Week 5: Spatial Point Pattern Analysis II

Statistical perspective of species distribution modeling

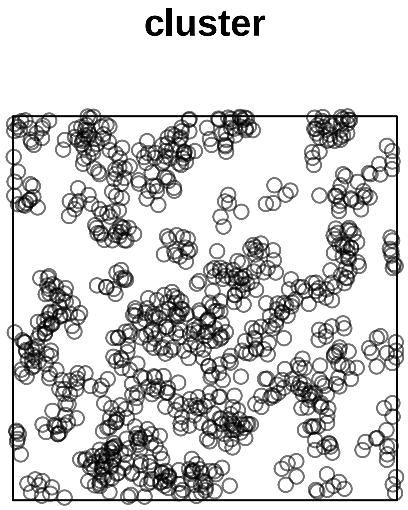
Poisson process

- Homogeneous Poisson process with intensity λ have two properties:
  - $N(A)$ is Poisson distributed with mean $\lambda|A|$, for all A
  - Condition on $N(A)$, the n points are independent and uniformly distributed in A
- model for complete spatial randomness and null model in a statistical analysis.

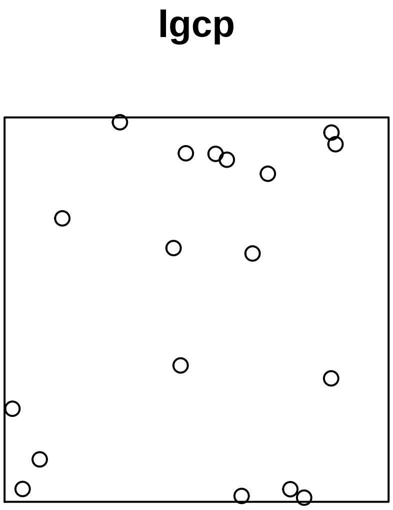
Non-Poisson Process

- Poisson cluster processes
  - Hierarchical processes: Parent Poisson processes with offspring point processes
  - Example, Matern cluster process, each parent has Poisson(μ) number of offsprings uniformly distributed around the parent.
- Cox processes - A Poisson process with a random intensity function - Example, log-Gaussian Cox processes (LGCP) in which intensity $\lambda(u)$ is a Gaussian random field.

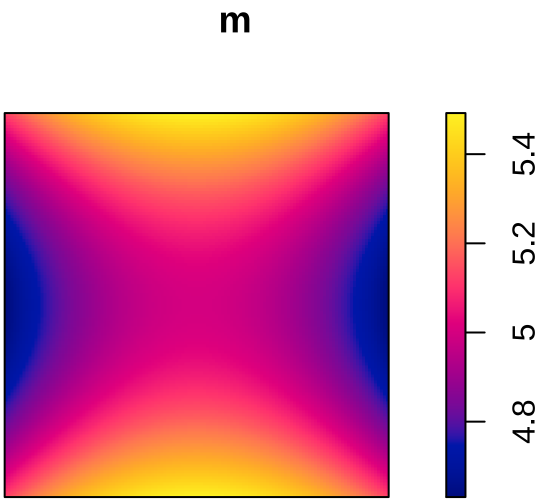
```
# Materm cluster proccess
cluster <- rMatClust(90, 0.05, 10)
plot(cluster)
```



```
# log-Gaussian Cox procces

lgcp <-  rLGCP("exp", 3, var=0.2, scale=.1 )
plot(lgcp)
```



```
# inhomogeneous LGCP with Gaussian covariance function
m <- as.im(function(x, y){5 - 1.5 * (x - 0.5)^2 + 2 * (y - 0.5)^2}, W=owin())
plot(m)
```



```
X <- rLGCP("gauss", m, var=0.15, scale =0.5)
plot(attr(X, "Lambda"))
points(X)
```

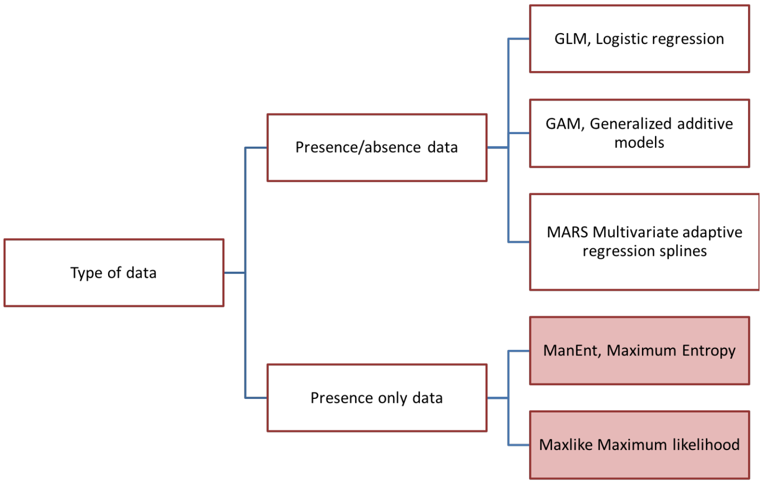
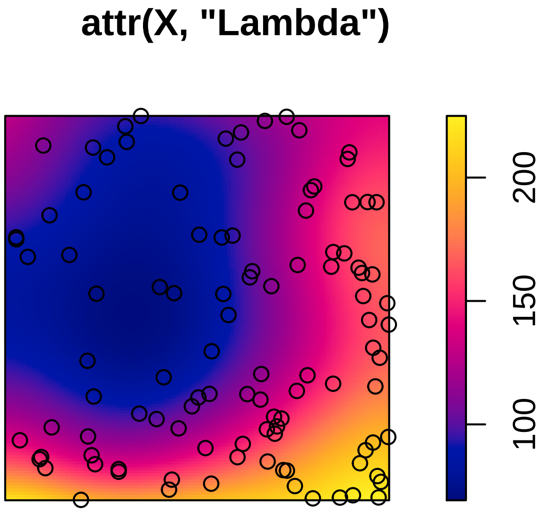

Type of data
Presence/absence data
GLM, Logistic regression
GAM, Generalized additive models
MARS Multivariate adaptive regression splines
Presence only data
ManEnt, Maximum Entropy
Maxlike Maximum likelihood

Figure 1: SDM methods



Species distribution modeling

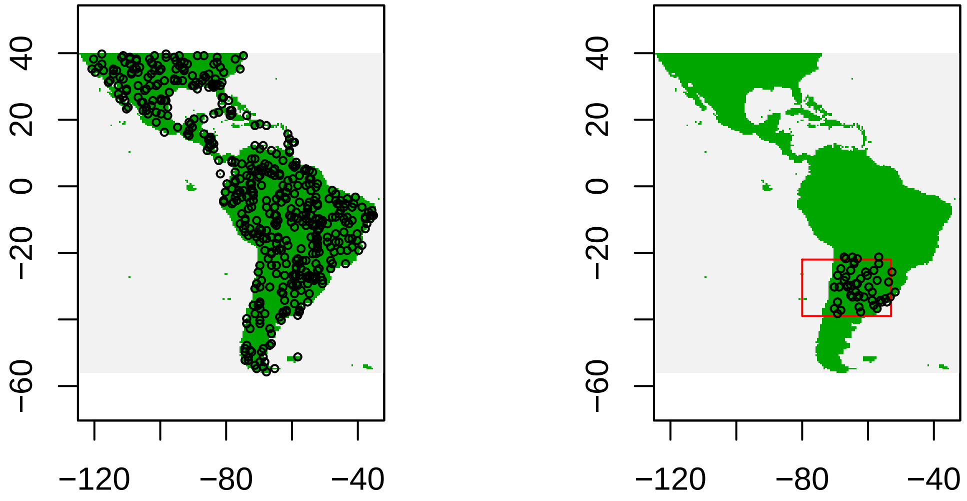
Species distribution models (SDMs) estimate the relationship between species records at sites and the environmental and/or spatial characteristics of those sites. See Figure 1 for commonly used SDM methods.

Absence and background data

- Background data are not attempting to guess at absence locations, but rather to characterize environments in the study region.
- Background data establishes the environmental domain of the study or regions where a specie should habitat but hasn't, whilst presence data should establish under which conditions a species is more likely to be present than on average.
- A closely related concept is "pseudo-absences", which is also used for generating the non-presence class. In this case, researchers try to guess where absences might occur they may sample the whole region

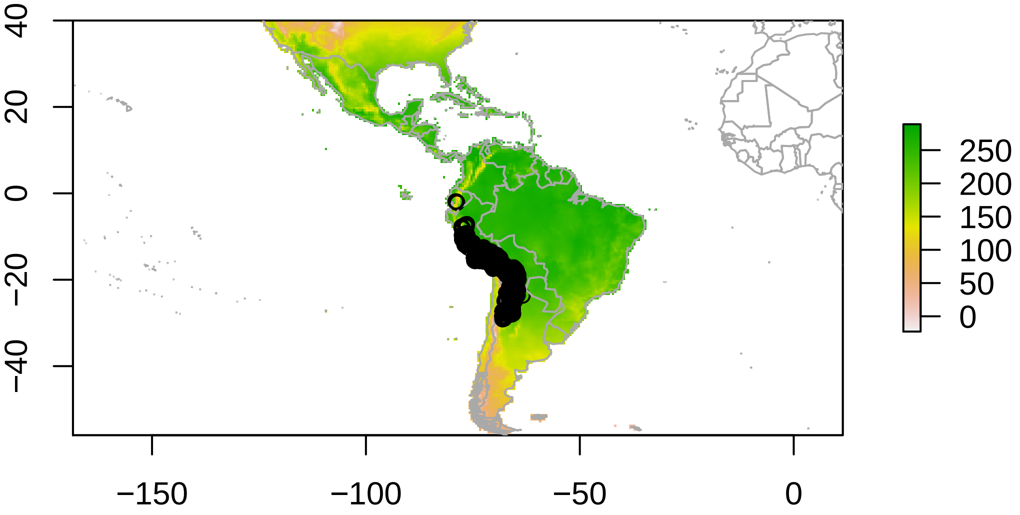
except at presence locations, or they might sample at places unlikely to be suitable for the species.

```
# Random background data

files <- list.files(path=paste(system.file(package="dismo"), '/ex' , sep= ''), pattern= 'grd', full.nam

mask <- raster(files[1])
set.seed(1963)
bg <- randomPoints(mask, 500 )

# set up the plotting area for two maps

par(mfrow=c(1,2))
plot(!is.na(mask), legend=FALSE)
points(bg, cex=0.5)
# now we repeat the sampling, but limit
# the area of sampling using a spatial extent
e <- extent(-80, -53, -39, -22)
bg2 <- randomPoints(mask, 50, ext=e)
plot(!is.na(mask), legend=FALSE)
plot(e, add=TRUE, col= ' red ')
points(bg2, cex=0.5)
```



```
# Pseudo-abasense

file <- paste(system.file(package="dismo"), '/ex/acaule.csv' , sep='')
ac <- read.csv(file)
coordinates(ac) <- ~lon+lat
projection(ac)<-CRS('+proj=longlat +datum=WGS84')

data(wrld_simpl)
plot(mask)
points(ac)
plot(wrld_simpl, add=TRUE, border='dark grey')

# Generate a cicule centered at each acaule
x <- circles(ac, d=50000, lonlat=TRUE)
pol <- polygons(x)
```

```r
# Now sample 250 random 'pseudo' location around each acaule sample locations
samp1 <- spsample(pol, 250, type= 'random' , iter=25)
points(samp1)
```



Regression models

- Converting a SDM problem into a generalized linear regression (GLM) or generalized additive models (GAM)

$$\eta(s) = \alpha + \sum_{p=1}^{P} \beta_i X_i(s) + \epsilon(s)$$

where $\eta(\cdot) = \frac{P(s)}{1-P(s)}$ is the logit link function, X_i is the $i-$th variable and $\epsilon(\cdot) \sim N(\mu, \sigma)$ is Gaussian distributed residuals.

- The diagnostic tools (e.g., AIC, k-fold methods) avaiable in GLM can be applied to here

How good are the models

- Confusion matrix

	+	-
+	True Positive	Faluse Positive
-	False Positive	True Negative

- Kappa statistics: Scales between 0 and 1; >0.7 good, 0.4 – 0.7 fair, <0.4 poor
- ROC curves and AUC: 0.8 good, 0.6 – 0.8 fair, 0.5 random, <0.6 poor

```r
# Regression models

# sample locations
file <- paste(system.file(package="dismo"), "/ex/bradypus.csv", sep="")
bradypus <- read.table(file,  header=TRUE,  sep= ',')
bradypus  <- bradypus[,-1]
```

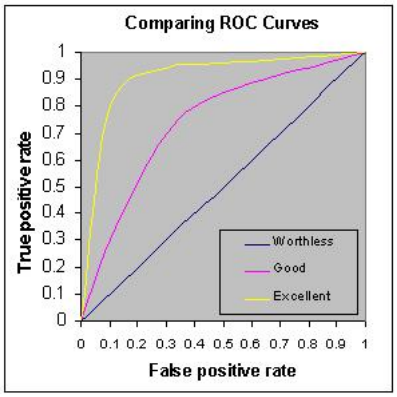
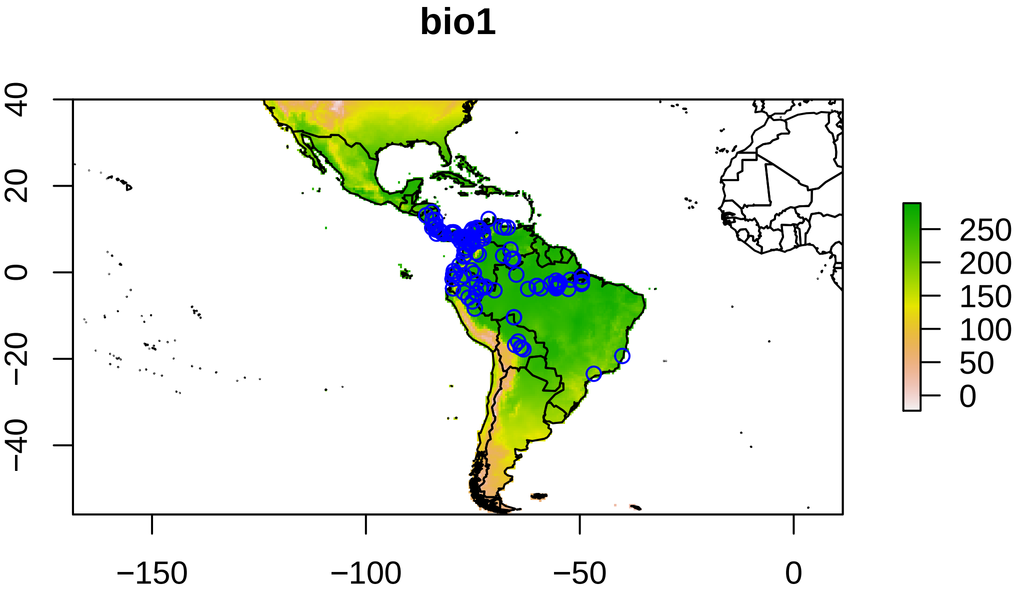


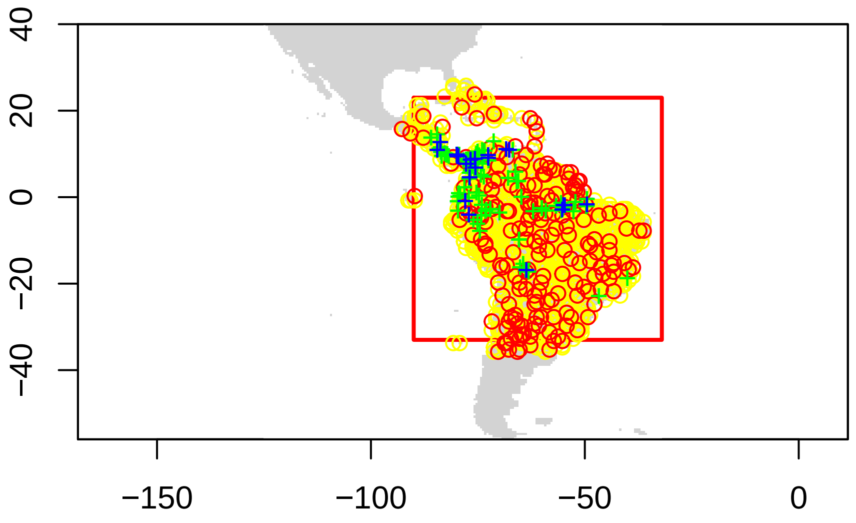
Figure 2: ROC curves and AUC

```
# environment conditions

files <- list.files(path=paste(system.file(package="dismo"), '/ex', sep= ''), pattern= 'grd' , full.name
predictors <- stack(files)

# first layer of the RasterStack
plot(predictors, 1)
#plot(predictors)
# note the "add=TRUE" argument with plot
plot(wrld_simpl, add=TRUE)
# with the points function, "add" is implicit
points(bradypus, col= ' blue ')
```



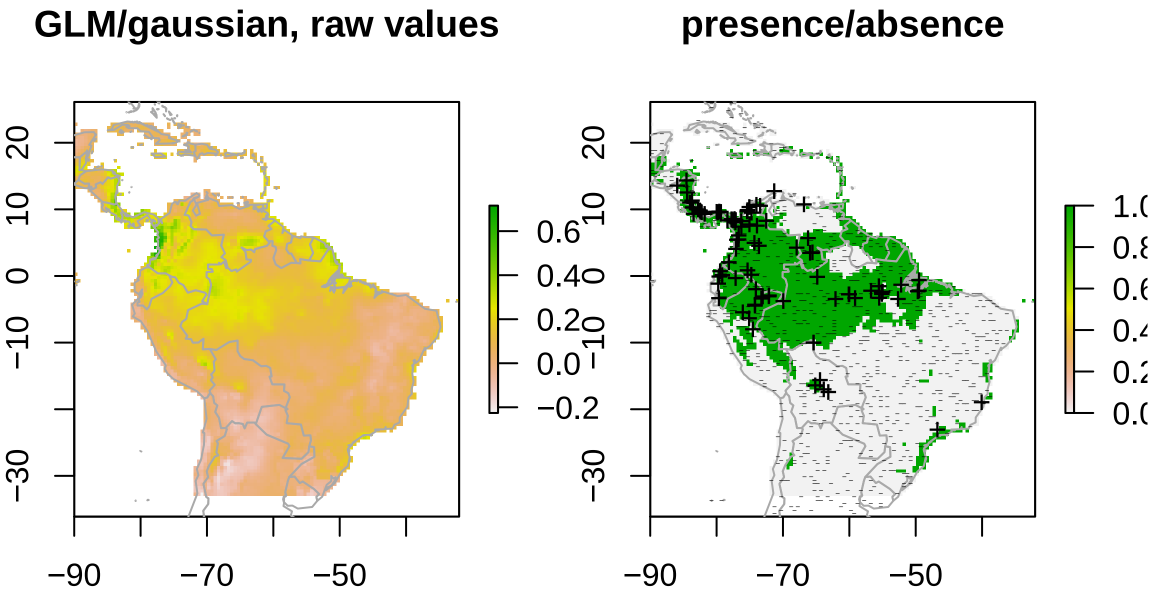
```
# 'biome' is a categorical data that needs special treatment in
# regression case, let's simply drop it from the predicator stacks.

pred_nf <- dropLayer(predictors, 'biome')
```

```
# Generate background data. To speed up processing, let's restrict the
# predictions to a more restricted area:

ext = extent(-90, -32, -33, 23)
backg <- randomPoints(pred_nf, n=1000, ext=ext)
colnames(backg) = c('lon', 'lat')
backg=as.data.frame(backg)

# Randomly seperate the bradypus observations into 5 groups and use
# four of them as training data and the rest one for validation

group <- kfold(bradypus, 5)
pres_train <- bradypus[group != 1, ]
pres_test <- bradypus[group == 1, ]

group <- kfold(backg, 5)
backg_train <- backg[group != 1, ]
backg_test <- backg[group == 1, ]

# Display the training and validation test data
r = raster(pred_nf, 1)
plot(!is.na(r), col=c(' white ' , ' light grey '), legend=FALSE)
plot(ext, add=TRUE, col= ' red ' , lwd=2)
points(backg_train$lon, backg_train$lat,  col= ' yellow ')
points(backg_test$lon, backg_test$lat,  col= ' red ')
points(pres_train$lon, pres_train$lat, pch= '+' , col= ' green ')
points(pres_test$lon, pres_test$lat, pch= '+' , col= 'blue')
```



```
# Combine sample locations and environment conditions into one data frame
train <- rbind(pres_train, backg_train)
pb_train <- c(rep(1, nrow(pres_train)), rep(0, nrow(backg_train)))
envtrain <- extract(predictors, train)
envtrain <- data.frame( cbind(pa=pb_train, envtrain) )
envtrain[,'biome'] = factor(envtrain[,'biome'], levels=1:14)
head(envtrain)

testpres <- data.frame( extract(predictors, pres_test) )
```

```r
testbackg <- data.frame( extract(predictors, backg_test) )
testpres[ ,'biome'] = factor(testpres[ ,'biome'], levels=1:14)
testbackg[ ,'biome'] = factor(testbackg[ ,'biome'], levels=1:14)

#In R , GLM is implemented in the 'glm' function, and the link function and
#error distribution are specified with the 'family' argument. Examples are:
#family = binomial(link = "logit")
#family = gaussian(link = "identity")
#family = poisson(link = "log")

# logistic regression:
gm1 <- glm(pa ~ bio1 + bio5 + bio6 + bio7 + bio8 + bio12 + bio16 + bio17,
family = binomial(link = "logit"), data=envtrain)
summary(gm1)

gm2 <- glm(pa ~ bio1+bio5 + bio6 + bio7 + bio8 + bio12 + bio16 + bio17,
family = gaussian(link = "identity"), data=envtrain)

# Model evaluation

# ROC curve (reveiver operating characterstic curve) and related AUC
# (area under the curve) are commonly used metrics for classification
# performance. The ROC curve is based on confusion matrix.  X is false
# positive rate (FP/(FP+TN))and Y is true positive rate (TP/(TP+FN)).
# Applying these two rate to different sets of classification
# threshold leads to the ROC curve

ge1=evaluate(testpres, testbackg, gm1)
ge2=evaluate(testpres, testbackg, gm2)

pg <- predict(predictors, gm2, ext=ext)
par(mfrow=c(1,2))
plot(pg, main='GLM/gaussian, raw values')
plot(wrld_simpl, add=TRUE, border='dark grey')
tr <- threshold(ge2, 'spec_sens')
plot(pg > tr, main='presence/absence')
plot(wrld_simpl, add=TRUE, border='dark grey')
points(pres_train, pch='+')
points(backg_train, pch='-', cex=0.25)
```

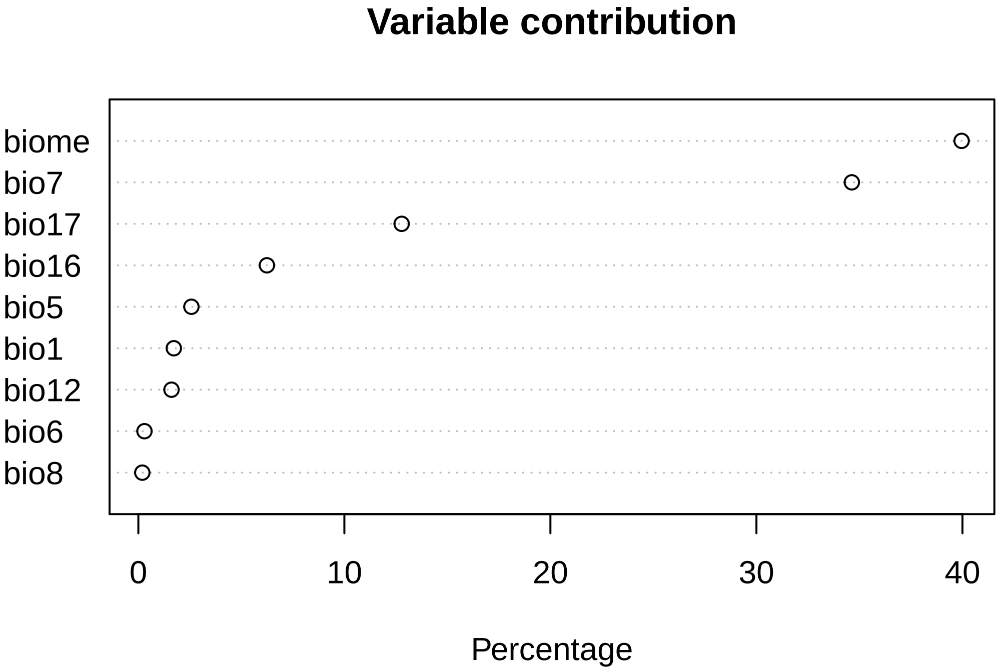

GLM/gaussian, raw values
presence/absence
20
10
0
−10
−30
−90
−70
−50
0.6
0.4
0.2
0.0
−0.2
1.(
0.8
0.6
0.4
0.2
0.0

MaxEnt

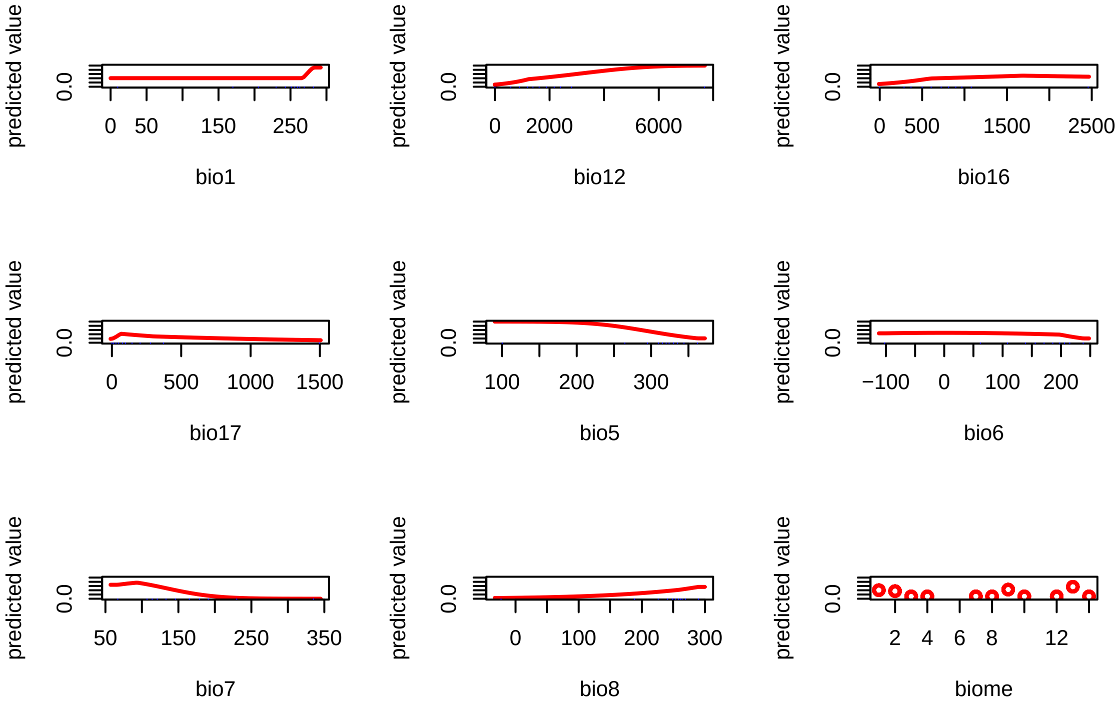
- One of the most widely used SDM framework with consistently competitive predictive performance, developed by: Phillips, Steven J., Robert P. Anderson, and Robert E. Schapire. "Maximum entropy modeling of species geographic distributions." Ecological modelling 190, no. 3-4 (2006): 231-259.
- **Premise:** the best approximation of a distribution is determined by maximum entropy, subject to constraints on it's moments. It agrees with everything that is known, but carefully avoids assuming anything that is not known (Jaynes 1990)
- The distribution π assign non-negative probability $\pi(x)$ to each point x, and these probabilities sum to 1. Our approximation of π is also a probability distribution, and we denote it $\hat{\pi}$. The entropy of $\hat{\pi}$ is defined as (Phillips et al. 2006):

$$H(\hat{\pi}(x)) = -\sum_{x \in X} \hat{\pi}(x) ln \hat{\pi}(x)$$

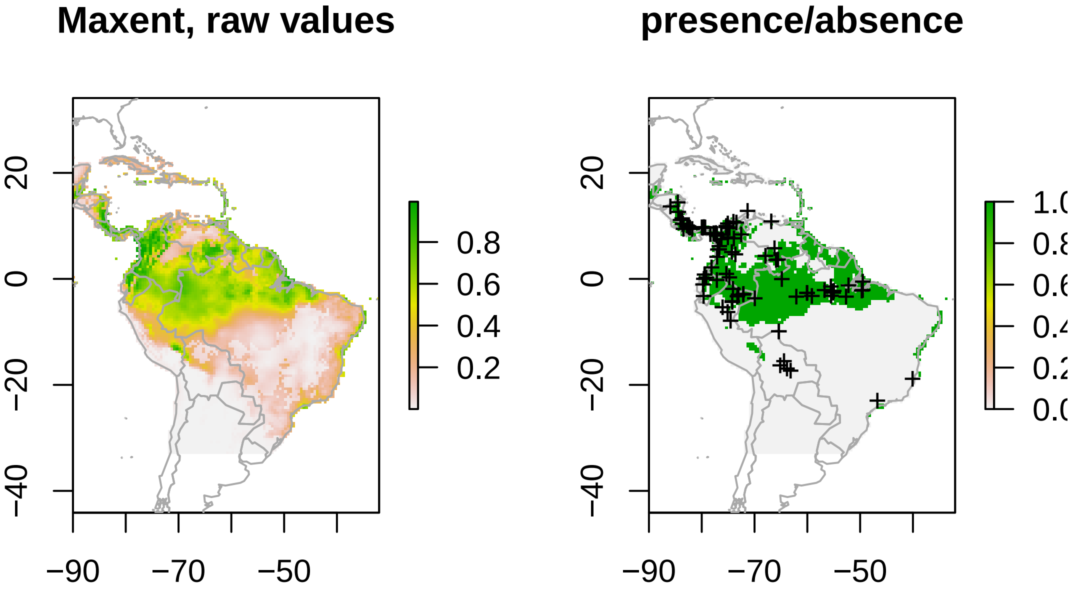
```
# MaxEnt, is a seperate package writtten in JAVA. Package 'dismo'
# provide the interface to Maxent

jar <- paste(system.file(package="dismo"), "/java/maxent.jar", sep= '')

xm <- maxent(predictors, p=pres_train, a= backg_train,factors= 'biome')

plot(xm)
```



```
# Check the response curve of each environmental conditions
response(xm)
```



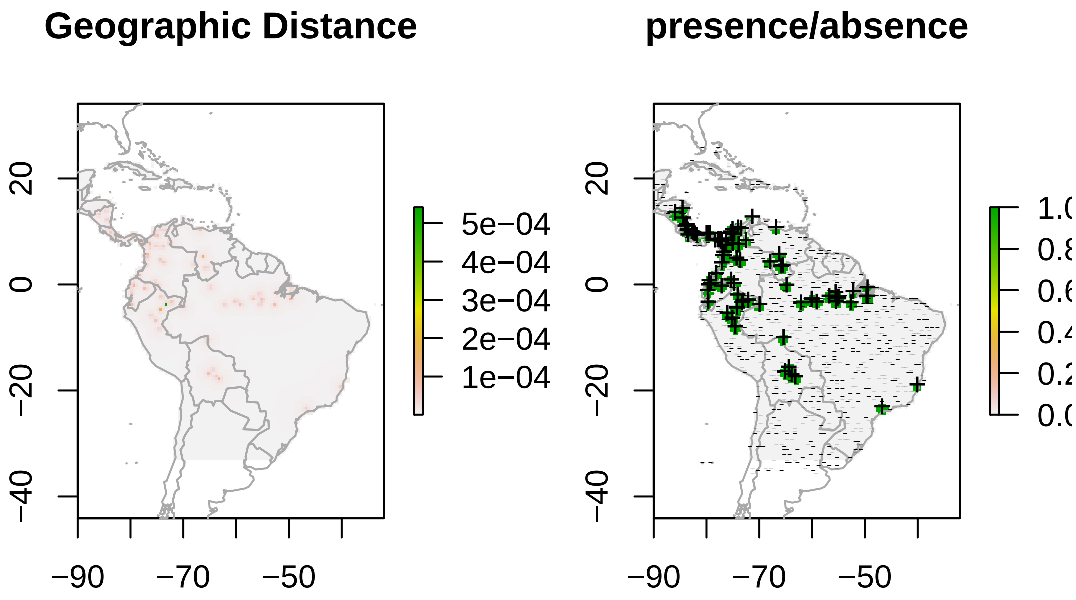
```
e <- evaluate(pres_test, backg_test, xm, predictors)
e
px <- predict(predictors, xm, ext=ext, progress='')
par(mfrow=c(1,2))
plot(px, main='Maxent, raw values')
plot(wrld_simpl, add=TRUE, border='dark grey')
tr <- threshold(e, 'spec_sens')
plot(px > tr, main='presence/absence')
plot(wrld_simpl, add=TRUE, border='dark grey')
points(pres_train, pch='+')
```



Geographic models

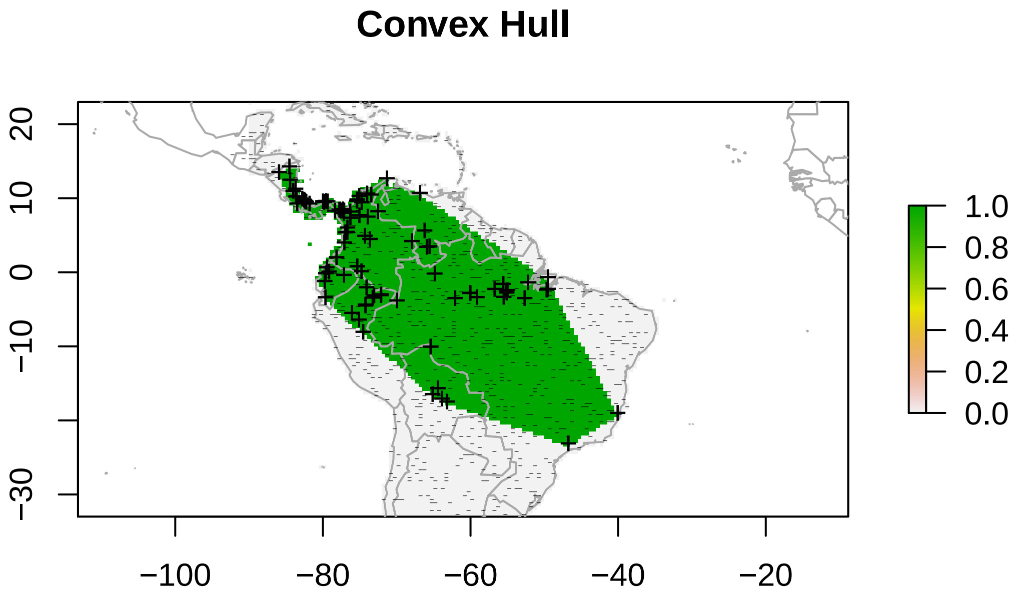
- Distance-based

```
# first create a mask to predict to, and to use as a mask
# to only predict to land areas
seamask <- crop(predictors[[1]], ext)
distm <- geoDist(pres_train, lonlat=TRUE)
ds <- predict(distm,seamask, mask=TRUE)
e <- evaluate(distm, p=pres_test, a=backg_test)
e

par(mfrow=c(1,2))
plot(ds, main='Geographic Distance')

plot(wrld_simpl, add=TRUE, border='dark grey')
tr <- threshold(e, 'spec_sens')
plot(ds > tr, main='presence/absence')
plot(wrld_simpl, add=TRUE, border='dark grey')
points(pres_train, pch='+')
points(backg_train, pch='-', cex=0.25)
```



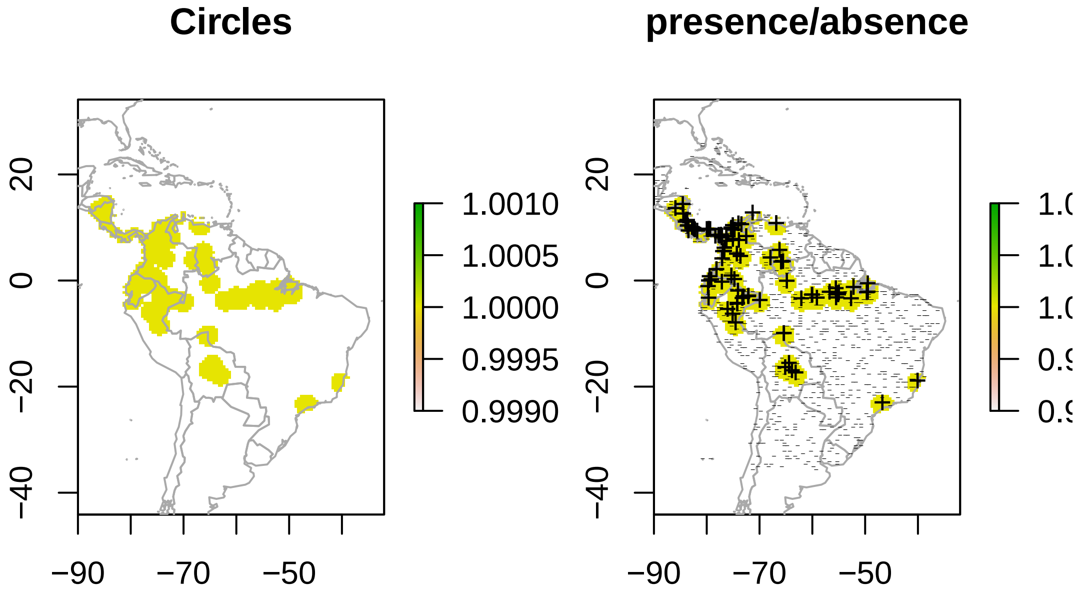
- Convex Hull

```
hull <- convHull(pres_train, lonlat=TRUE)
e <- evaluate(hull, p=pres_test, a=backg_test)
e

h <- predict(seamask, hull, mask=TRUE)
plot(h, main='Convex Hull')
plot(wrld_simpl, add=TRUE, border='dark grey')
points(pres_train, pch='+')
points(backg_train, pch='-', cex=0.25)
```



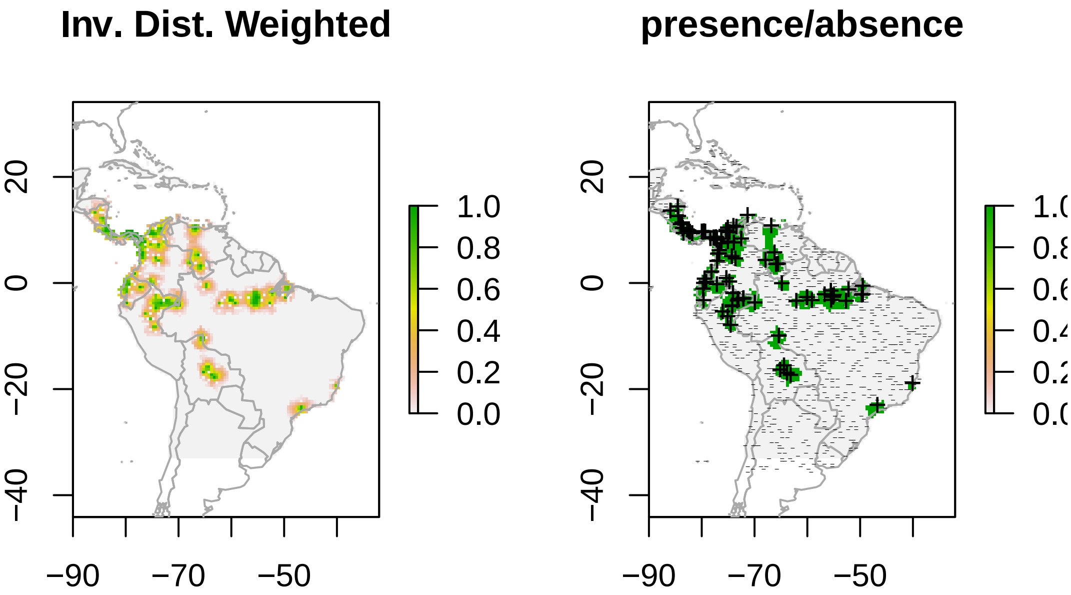
- Geographic circles

```
circ <- circles(pres_train, lonlat=TRUE)
pc <- predict(seamask, circ, mask=TRUE)
e <- evaluate(circ, p=pres_test, a=backg_test)
e
par(mfrow=c(1,2))
plot(pc, main='Circles')
plot(wrld_simpl, add=TRUE, border='dark grey')
tr <- threshold(e, 'spec_sens')
plot(pc > tr, main='presence/absence')
plot(wrld_simpl, add=TRUE, border='dark grey')
points(pres_train, pch='+')
points(backg_train, pch='-', cex=0.25)
```



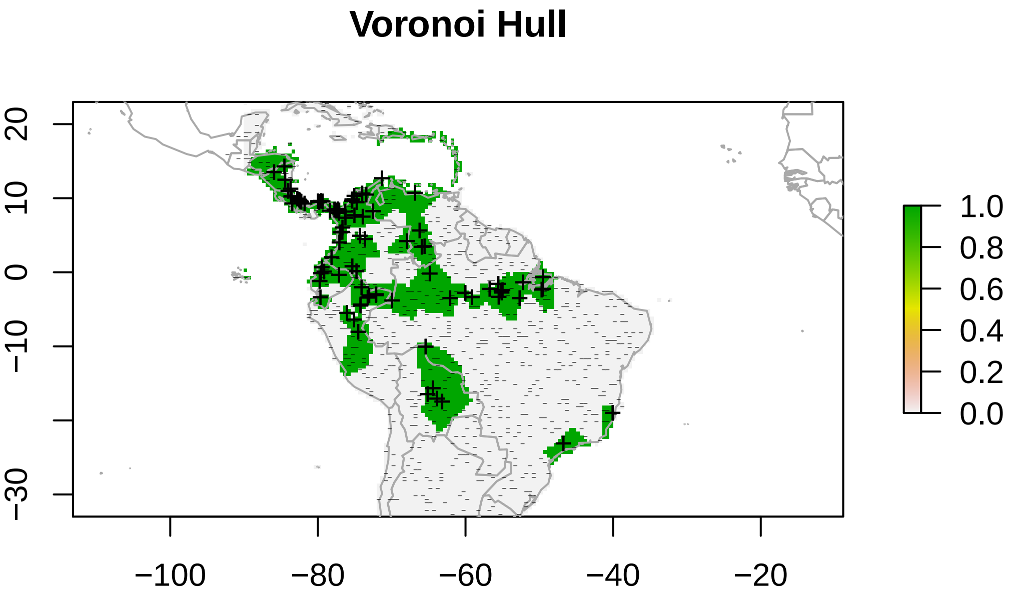
- Interpolation

```
idwm <- geoIDW(p=pres_train, a=data.frame(backg_train))
e <- evaluate(idwm, p=pres_test, a=backg_test)
e

iw <- predict(seamask, idwm, mask=TRUE)
par(mfrow=c(1,2))
plot(iw, main='Inv. Dist. Weighted')
plot(wrld_simpl, add=TRUE, border='dark grey')
tr <- threshold(e, 'spec_sens')
pa <- mask(iw > tr, seamask)
plot(pa, main='presence/absence')
plot(wrld_simpl, add=TRUE, border='dark grey')
points(pres_train, pch='+')
points(backg_train, pch='-', cex=0.25)
```



- Voronoi diagram

```
# take a smallish sample of the background training data
va <- data.frame(backg_train[sample(nrow(backg_train), 100), ])
vorm <- voronoiHull(p=pres_train, a=va)
e <- evaluate(vorm, p=pres_test, a=backg_test)
e
vo <- predict(seamask, vorm, mask=T)
plot(vo, main='Voronoi Hull')
plot(wrld_simpl, add=TRUE, border='dark grey')
points(pres_train, pch='+')
points(backg_train, pch='-', cex=0.25)
```



Reading:

Phillips et al. 2006: Maximum entropy modeling of species geographic distributions

https://cran.r-project.org/web/packages/dismo/vignettes/sdm.pdf