### 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")</pre> 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

sstsd=tur\$SST\_SD\_1
plot(sstsd,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

dispersiontest(glmbase\_p)
dispersiontest(glmbase\_o)
dispersiontest(glmbase\_f)

#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")

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

##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))</pre>

```
#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))</pre>
```

```
##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 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</pre>

psd.r21apglm <- lm(tur\$OCC\_TUR~ fitted(glmbase\_f))
summary(psd.r21apglm)\$r.square</pre>

### #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")</pre>

#GLM residuals
ressevglm1 <- residuals.glm(sevglm\_f3, type="pearson")
write.csv(ressevglm1,file="residualstursiopsPHYSsevglm17.csv")</pre>

\*\*\*\*\*

##End of coding