colour = NA)
)+geom_point()+
  stat_smooth(method = "glm", col="black", bg="black", family = "poisson", se = TRUE) +
  labs(x = "Distance to anchorage areas (m)",
       y = "Bryde's whale sighting prediction")
fundpredbry
ggsave(fundpredbry, file="fundpredbry.jpg", dpi=600)
##################################################################################
######################
##                    Spatially predicting Bryde habitat use        ##
##################################################################################
######################
#SEV-GLM
sevglmpredbry=predict.glm(sevglmbrybest,type="response")
write.csv(sevglmpredbry,file="sevglmpredbry.csv")
#Residuals mapping
#SEV-GLM residuals
ressevglmbry <- residuals.glm(sevglmbrybest, type="pearson")
write.csv(ressevglmbry,file="ressevglmbry.csv")
```

```
##############################################################################
#####################
##                    Eigenvector Mapping                              ##
##############################################################################
#####################
betabry <- matrix(coefficients(sevglmbrybest)[7])
xbry<-as.matrix(fitted(eigfbry))
sfbry <- x%*%beta
write.csv(sfbry,file="spatialfilterbry.csv")
##############################################################################
#########################
####
###                 Humpback whales                              #########
##############################################################################
#########################
#Overdispersion check
dispersiontest(sevglmfhump)
##############################################################################
###
### Spatial Eigenvector Modelling                          ########
##############################################################################
###
names(cagarras)
## Moran Eigenvectors
#Environmental
eigehump  <-  ME(HUMPTOTAL ~
CHLMEAN+DEPTHCM+I(DEPTHCM^2)+DISTCOAST +
Slope+DISTILHAS+SSTMEANFUL,
            data=cagarras, family="poisson", listw=cagarras.lw.q1,offset=log(KM_TOTAL),
alpha=0.05,
            verbose=TRUE)
```

```
#Anthropogenic

eigahump <- ME(HUMPTOTAL ~ EMISSARIO+FSHGRD+FUND,

        data=cagarras, family="poisson", offset=log(KM_TOTAL),listw=cagarras.lw.q1,
alpha=0.05,

        verbose=TRUE,)

#Full

eigfhump <- ME(HUMPTOTAL ~
CHLMEAN+DEPTHCM+I(DEPTHCM^2)+DISTCOAST+
Slope+DISTILHAS+SSTMEANFUL+EMISSARIO+FSHGRD+FUND,

        data=cagarras, family="poisson", listw=cagarras.lw.q1,offset=log(KM_TOTAL),
alpha=0.05,

        verbose=TRUE)

######### SEV-GLM #################

#Environmental

sevglmehump <- step(glm(HUMPTOTAL ~ CHLMEAN+DEPTHCM+I(DEPTHCM^2)
+DISTCOAST+ Slope+SSTMEANFUL+fitted(eigehump), data=cagarras,

family="poisson",

            offset=log(KM_TOTAL)))

#Anthropogenic

sevglmahump <- step(glm(HUMPTOTAL ~
EMISSARIO+FSHGRD+FUND+fitted(eigahump), data=cagarras, family="poisson",

            offset=log(KM_TOTAL)))

#Fullsevglmfhump <- step(glm(HUMPTOTAL ~
CHLMEAN+DEPTHCM+I(DEPTHCM^2)+DISTCOAST +
Slope+DISTILHAS+SSTMEANFUL+EMISSARIO+FSHGRD+FUND+fitted(eigfhump),

data=cagarras, family="poisson",

            offset=log(KM_TOTAL)) )

sevglmbesthump1=glm(HUMPTOTAL ~ I(DEPTHCM^2) + DISTCOAST + Slope +
EMISSARIO + FSHGRD +

             fitted(eigfhump), data=cagarras, family="poisson",

           offset=log(KM_TOTAL))

sevglmbesthump2=glm(HUMPTOTAL ~ I(DEPTHCM^2) + DISTCOAST + Slope +
fitted(eigehump), data=cagarras, family="poisson",
```

```
offset=log(KM_TOTAL))
#Model Selection - full period
summary(sevglmbesthump1)
summary(sevglmbesthump2)
tableodo=xtable(summary(sevglmfodo))
print(tableodo)
write.csv(tableodo, file="tableodo.csv")
##Hierarchical partitioning analysis
#Full period
names(cagarras)
slope1=as.data.frame(slope)
distcoast1=as.data.frame(distcoast)
envhump<-c(slope1,distcoast1)
env1hump<-as.data.frame(envhump)
hier.part(cagarras$HUMPTOTAL, env1hump)
## test if the fitted values explain the observed value
glmME <- glm(cagarras$HUMPTOTAL ~ fitted(sevglmfodo),
        family="poisson")
anova(glmME, test="Chisq")
#PSeudoR
psdr.sevglmhump1 <- lm(cagarras$HUMPTOTAL~ fitted(sevglmbesthump1))
summary(psdr.sevglmhump1)$r.square
#0.35
psdr.sevglmhump2 <- lm(cagarras$HUMPTOTAL~ fitted(sevglmbesthump2))
summary(psdr.sevglmhump2)$r.square
#0.38
summary(sevglmbesthump2)
# Model predictions in relation to each explanatory variable selected from the best SEV-GLM
neo.pred2 <- predict(sevglmbesthump2, type = "response", se.fit = F)
```

```
distcoastpredhump<-ggplot(as.data.frame(cagarras), aes(x = distcoast, y = neo.pred2)) +
theme_bw() + theme(

  panel.grid.major = element_line(size = 0.5, colour = 'NA'),

  panel.grid.minor = element_line(colour = NA),axis.line = element_line(colour =
"black"),panel.border = element_blank(),

  panel.background = element_rect(colour = NA),

  axis.ticks = element_line(colour = NA)

)+geom_point()+

  stat_smooth(method = "glm", col="black", bg="black", family = "poisson", se = TRUE) +

  labs(x = "Distance to coast (m)",

       y = "Humpback whale sighting prediction")

distcoastpredhump

ggsave(distcoastpredhump, file="distcoastpredhump.jpg", dpi=600)

slopepredhump<-ggplot(as.data.frame(cagarras), aes(x = cagarras$Slope, y = neo.pred2)) +
theme_bw() + theme(

  panel.grid.major = element_line(size = 0.5, colour = 'NA'),

  panel.grid.minor = element_line(colour = NA),axis.line = element_line(colour =
"black"),panel.border = element_blank(),

  panel.background = element_rect(colour = NA),

  axis.ticks = element_line(colour = NA)

)+geom_point()+

  stat_smooth(method = "glm", col="black", bg="black", family = "poisson", se = TRUE) +

  labs(x = "Slope (m)",

       y = "Humpback whale sighting prediction")

slopepredhump

ggsave(slopepredhump, file="slopepredhump.jpg", dpi=600)

##################################################################################

#######################

##                    Spatially predicting Humpback habitat use      ##

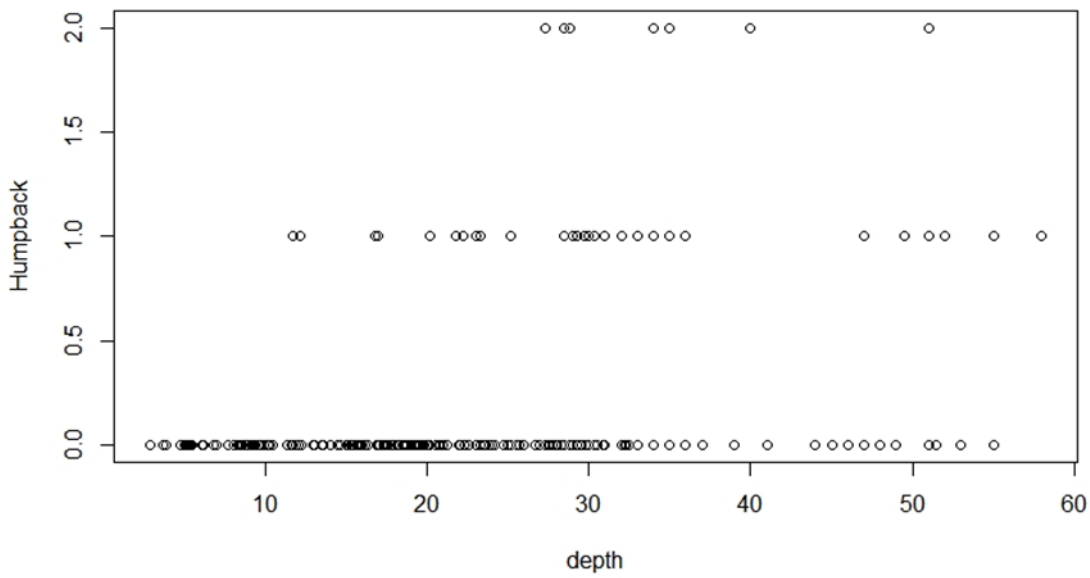
##################################################################################
```

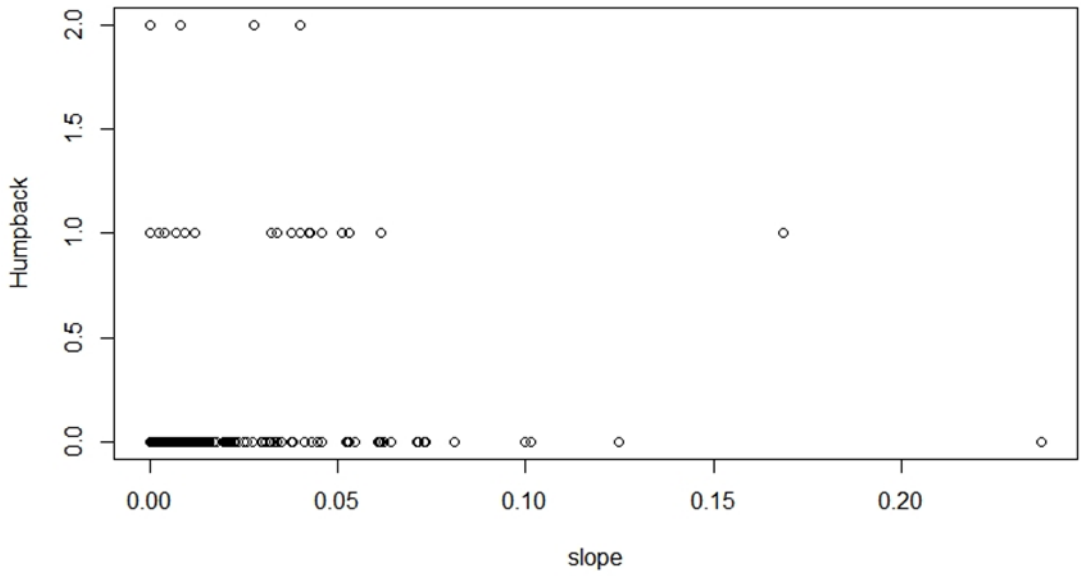
```
######################
#SEV-GLM
sevglmpredhump1=predict.glm(sevglmbesthump1,type="response")
write.csv(sevglmpredhump1,file="sevglmpredhump1.csv")
sevglmpredhump2=predict.glm(sevglmbesthump2,type="response")
write.csv(sevglmpredhump2,file="sevglmpredhump2.csv")
#Residuals mapping
#SEV-GLM residuals
ressevglmbesthump2 <- residuals.glm(sevglmbesthump2, type="pearson")
write.csv(ressevglmbesthump2,file="ressevglmbesthump2.csv")
##############################################################################
######################
##                    Eigenvector Mapping                                  ##
##############################################################################
######################
betahump <- matrix(coefficients(sevglmbesthump2)[5:6])
xhump<-as.matrix(fitted(eigfhump))
sfhump <- x%*%beta
write.csv(sfhump,file="spatialfilterhump.csv")
##End of coding
```

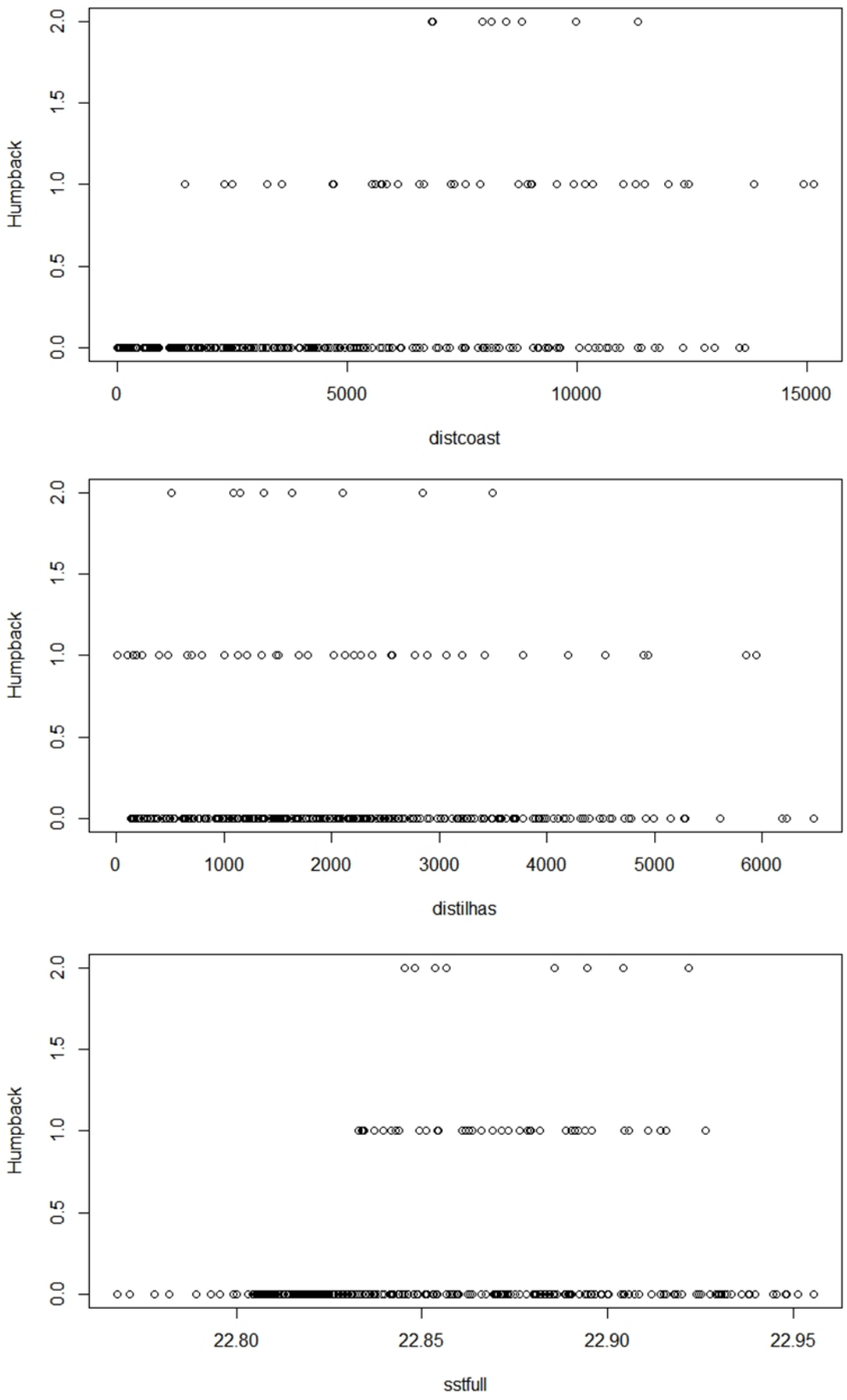
Supplement 3

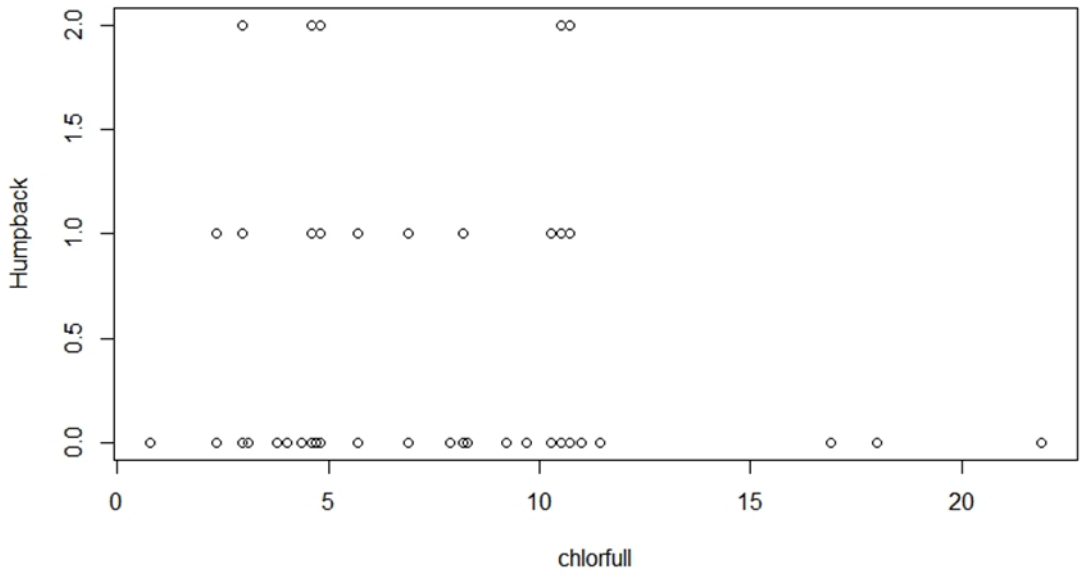
Data exploration for linear or quadratic terms the data sets on each of the two species investigated in this study:

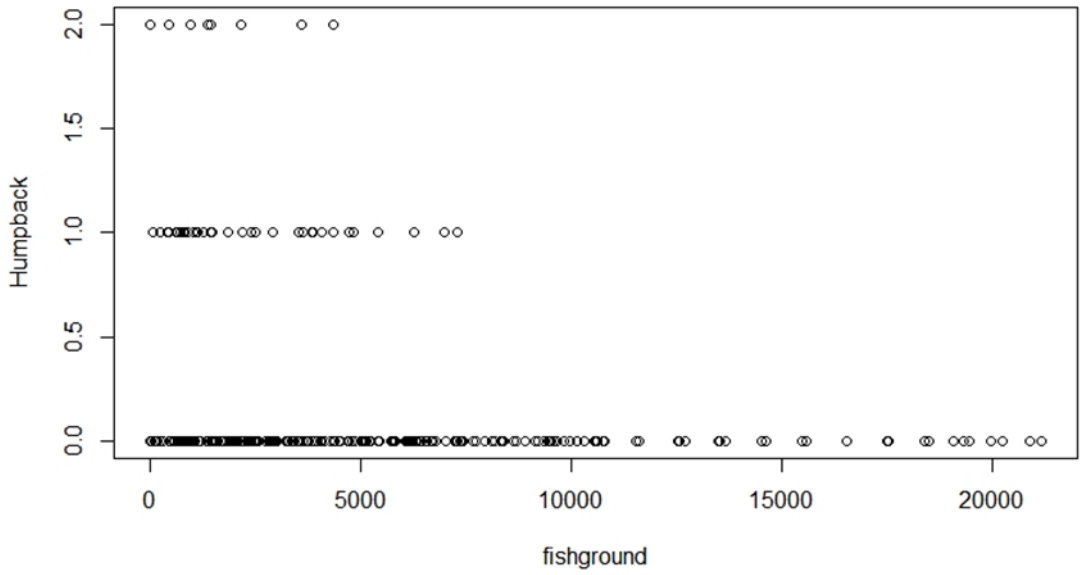
1. Humpback whales






Humpback
0.0
0.5
1.0
1.5
2.0
0
5000
10000
15000
distcoast
Humpback
0.0
0.5
1.0
1.5
2.0
0
1000
2000
3000
4000
5000
6000
distilhas
Humpback
0.0
0.5
1.0
1.5
2.0
22.80
22.85
22.90
22.95
sstfull


Humpback
0.0
0.5
1.0
1.5
2.0
0
5
10
15
20
chlorfull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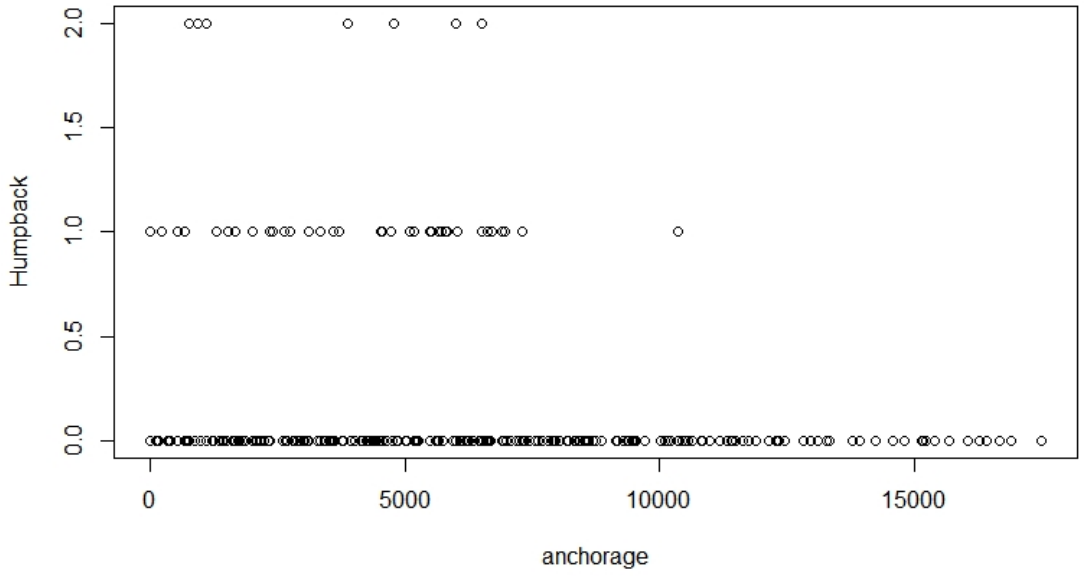
0.5
1.0
1.5
2.0
0
5000
10000
15000
20000
fishground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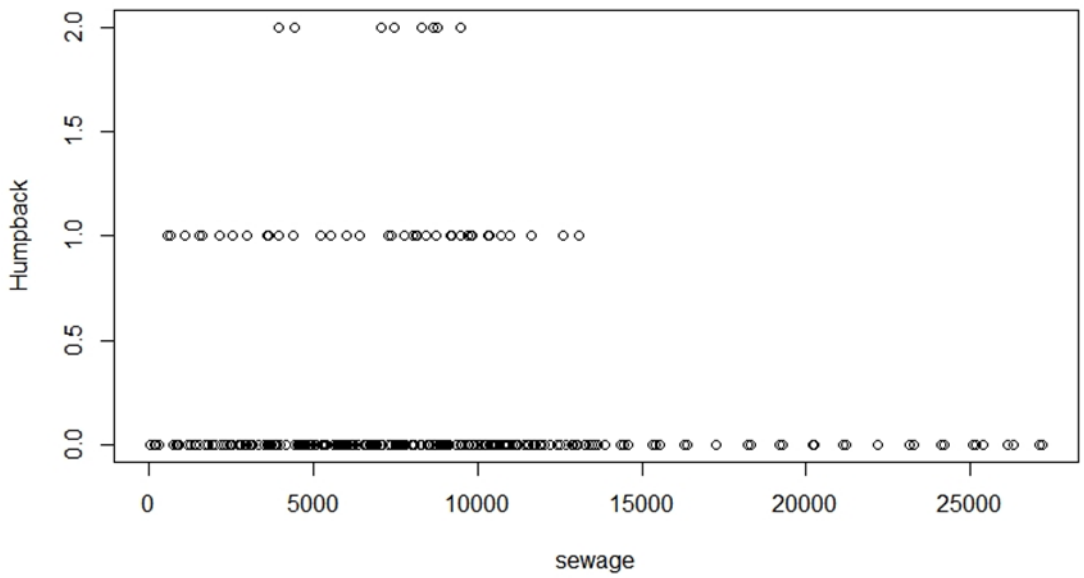
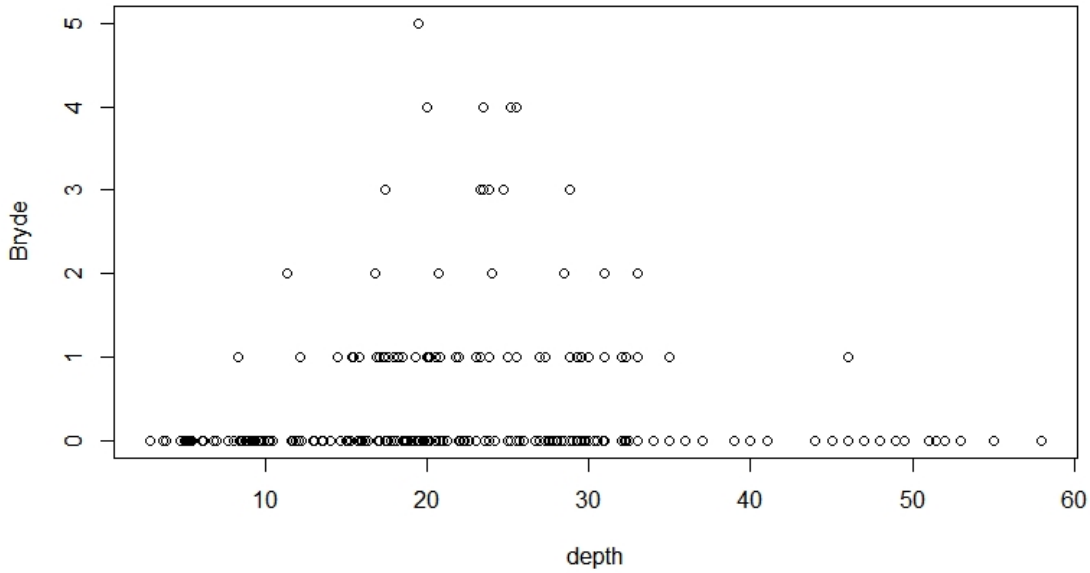
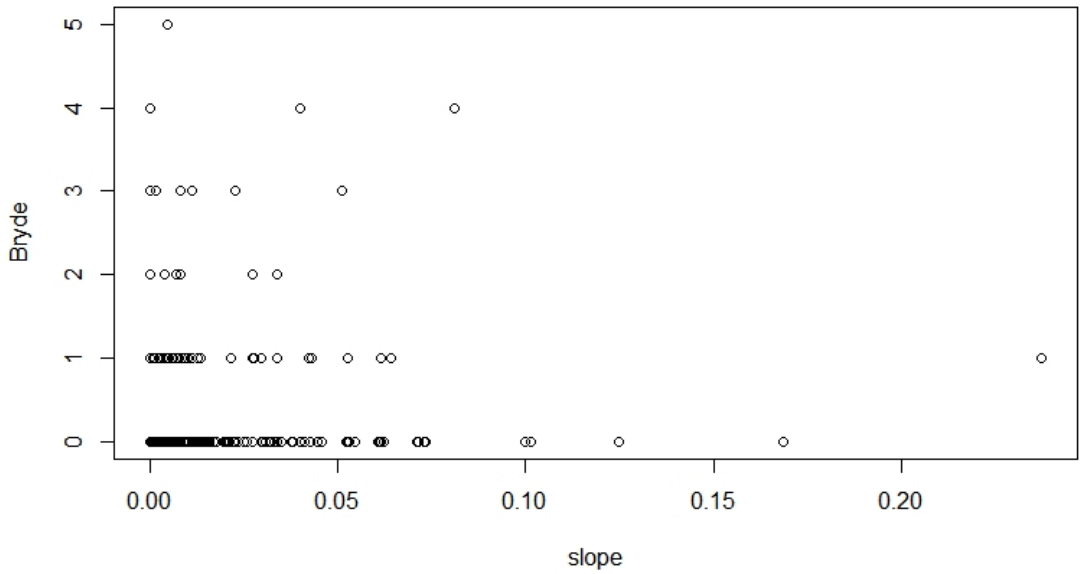
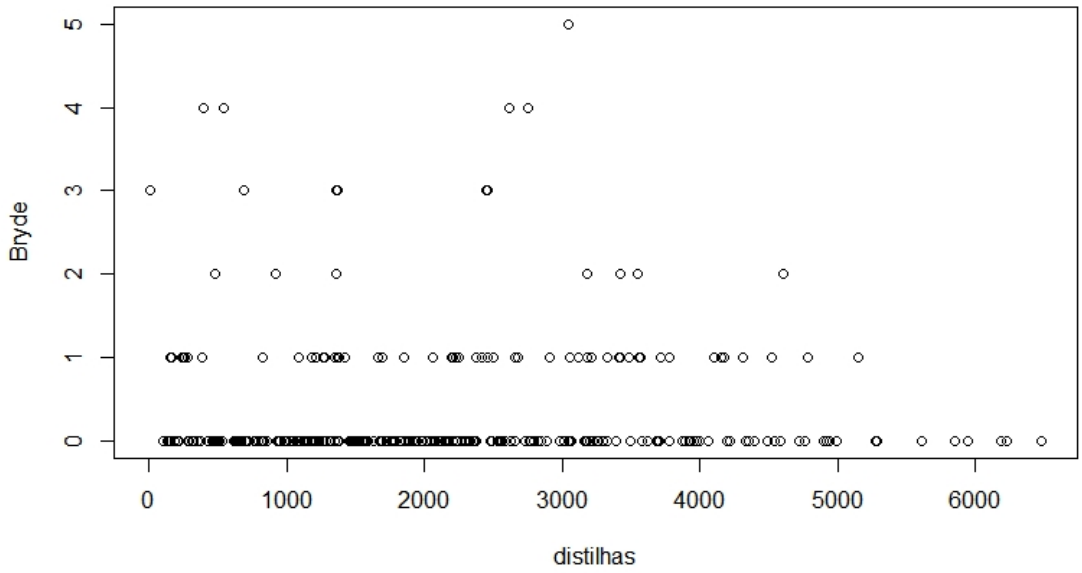
0.5
1.0
1.5
2.0
0
5000
10000
15000
anchorage

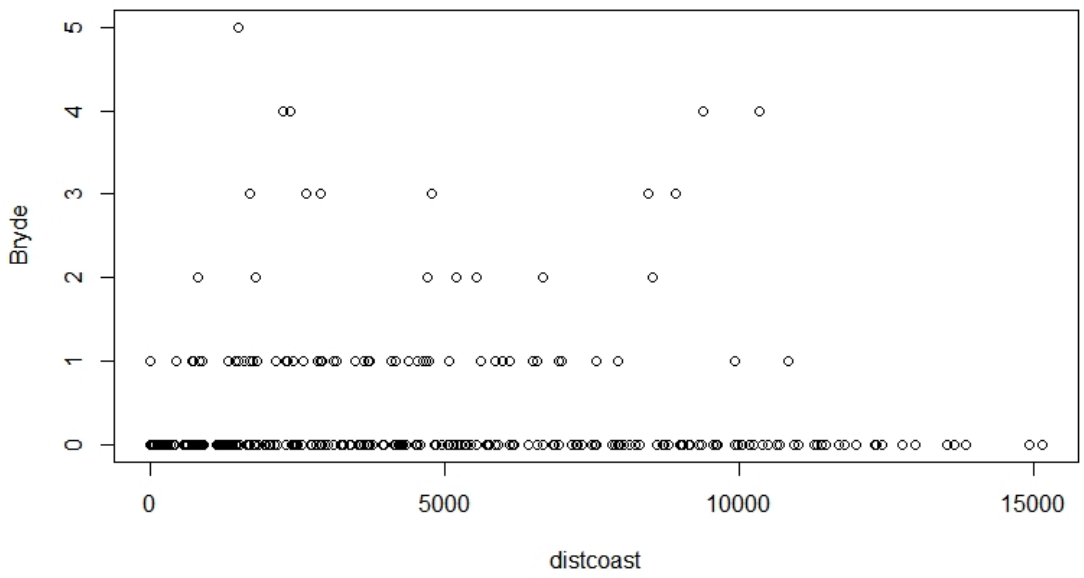

Humpback
0.0
0.5
1.0
1.5
2.0
0
5000
10000
15000
20000
25000
sewage

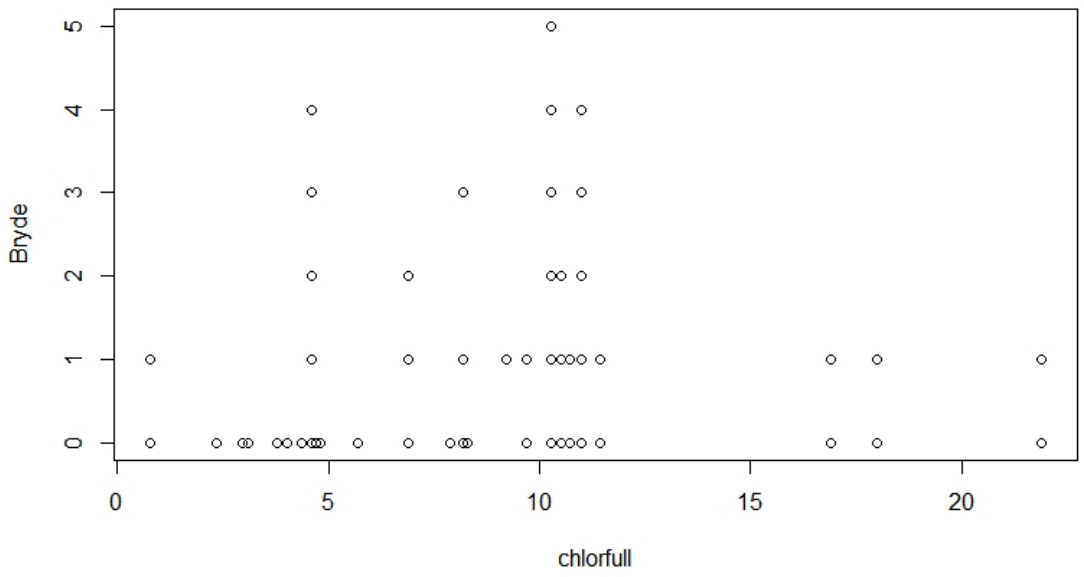
2. Bryde's whale








Bryde
0
1
2
3
4
5
0
5000
10000
15000
distcoast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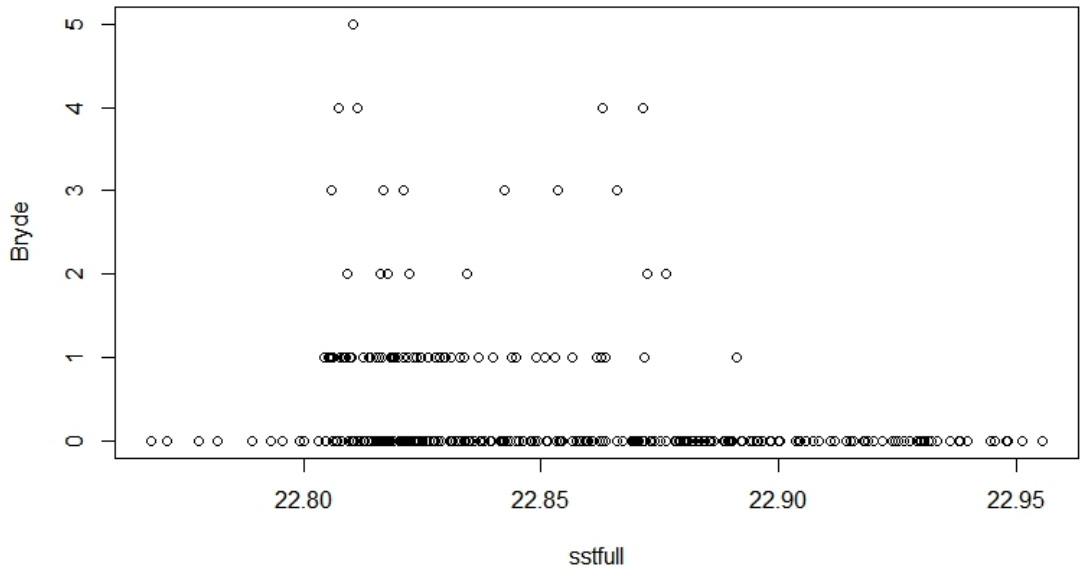
0
1
2
3
4
5
0
5
10
15
20
chlorfull


Bryde
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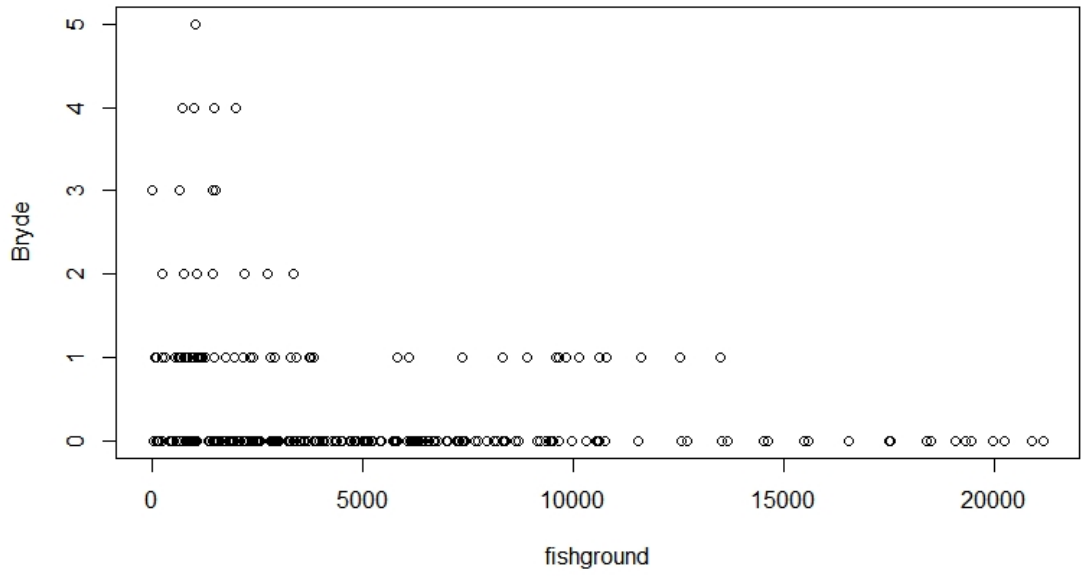
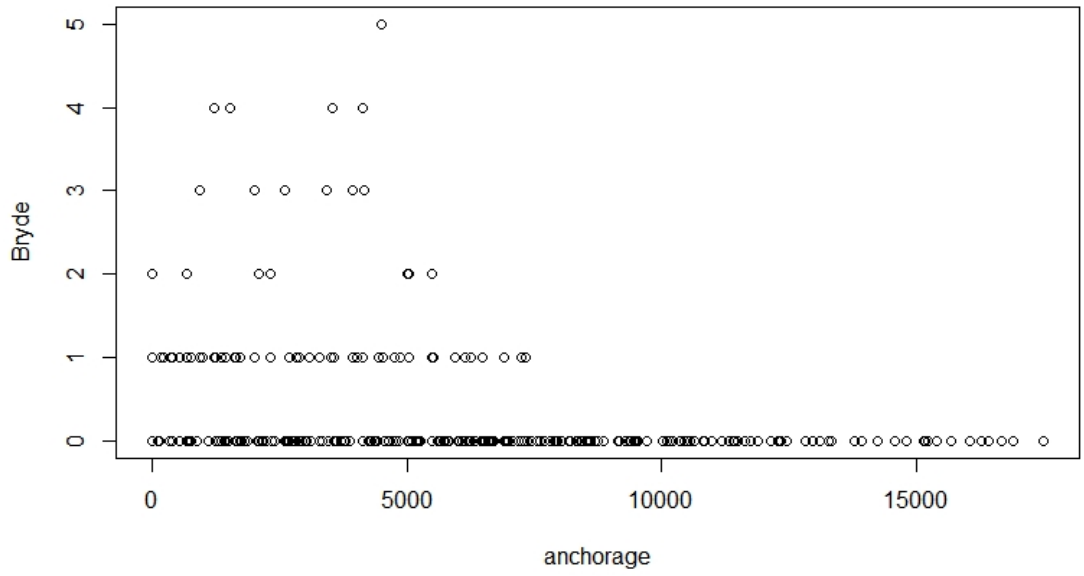
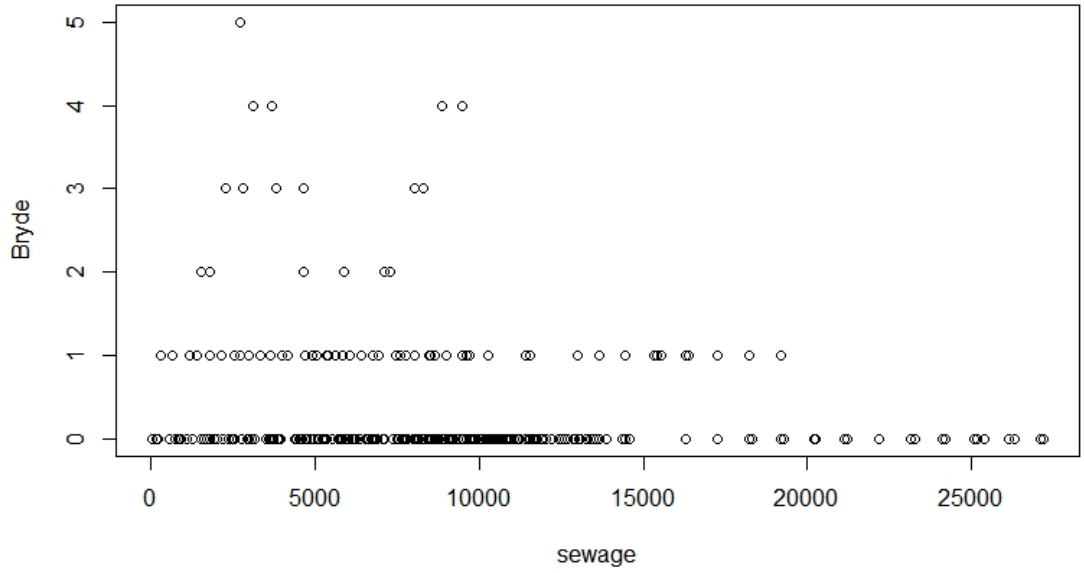
1
2
3
4
5
22.80
22.85
22.90
22.95
sstfull


Bryde
0
1
2
3
4
5
0
5000
10000
15000
20000
fishground


Bryde
0
1
2
3
4
5
0
5000
10000
15000
anchorage


Bryde
0
1
2
3
4
5
0
5000
10000
15000
20000
25000
sewage

Generalized Inflation Variance (GVIF) test to investigate for multicollinearity

Explanatory variables	Df	GVIF^(1/(2*Df))
Mean chl-a	1	2.446457
Squared mean chl-a	1	1.648105
Depth	1	1.989875
Squared depth	1	1.831268
Distance to coast	1	3.961737
Squared distance to coast	1	2.386277
Slope	1	1.330291
Distance to islands	1	1.631218
Mean SST	1	2.820251
Distance to submarine outfall	1	3.17623
Distance to fishing grounds	1	2.949521
Distance to anchorage areas	1	3.350306
Squared Distance to anchorage areas	1	1.605762
fitted(eigfcet)	6	1.096296

Supplement 4

All model combination from each pre-defined subset (environmental, anthropogenic and full) using a stepwise backward procedure for both species (Bryde's and humpback whales). Models in bold indicates the lowest AIC value, thus, the more parsimonious models that are presented in details in the main text.

```
BRYDE - ENVIRONMENTAL

Start:  AIC=341.21
Model 1:
BRYDETOTAL ~ CHLMEANCM + I(CHLMEANCM^2) + DEPTHCM + I(DEPTHCM^2) +
    DISTCOASTCM + I(DISTCOASTCM^2) + Slope + SSTMEANFUL + fitted(eigeb
ry)

                    Df Deviance    AIC
- Slope              1   158.58 339.37
- I(CHLMEANCM^2)     1   158.90 339.69
- I(DISTCOASTCM^2)   1   158.99 339.78
- CHLMEANCM          1   159.59 340.38
<none>                  158.42 341.21
- DEPTHCM            1   160.59 341.39
- fitted(eigebry)    2   178.45 357.24
- DISTCOASTCM        1   179.31 360.10
- I(DEPTHCM^2)       1   180.15 360.94
- SSTMEANFUL         1   214.01 394.80

Step:  AIC=339.37
Model 2:
BRYDETOTAL ~ CHLMEANCM + I(CHLMEANCM^2) + DEPTHCM + I(DEPTHCM^2) +
    DISTCOASTCM + I(DISTCOASTCM^2) + SSTMEANFUL + fitted(eigebry)

                    Df Deviance    AIC
- I(CHLMEANCM^2)     1   159.04 337.83
- I(DISTCOASTCM^2)   1   159.16 337.96
- CHLMEANCM          1   159.71 338.50
<none>                  158.58 339.37
- DEPTHCM            1   160.73 339.52
- fitted(eigebry)    2   178.72 355.51
- DISTCOASTCM        1   179.88 358.67
- I(DEPTHCM^2)       1   180.77 359.56
- SSTMEANFUL         1   222.18 400.97

Step:  AIC=337.83
Model 3:
BRYDETOTAL ~ CHLMEANCM + DEPTHCM + I(DEPTHCM^2) + DISTCOASTCM +
    I(DISTCOASTCM^2) + SSTMEANFUL + fitted(eigebry)

                    Df Deviance    AIC
- I(DISTCOASTCM^2)   1   160.27 337.06
- CHLMEANCM          1   160.53 337.33
- DEPTHCM            1   160.80 337.59
<none>                  159.04 337.83
- fitted(eigebry)    2   179.40 354.19
- DISTCOASTCM        1   181.08 357.87
- I(DEPTHCM^2)       1   181.70 358.49
- SSTMEANFUL         1   222.71 399.50

Step:  AIC=337.06
Model 4:BRYDETOTAL ~ CHLMEANCM + DEPTHCM + I(DEPTHCM^2) + DISTCOASTCM
+
    SSTMEANFUL + fitted(eigebry)

                   Df Deviance    AIC
- DEPTHCM           1   161.46 336.25
```

```
- CHLMEANCM        1   161.62 336.41
<none>                 160.27 337.06
- fitted(eigebry)  2   180.52 353.31
- I(DEPTHCM^2)     1   182.84 357.63
- DISTCOASTCM      1   185.55 360.34
- SSTMEANFUL       1   222.72 397.51

Step:  AIC=336.25
Model 5:
BRYDETOTAL ~ CHLMEANCM + I(DEPTHCM^2) + DISTCOASTCM + SSTMEANFUL +
    fitted(eigebry)

                  Df Deviance    AIC
- CHLMEANCM        1   163.15 335.94
<none>                 161.46 336.25
- fitted(eigebry)  2   182.15 352.94
- I(DEPTHCM^2)     1   185.41 358.20
- DISTCOASTCM      1   197.12 369.91
- SSTMEANFUL       1   225.72 398.51

Step:  AIC=335.94
Model 6:
BRYDETOTAL ~ I(DEPTHCM^2) + DISTCOASTCM + SSTMEANFUL + fitted
(eigebry)

                  Df Deviance    AIC
<none>                 163.15 335.94
- fitted(eigebry)  2   182.96 351.75
- I(DEPTHCM^2)     1   187.01 357.81
- DISTCOASTCM      1   210.37 381.16
- SSTMEANFUL       1   250.74 421.53
```

BRYDE – ANTHROPOGENIC

```
Start:  AIC=349.92
Model 7:BRYDETOTAL ~ EMISSARIO + FSHGRD + FUNDCM + I(FUNDCM^2)
+ fitted(eigabry)

                  Df Deviance      AIC
<none>                 171       350
- FSHGRD           1      173       350
- EMISSARIO        1      175       352
- fitted(eigabry)  4      219       390
- FUNDCM           1      240       417
- I(FUNDCM^2)      1 19885452 19885629
```

BRYDE - FULL

```
Start:  AIC=341.68
Model 8:
BRYDETOTAL ~ CHLMEANCM + I(CHLMEANCM^2) + DEPTHCM + I(DEPTHCM^2) +
    DISTCOASTCM + I(DISTCOASTCM^2) + Slope + DISTILHAS + SSTMEANFUL +
    EMISSARIO + FSHGRD + FUNDCM + I(FUNDCM^2) + fitted(eigfbry)

                  Df Deviance    AIC
- Slope            1   150.89 339.68
- DEPTHCM          1   150.91 339.70
- FSHGRD           1   150.91 339.70
- DISTCOASTCM      1   150.96 339.75
```

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- EMISSARIO          1   151.05 339.84
- CHLMEANCM          1   151.57 340.36
- I(FUNDCM^2)        1   151.91 340.70
- I(DISTCOASTCM^2)   1   152.17 340.96
- I(CHLMEANCM^2)     1   152.17 340.96
<none>                   150.89 341.68
- SSTMEANFUL         1   155.22 344.01
- DISTILHAS          1   156.24 345.03
- fitted(eigfbry)    1   156.28 345.07
- FUNDCM             1   162.58 351.37
- I(DEPTHCM^2)       1   169.30 358.09

Step:  AIC=339.68
Model 9:
BRYDETOTAL ~ CHLMEANCM + I(CHLMEANCM^2) + DEPTHCM + I(DEPTHCM^2) +
    DISTCOASTCM + I(DISTCOASTCM^2) + DISTILHAS + SSTMEANFUL +
    EMISSARIO + FSHGRD + FUNDCM + I(FUNDCM^2) + fitted(eigfbry)

                    Df Deviance    AIC
- DEPTHCM            1   150.91 337.70
- FSHGRD             1   150.93 337.72
- DISTCOASTCM        1   150.99 337.78
- EMISSARIO          1   151.08 337.87
- CHLMEANCM          1   151.57 338.36
- I(FUNDCM^2)        1   151.93 338.72
- I(DISTCOASTCM^2)   1   152.18 338.97
- I(CHLMEANCM^2)     1   152.19 338.98
<none>                   150.89 339.68
- SSTMEANFUL         1   155.26 342.05
- fitted(eigfbry)    1   156.50 343.29
- DISTILHAS          1   156.64 343.43
- FUNDCM             1   162.60 349.39
- I(DEPTHCM^2)       1   169.30 356.09

Step:  AIC=337.7
Model 10:
BRYDETOTAL ~ CHLMEANCM + I(CHLMEANCM^2) + I(DEPTHCM^2) + DISTCOASTCM +
    I(DISTCOASTCM^2) + DISTILHAS + SSTMEANFUL + EMISSARIO + FSHGRD +
    FUNDCM + I(FUNDCM^2) + fitted(eigfbry)

                    Df Deviance    AIC
- FSHGRD             1   150.95 335.74
- DISTCOASTCM        1   151.02 335.81
- EMISSARIO          1   151.09 335.88
- CHLMEANCM          1   151.60 336.39
- I(FUNDCM^2)        1   151.93 336.72
- I(DISTCOASTCM^2)   1   152.20 336.99
- I(CHLMEANCM^2)     1   152.20 336.99
<none>                   150.91 337.70
- SSTMEANFUL         1   155.32 340.11
- fitted(eigfbry)    1   156.54 341.33
- DISTILHAS          1   157.57 342.36
- FUNDCM             1   162.77 347.56
- I(DEPTHCM^2)       1   169.34 354.13

Step:  AIC=335.74
Model 11:
BRYDETOTAL ~ CHLMEANCM + I(CHLMEANCM^2) + I(DEPTHCM^2) + DISTCOASTCM +
    I(DISTCOASTCM^2) + DISTILHAS + SSTMEANFUL + EMISSARIO + FUNDCM +
    I(FUNDCM^2) + fitted(eigfbry)

                    Df Deviance    AIC
- DISTCOASTCM        1   151.02 333.81
- EMISSARIO          1   151.56 334.35
- CHLMEANCM          1   151.68 334.47
- I(FUNDCM^2)        1   152.11 334.90
- I(DISTCOASTCM^2)   1   152.21 335.00
- I(CHLMEANCM^2)     1   152.27 335.06
```

```
<none>                    150.95 335.74
- SSTMEANFUL        1    155.73 338.52
- fitted(eigfbry)   1    156.99 339.78
- DISTILHAS         1    159.11 341.90
- FUNDCM            1    163.04 345.83
- I(DEPTHCM^2)      1    169.45 352.24

Step:  AIC=333.81
Model 12:
BRYDETOTAL ~ CHLMEANCM + I(CHLMEANCM^2) + I(DEPTHCM^2) + I(DISTCOASTCM
^2) +
    DISTILHAS + SSTMEANFUL + EMISSARIO + FUNDCM + I(FUNDCM^2) +
    fitted(eigfbry)

                    Df Deviance    AIC
- EMISSARIO          1   151.73 332.52
- CHLMEANCM          1   151.79 332.58
- I(FUNDCM^2)        1   152.37 333.16
- I(DISTCOASTCM^2)   1   152.54 333.33
- I(CHLMEANCM^2)     1   152.63 333.42
<none>                   151.02 333.81
- fitted(eigfbry)    1   156.99 337.78
- SSTMEANFUL         1   159.50 340.29
- DISTILHAS          1   163.56 344.36
- FUNDCM             1   171.35 352.14
- I(DEPTHCM^2)       1   173.07 353.86

Step:  AIC=332.52
Model 13:
BRYDETOTAL ~ CHLMEANCM + I(CHLMEANCM^2) + I(DEPTHCM^2) + I(DISTCOASTCM
^2) +
    DISTILHAS + SSTMEANFUL + FUNDCM + I(FUNDCM^2) + fitted(eigfbry)

                    Df Deviance    AIC
- I(DISTCOASTCM^2)   1   152.86 331.65
- I(CHLMEANCM^2)     1   153.11 331.90
- CHLMEANCM          1   153.24 332.03
<none>                   151.73 332.52
- I(FUNDCM^2)        1   153.90 332.69
- fitted(eigfbry)    1   157.18 335.97
- SSTMEANFUL         1   160.78 339.57
- DISTILHAS          1   164.56 343.35
- I(DEPTHCM^2)       1   173.08 351.87
- FUNDCM             1   173.71 352.50

Step:  AIC=331.65
Model 14:
BRYDETOTAL ~ CHLMEANCM + I(CHLMEANCM^2) + I(DEPTHCM^2) + DISTILHAS +
    SSTMEANFUL + FUNDCM + I(FUNDCM^2) + fitted(eigfbry)

                   Df Deviance    AIC
- I(FUNDCM^2)       1   154.45 331.24
<none>                 152.86 331.65
- CHLMEANCM         1   156.17 332.96
- I(CHLMEANCM^2)    1   156.25 333.04
- fitted(eigfbry)   1   159.62 336.41
- SSTMEANFUL        1   162.03 338.82
- DISTILHAS         1   165.27 342.06
- I(DEPTHCM^2)      1   173.23 350.02
- FUNDCM            1   174.85 351.64

Step:  AIC=331.24
Model 15:
BRYDETOTAL ~ CHLMEANCM + I(CHLMEANCM^2) + I(DEPTHCM^2) + DIST
ILHAS +
    SSTMEANFUL + FUNDCM + fitted(eigfbry)

                    Df Deviance    AIC
```

```
<none>                    154.45 331.24
- I(CHLMEANCM^2)    1    158.63 333.42
- CHLMEANCM         1    158.98 333.77
- fitted(eigfbry)   1    162.35 337.14
- SSTMEANFUL        1    166.45 341.24
- DISTILHAS         1    168.02 342.81
- I(DEPTHCM^2)      1    176.34 351.13
- FUNDCM            1    183.92 358.71
```

HUMPBACK WHALE

```
Start:  AIC=212.17
Model 1:
HUMPTOTAL ~ CHLMEAN + DEPTHCM + I(DEPTHCM^2) + DISTCOAST + Slope +
    SSTMEANFUL + fitted(eigehump)

                    Df Deviance    AIC
- SSTMEANFUL         1   97.266 210.18
- CHLMEAN            1   97.550 210.46
- DEPTHCM            1   97.979 210.89
- I(DEPTHCM^2)       1   97.985 210.90
<none>                   97.261 212.17
- Slope              1   99.356 212.27
- fitted(eigehump)   2  121.084 231.99
- DISTCOAST          1  122.815 235.72

Step:  AIC=210.18
Model 2:
HUMPTOTAL ~ CHLMEAN + DEPTHCM + I(DEPTHCM^2) + DISTCOAST + Slope +
    fitted(eigehump)

                    Df Deviance    AIC
- CHLMEAN            1   97.647 208.56
- I(DEPTHCM^2)       1   97.987 208.90
- DEPTHCM            1   98.090 209.00
<none>                   97.266 210.18
- Slope              1   99.761 210.67
- fitted(eigehump)   2  121.468 230.38
- DISTCOAST          1  123.011 233.92

Step:  AIC=208.56
Model 3:
HUMPTOTAL ~ DEPTHCM + I(DEPTHCM^2) + DISTCOAST + Slope + fitted(eigehu
mp)

                    Df Deviance    AIC
- DEPTHCM            1   98.261 207.17
- I(DEPTHCM^2)       1   98.569 207.48
<none>                   97.647 208.56
- Slope              1  100.938 209.85
- fitted(eigehump)   2  123.799 230.71
- DISTCOAST          1  124.220 233.13

Step:  AIC=207.17
Model 4:HUMPTOTAL ~ I(DEPTHCM^2) + DISTCOAST + Slope + fitted(
eigehump)

                      Df Deviance    AIC
<none>                     98.261 207.17
- I(DEPTHCM^2)         1  101.224 208.13
- Slope                1  112.630 219.54
- fitted(eigehump)     2  124.086 229.00
- DISTCOAST            1  204.630 311.54
```

ANTHROPOGENIC

```
Start:  AIC=1.211,84
Model 5:
HUMPTOTAL ~ EMISSARIO + FSHGRD + FUND + fitted(eigahump)

                   Df   Deviance        AIC
- fitted(eigahump)  1 2.2400e+02 3.2900e+02
<none>                1.2118e+10 1.2118e+10
- EMISSARIO         1 9.6567e+11 9.6567e+11
- FSHGRD            1 1.0095e+12 1.0095e+12
- FUND              1 7.3374e+21 7.3374e+21

Step:  AIC=329.34
Model 6:
HUMPTOTAL ~ EMISSARIO + FSHGRD + FUND

             Df Deviance    AIC
<none>            224.43 329.34
- FSHGRD     1   227.01 329.92
- EMISSARIO  1   229.51 332.42
- FUND       1   236.42 339.33
```

FULL

```
Start:  AIC=216.83
Model 7:
HUMPTOTAL ~ CHLMEAN + DEPTHCM + I(DEPTHCM^2) + DISTCOAST + Slope +
    DISTILHAS + SSTMEANFUL + EMISSARIO + FSHGRD + FUND + fitted(eigfhu
mp)

                   Df Deviance    AIC
- FUND              1   93.936 214.84
- DEPTHCM           1   93.937 214.85
- SSTMEANFUL        1   94.014 214.92
- DISTILHAS         1   94.120 215.03
- CHLMEAN           1   94.666 215.58
- I(DEPTHCM^2)      1   94.814 215.72
<none>                 93.923 216.83
- FSHGRD            1   97.112 218.02
- Slope             1   97.239 218.15
- EMISSARIO         1  107.101 228.01
- fitted(eigfhump)  2  109.867 228.78
- DISTCOAST         1  108.679 229.59

Step:  AIC=214.85
Model 8:
HUMPTOTAL ~ CHLMEAN + DEPTHCM + I(DEPTHCM^2) + DISTCOAST + Slope +
    DISTILHAS + SSTMEANFUL + EMISSARIO + FSHGRD + fitted(eigfhump)

                   Df Deviance    AIC
- DEPTHCM           1   93.943 212.85
- DISTILHAS         1   94.149 213.06
- SSTMEANFUL        1   94.318 213.23
- CHLMEAN           1   94.674 213.58
- I(DEPTHCM^2)      1   95.216 214.12
<none>                 93.936 214.84
- Slope             1   97.284 216.19
- FSHGRD            1   98.136 217.05
- EMISSARIO         1  107.237 226.15
- fitted(eigfhump)  2  111.295 228.21
- DISTCOAST         1  116.929 235.84
```

```
Step:  AIC=212.85
Model 9:
HUMPTOTAL ~ CHLMEAN + I(DEPTHCM^2) + DISTCOAST + Slope + DISTILHAS +
    SSTMEANFUL + EMISSARIO + FSHGRD + fitted(eigfhump)

                   Df Deviance    AIC
- DISTILHAS         1   94.168 211.08
- SSTMEANFUL        1   94.462 211.37
- CHLMEAN           1   94.675 211.59
<none>                 93.943 212.85
- I(DEPTHCM^2)      1   96.034 212.94
- FSHGRD            1   98.137 215.05
- Slope             1  101.402 218.31
- EMISSARIO         1  107.767 224.68
- fitted(eigfhump)  2  111.766 226.68
- DISTCOAST         1  124.484 241.39

Step:  AIC=211.08
Model 10:
HUMPTOTAL ~ CHLMEAN + I(DEPTHCM^2) + DISTCOAST + Slope + SSTMEANFUL +
    EMISSARIO + FSHGRD + fitted(eigfhump)

                   Df Deviance    AIC
- SSTMEANFUL        1   94.522 209.43
- CHLMEAN           1   95.083 209.99
<none>                 94.168 211.08
- I(DEPTHCM^2)      1   96.709 211.62
- FSHGRD            1  101.969 216.88
- Slope             1  105.285 220.19
- fitted(eigfhump)  2  113.676 226.59
- EMISSARIO         1  111.789 226.70
- DISTCOAST         1  132.478 247.39

Step:  AIC=209.43
Model 11:
HUMPTOTAL ~ CHLMEAN + I(DEPTHCM^2) + DISTCOAST + Slope + EMISSARIO +
    FSHGRD + fitted(eigfhump)

                   Df Deviance    AIC
- CHLMEAN           1   95.124 208.03
<none>                 94.522 209.43
- I(DEPTHCM^2)      1   96.710 209.62
- FSHGRD            1  103.847 216.76
- Slope             1  105.779 218.69
- fitted(eigfhump)  2  114.129 225.04
- EMISSARIO         1  115.498 228.41
- DISTCOAST         1  139.212 252.12

Step:  AIC=208.03
Model 12:
HUMPTOTAL ~ I(DEPTHCM^2) + DISTCOAST + Slope + EMISSARIO + FS
HGRD +
    fitted(eigfhump)

                   Df Deviance    AIC
<none>                 95.124 208.03
- I(DEPTHCM^2)      1   97.960 208.87
- Slope             1  106.146 217.06
- FSHGRD            1  109.207 220.12
- EMISSARIO         1  115.830 226.74
- fitted(eigfhump)  2  120.603 229.51
- DISTCOAST         1  201.748 312.66
```

Supplement 5

Humpback and Bryde's whale model residuals and Moran eigenvectors

Humpback whales model residuals

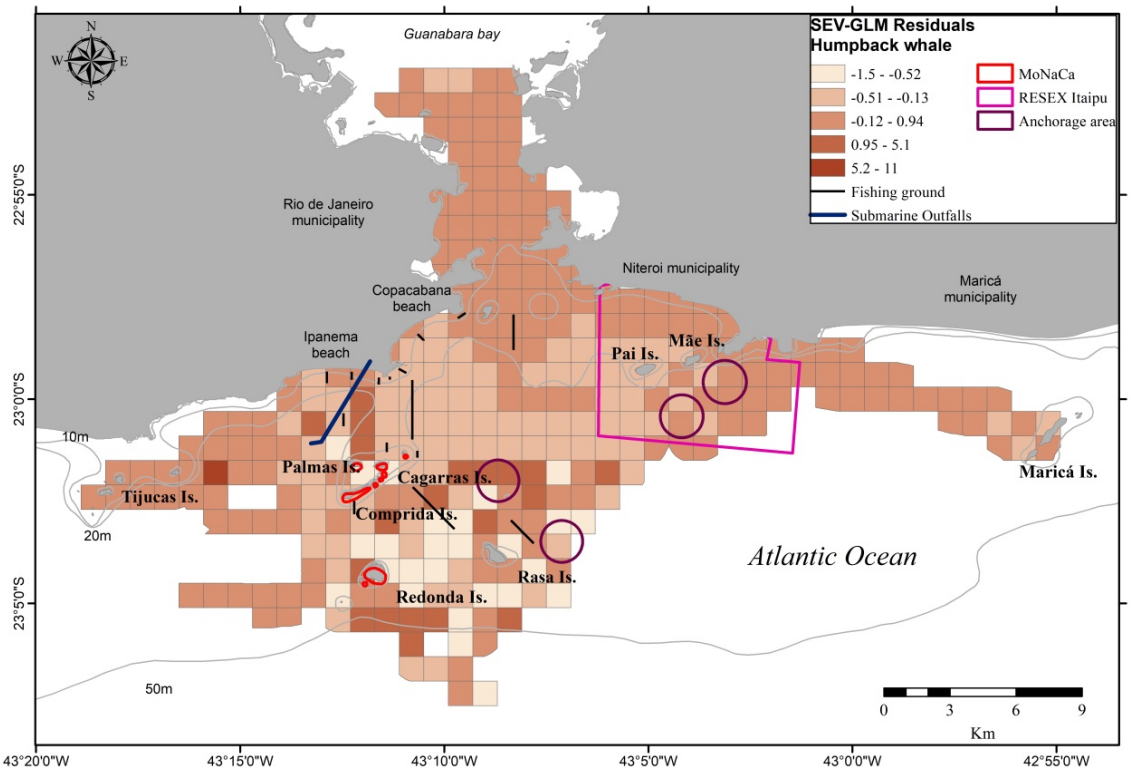

Fig. S 5.1. Humpback whale model residuals for each grid cell along off the coast of the city of Rio de Janeiro, in southeastern Brazil, from Poisson Spatial Eigenvector Generalized Linear Models.

Bryde´s whales model residuals

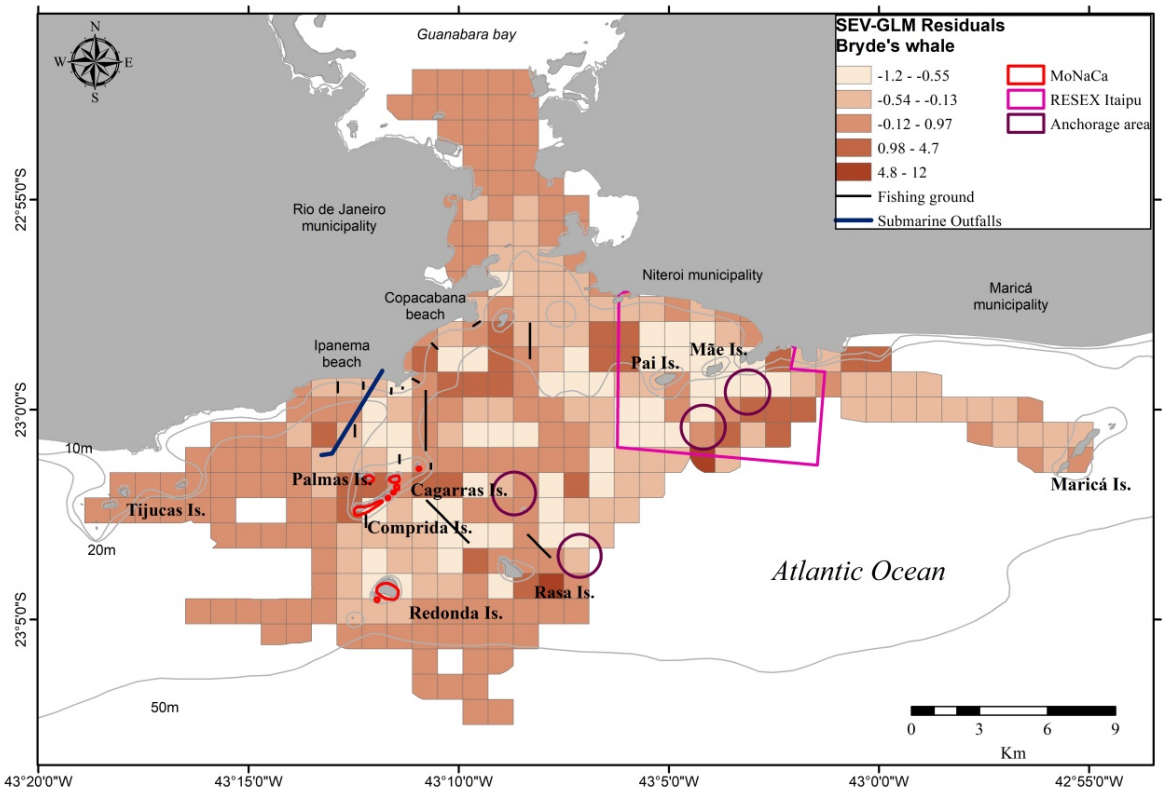

Fig. S 5.2. Bryde's whale model residuals for each grid cell along off the coast of the city of Rio de Janeiro, in southeastern Brazil, from Poisson Spatial Eigenvector Generalized Linear Models.

Humpback whales Moran eigenvectors

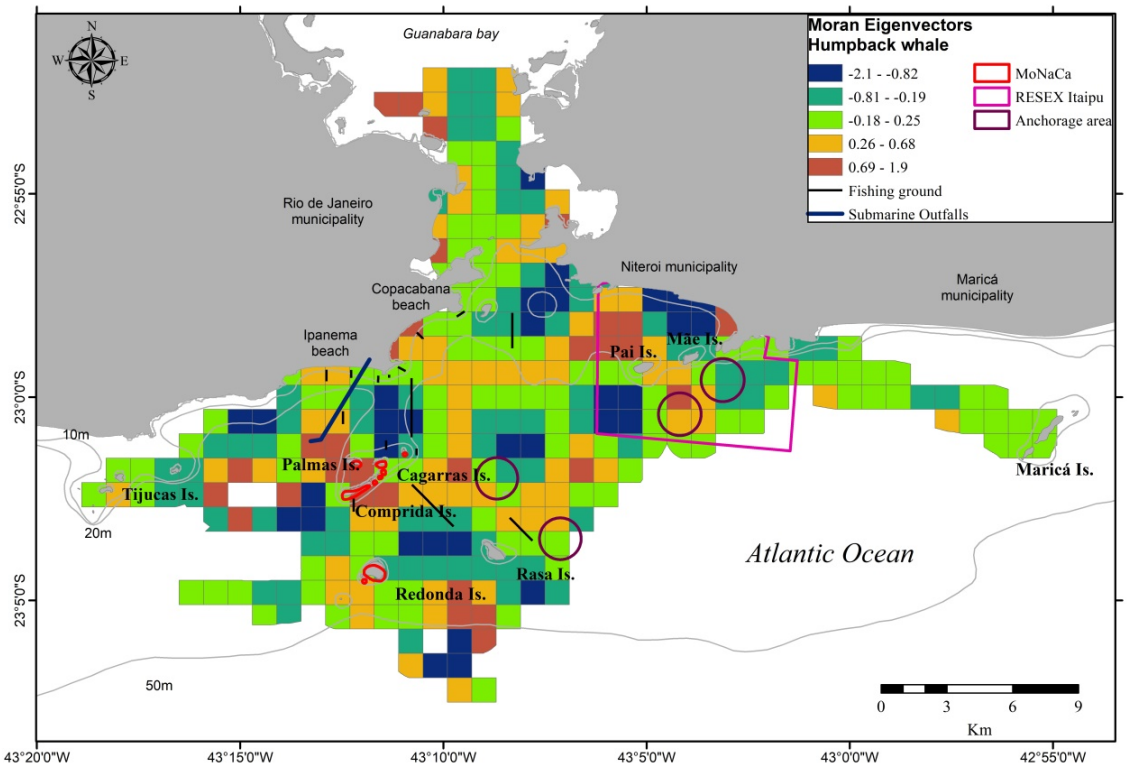

Fig. S 5.3. Map of the linear combination for the two Moran's I eigenvectors with estimated coefficient values retained of the best spatial eigenvector generalized linear models for humpback whales off the coast of the city of Rio de Janeiro, in southeastern Brazil.

Bryde´s whales Moran eigenvectors

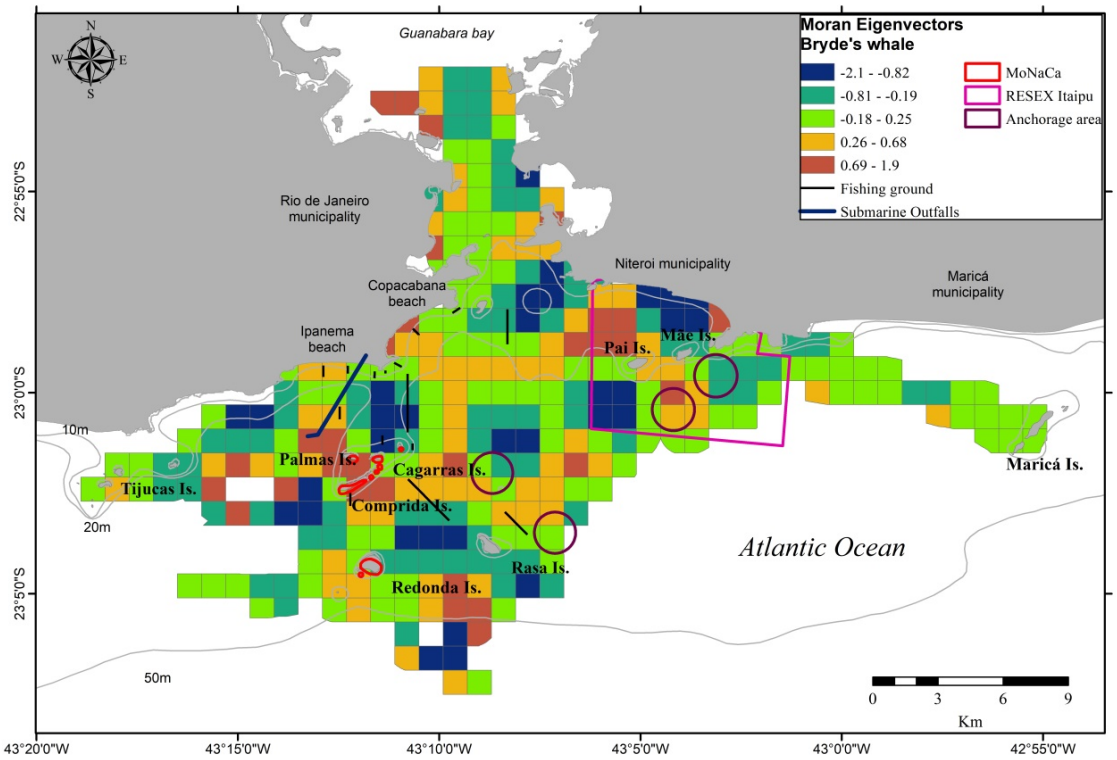

Fig. S 5.4. Map of the only Moran's I eigenvector with estimated coefficient values retained of the best spatial eigenvector generalized linear models for Bryde's whales off the coast of the city of Rio de Janeiro, in southeastern Brazil.