[Testing some functionalities]

1. Habitat and environment from localities

Getting some climatic variables and biomes for each point, then summarizing for each species

```
# Load packages you will need for this workflow:
library(ape)
library(maptools)
library(raster)
library(phylolm)

# Load function:
source("R/miscellaneous.R")
source("R/GetRanges.R")
source("R/GetTraitDistribution.R")

# Load files you will need for this workflow:
tree <- read.tree("example_datasets/tree.tre")
points <- read.csv("example_datasets/points.csv")
traits <- read.csv("example_datasets/traits.csv")
```

Gets biomes and ecoregion for each point and summary for each species:

```
# Gets biomes and eco_region for each point
all_biomes <- localityToBiome(points)
summary_biomes <- getBiomes(all_biomes)
```

2. PGLS

```
# Get variables from layers
# Load layer
layer <- raster("example_datasets/bio12.bil")
# plot(predictor)
climate_dataset <- GetClimateSummStats(points, layer)

combined_dataset <- merge(climate_dataset, traits, by="species")
rownames(combined_dataset) <- combined_dataset$species
combined_dataset$mean <- as.numeric(combined_dataset$mean)

# pgls?

model <- phylolm(B~mean, data=combined_dataset, tree)
summary(model)
plot(combined_dataset$B~combined_dataset$mean)
abline(model)
```

3. Ploting maps

Function GetRanges is a wrapper of dismo::maxent to perform sdms in many species.

```r
all_ranges <- GetRanges(points, species="species", lat="lat", lon="lon", threshold=0.75, buffer=25, res=

# merging ranges with trait data
trait_data <- combined_dataset[,c("species","B")]
trait_data <- subset(trait_data, !is.na(trait_data$B))
all_ranges[!names(all_ranges) %in% trait_data$species] <- NULL

traitB_dist <- GetTraitDistribution(all_ranges, trait_data, type=c("continuous"))

# we can plot
plot(traitB_dist)
plot(wrld_simpl, add=T)
```