

Supplementary Code 1

Late Pleistocene South American megafaunal extinctions associated with rise of Fishtail points and human population

Luciano Prates and S. Ivan Perez

##The data for running temporal and spatial analyses in R packages are provided in the Supplementary Data 1 to 4

##R script for analyzing radiocarbon dates in *rcarbon* package

```
require(rcarbon)
```

```
#Open radiocarbon data - example
```

```
nqn<-read.csv("FPP.csv", h=T)
```

```
nqn
```

```
attach(nqn)
```

```
#Radiocarbon data preparation
```

```
bins <- binPrep(Site,C14Age,h=200)
```

```
bins
```

```
#Calibrate radiocarbon data for SPD
```

```
x <- calibrate(C14Age,C14SD, calCurves='shcal20')
```

```
x
```

```
#Calculate empirical SPD
```

```
spd.nqn5 <- spd(x,bins=bins, runm=500,timeRange=c(14000,10500))
```

```
plot(spd.nqn5)
```

```
#Comparing empirical SPDs against each other
```

```
perm.NPat=permTest(x=x,marks=as.character(Region),
```

```
timeRange=c(14000,10500),bins=bins,nsim=100,runm=500)
```

```
#Ploting results
```

```
par(mfrow=c(3,1))
```

```
plot(spd.nqn5, main="Global")
```

```
plot(perm.NPat, focalm = "Andes", main="Andes")
```

```
plot(perm.NPat, focalm = "Pampa", main="Pampa")
```

```
plot(perm.NPat, focalm = "Patagonia ", main="Patagonia")
```

##R script for analyzing occurrence data in SSDM package

```
require(dismo)
require(SSDM)
# only run if the maxent.jar file is available, in the right folder
jar <- paste(system.file(package="dismo"), "/java/maxent.jar", sep=")

####Read files
# File with presence points or occurrence data
occ <- read.table("TodosGenerosFinal.csv", header=TRUE, sep=',')

occ2<-load_occ(path = getwd(), predictors, Xcol = 'LONGITUDE', Ycol = 'LATITUDE', Spcol =
'SPECIES', file = 'TodosGenerosFinal.csv', sep = ',')

occ2

# Get predictor variables. All .GTiff images obtained from http://www.paleoclim.org/ must to be
available in the same folder than the .csv file. We crop the GTiff images in QGIS 3.14 using a South
American shapefile

fnames <- list.files(pattern='tif', full.names=TRUE)
fnames

predictors <- stack(fnames)
plot(predictors)

# Stacked distribution (SSDM) building
SSDM2 <- stack_modelling('MAXENT', occ2, predictors, rep = 1,
                        Xcol = 'LONGITUDE', Ycol = 'LATITUDE',
                        Spcol = 'SPECIES', cores = 6)

# SSDM results plotting
plot(SSDM2)

# Saving SDM results
save.stack(SSDM2, name = strsplit(SSDM2@name, ".Stacked2.SDM", fixed = TRUE)[[1]][1], path =
getwd(), verbose = TRUE, GUI = FALSE)
```

##R script for estimating niche overlap index

#Example niche overlapping. The raster files in GTiff format are saving or obtaining from the
stack_modelling estimation

```
arP <- writeRaster(rP, filename="MaxentPuntasocc.tif", format="GTiff", overwrite=TRUE)
arH <- writeRaster(r, filename="MaxentMegatheriumFinal_new.tif", format="GTiff",
overwrite=TRUE)
```

```
nicheOverlap(rP, rH, stat = "I")
```