

## Supplement #2

### R script

Habitat use models of spatially auto-correlated data: a case study of the bottlenose dolphin, *Tursiops truncatus truncatus*, in southeastern Brazil

Rodrigo H. Tardin, Yongwan Chun, Sheila M. Simão, Maria Alice S. Alves

```
##Getting libraries
```

```
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
```

```
tur <- readShapePoly("Fishnet_Tursiops_paper4.shp")
```

```
names(tur)
```

```
nrow(tur)
```

```
#####
```

```
#          Data exploration                #####
```

```
#####
```

```
#Visual inspection to include or not a polynomial term
```

```
depth=tur$DEPTH
```

```
occtursiops=tur$OCC_TUR
```

```
plot(depth,occtursiops)
```

```
#linear
```

```
distcoast=tur$DISTCOAST
plot(distcoast,occtursiops)
#Linear
```

```
sstd=tur$SST_SD_1
plot(sstd,occtursiops)
#Linear
```

```
sstmean=tur$SST_MEAN_1
plot(sstmean,occtursiops)
#Linear
```

```
sstmin=tur$SST_MIN_1
plot(sstmin,occtursiops)
#Curvilinear
```

```
sstmax=tur$SST_MAX_1
plot(sstmax,occtursiops)
#Linear
```

```
chlormean=tur$CHLOR_ME_1
plot(chlormean,occtursiops)
#Curvilinear
```

```
chlormin=tur$CHLOR_MI_1
plot(chlormin,occtursiops)
#Curvilinear
```

```
#####
##                      GLM modelling                      ##
#####
##Overdispersion check
```

```
dispersiontest(glmbase_p)
```

```
dispersiontest(glmbase_o)
```

```
dispersiontest(glmbase_f)
```

```
# Physiographic model
```

```
glmbase_p= glm(OCC_TUR~ DEPTH+ DISTCOAST,  
               data=tur, offset=log(Effort_KM),family="poisson",maxit=100)
```

```
#Oceanographic model
```

```
glmbase_o <- glm(OCC_TUR~  
SST_SD+SST_MEAN+SST_MIN_1+SST_MIN_1^2+SST_MAX_1+CHLOR_MEAN  
+CHLOR_MEAN^2+CHLOR_MIN+CHLOR_MIN^2,  
data=tur,offset=log(Effort_KM),family="poisson",maxit=100)
```

```
#Full model
```

```
glmbase_f <- glm(OCC_TUR~ DEPTH +  
DISTCOAST+SST_SD_1+SST_MEAN+SST_MIN_1+SST_MIN_1^2+SST_MAX_1+  
CHLOR_MEAN+CHLOR_MEAN^2+CHLOR_MIN+CHLOR_MIN^2, data=tur,  
offset=log(Effort_KM),family="poisson",maxit=100)
```

```
# GLM Model Selection
```

```
#Model selection
```

```
AIC(glmbase_p,glmbase_f,glmbase_o)
```

```
#Best GLM summary
```

```
bestglm=summary(glmbase_f)
```

```
bestglmtable=xtable(bestglm)
```

```
print.xtable(bestglmtable, type="html", file="bestglmtable.html")
```

```
#####
```

```
#                SEV-GLM modelling                ##
```

```
#####
```

```

##Neighbourhood with Queen specification
tursiops.nb.q1 <- poly2nb(tur, queen=TRUE)
tursiops.lw.q1 <- nb2listw(tursiops.nb.q1, style="W")

##Moran Test check for spatial autocorrelation
moran.test(tur$OCC_TUR,nb2listw(tursiops.nb.q1, style="W"))
#Existence of spatial autocorrelation

#Variance Inflation Check
sevglm_vif<- glm(OCC_TUR ~ DEPTH + DISTCOAST+
SST_SD+SST_MEAN+SST_MINCS+SSTMIN2CS+SST_MAX_1+CHLMEANCS+C
HLMEANCS2+CHLMINCS+CHLMINCS2+CHLOR_MAX+ CHLOR_SD+
fitted(errcol2.q_f), data=tur, family="poisson", offset=log(Effort_KM))
vif=vif(sevglm_vif)
viftable=xtable(vif)
print.xtable(viftable, type="html", file="viftable.html")

##Spatial filtering with ME
# Moran Eigenvectors

#Physiographic
errcol2.p <- ME(OCC_TUR ~ DEPTH + DISTCOAST,data=tur, family="poisson",
listw=tursiops.lw.q1,offset=log(Effort_KM), alpha=0.05, verbose=TRUE)

#Oceanographic
errcol2.o3 <- ME(OCC_TUR ~
SST_SD+SST_MEAN+SST_MINCS+SSTMIN2CS+SST_MAX_1+CHLOR_MEAN+
CHLMEANCS+CHLMINCS+CHLMINCS2,data=tur, family="poisson",
listw=tursiops.lw.q1,offset=log(Effort_KM), alpha=0.05, verbose=TRUE)

#Full
errcol2.q_f3 <- ME(OCC_TUR ~ DEPTH+ DISTCOAST+
SST_SD+SST_MEAN+SST_MINCS+SSTMIN2CS+SST_MAX_1+CHLMEANCS+C

```

```
HLMEANCS2+CHLMINCS+CHLMINCS2,data=tur, family="poisson",  
listw=tursiops.lw.q1,offset=log(Effort_KM), alpha=0.05, verbose=TRUE)
```

```
## SEV-GLM
```

```
#Physiographic
```

```
sevglm_p <- glm(OCC_TUR ~ DEPTH+DISTCOAST+fitted(errcol2.p), data=tur,  
family="poisson", offset=log(Effort_KM))
```

```
#Oceanographic
```

```
sevglm_o3<- glm(OCC_TUR ~  
SST_SD+SST_MEAN+SST_MINCS+SSTMIN2CS+SST_MAX_1+CHLOR_MEAN+  
CHLMEANCS+CHLMINCS+CHLMINCS2+fitted(errcol2.o3), data=tur,  
family="poisson", offset=log(Effort_KM))
```

```
#Full
```

```
sevglm_f3<- glm(OCC_TUR ~ DEPTH+ DISTCOAST+  
SST_SD+SST_MEAN+SST_MINCS+SSTMIN2CS+SST_MAX_1+CHLMEANCS+C  
HLMEANCS2+CHLMINCS+CHLMINCS2+fitted(errcol2.q_f3), data=tur,  
family="poisson", offset=log(Effort_KM))
```

```
##Overdispersion check
```

```
dispersiontest(sevglm_p)
```

```
dispersiontest(sevglm_o)
```

```
dispersiontest(sevglm_f)
```

```
## Model Selection
```

```
AIC(sevglm_p,sevglm_o3,sevglm_f3)
```

```
##Summary for best model
```

```
summary(sevglm_f3)
```

```
bestsevglm3=summary(sevglm_f3)
```

```
bestsevglmtable3=xtable(bestsevglm3)
```

```
print.xtable(bestsevglmtable3, type="html", file="bestsevglmtable3.html")
```

```
##Hierarchical partitioning analysis
```

```
names(tur)
```

```
depth4=as.data.frame(tur$DEPTH)
```

```
discoast4=as.data.frame(tur$DISTCOAST)
```

```
sst_mean4=as.data.frame(tur$SST_MEAN)
```

```
sst_min4=as.data.frame(tur$SST_MINCS)
```

```
chlor_mean4=as.data.frame(tur$CHLMEANCS)
```

```
chlor_min4=as.data.frame(tur$CHLMINCS)
```

```
env4=c(depth4,discoast4,sst_mean4,sst_min4,chlor_mean4,chlor_min4)
```

```
env5=as.data.frame(env4)
```

```
hier.part(tur$OCC_TUR, env5,family="poisson")
```

```
## test if the fitted values explain the observed value
```

```
glmME <- glm(tur$OCC_TUR ~ fitted(sevglm_f3),  
             family="poisson")
```

```
anova(glmME, test="Chisq")
```

```
# Test if SEVGLM is best than GLM
```

```
ln.lr <- -2*(logLik(glmbase_f)[1]-logLik(sevglm_f3)[1])
```

```
1-pchisq(ln.lr, df=13)
```

```
#PSeudoR
```

```
psd.r21ap3 <- lm(tur$OCC_TUR~ fitted(sevglm_f3))
```

```
summary(psd.r21ap3)$r.square
```

```
psd.r21apglm <- lm(tur$OCC_TUR~ fitted(glmbase_f))
```

```
summary(psd.r21apglm)$r.square
```

```
#####
```

```
##           Spatially predicting T. truncatus habitat use           ##
```

```
#####
```

```

#GLM
predtursiopsglm171=predict.glm(glmbase_f,type='response')
which(predtursiopsglm171>2)
write.csv(predtursiopsglm171,file="predtursiopsglm171.csv")

#SEV-GLM
predtursiopssevglm171CS=predict.glm(sevglm_f3,type="response")
which(predtursiopssevglm171CS>2)
write.csv(predtursiopssevglm171CS,file="predtursiopssevglm171CS.csv")

#Residualas mapping
#SEV-GLM residuals
resglm1 <- residuals.glm(glmbase_f3, type="pearson")
write.csv(resglm1,file="residualstursiopsPHYSglm17.csv")

#GLM residuals
ressevglm1 <- residuals.glm(sevglm_f3, type="pearson")
write.csv(ressevglm1,file="residualstursiopsPHYSsevglm17.csv")

#####
##                               Eigenvector Mapping                               ##
#####
beta <- matrix(coefficients(sevglm_f3)[9:15])
x<-as.matrix(fitted(errcol2.q_f))
sf <- x%*%beta
write.csv(sf,file="spatialfiltertursiops17.csv")

##End of coding

```