

# Species distribution modeling with R

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# Chapter 1

## Introduction

This document provides an introduction to species distribution modeling with R. Species distribution modeling (SDM) is also known under other names including climate envelope-modeling, habitat modeling, and (environmental or ecological) niche-modeling. The assumption of SDM is that you can predict the entire, or potential, spatial distribution of a phenomenon, by relating sites of known occurrence (and perhaps non-occurrence) with predictor variables known for these sites and for all other sites. The common application of this method is to predict species ranges with climate data as predictors.

In SDM, the following steps are usually taken: (1) locations of occurrence (and perhaps non-occurrence) of a species (or other phenomenon) are compiled. (2) values of environmental predictor variables (such as climate) at these locations are determined. (3) the environmental values are used to fit a model predicting likelihood of presence, or another measure such as abundance of the species. (4) The model is used to predict the likelihood of presence at all locations of an area of interest (and perhaps in a future climate).

In this text we assume that you are familiar with most of the concepts in SDM. If in doubt, you could consult, for example, Richard Pearson's introduction to the subject: [http://biodiversityinformatics.amnh.org/index.php?section\\_id=111](http://biodiversityinformatics.amnh.org/index.php?section_id=111), the book by Janet Franklin (2009), and the recent review by Elith and Leathwick (2009). It is important to have a good understanding of the interplay of environmental (niche) and geographic (biotope) space – see Colwell and Rangel (2009) for a good overview. SDM is a widely used approach but there is much debate on when and how to best use this method. While we refer to some of these issues, in this document we do not provide an in-depth discussion of this scientific debate. Rather, our objective is to provide practical guidance to implementing the basic steps of SDM. We leave it to you to use other sources to determine the appropriate methods for their research; and to use the ample opportunities provided by the R environment to improve existing approaches and to develop new ones.

We also assume that you are already familiar with the R language and environment. It would be particularly useful if you already had some experience

with statistical model fitting (e.g. the `glm` function) and with the `'raster'` package. To familiarize yourself with model fitting see, for instance, the Documentation section on the CRAN webpage (<http://cran.r-project.org/>) and any introduction to R txt. For the `'raster'` package you could consult its vignette. When we present code we will give some hints on how to understand the code, if we think it might be confusing. We will do more of this earlier on in this document, so if you are relatively inexperienced with R and would like to ease into it, read this text in the presented order.

SDM have been implemented in R in many different ways. Here we focus on the functions in the `'dismo'` and the `'raster'` packages (but we also refer to other packages). If you want to test, or build on, some of the examples presented here, make sure you have the latest versions of these packages, and their dependencies, installed. If you are using a recent version of R, you can do that with:

```
install.packages(c('raster', 'rgdal', 'dismo', 'rJava'))
```

This document consists of 4 main parts. Part I is concerned with data preparation. This is often the most time consuming part of a species distribution modeling project. You need to collect a sufficient number of occurrence records that document presence (and perhaps absence or abundance) of the species of interest. You also need to have accurate and relevant spatial predictor variables at a sufficiently high spatial resolution. We first discuss some aspects of assembling and cleaning species records, followed by a discussion of aspects of choosing and using the predictor variables. A particularly important concern in species distribution modeling is that the species occurrence data adequately represent the species' distribution. For instance, the species should be correctly identified, the coordinates of the location data need to be accurate enough to allow the general species/environment to be established, and the sample unbiased, or accompanied by information on known biases such that these can be taken into account. Part II introduces the main steps in SDM: fitting a model, making a prediction, and evaluating the result. Part III introduces different modeling methods in more detail (profile methods, regression methods, machine learning methods, and geographic methods). In Part IV we discuss a number of applications (e.g. predicting the effect of climate change), and a number of more advanced topics.

This is a work in progress. Suggestions are welcomed.

## Part I

# Data preparation

## Chapter 2

# Species occurrence data

Importing occurrence data into R is easy. But collecting, georeferencing, and cross-checking coordinate data is tedious. Discussions about species distribution modeling often focus on comparing modeling methods, but if you are dealing with species with few and uncertain records, your focus probably ought to be on improving the quality of the occurrence data (Lobo, 2008). All methods do better if your occurrence data is unbiased and free of error (Graham *et al.*, 2007) and you have a relatively large number of records (Wisz *et al.*, 2008). While we'll show you some useful data preparation steps you can do in R, it is necessary to use additional tools as well. For example, Quantum GIS, <http://www.qgis.org/>, is a very useful program for interactive editing of point data sets.

### 2.1 Importing occurrence data

In most cases you will have a file with point locality data representing the known distribution of a species. Below is an example of using `read.table` to read records that are stored in a text file. The R commands used are in *italics* and preceded by a `'>'`. Comments are preceded by a hash (`#`). We are using an example file that is installed with the `'dismo'` package, and for that reason we use a complex way to construct the filename, but you can replace that with your own filename. (remember to use forward slashes in the path of filenames!). `system.file` inserts the file path to where `dismo` is installed. If you haven't used the `paste` function before, it's worth familiarizing yourself with it (type `?paste` in the command window). It's very useful.

```
> # loads the dismo library
> library(dismo)
> file <- paste(system.file(package="dismo"), "/ex/bradypus.csv", sep="")
> # this is the file we will use:
> file
```

```
[1] "c:/temp/Rtmpodl0ka/Rinste756f2/dismo/ex/bradypus.csv"

> # let's read it
> bradypus <- read.table(file, header=TRUE, sep=',')
> # let's inspect the values of the file
> # first rows
> head(bradypus)

      species      lon      lat
1 Bradypus variegatus -65.4000 -10.3833
2 Bradypus variegatus -65.3833 -10.3833
3 Bradypus variegatus -65.1333 -16.8000
4 Bradypus variegatus -63.6667 -17.4500
5 Bradypus variegatus -63.8500 -17.4000
6 Bradypus variegatus -64.4167 -16.0000

> # we only need columns 2 and 3:
> bradypus <- bradypus[,2:3]
> head(bradypus)

      lon      lat
1 -65.4000 -10.3833
2 -65.3833 -10.3833
3 -65.1333 -16.8000
4 -63.6667 -17.4500
5 -63.8500 -17.4000
6 -64.4167 -16.0000
```

You can also read such data directly out of Excel or from a database (see e.g. the `RODBC` package). Because this is csv (comma separated values) file, we could also have used the `read.csv` function. No matter how you do it, the objective is to get a matrix (or a **data.frame**) with at least 2 columns to hold the coordinates. Coordinates are typically longitude and latitude, but they could also be Easting and Northing in UTM or another coordinate reference system (map projection). The convention used here is to organize the coordinates columns so that longitude is the first and latitude the second column (think x and y axes in a plot; longitude is x, latitude is y); they often are in the reverse order, leading to undesired results. In many cases you will have additional columns, e.g., a column to indicate the species if you are modeling multiple species; and a column to indicate whether this is a 'presence' or an 'absence' record (a much used convention is to code presence with a 1 and absence with a 0).

If you do not have any species distribution data you can get started by downloading data from the Global Biodiversity Inventory Facility (GBIF) (<http://www.gbif.org/>). In the `dismo` package there is a function `'gbif'` that you can use for this. The data used below were downloaded (and saved to a permanent data set for use in this vignette) using the `gbif` function like this:

```
acaule = gbif("solanum", "acaule", geo=FALSE)
```

If you want to understand the order of the arguments given here to `gbif` or find out what other arguments you can use with this function, check out the help file (remember you can't access help files if the library is not loaded), by typing: `?gbif` or `help(gbif)`

Many species occurrence records may not have geographic coordinates. Out of the 699 records that GBIF returned (March 2010), there were only 54 records with coordinates.

```
> # load the saved acaule data
> data(acaule)
> # how many rows and columns?
> dim(acaule)

[1] 699 23

> #select the records that have longitude and latitude data
> colnames(acaule)

[1] "species"           "continent"
[3] "country"           "adm1"
[5] "adm2"              "locality"
[7] "lat"               "lon"
[9] "coordUncertaintyM" "alt"
[11] "institution"       "collection"
[13] "catalogNumber"     "basisOfRecord"
[15] "collector"         "earliestDateCollected"
[17] "latestDateCollected" "gbifNotes"
[19] "downloadDate"      "maxElevationM"
[21] "minElevationM"     "maxDepthM"
[23] "minDepthM"

> acgeo <- subset(acaule, !is.na(lon) & !is.na(lat))
> dim(acgeo)

[1] 54 23

> # show some values
> acgeo[1:4, c(1:5,7:10)]
```

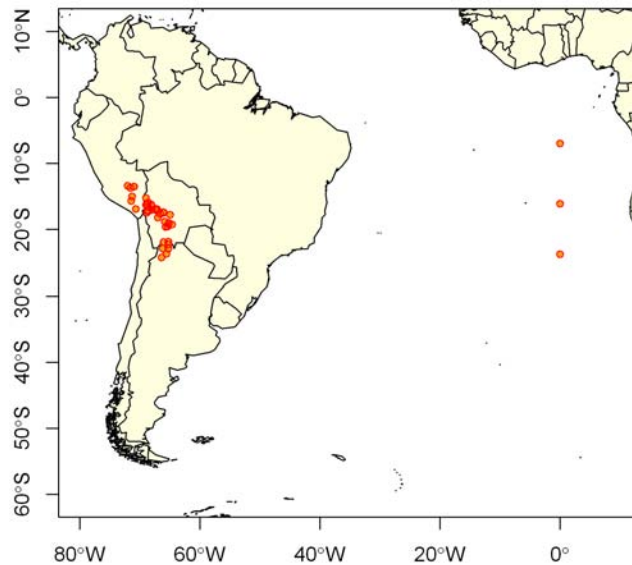
	species	continent	country	adm1
13	Solanum acaule	<NA>	BOL	<NA>
426	Solanum acaule Bitter	America	Argentina	Jujuy
428	Solanum acaule Bitter	America	Bolivia	La Paz
429	Solanum acaule Bitter	America	Bolivia	La Paz

```

      adm2      lat      lon coordUncertaintyM alt
13      <NA> -18.8167 -65.90                NA 3960
426      -22.9000 -66.24                NA 4050
428 Pacajes -17.4200 -68.85                NA 3811
429 Pacajes -17.1200 -68.77                NA 3800
```

Below is a simple way to make a map of the occurrence localities of *Solanum acaule*. It is important to make such maps to assure that the points are, at least roughly, in the right location.

```
> library(maptools)
> data(wrld_simpl)
> plot(wrld_simpl, xlim=c(-80,10), ylim=c(-60,10), axes=TRUE,
+       col='light yellow')
> # restore the box around the map
> box()
> # plot points
> points(acgeo$lon, acgeo$lat, col='orange', pch=20, cex=0.75)
> # plot points again to add a border, for better visibility
> points(acgeo$lon, acgeo$lat, col='red', cex=0.75)
```



The "wrld\_simpl" dataset contains rough country outlines. You can use other datasets of polygons (or lines or points) as well. For example, you can download higher resolution data country and subnational administrative boundaries data with the `getData` function of the `raster` package. You can also read your own shapefile data into R using the `readOGR` function in the `rgdal` package or the `readShapePoly` function in the `maptools` package.



## 2.2 Data cleaning

Data 'cleaning' is particularly important for data sourced from species distribution data warehouses such as GBIF. Such efforts do not specifically gather data for the purpose of species distribution modeling, so you need to understand the data and clean them appropriately, for your application. Here we provide an example.

*Solanum acaule* is a species that occurs in the higher parts of the Andes mountains of Peru and Bolivia. Do you see any errors on the map? There are three records that have plausible latitudes, but longitudes that are clearly wrong, as they are in the Atlantic Ocean, south of West Africa. It looks like they have a longitude that is zero. In many data-bases you will find values that are 'zero' where 'no data' was intended. The `gbif` function (when using the default arguments) sets coordinates that are (0, 0) to NA, but not if one of the coordinates is zero. Let's see if we find them by searching for records with longitudes of zero.

Let's have a look at these records:

```
> lonzero = subset(acgeo, lon==0)
> # show all records, only the first 13 columns
> lonzero[, 1:13]
```

	species	continent	country
544	Solanum acaule Bitter subsp. acaule	<NA>	BOL
551	Solanum acaule Bitter subsp. acaule	<NA>	BOL
567	Solanum acaule Bitter subsp. acaule	<NA>	PER
638	Solanum acaule Bitter subsp. acaule	<NA>	PER
640	Solanum acaule Bitter subsp. acaule	<NA>	ARG
641	Solanum acaule Bitter subsp. acaule	<NA>	ARG

	adm1	adm2
544	<NA>	<NA>
551	<NA>	<NA>
567	<NA>	<NA>
638	<NA>	<NA>
640	<NA>	<NA>
641	<NA>	<NA>

	locality
544	Llave
551	Llave
567	km 205 between Puno and Cuzco
638	km 205 between Puno and Cuzco
640	between Quelbrada del Chorro and Laguna Colorada
641	between Quelbrada del Chorro and Laguna Colorada

	lat	lon	coordUncertaintyM	alt	institution
544	-16.083333	0	NA	3900	IPK
551	-16.083333	0	NA	3900	IPK
567	-6.983333	0	NA	4250	IPK

638	-6.983333	0	NA	4250	IPK
640	-23.716667	0	NA	3400	IPK
641	-23.716667	0	NA	3400	IPK
	collection	catalogNumber			
544	WKS 30050	304711			
551	GB	WKS 30050			
567	WKS 30048	304709			
638	GB	WKS 30048			
640	WKS 30027	304688			
641	GB	WKS 30027			

The records are from Bolivia (BOL), Peru (PER) and Argentina (ARG), confirming that coordinates are in error (it could have been that the coordinates were correct for a location in the Ocean, perhaps referring to a location a fish was caught rather than a place where *S. acaule* was collected).

### 2.2.1 Duplicate records

Interestingly, another data quality issue is revealed above: each record occurs twice. This could happen because plant samples are often split and sent to multiple herbariums. But in this case it seems that the data from IPK are duplicated in the GBIF database. Duplicates can be removed with the `duplicated` function.

```
> # which records are duplicates (only for the first 10 columns)?
> dups <- duplicated(lonzero[, 1:10])
> # remove duplicates
> lonzero <- lonzero[dups, ]
> lonzero[,1:13]
```

	species	continent	country
551	Solanum acaule Bitter subsp. acaule	<NA>	BOL
638	Solanum acaule Bitter subsp. acaule	<NA>	PER
641	Solanum acaule Bitter subsp. acaule	<NA>	ARG
	adm1	adm2	
551	<NA>	<NA>	
638	<NA>	<NA>	
641	<NA>	<NA>	
		locality	
551		Llave	
638		km 205 between Puno and Cuzco	
641		between Quelbrada del Chorro and Laguna Colorada	
	lat	lon	coordUncertaintyM alt institution
551	-16.083333	0	NA 3900 IPK
638	-6.983333	0	NA 4250 IPK
641	-23.716667	0	NA 3400 IPK
	collection	catalogNumber	

551	GB	WKS 30050
638	GB	WKS 30048
641	GB	WKS 30027

Another approach might be to detect duplicates for the same species and some coordinates in the data, even if the records were from collections by different people or in different years. (in our case, using species is redundant as we have data for only species)

```
> dups2 <- duplicated(acgeo[, c('species', 'lon', 'lat')])
> # number of duplicates
> sum(dups2)

[1] 8

> # keep the records that are _not_ duplicated
> acg <- acgeo[!dups2, ]
> # let's also remove the records with longitude=0
> acg <- acg[acg$lon != 0, ]
```

## 2.3 Cross-checking

It is important to cross-check coordinates by visual and other means. One approach is to compare the country (and lower level administrative subdivisions) of the site as specified by the records, with the country implied by the coordinates (Hijmans *et al.*, 1999). In the example below we use the `coordinates` function from the 'sp' package to create a `SpatialPointsDataFrame`, and then the `overlay` function, also from 'sp', to do a point-in-polygon query with the countries polygons.

```
> library(sp)
> # make a SpatialPointsDataFrame
> coordinates(acgeo) <- ~lon+lat
> class(acgeo)

[1] "SpatialPointsDataFrame"
attr(,"package")
[1] "sp"

> # use the coordinates to do a spatial query of the polygons
> # in wrld_simpl wich is a SpatialPolygonsDataFrame object
> class(wrld_simpl)

[1] "SpatialPolygonsDataFrame"
attr(,"package")
[1] "sp"
```

```

> ov <- overlay(acgeo, wrld_simpl)
> # ov has, for each point, the record number of wrld_simpl
> # we can use the record number to extract the country name
> # first find the variable name
> names(wrld_simpl@data)

[1] "FIPS"      "ISO2"      "ISO3"      "UN"
[5] "NAME"      "AREA"      "POP2005"   "REGION"
[9] "SUBREGION" "LON"       "LAT"

> head(wrld_simpl@data)

      FIPS ISO2 ISO3 UN      NAME      AREA POP2005
ATG   AC   AG  ATG 28 Antigua and Barbuda    44    83039
DZA   AG   DZ  DZA 12      Algeria 238174 32854159
AZE   AJ   AZ  AZE 31      Azerbaijan 8260  8352021
ALB   AL   AL  ALB 8      Albania 2740  3153731
ARM   AM   AM  ARM 51      Armenia 2820  3017661
AGO   AO   AO  AGO 24      Angola 124670 16095214
      REGION SUBREGION      LON      LAT
ATG      19      29 -61.783  17.078
DZA      2      15  2.632  28.163
AZE     142     145  47.395  40.430
ALB     150      39  20.068  41.143
ARM     142     145  44.563  40.534
AGO      2      17  17.544 -12.296

> # We clearly need the variable 'NAME' in the data.frame
> # (stored in the 'data' slot) of wrld_simpl
>
> cntr <- as.character(wrld_simpl@data$NAME[ov])
> # which points (identified by their record numbers) do not match
> # any country (i.e. are in an ocean)
> i <- which(is.na(cntr))
> i

[1] 43 44 45 46 47 48

> # these are the same records, with longitude=0, as identified above:
> acgeo@data[i, 'catalogNumber']

[1] "304711"      "WKS 30050" "304709"      "WKS 30048"
[5] "304688"      "WKS 30027"

> # which points has coordinates that are in a different country than
> # listed in the 'country' field of the gbif record
> j <- which(cntr != acgeo@data$country)
> j

```

```
[1] 1 49 50 51 52

> # for the mismatches, bind the country names of the polygons and points
> cbind(cntr, acgeo@data$country)[j,]

      cntr
[1,] "Bolivia" "BOL"
[2,] "Bolivia" "BOL"
[3,] "Peru"    "PER"
[4,] "Peru"    "PER"
[5,] "Peru"    "PER"

> # fortunately the mismatch is simply because of the use of abbreviations
> # instead of full country names in these records.
```

See the `sp` package for more information on the `overlay` function and the related function `over`. At first it may be confusing that it returns indices (row numbers). These indices, stored in variables `i` and `j` were used to get the relevant records. Note that the polygons that we used in the example above are not very precise, and they should not be used in a real analysis. See <http://www.gadm.org/> for more detailed administrative division files, or use the `'getData'` function from the `raster` package (e.g. `getData('gadm', country='PER', level=0)` to get the national borders of Peru.

```
> # now let's remove the records that have a longitude of 0
> acgeo <- acgeo[ coordinates(acgeo)[,'lon'] != 0, ]
```

## 2.4 Georeferencing

If you have records with locality descriptions but no coordinates, you should consider georeferencing these. Not all the records can be georeferenced. Sometimes even the country is unknown (`country=="UNK"`). Here we select only records that do not have coordinates, but that do have a locality description.

```
> georef <- subset(acaule, (is.na(lon) | is.na(lat)) & ! is.na(locality) )
> dim(georef)
```

```
[1] 89 23
```

```
> georef[1:3,1:13]
```

```

                                species
30 Solanum acaule Bitter subsp. acaule (Juz.) Hawkes & Hjert.
42 Solanum acaule Bitter subsp. acaule (Juz.) Hawkes & Hjert.
81 Solanum acaule Bitter subsp. acaule (Juz.) Hawkes & Hjert.
  continent country adm1 adm2
30      <NA>      PER <NA> <NA>
```

```

42      <NA>      BOL <NA> <NA>
81      <NA>      ARG <NA> <NA>

      locality lat lon coordUncertaintyM
30 km 205 between Puno and Cuzco NA NA NA
42      Llave NA NA NA
81      da Pena NA NA NA

      alt institution collection catalogNumber
30 4250      DEU159      DEU      WKS 30048
42 3900      DEU159      DEU      WKS 30050
81  NA      DEU159      DEU      WKS 30417

```

Among the first records is an old acquaintance. The record, with catalog number WKS 30048 was also in the set of records that had a longitude of zero degrees.

We recommend using a tool like BioGeomancer: <http://bg.berkeley.edu/latest> (Guralnick *et al.*, 2006) to georeference textual locality descriptions. An important feature of BioGeomancer is that it attempts to capture the uncertainty associated with each georeference (Wieczorek *et al.*, 2004). The dismo package has a function `biogeomancer` that you can use for this, and that we demonstrate below, but its use is generally not recommended because you really need a detailed map interface for accurate georeferencing.

Here is an example for one of the records with longitude = 0. We put the `biogeomancer` function into a 'try' function, to assure elegant error handling if the computer is not connected to the Internet.

```

> args(biogeomancer)

function (country = "", adm1 = "", adm2 = "", locality = "",
      singleRecord = TRUE, progress = "text")
NULL

> # the first locality:
> lonzero$locality[1]

[1] "Llave"

> b <- try( biogeomancer('Peru', locality=lonzero$locality[1], progress=''))
> b

      id lon lat coordUncertaintyM
1  1  NA  NA      NA

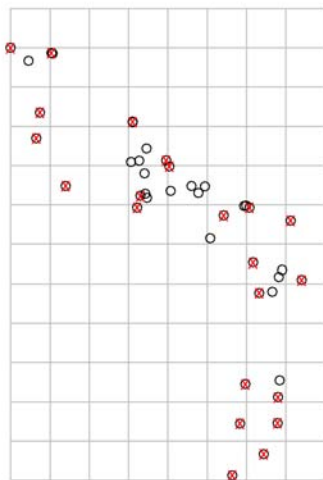
```

## 2.5 Sampling bias

Sampling bias is frequently present in occurrence records (Hijmans *et al.*, 2001). One can attempt to remove some of the bias by subsampling records, and this is illustrated below. However, subsampling reduces the number of

records, and it cannot correct the data for areas that have not been sampled at all. It also suffers from the problem that locally dense records might be a true reflection of the relative suitability of habitat. The example below illustrates how one could go about subsampling. This is not a general recommendation to subsample, or to subsample in this way. See Phillips *et al.* (2009) for an approach with MaxEnt to deal with bias in occurrence records used in SDM.

```
> # create a RasterLayer with the extent of acgeo
> r <- raster(acgeo)
> # set the resolution of the cells to 1 degrees
> res(r) <- 1
> # expand the RasterLayer a little
> r <- expand(r, extent(r)+1)
> # get the cell number for each point
> cell <- cellFromXY(r, acgeo)
> dup <- duplicated(cell)
> # select the records that are not duplicated. A random selection
> # within duplicates might be better (but more elaborate).
> acsel <- acgeo[!dup, ]
> # display the results
> p <- rasterToPolygons(r)
> plot(p, border='gray')
> points(acgeo)
> # selected points in red
> points(acsel, cex=1, col='red', pch='x')
```





## Chapter 3

# Absence and background points

Some of the early species distribution model algorithms, such as Bioclim and Domain only use 'presence' data in the modeling process. Other methods also use 'absence' data or 'background' data. Logistic regression is the classical approach to analyzing presence and absence data (and it is still much used, often implemented in a generalized linear modeling (GLM) framework). If you have a large dataset with presence/absence from a well designed survey, you should use a method that can use these data (i.e. do not use a modeling method that only considers presence data). If you only have presence data, you can still use a method that needs absence data, by substituting absence data with background data.

Background data (e.g. Phillips *et al.* 2009) are not attempting to guess at absence locations, but rather to characterize environments in the study region. In this sense, background is the same, irrespective of where the species has been found. Background data establishes the environmental domain of the study, whilst presence data should establish under which conditions a species is more likely to be present than on average. A closely related but different concept, that of "pseudo-absences", is also used for generating the non-presence class for logistic models. In this case, researchers sometimes 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. We prefer the background concept because it requires fewer assumptions and has some coherent statistical methods for dealing with the "overlap" between presence and background points (e.g. Ward et al. 2009; Phillips and Elith, 2011).

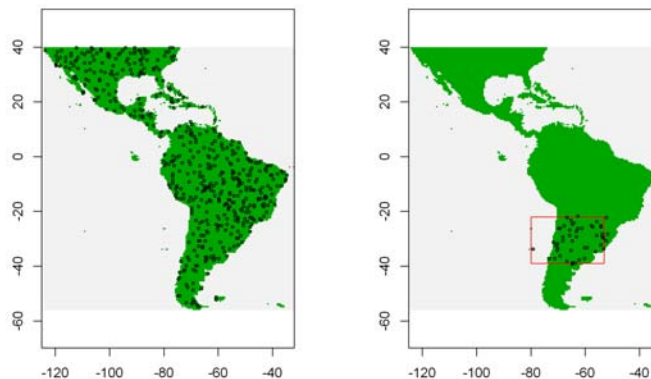
Survey-absence data has value. In conjunction with presence records, it establishes where surveys have been done, and the prevalence of the species given the survey effort. That information is lacking for presence-only data, a fact that can cause substantial difficulties for modeling presence-only data well. However, absence data can also be biased and incomplete, as discussed in the

literature on detectability (e.g., Kéry et al., 2010).

`dismo` has a function to sample random points (background data) from a study area. You can use a 'mask' to exclude area with no data NA, e.g. areas not on land. You can use an 'extent' to further restrict the area from which random locations are drawn. In the example below, we first get the list of filenames with the predictor raster data (discussed in detail in the next chapter). We use a raster as a 'mask' in the `randomPoints` function such that the background points are from the same geographic area, and only for places where there are values (land, in our case).

Note that if the mask has the longitude/latitude coordinate reference system, function `randomPoints` selects cells according to cell area, which varies by latitude (as in Elith et al., 2011)

```
> files <- list.files(path=paste(system.file(package="dismo"), '/ex',
+                               sep=''), pattern='grd', full.names=TRUE )
> mask <- raster(files[[1]])
> # select 500 random points
> # set seed to assure that the examples will always
> # have the same random sample.
> 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 limiting the area of sampling by 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)
```



There are several approaches one could use to sample 'pseudo-absence' points, i.e. points from more restricted area than 'background'. VanDerWal et al. (2009) sampled within a radius of presence points. Here is one way to implement that, using the *Solanum acaule* data.

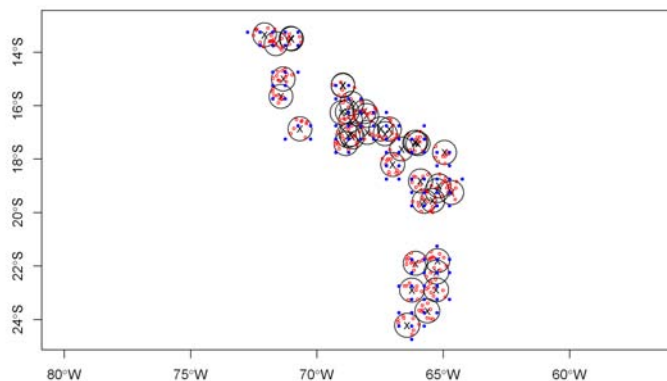
```
> pts <- acg[, c('lon', 'lat')]
> # circles with a radius of 50 km
> x <- circles(pts, d=50000, lonlat=T, col='light gray')
> plot(x@polygons, axes=T)
> points(pts, pch='x')
> # sample randomly from all circles
> samp1 <- spsample(x@polygons, 250, type='random', iter=25)
> points(samp1, cex=0.5, col='red')
> # get unique cells
> cells <- cellFromXY(mask, samp1)
> length(cells)

[1] 250

> cells <- unique(cells)
> length(cells)

[1] 92

> xy <- xyFromCell(mask, cells)
> points(xy, cex=0.75, pch=20, col='blue')
```



Note that the blue points are not all within the circles, as they now represent the centers of the selected cells from mask. We could choose to select only those cells that have their centers within the circles, using the `overlay` function.

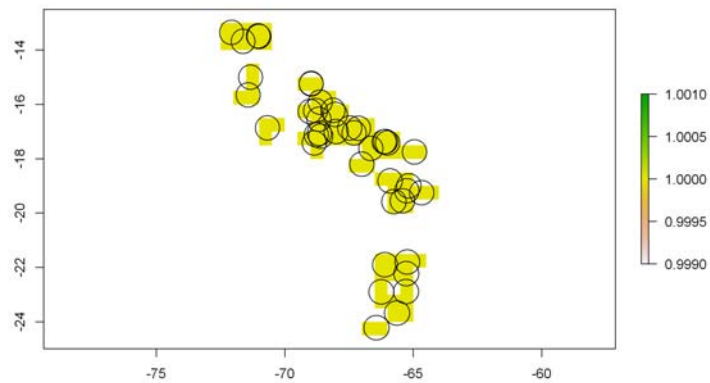
```
> o <- overlay(x@polygons, SpatialPoints(xy))
> xyInside <- xy[!is.na(o), ]
```

Similar results could also be achieved via the raster functions `rasterize` or `extract`.

```
> # extract cell numbers for the circles
> v <- extract(mask, x@polygons, cellnumbers=T)
> # use rbind to combine the elements in list v
> v <- do.call(rbind, v)
> # get unique cell numbers from which you could sample
> v <- unique(v[,1])
> v

[1] 21880 21881 23368 23554 21316 21317 21503 21131 21321
[10] 21507 21508 19822 19823 20008 20946 20947 22067 22253
[19] 21132 23183 23184 23925 23926 20009 20010 21510 21511
[28] 21134 21135 21320 20572 20573 20382 20568 21692 21693
[37] 21322 21323 21133 21509 23555 23741 23742 21318 20759
[46] 20760 20945 20944 22069 22070 21882 22068 22998 22999
[55] 19824 19825 20011 22254 23370 23556 21319 20753 20754
[64] 21127 21128 21313 22996 22997 23182

> # to display the results
> m <- mask
> m[] <- NA
> m[v] <- 1
> plot(m, ext=extent(x@polygons)+1)
> plot(x@polygons, add=T)
```



## Chapter 4

# Environmental data

### 4.1 Raster data

In species distribution modeling, predictor variables are typically organized as raster (grid) type files. Each predictor should be a 'raster' representing a variable of interest. Variables can include climatic, soil, terrain, vegetation, land use, and other variables. These data are typically stored in files in some kind of GIS format. Almost all relevant formats can be used (including ESRI grid, geoTiff, netCDF, IDRISI). Avoid ASCII files if you can, as they tend to considerably slow down processing speed. For any particular study the layers should all have the same spatial extent, resolution, origin, and projection. If necessary, use functions like `crop`, `expand`, `aggregate`, `resample`, and `projectRaster` from the 'raster' package to prepare your predictor variable data. See the help files and the vignette of the raster package for more info on how to do this. The set of predictor variables (rasters) can be used to make a 'RasterStack', which is a collection of 'RasterLayer' objects (see the `raster` package for more info).

Here we make a list of files that are installed with the `dismo` package and then create a `rasterStack` from these, show the names of each layer, and finally plot them all.

```
> files <- list.files(path=paste(system.file(package="dismo"),
+                               '/ex', sep=''), pattern='grd', full.names=TRUE )
> # The above finds all the files with extension "grd" in the
> # examples ("ex") directory of the dismo package. You do not
> # need such a complex statement to get your own files.
> files

[1] "c:/temp/Rtmpodl0ka/Rinste756f2/dismo/ex/bio1.grd"
[2] "c:/temp/Rtmpodl0ka/Rinste756f2/dismo/ex/bio12.grd"
[3] "c:/temp/Rtmpodl0ka/Rinste756f2/dismo/ex/bio16.grd"
[4] "c:/temp/Rtmpodl0ka/Rinste756f2/dismo/ex/bio17.grd"
```

```

[5] "c:/temp/Rtmpodl0ka/Rinste756f2/dismo/ex/bio5.grd"
[6] "c:/temp/Rtmpodl0ka/Rinste756f2/dismo/ex/bio6.grd"
[7] "c:/temp/Rtmpodl0ka/Rinste756f2/dismo/ex/bio7.grd"
[8] "c:/temp/Rtmpodl0ka/Rinste756f2/dismo/ex/bio8.grd"
[9] "c:/temp/Rtmpodl0ka/Rinste756f2/dismo/ex/biome.grd"

> predictors <- stack(files)
> predictors

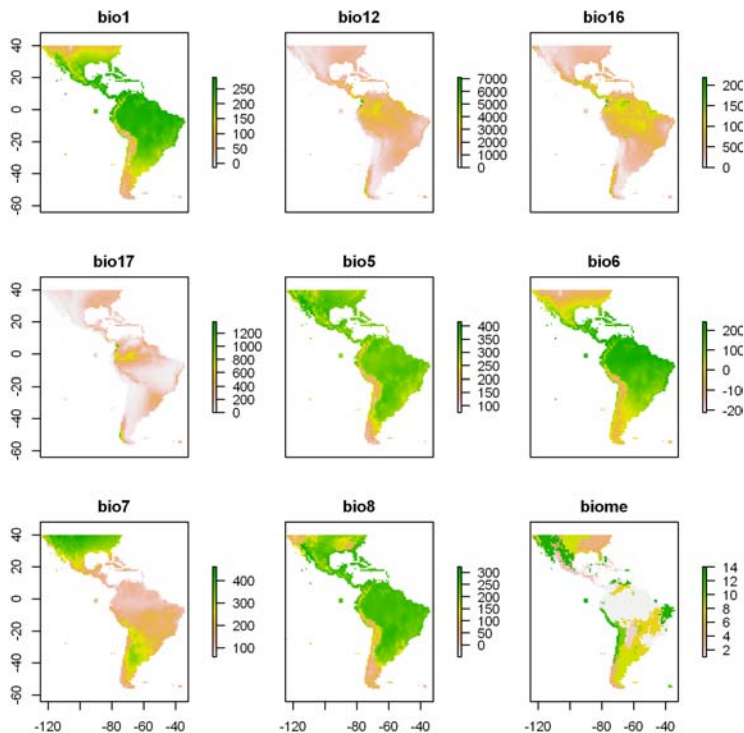
class       : RasterStack
dimensions  : 192, 186, 35712, 9  (nrow, ncol, ncell, nlayers)
resolution  : 0.5, 0.5  (x, y)
extent      : -125, -32, -56, 40  (xmin, xmax, ymin, ymax)
coord. ref. : +proj=longlat +datum=WGS84 +ellps=WGS84 +towgs84=0,0,0
min values  : -23  0  0  0  61 -212  60 -66  1
max values  : 289 7682 2458 1496 422 242 461 323 14

> layerNames(predictors)

[1] "bio1" "bio12" "bio16" "bio17" "bio5" "bio6" "bio7"
[8] "bio8" "biome"

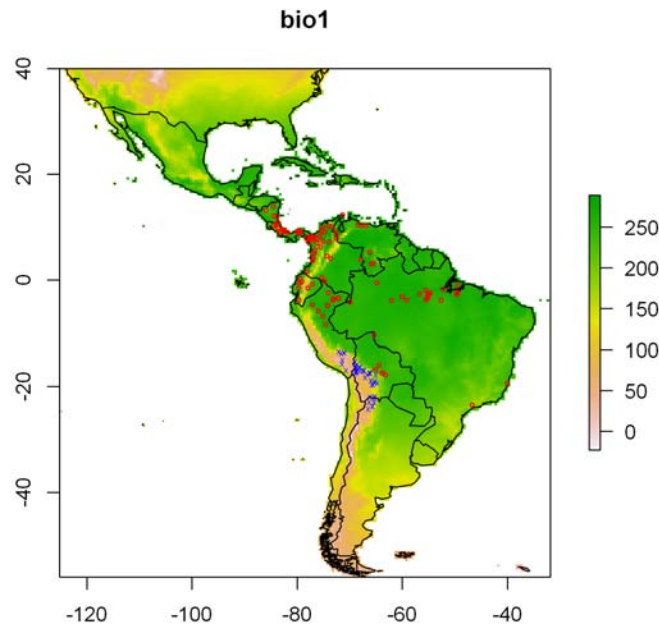
> plot(predictors)

```



We can also make a plot of a single layer in a RasterStack, and plot some additional data on top of it:

```
> plot(predictors, 1)
> plot(wrld_simpl, add=TRUE)
> points(bradypus, col='red', cex=0.5)
> points(acgeo, col='blue', pch='x', cex=0.5)
```



The example above uses data representing 'bioclimatic variables' from the WorldClim database (<http://www.worldclim.org>, Hijmans *et al.*, 2004) and 'terrestrial biome' data from the WWF. (<http://www.worldwildlife.org/science/data/item1875.html>, Olsen *et al.*, 2001). You can go to these websites if you want higher resolution data. You can also use the `getData` function from the `raster` package to download WorldClim climate data.

Predictor variable selection can be important, particularly if the objective of a study is explanation. See, e.g., Austin and Smith (1987), Austin (2002), Mellert *et al.*, (2011). The early applications of species modeling tended to focus on explanation (Elith and Leathwick 2009). Nowadays, the objective of SDM tends to be prediction. For prediction within the same geographic area, variable selection might arguably be relatively less important, but for many prediction tasks (e.g. to new times or places, see below) variable selection is critically important. In all cases it is important to use variables that are relevant to the ecology of the species (rather than with the first data that can be found on the

web!). In some cases it can be useful to develop new, more ecologically relevant, predictor variables from existing data. For example, one could use land cover data and the `focal` function in the `raster` package to create a new variable that indicates how much forest area is available within x km of a grid cell, for a species that might have a home range of x.

## 4.2 Extracting values from rasters

We now have a set of predictor variables (rasters) and occurrence points. The next step is to extract the values of the predictors at the locations of the points. (This step can be skipped for the modeling methods that are implemented in the `dismo` package). This is a very straightforward thing to do using the `'extract'` function from the `raster` package. In the example below we use that function first for the *Bradypus* occurrence points, then for 500 random background points. We combine these into a single `data.frame` in which the first column (variable `'pb'`) indicates whether this is a presence or a background point. `'biome'` is categorical variable (called a `'factor'` in R) and it is important to explicitly define it that way, so that it won't be treated like any other numerical variable.

```
> presvals <- extract(predictors, bradypus)
> backgr <- randomPoints(predictors, 500)
> absvals <- extract(predictors, backgr)
> pb <- c(rep(1, nrow(presvals)), rep(0, nrow(absvals)))
> sdmdata <- data.frame(cbind(pb, rbind(presvals, absvals)))
> sdmdata[, 'biome'] = as.factor(sdmdata[, 'biome'])
> head(sdmdata)
```

	pb	bio1	bio12	bio16	bio17	bio5	bio6	bio7	bio8	biome
1	1	263	1639	724	62	338	191	147	261	1
2	1	263	1639	724	62	338	191	147	261	1
3	1	253	3624	1547	373	329	150	179	271	1
4	1	243	1693	775	186	318	150	168	264	1
5	1	243	1693	775	186	318	150	168	264	1
6	1	252	2501	1081	280	326	154	172	270	1

```
> tail(sdmdata)
```

	pb	bio1	bio12	bio16	bio17	bio5	bio6	bio7	bio8	biome
611	0	256	1208	503	144	315	200	115	255	1
612	0	269	2346	977	115	348	217	130	259	7
613	0	103	29	17	1	188	15	172	75	12
614	0	241	1482	1031	22	339	130	209	254	3
615	0	229	2943	1194	342	294	169	125	224	1
616	0	261	2796	964	322	319	206	113	258	1

```
> summary(sdmdata)
```



pb	bio1	bio12
Min. :0.0000	Min. : 5.0	Min. : 1.0
1st Qu.:0.0000	1st Qu.:178.0	1st Qu.: 739.8
Median :0.0000	Median :241.5	Median :1489.0
Mean :0.1883	Mean :212.2	Mean :1614.6
3rd Qu.:0.0000	3rd Qu.:260.0	3rd Qu.:2259.8
Max. :1.0000	Max. :286.0	Max. :7682.0

bio16	bio17	bio5
Min. : 1.0	Min. : 0.0	Min. : 75.0
1st Qu.: 330.8	1st Qu.: 36.0	1st Qu.:300.0
Median : 626.5	Median : 106.5	Median :318.0
Mean : 654.9	Mean : 166.2	Mean :306.7
3rd Qu.: 916.2	3rd Qu.: 232.0	3rd Qu.:332.0
Max. :2458.0	Max. :1496.0	Max. :405.0

bio6	bio7	bio8
Min. : -177.00	Min. : 60.0	Min. : 3.0
1st Qu.: 48.75	1st Qu.:117.0	1st Qu.:213.0
Median : 157.00	Median :158.5	Median :250.0
Mean : 118.06	Mean :188.6	Mean :224.2
3rd Qu.: 200.00	3rd Qu.:235.0	3rd Qu.:262.0
Max. : 242.00	Max. :449.0	Max. :319.0

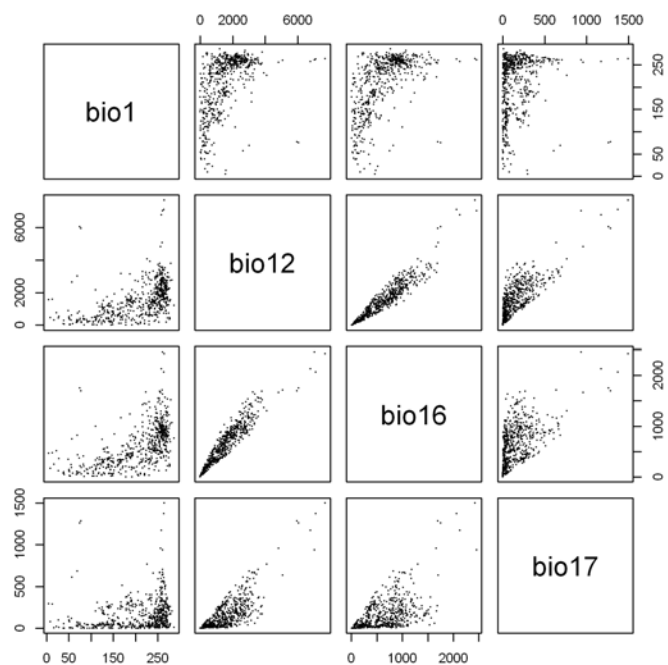
  

biome
1 :281
13 : 77
7 : 60
8 : 53
2 : 42
(Other):102
NA's : 1

There are alternative approaches possible here. For example, one could extract multiple points in a radius as a potential means for dealing with mismatch between location accuracy and grid cell size. If one would make 10 datasets that represent 10 equally valid "samples" of the environment in that radius, that could be then used to fit 10 models and explore the effect of uncertainty in location.

To visually investigate colinearity in the environmental data (at the occurrence points) you can use a pairs plot. See Dormann *et al.* (2011) for a discussion of methods to remove colinearity.

```
> # pairs plot of the values of the climate data
> # at the bradypus occurrence sites.
> pairs(sdmdata[,2:5], cex=0.1, fig=TRUE)
```



## Part II

# Model fitting, prediction, and evaluation

## Chapter 5

# Model fitting

Model fitting is technically quite similar across the modeling methods that exist in R. Most methods take a 'formula' identifying the dependent and independent variables, accompanied with a `data.frame` that holds these variables. Details on specific methods are provided further down on this document, in part III.

A simple formula could look like:  $y \sim x1 + x2 + x3$ , i.e.  $y$  is a function of  $x1$ ,  $x2$ , and  $x3$ . Another example is  $y \sim .$ , which means that  $y$  is a function of all other variables in the `data.frame` provided to the function. See `help('formula')` for more details about the formula syntax. In the example below, the function 'glm' is used to fit generalized linear models. `glm` returns a model object.

```
> m1 = glm(pb ~ bio1 + bio5 + bio12, data=sdmdata)
> class(m1)

[1] "glm" "lm"

> summary(m1)

Call:
glm(formula = pb ~ bio1 + bio5 + bio12, data = sdmdata)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.82681 -0.24010 -0.09947  0.07679  0.86667

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.104e-01  1.021e-01   1.082  0.27959
bio1         1.682e-03  3.840e-04   4.381 1.39e-05 ***
bio5        -1.454e-03  4.538e-04  -3.205  0.00142 **
bio12        1.034e-04  1.564e-05   6.616 8.09e-11 ***
```

```

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 0.1233405)

Null deviance: 94.156  on 615  degrees of freedom
Residual deviance: 75.484  on 612  degrees of freedom
AIC: 464.95

Number of Fisher Scoring iterations: 2

> m2 = glm(pb ~ ., data=sdmdata)
> m2

Call:  glm(formula = pb ~ ., data = sdmdata)

Coefficients:
(Intercept)      bio1      bio12      bio16
  3.026e-01  -1.889e-03   3.147e-04  -4.269e-04
      bio17      bio5      bio6      bio7
 -5.908e-04  -2.029e-04   1.619e-03   9.427e-05
      bio8      biome2      biome3      biome4
  3.565e-04  -1.173e-01  -1.908e-01  -1.647e-01
      biome5      biome7      biome8      biome9
 -9.556e-02  -2.441e-01  -9.018e-02   2.952e-02
      biome10      biome11      biome12      biome13
 -1.145e-01  -3.197e-01  -1.281e-01  -5.218e-02
      biome14
 -2.195e-01

Degrees of Freedom: 614 Total (i.e. Null);  594 Residual
(1 observation deleted due to missingness)
Null Deviance:      94.12
Residual Deviance: 70.15      AIC: 454.1

Models that are implemented in dismo do not use a formula (and most
models only take presence points). For example:

> bc = bioclim(sdmdata[,c('bio1', 'bio5', 'bio12')])
> class(bc)

[1] "Bioclim"
attr(,"package")
[1] "dismo"

> bc

```

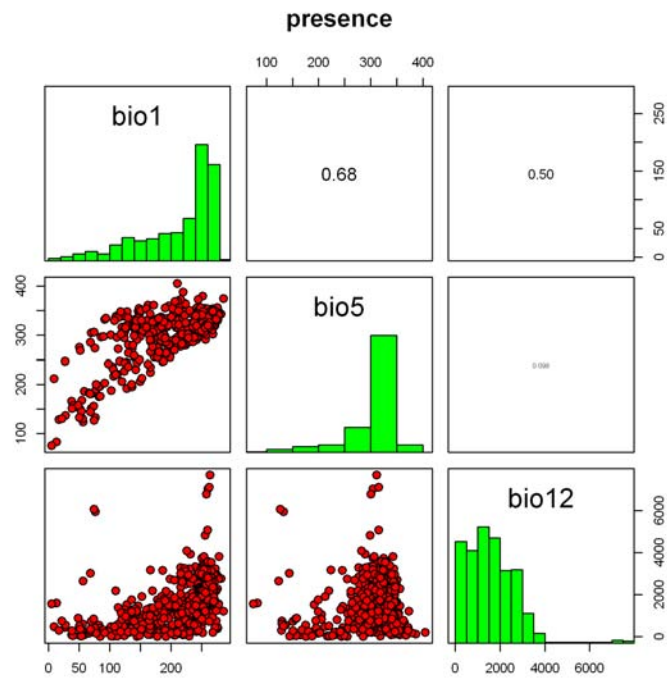
```
class      : Bioclim
```

```
variables: bio1 bio5 bio12
```

```
presence points: 616
```

```
      bio1 bio5 bio12  
1    263  338 1639  
2    263  338 1639  
3    253  329 3624  
4    243  318 1693  
5    243  318 1693  
6    252  326 2501  
7    240  317 1214  
8    275  335 2259  
9    271  327 2212  
10   274  329 2233  
(... ... ...)
```

```
> pairs(bc)
```



## Chapter 6

# Model prediction

Different modeling methods return different type of 'model' objects (typically they have the same name as the modeling method used). All of these 'model' objects, irrespective of their exact class, can be used to with the `predict` function to make predictions for any combination of values of the independent variables. This is illustrated in the example below where we make predictions with the glm model object 'm1' and for bioclim model 'bc', for three records with values for variables bio1, bio5 and bio12 (the variables used in the example above to create the model objects).

```
> bio1 = c(40, 150, 200)
> bio5 = c(60, 115, 290)
> bio12 = c(600, 1600, 1700)
> pd = data.frame(cbind(bio1, bio5, bio12))
> pd
```

	bio1	bio5	bio12
1	40	60	600
2	150	115	1600
3	200	290	1700

```
> predict(m1, pd)
```

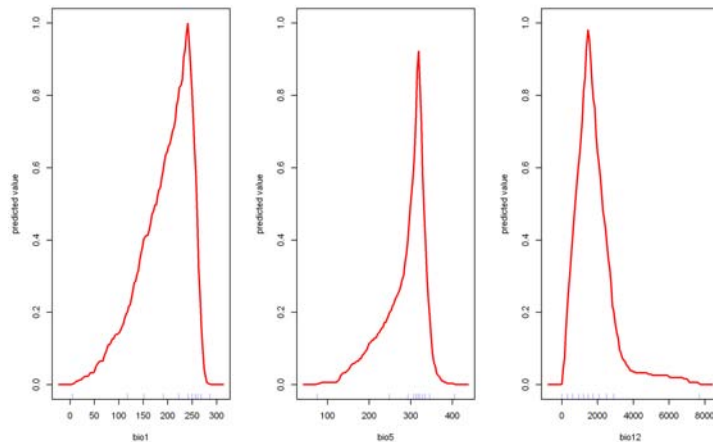
	1	2	3
	0.1525364	0.3610495	0.2010020

```
> predict(bc, pd)
```

```
[1] 0.000000000 0.006493506 0.375000000
```

Making such predictions for a few environments can be very useful to explore and understand model predictions. For example it used in the `response` function that creates response plots for each variable, with the other variables at their median value.

```
> response(bc)
```

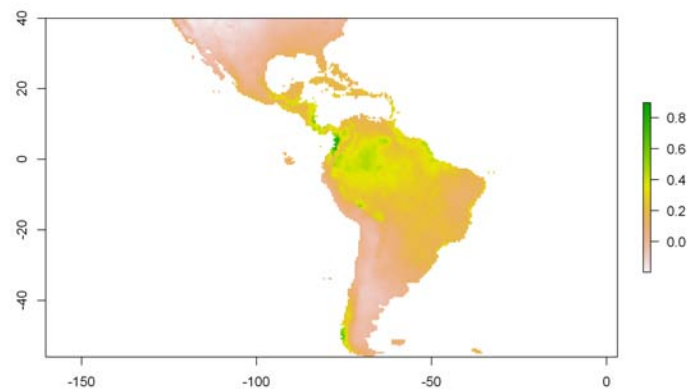


In most cases, however, the purpose is SDM is to create a map of suitability scores. We can do that by providing the predict function with a Raster\* object and a model object. As long as the variable names in the model object are available as layers (layerNames) in the Raster\* object.

```
> layerNames(predictors)
```

```
[1] "bio1" "bio12" "bio16" "bio17" "bio5" "bio6" "bio7"
[8] "bio8" "biome"
```

```
> p <- predict(predictors, m1)
> plot(p)
```





## Chapter 7

# Model evaluation

It is much easier to create a model and make a prediction than to assess how good the model is, and whether it can be used for a specific purpose. Most model types have different measures that can help to assess how good the model fits the data. It is worth becoming familiar with these and understanding their role, because they help you to assess whether there is anything substantially wrong with your model. Most statistics or machine learning texts will provide some details. For instance, for a GLM one can look at how much deviance is explained, whether there are patterns in the residuals, whether there are points with high leverage and so on. However, since many models are to be used for prediction, much evaluation is focused on how well the model predicts to points not used in model training (see following section on data partitioning). Before we start to give some examples of statistics used for this evaluation, it is worth considering what else can be done to evaluate a model. Useful questions include:

- does the model seem sensible, ecologically?
- do the fitted functions (the shapes of the modeled relationships) make sense?
- do the predictions seem reasonable? (map them, and think about them)
- are there any spatial patterns in model residuals? (see Leathwick and Whitehead 2001 for an interesting example)

Most modelers rely on cross-validation. This consists of creating a model with one 'training' data set, and testing it with another data set of known occurrences. Typically, training and testing data are created through random sampling (without replacement) from a single data set. Only in a few cases, e.g. Elith *et al.*, 2006, training and test data are from different sources and pre-defined.

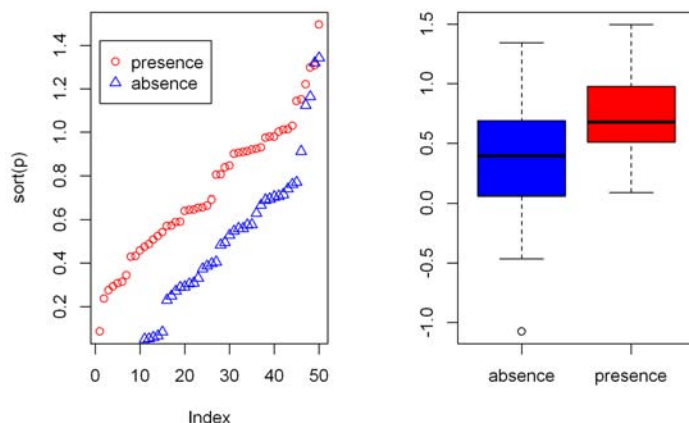
Different measures can be used to evaluate the quality of a prediction (Fielding and Bell, 1997, Liu *et al.*, 2011; and Potts and Elith (2006) for abundance data), perhaps depending on the goal of the study. Many measures for evaluating models based on presence-absence or presence-only data are 'threshold dependent'. That means that a threshold must be set first (e.g., 0.5, though 0.5 is rarely a sensible choice – e.g. see Lui *et al.* 2005). Predicted values above

that threshold indicate a prediction of 'presence', and values below the threshold indicate 'absence'. Some measures emphasize the weight of false absences; others give more weight to false presences.

Much used statistics that are threshold independent are the correlation coefficient and the Area Under the Receiver Operator Curve (AUROC, generally further abbreviated to AUC). AUC is a measure of rank-correlation. In unbiased data, a high AUC indicates that sites with high predicted suitability values tend to be areas of known presence and locations with lower model prediction values tend to be areas where the species is not known to be present (absent or a random point). An AUC score of 0.5 means that the model is as good as a random guess. See Phillips *et al.* (2006) for a discussion on the use of AUC in the context of presence-only rather than presence/absence data.

Here we illustrate the computation of the correlation coefficient and AUC with two random variables. **p** (presence) has higher values, and represents the predicted value for 50 known cases (locations) where the species is present, and **a** (absence) has lower values, and represents the predicted value for 50 known cases (locations) where the species is absent.

```
> p <- rnorm(50, mean=0.7, sd=0.3)
> a <- rnorm(50, mean=0.4, sd=0.4)
> par(mfrow=c(1, 2))
> plot(sort(p), col='red', pch=21)
> points(sort(a), col='blue', pch=24)
> legend(1, 0.95 * max(a,p), c('presence', 'absence'),
+       pch=c(21,24), col=c('red', 'blue'))
> comb = c(p,a)
> group = c(rep('presence', length(p)), rep('absence', length(a)))
> boxplot(comb~group, col=c('blue', 'red'))
```



We created two variables with random normally distributed values, but with different mean and standard deviation. The two variables clearly have different distributions, and the values for 'presence' tend to be higher than for 'absence'. Here is how you can compute the correlation coefficient and the AUC:

```
> group = c(rep(1, length(p)), rep(0, length(a)))
> cor.test(comb, group)$estimate

      cor
0.4259716

> mv <- wilcox.test(p,a)
> auc <- as.numeric(mv$statistic) / (length(p) * length(a))
> auc

[1] 0.7428
```

Below we show how you can compute these, and other statistics more conveniently, with the `evaluate` function in the `dismo` package. See `?evaluate` for info on additional evaluation measures that are available. ROC/AUC can also be computed with the `ROCR` package.

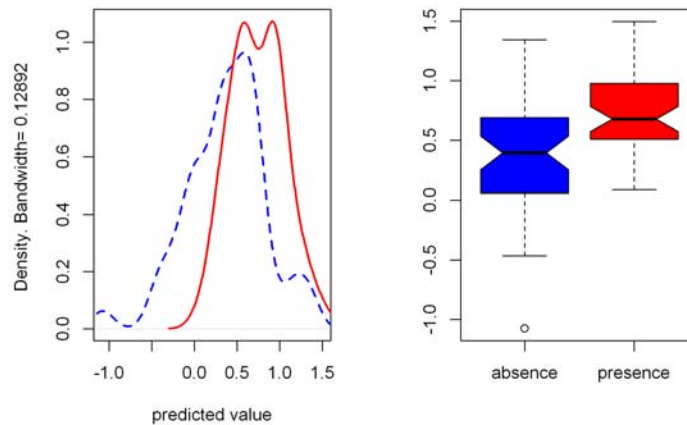
```
> e = evaluate(p=p, a=a)
> class(e)

[1] "ModelEvaluation"
attr(,"package")
[1] "dismo"

> e

class           : ModelEvaluation
n presences     : 50
n absences      : 50
AUC              : 0.7428
cor             : 0.4259716
max TPR+TNR at : 0.4288114

> par(mfrow=c(1, 2))
> density(e)
> boxplot(e, col=c('blue', 'red'))
```

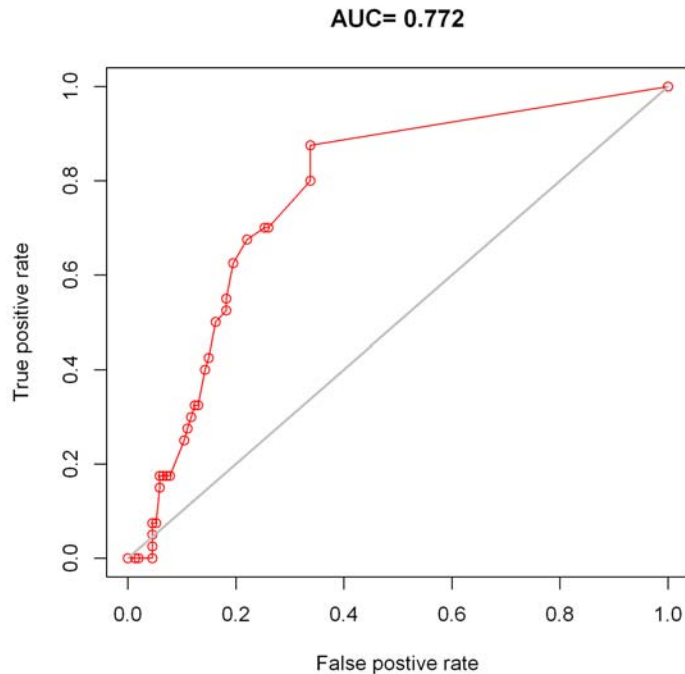


Now back to some real data, presence-only in this case. We'll divide the data in two random sets, one for training a Bioclim model, and one for evaluating the model.

```
> rand <- round(0.75 * runif(nrow(sdmdata)))
> traindata <- sdmdata[rand==0,]
> traindata <- traindata[traindata[,1] == 1, 2:9]
> testdata <- sdmdata[rand==1,]
> bc <- bioclim(traindata)
> e <- evaluate(testdata[testdata==1,], testdata[testdata==0,], bc)
> e

class          : ModelEvaluation
n presences    : 30
n absences     : 168
AUC            : 0.8202381
cor            : 0.3169584
max TPR+TNR at : 0.03478372

> plot(e, 'ROC')
```



In real projects, you would want to use *k-fold* data partitioning instead of a single random sample. The `dismo` function `kfold` facilitates that type of data partitioning. It creates a vector that assigns each row in the data matrix to a group (between 1 to *k*).

Let's first create presence and background data.

```
> pres <- sdmdata[sdmdata[,1] == 1, 2:9]
> back <- sdmdata[sdmdata[,1] == 0, 2:9]
```

The background data will only be used for model testing and does not need to be partitioned. We now partition the data into 5 groups.

```
> k <- 5
> group <- kfold(pres, k)
> group[1:10]

[1] 4 2 3 1 5 3 2 5 5 1

> unique(group)

[1] 4 2 3 1 5
```

Now we can fit and test our model five times. In each run, the records corresponding to one of the five groups is only used to evaluate the model, while the other four groups are only used to fit the model. The results are stored in a list called 'e'.

```

> e <- list()
> for (i in 1:k) {
+   train <- pres[group != i,]
+   test <- pres[group == i,]
+   bc <- bioclim(train)
+   e[[i]] <- evaluate(p=test, a=back, bc)
+ }

```

We can extract several things from the objects in 'e', but let's restrict ourselves to the AUC values and the "maximum of the sum of the sensitivity (true positive rate) and specificity (true negative rate)" (this is sometimes used as a threshold for setting cells to presence or absence).

```

> auc <- sapply( e, function(x){slot(x, 'auc')} )
> auc

[1] 0.8070435 0.8378696 0.7332500 0.7101304 0.7925652

> mean(auc)

[1] 0.7761717

> sapply( e, function(x){ x@t[which.max(x@TPR + x@TNR)] } )

[1] 0.03215806 0.08592151 0.01076957 0.01065269 0.06441613

```

The use of AUC in evaluating SDMs has been criticized (Lobo et al. 2008, Jiménez-Valverde 2011). A particularly sticky problem is that the values of AUC vary with the spatial extent used to select background points. Generally, the larger that extent, the higher the AUC value. Therefore, AUC values are generally biased and cannot be directly compared. Hijmans (2011) suggested that one could remove "spatial sorting bias" (the difference between the distance from testing-presence to training-presence and testing-absence to training-absence points) through "point-wise distance sampling".

```

> nr <- nrow(bradypus)
> s <- sample(nr, 0.25 * nr)
> pres_train <- bradypus[-s, ]
> pres_test <- bradypus[s, ]
> nr <- nrow(backgr)
> s <- sample(nr, 0.25 * nr)
> back_train <- backgr[-s, ]
> back_test <- backgr[s, ]

> sb <- ssb(pres_test, back_test, pres_train)
> sb[,1] / sb[,2]

[1] 0.1040448

```

$sb[1] / sb[2]$  is an indicator of spatial sorting bias (SSB). If there is no SSB this value should be 1, in these data it is close to zero, indicating that SSB is very strong. Let's create a subsample in which SSB is removed.

```
> i <- pwdSample(pres_test, back_test, pres_train, n=1, tr=0.1)
> pres_test_pwd <- pres_test[!is.na(i[,1]), ]
> back_test_pwd <- back_test[na.omit(as.vector(i)), ]
> sb2 <- ssb(pres_test_pwd, back_test_pwd, pres_train)
> sb2[1]/ sb2[2]

[1] 0.9987177
```

Spatial sorting bias is much reduced now; notice how the AUC dropped!

```
> bc <- bioclim(predictors, pres_train)
> evaluate(bc, p=pres_test, a=back_test, x=predictors)

class          : ModelEvaluation
n presences    : 29
n absences     : 125
AUC            : 0.6917241
cor            : 0.2043
max TPR+TNR at : 0.03438276

> evaluate(bc, p=pres_test_pwd, a=back_test_pwd, x=predictors)

class          : ModelEvaluation
n presences    : 17
n absences     : 17
AUC            : 0.3823529
cor            : -0.1501684
max TPR+TNR at : 0.2642678
```

**Part III**

**Modeling methods**



## Chapter 8

# Types of algorithms & data used in examples

A large number of algorithms has been used in species distribution modeling. They can be classified as 'profile', 'regression', and 'machine learning' methods. Profile methods only consider 'presence' data, not absence or background data. Regression and machine learning methods use both presence and absence or background data. The distinction between regression and machine learning methods is not sharp, but it is perhaps still useful as way to classify models. Another distinction that one can make is between presence-only and presence-absence models. Profile methods are always presence-only, other methods can be either, depending if they are used with survey-absence or with pseudo-absence/background data. An entirely different class of models consists of models that only, or primarily, use the geographic location of known occurrences, and do not rely on the values of predictor variables at these locations. We refer to these models as 'geographic models'. Below we discuss examples of these different types of models.

We will use the same data to illustrate all models, except that some models cannot use categorical variables. So for those models we drop the categorical variables from the predictors stack.

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

We'll use the *Bradypus* data for presence of a species. Let's make a training and a testing set.

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

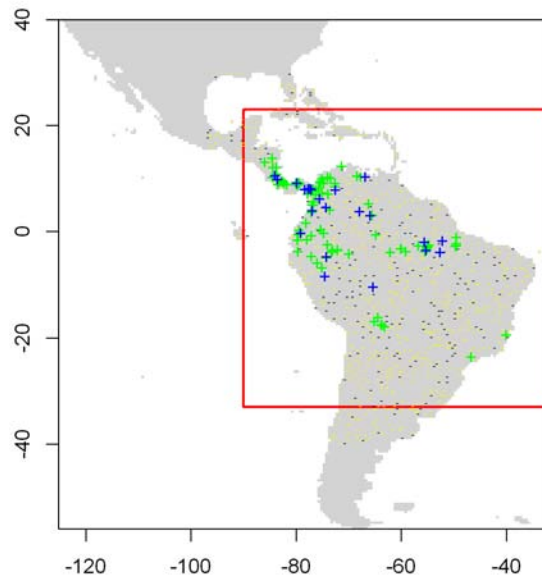
To speed up processing, let's restrict the predictions to a more restricted area (defined by a rectangular extent):

```
> ext = extent(-90, -32, -33, 23)
```

Background data for training and a testing set. The first layer in the Raster-Stack is used as a 'mask'. That ensures that random points only occur within the spatial extent of the rasters, and within cells that are not NA, and that there is only a single absence point per cell. Here we further restrict the background points to be within 12.5% of our specified extent 'ext'.

```
> backg <- randomPoints(pred_nf, n=1000, ext=ext, extf = 1.25)
> colnames(backg) = c('lon', 'lat')
> group <- kfold(backg, 5)
> backg_train <- backg[group != 1, ]
> backg_test <- backg[group == 1, ]

> 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, pch='-', cex=0.5, col='yellow')
> points(backg_test, pch='-', cex=0.5, col='black')
> points(pred_train, pch='+', col='green')
> points(pred_test, pch='+', col='blue')
```



## Chapter 9

# Profile methods

The three methods described here, Bioclim, Domain, and Mahal. These methods are implemented in the `dismo` package, and the procedures to use these models are the same for all three.

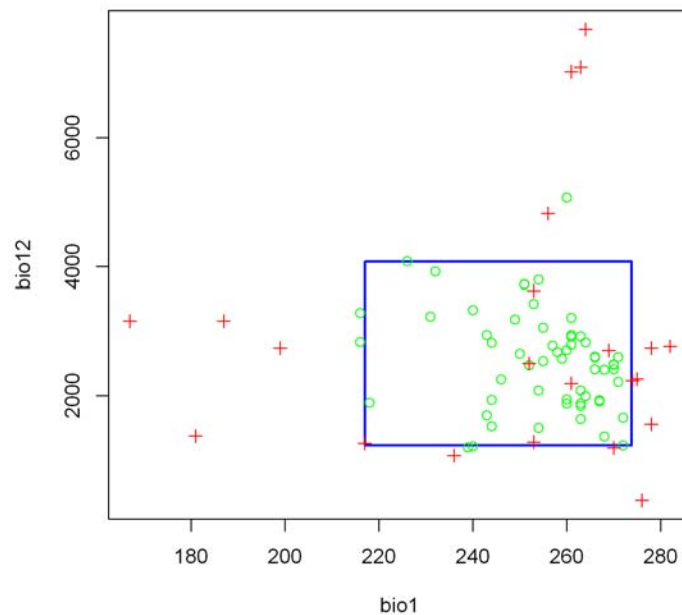
### 9.1 Bioclim

The BIOCLIM algorithm has been extensively used for species distribution modeling. BIOCLIM is a classic 'climate-envelope-model'. Although it generally does not perform as good as some other modeling methods (Elith *et al.* 2006), particularly in the context of climate change (Hijmans and Graham, 2006), it is still used, among other reasons because the algorithm is easy to understand and thus useful in teaching species distribution modeling. The BIOCLIM algorithm computes the similarity of a location by comparing the values of environmental variables at any location to a percentile distribution of the values at known locations of occurrence ('training sites'). The closer to the 50th percentile (the median), the more suitable the location is. The tails of the distribution are not distinguished, that is, 10 percentile is treated as equivalent to 90 percentile. In the 'dismo' implementation, the values of the upper tail values are transformed to the lower tail, and the minimum percentile score across all the environmental variables is used (i.e., BIOCLIM uses an approach like Liebig's law of the minimum). This value is subtracted from 1 and then multiplied with two so that the results are between 0 and 1. The reason for scaling this way is that the results become more like that of other distribution modeling methods and are thus easier to interpret. The value 1 will rarely be observed as it would require a location that has the median value of the training data for all the variables considered. The value 0 is very common as it is assigned to all cells with a value of an environmental variable that is outside the percentile distribution (the range of the training data) for at least one of the variables.

Earlier on, we fitted a Bioclim model using `data.frame` with each row representing the environmental data at known sites of presence of a species. Here we

fit a bioclim model simply using the predictors and the occurrence points (the function will do the extracting for us).

```
> bc <- bioclim(pred_nf, pres_train)
> plot(bc, a=1, b=2, p=0.85)
```



We evaluate the model in a similar way, by providing presence and background (absence) points, the model, and a RasterStack:

```
> e <- evaluate(pres_test, backg_test, bc, pred_nf)
> e
```

```
class          : ModelEvaluation
n presences    : 23
n absences     : 200
AUC            : 0.7209783
cor            : 0.1589782
max TPR+TNR at : 0.04291075
```

And we use the RasterStack with predictor variables to make a prediction to a RasterLayer:

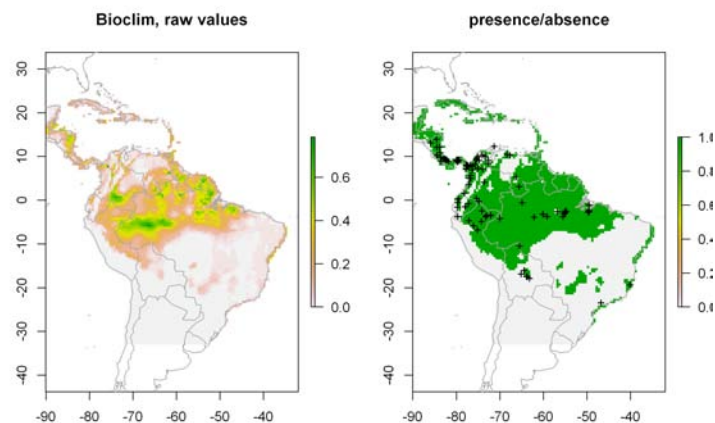
```
> pb <- predict(pred_nf, bc, ext=ext, progress='')
> pb
```

```

class      : RasterLayer
dimensions : 112, 116, 12992 (nrow, ncol, ncell)
resolution : 0.5, 0.5 (x, y)
extent     : -90, -32, -33, 23 (xmin, xmax, ymin, ymax)
coord. ref.: +proj=longlat +datum=WGS84 +ellps=WGS84 +towgs84=0,0,0
values     : in memory
min value  : 0
max value  : 0.7849462

> par(mfrow=c(1,2))
> plot(pb, main='Bioclim, raw values')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> threshold <- e@t[which.max(e@TPR + e@TNR)]
> plot(pb > threshold, main='presence/absence')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> points(pres_train, pch='+')

```



Please note the order of the arguments in the `predict` function. In the example above, we used `predict(pred_nf, bc)` (first the `RasterStack`, then the model object), which is little bit less efficient than `predict(bc, pred_nf)` (first the model, then the `RasterStack`). The reason for using the order we have used, is that this will work for all models, whereas the other option only works for the models defined in the `dismo` package, such as `Bioclim`, `Domain`, and `Maxent`, but not for models defined in other packages (random forest, boosted regression trees, glm, etc.).

## 9.2 Domain

The `Domain` algorithm (Carpenter *et al.* 1993) has been extensively used for species distribution modeling. It did not perform very well in a model

comparison (Elith *et al.* 2006) and very poorly when assessing climate change effects (Hijmans and Graham, 2006). The Domain algorithm computes the Gower distance between environmental variables at any location and those at any of the known locations of occurrence ('training sites').

The distance between the environment at point A and those of the known occurrences for a single climate variable is calculated as the absolute difference in the values of that variable divided by the range of the variable across all known occurrence points (i.e., the distance is scaled by the range of observations). For each variable the minimum distance between a site and any of the training points is taken. The Gower distance is then the mean of these distances over all environmental variables. The algorithm assigns to a place the distance to the closest known occurrence (in environmental space).

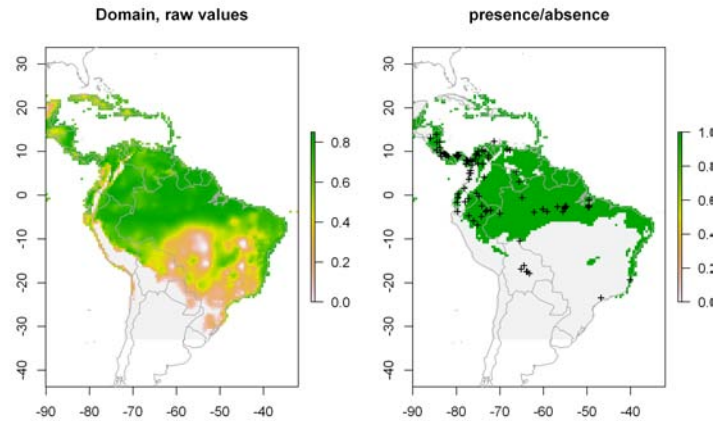
To integrate over environmental variables, the distance to any of the variables is used. This distance is subtracted from one, and (in this R implementation) values below zero are truncated so that the scores are between 0 (low) and 1 (high).

Below we fit a domain model, evaluate it, and make a prediction. We map the prediction, as well as a map subjectively classified into presence / absence.

```
> dm <- domain(pred_nf, pres_train)
> e <- evaluate(pres_test, backg_test, dm, pred_nf)
> e

class           : ModelEvaluation
n presences     : 23
n absences      : 200
AUC              : 0.7367391
cor              : 0.2445056
max TPR+TNR at  : 0.6591056

> pd = predict(pred_nf, dm, ext=ext, progress='')
> par(mfrow=c(1,2))
> plot(pd, main='Domain, raw values')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> threshold <- e@t[which.max(e@TPR + e@TNR)]
> plot(pd > threshold, main='presence/absence')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> points(pres_train, pch='+')
```



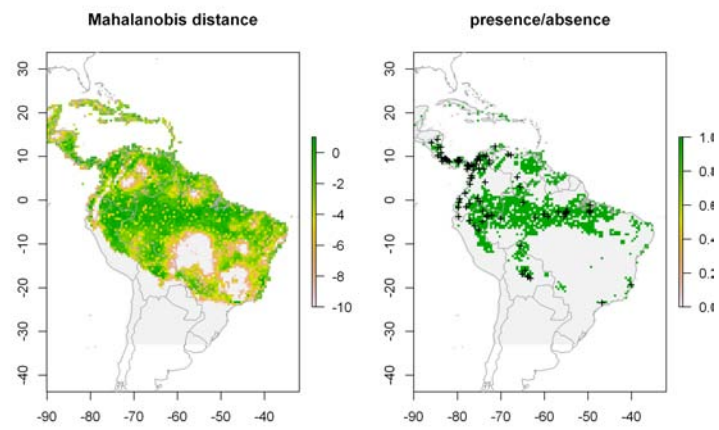
### 9.3 Mahalanobis

The `mahal` function implements a species distribution model based on the Mahalanobis distance (Mahalanobis, 1936). Mahalanobis distance takes into account the correlations of the variables in the data set, and it is not dependent on the scale of measurements.

```
> mm <- mahal(pred_nf, pres_train)
> e <- evaluate(pres_test, backg_test, mm, pred_nf)
> e

class          : ModelEvaluation
n presences    : 23
n absences     : 200
AUC            : 0.838587
cor            : 0.1310426
max TPR+TNR at : -1.058378

> pm = predict(pred_nf, mm, ext=ext, progress='')
> par(mfrow=c(1,2))
> pm[pm < -10] <- -10
> plot(pm, main='Mahalanobis distance')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> threshold <- e@t[which.max(e@TPR + e@TNR)]
> plot(pm > threshold, main='presence/absence')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> points(pres_train, pch='+')
```





## Chapter 10

# Regression models

The remaining models need to be fit presence textifand absence (background) data. With the exception of 'maxent', we cannot fit the model with a Raster-Stack and points. Instead, we need to extract the environmental data values ourselves, and fit the models with these values.

```
> 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)
```

	pa	bio1	bio12	bio16	bio17	bio5	bio6	bio7	bio8	biome
1	1	263	1639	724	62	338	191	147	261	1
2	1	253	3624	1547	373	329	150	179	271	1
3	1	243	1693	775	186	318	150	168	264	1
4	1	243	1693	775	186	318	150	168	264	1
5	1	252	2501	1081	280	326	154	172	270	1
6	1	240	1214	516	146	317	150	168	261	2

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

### 10.1 Generalized Linear Models

A generalized linear model (GLM) is a generalization of ordinary least squares regression. Models are fit using maximum likelihood and by allowing the linear model to be related to the response variable via a link function and by allowing the magnitude of the variance of each measurement to be a function of its

predicted value. Depending on how a GLM is specified it can be equivalent to (multiple) linear regression, logistic regression or Poisson regression. See Guisan *et al* (2002) for an overview of the use of GLM in species distribution modeling.

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")
```

Here we fit two basic glm models. All variables are used, but without interaction terms.

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

Call:

```
glm(formula = pa ~ bio1 + bio5 + bio6 + bio7 + bio8 + bio12 +
    bio16 + bio17, family = binomial(link = "logit"), data = envtrain)
```

Deviance Residuals:

	Min	1Q	Median	3Q	Max
	-1.67389	-0.47627	-0.24289	-0.04145	2.73857

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	1.6609816	1.8232604	0.911	0.362298
bio1	0.1007418	0.0561639	1.794	0.072859 .
bio5	0.1432002	0.2608487	0.549	0.583021
bio6	-0.2528950	0.2607172	-0.970	0.332048
bio7	-0.2418984	0.2598453	-0.931	0.351888
bio8	0.0110994	0.0246434	0.450	0.652421
bio12	0.0020291	0.0006768	2.998	0.002718 **
bio16	-0.0018960	0.0014029	-1.351	0.176557
bio17	-0.0052624	0.0015772	-3.336	0.000849 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 596.69 on 892 degrees of freedom  
Residual deviance: 439.41 on 884 degrees of freedom  
AIC: 457.41

Number of Fisher Scoring iterations: 8

```
> coef(gm1)
```

```

(Intercept)      bio1      bio5      bio6
1.660981573 0.100741766 0.143200190 -0.252894973
      bio7      bio8      bio12      bio16
-0.241898406 0.011099417 0.002029095 -0.001895976
      bio17
-0.005262384

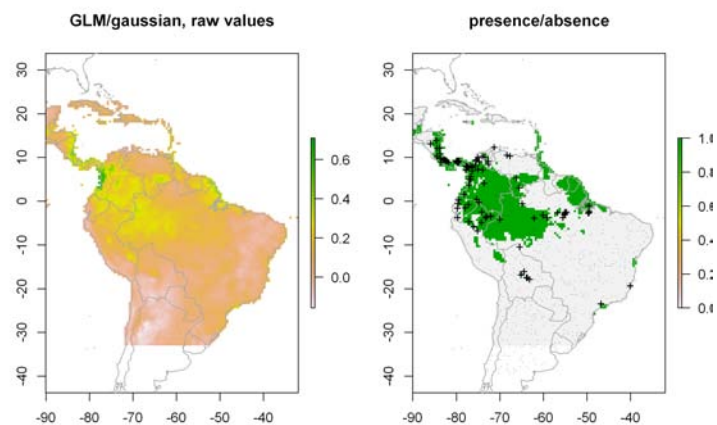
> gm2 <- glm(pa ~ bio1+bio5 + bio6 + bio7 + bio8 + bio12 + bio16 + bio17,
+           family = gaussian(link = "identity"), data=envtrain)
> evaluate(testpres, testbackg, gm1)

class          : ModelEvaluation
n presences    : 23
n absences     : 200
AUC            : 0.8325
cor            : 0.2966887
max TPR+TNR at : -2.780695

> e2 <- 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')
> threshold <- e2@t[which.max(e2@TPR + e2@TNR)]
> plot(pg > threshold, main='presence/absence')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> points(pres_train, pch='+')
> points(backg_train, pch='-', cex=0.25)

```



## 10.2 Generalized Additive Models

Generalized additive models (GAMs; Hastie and Tibshirani, 1990; Wood, 2006) are an extension to GLMs. In GAMs, the linear predictor is the sum of smoothing functions. This makes GAMs very flexible, and they can fit very complex functions. It also makes them very similar to machine learning methods. In R, GAMs are implemented in the 'mgcv' package.

## Chapter 11

# Machine learning methods

There is a variety of machine learning (sometimes referred to data mining) methods in R. For a long time there have been packages to do Artificial Neural Networks (ANN) and Classification and Regression Trees (CART). More recent methods include Random Forests, Boosted Regression Trees, and Support Vector Machines. Through the *dismo* package you can also use the Maxent program, that implements the most widely used method (maxent) in species distribution modeling. Breiman (2001a) provides a accessible introduction to machine learning, and how it contrasts with 'classical statistics' (model based probabilistic inference). Hastie *et al.*, 2009 provide what is probably the most extensive overview of these methods.

All the model fitting methods discussed here can be tuned in several ways. We do not explore that here, and only show the general approach. If you want to use one of the methods, then you should consult the R help pages (and other sources) to find out how to best implement the model fitting procedure.

### 11.1 Maxent

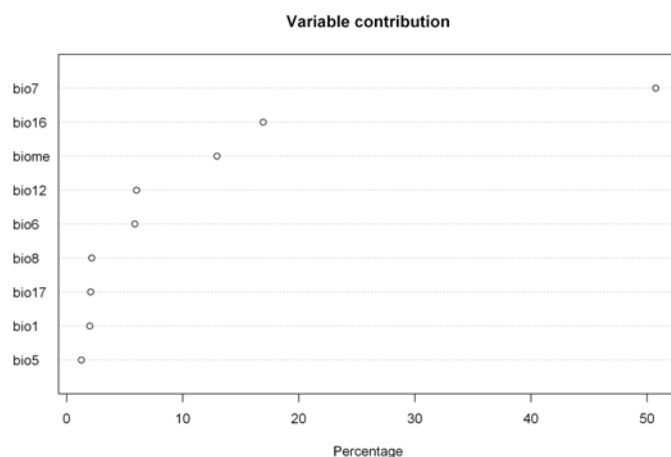
MaxEnt (Maximum Entropy; Phillips *et al.*, 2004, 2006) is the most widely used SDM algorithm. Elith *et al.*, 2010,) provide an explanation of the algorithm (and software) geared towards ecologists. MaxEnt is available as a stand-alone Java program. *Dismo* has a function 'maxent' that communicates with this program. To use it you must first download the program from <http://www.cs.princeton.edu/~schapire/maxent/>. Put the file 'maxent.jar' in the 'java' folder of the 'dismo' package. That is the folder returned by `system.file("java", package="dismo")`. Please note that this program (`maxent.jar`) cannot be redistributed or used for commercial purposes.

Because MaxEnt is implemented in *dismo* you can fit it like the profile methods (e.g. Bioclim). That is, you can provide presence points and a RasterStack. However, you can also first fit a model, like with the other methods such as glm. But in the case of MaxEnt you cannot use the formula notation.

```

> # checking if the jar file is present. If not, skip this bit
> jar <- paste(system.file(package="dismo"), "/java/maxent.jar", sep='')
> if (file.exists(jar)) {
+     xm <- maxent(predictors, pres_train, factors='biome')
+     plot(xm)
+ } else {
+     cat('cannot run this example because maxent is not available')
+     plot(1)
+ }

```

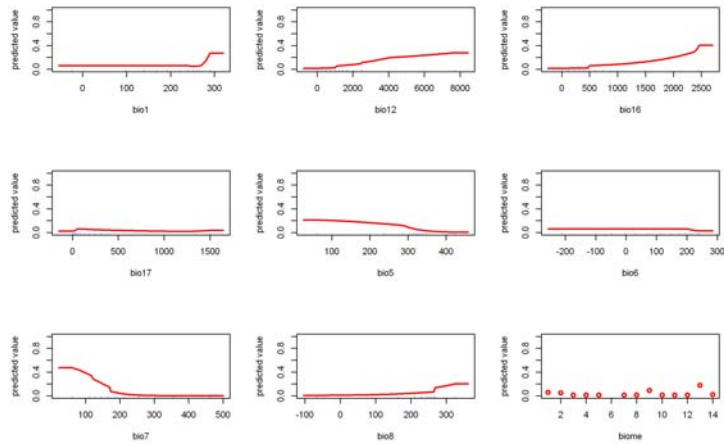


A response plot:

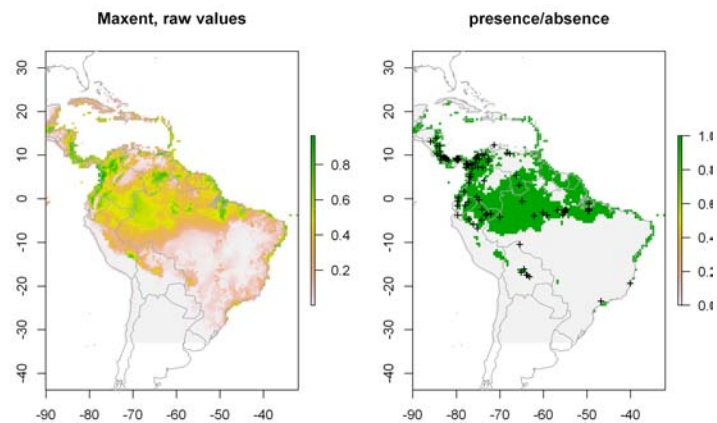
```

> # checking if the jar file is present. If not, skip this bit
> jar <- paste(system.file(package="dismo"), "/java/maxent.jar", sep='')
> if (file.exists(jar)) {
+     response(xm)
+ } else {
+     cat('cannot run this example because maxent is not available')
+     plot(1)
+ }

```



```
> if (file.exists(jar)) {
+   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')
+   threshold <- e@t[which.max(e@TPR + e@TNR)]
+   plot(px > threshold, main='presence/absence')
+   plot(wrld_simpl, add=TRUE, border='dark grey')
+   points(pres_train, pch='+')
+ } else {
+   plot(1)
+ }
```



## 11.2 Boosted Regression Trees

Boosted Regression Trees (BRT) is, unfortunately, known by a large number of different names. It was developed by Friedman (2001), who referred to it as a "Gradient Boosting Machine" (GBM). It is also known as "Gradient Boost", "Stochastic Gradient Boosting", "Gradient Tree Boosting". The method is implemented in the 'gbm' package in R.

The article by Elith, Leathwick and Hastie (2009) describes the use of BRT in the context of species distribution modeling. Their article is accompanied by a number of R functions and a tutorial that have been slightly adjusted and incorporated into the 'dismo' package. These functions extend the functions in the 'gbm' package, with the goal to make these easier to apply to ecological data, and to enhance interpretation. The adapted tutorial is available as a vignette to the dismo package. You can access it via the index of the help pages, or with this command: `vignette('gbm', 'dismo')`

## 11.3 Random Forest

The Random Forest (Breiman, 2001b) method is an extension of Classification and regression trees (CART; Breiman *et al.*, 1984). In R it is implemented in the function 'randomForest' in a package with the same name. The function randomForest can take a formula or, in two separate arguments, a data.frame with the predictor variables, and a vector with the response. If the response variable is a factor (categorical), randomForest will do classification, otherwise it will do regression. Whereas with species distribution modeling we are often interested in classification (species is present or not), it is my experience that using regression provides better results. rf1 does regression, rf2 and rf3 do classification (they are exactly the same models). See the function tuneRF for optimizing the model fitting procedure.

```
> library(randomForest)
> model <- pa ~ bio1 + bio5 + bio6 + bio7 + bio8 + bio12 + bio16 + bio17
> rf1 <- randomForest(model, data=envtrain)
> model <- factor(pa) ~ bio1 + bio5 + bio6 + bio7 + bio8 + bio12 + bio16 + bio17
> rf2 <- randomForest(model, data=envtrain)
> rf3 <- randomForest(envtrain[,1:8], factor(pb_train))
> e = evaluate(testpres, testbackg, rf1)
> e

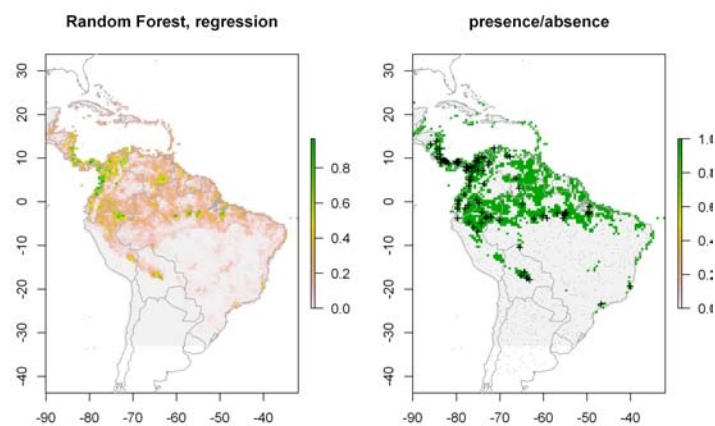
class           : ModelEvaluation
n presences     : 23
n absences      : 200
AUC             : 0.8609783
cor             : 0.4716929
max TPR+TNR at : 0.0773
```



```

> pr <- predict(predictors, rf1, ext=ext)
> par(mfrow=c(1,2))
> plot(pr, main='Random Forest, regression')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> threshold <- e@t[which.max(e@TPR + e@TNR)]
> plot(pr > threshold, main='presence/absence')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> points(pres_train, pch='+')
> points(backg_train, pch='-', cex=0.25)

```



## 11.4 Support Vector Machines

Support Vector Machines (SVMs; Vapnik, 1998) apply a simple linear method to the data but in a high-dimensional feature space non-linearly related to the input space, but in practice, it does not involve any computations in that high-dimensional space. This simplicity combined with state of the art performance on many learning problems (classification, regression, and novelty detection) has contributed to the popularity of the SVM (Karatzoglou *et al.*, 2006). They were first used in species distribution modeling by Guo *et al.* (2005).

There are a number of implementations of svm in R. The most useful implementations in our context are probably function 'ksvm' in package 'kernlab' and the 'svm' function in package 'e1071'. 'ksvm' includes many different SVM formulations and kernels and provides useful options and features like a method for plotting, but it lacks a proper model selection tool. The 'svm' function in package 'e1071' includes a model selection tool: the 'tune' function (Karatzoglou *et al.*, 2006)

```

> library(kernlab)
> svm <- ksvm(pa ~ bio1+bio5+bio6+bio7+bio8+bio12+bio16+bio17, data=envtrain)

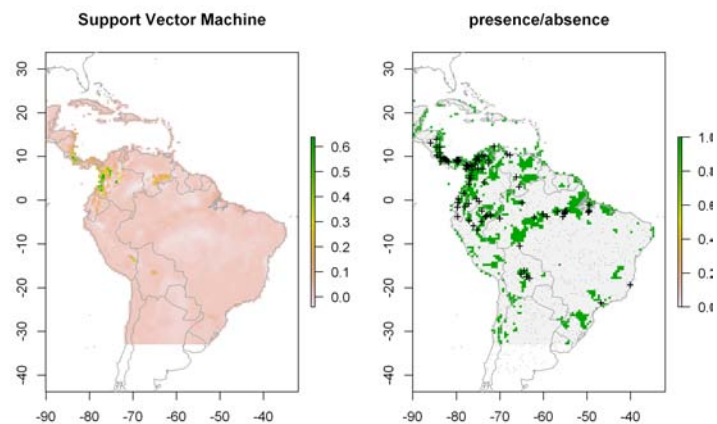
```

Using automatic sigma estimation (sigest) for RBF or laplace kernel

```
> e <- evaluate(testpres, testbackg, svm)
> e

class          : ModelEvaluation
n presences    : 23
n absences     : 200
AUC            : 0.7251087
cor            : 0.3750896
max TPR+TNR at : 0.03088595

> ps <- predict(predictors, svm, ext=ext)
> par(mfrow=c(1,2))
> plot(ps, main='Support Vector Machine')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> threshold <- e@t[which.max(e@TPR + e@TNR)]
> plot(ps > threshold, main='presence/absence')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> points(pres_train, pch='+')
> points(backg_train, pch='-', cex=0.25)
```



## Chapter 12

# Geographic models

The 'geographic models' described here are not commonly used in species distribution modeling. They use the geographic location of known occurrences, and do not rely on the values of predictor variables at these locations. We are exploring their use in comparing and contrasting them with the other approaches (Bahn and McGill, 2007); in model evaluation as null-models (Hijmans 2011); to sample background points; and generally to help think about the duality between geographic and environmental space (Colwell and Rangel, 2009). Below we show examples of these different types of models.

### 12.1 Geographic Distance

Simple model based on the assumption that the closer to a known presence point, the more likely it is to find the species.

```
> # 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(seamask, distm, mask=TRUE)
> e <- evaluate(distm, p=pres_test, a=backg_test, tr=quantile(ds, c(1:50/50)))
> e

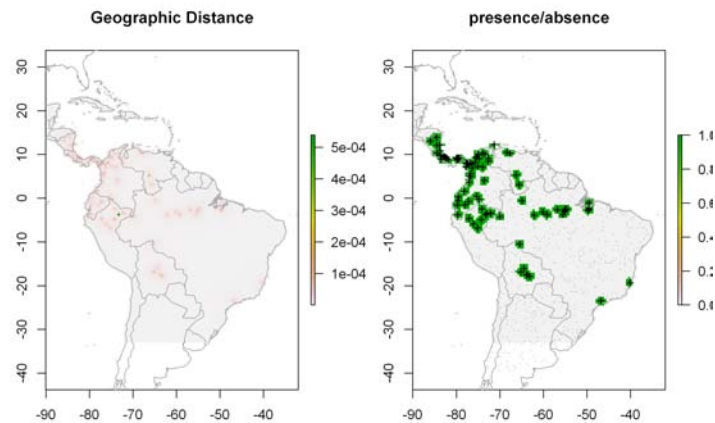
class          : ModelEvaluation
n presences    : 23
n absences     : 200
AUC            : 0.9286957
cor            : 0.429343
max TPR+TNR at : 8.117192e-06

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

```

> plot(wrld_simpl, add=TRUE, border='dark grey')
> threshold <- e@t[which.max(e@TPR + e@TNR)]
> plot(ds > threshold, main='presence/absence')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> points(pres_train, pch='+')
> points(backg_train, pch='-', cex=0.25)

```



## 12.2 Convex hulls

This model draws a convex hull around all 'presence' points.

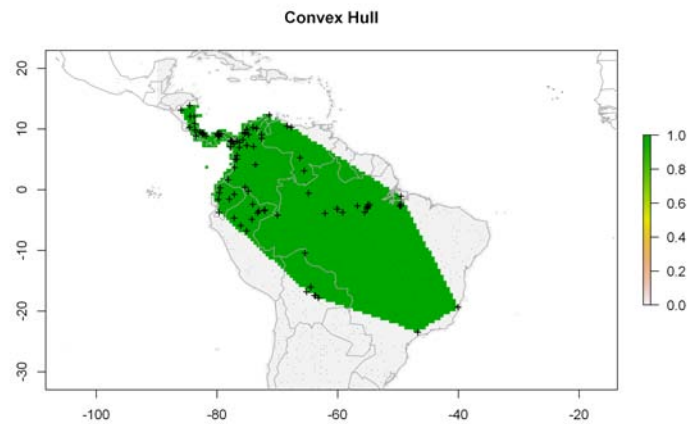
```

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

class          : ModelEvaluation
n presences    : 23
n absences     : 200
AUC            : 0.7115217
cor            : 0.2579133
max TPR+TNR at : 0.9999

> 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)

```



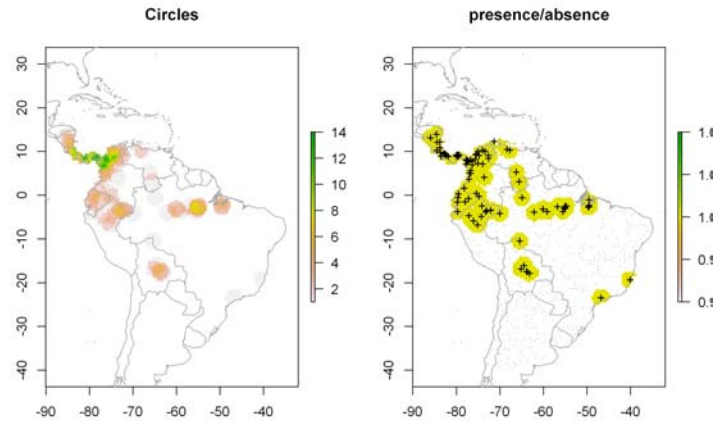
## 12.3 Circles

This model draws circles around all 'presence' points.

```
> circ <- circles(pres_train, lonlat=TRUE)
> pc <- predict(seamask, circ, mask=TRUE)
> e <- evaluate(circ, p=pres_test, a=backg_test, tr=quantile(ds, c(1:50/50)))
> e
```

```
class          : ModelEvaluation
n presences    : 23
n absences     : 200
AUC            : 0.8855435
cor            : 0.6063209
max TPR+TNR at : 6.537932e-07
```

```
> par(mfrow=c(1,2))
> plot(pc, main='Circles')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> threshold <- e@t[which.max(e@TPR + e@TNR)]
> plot(pc > threshold, main='presence/absence')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> points(pres_train, pch='+')
> points(backg_train, pch='-', cex=0.25)
```



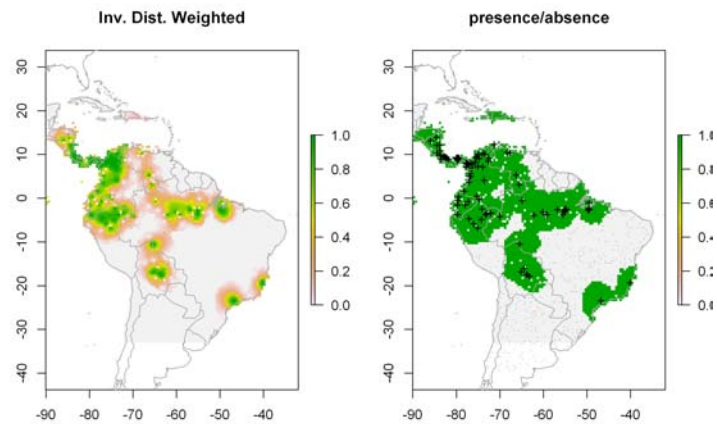
## 12.4 Presence/absence

Spatial-only models for presence/background (or absence) data are also available through functions `geoIDW`, `voronoiHull`, and general geostatistical methods such as indicator kriging (available in the `gstat` package).

```
> idwm <- geoIDW(p=pres_train, a=data.frame(back_train))
> e <- evaluate(idwm, p=pres_test, a=backg_test, tr=quantile(ds, c(1:50/50)))
> e
```

```
class          : ModelEvaluation
n presences    : 23
n absences     : 200
AUC            : 0.9223913
cor            : 0.5576616
max TPR+TNR at : 6.537932e-07
```

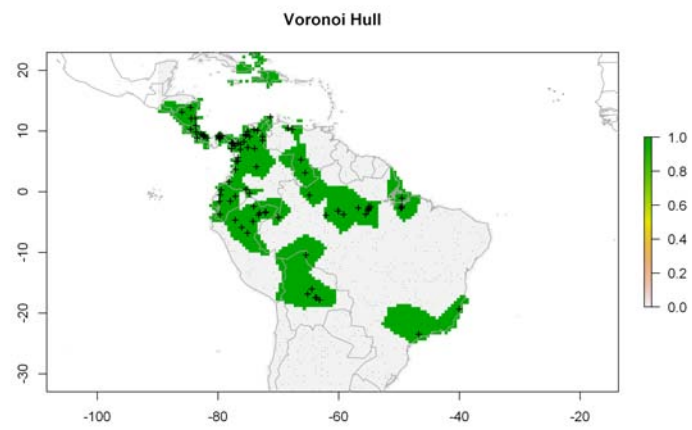
```
> iw <- predict(seamask, idwm, mask=TRUE)
> par(mfrow=c(1,2))
> plot(iw, main='Inv. Dist. Weighted')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> threshold <- e@t[which.max(e@TPR + e@TNR)]
> pa <- mask(iw > threshold, seamask)
> plot(pa, main='presence/absence')
> plot(wrld_simpl, add=TRUE, border='dark grey')
> points(pres_train, pch='+')
> points(backg_train, pch='-', cex=0.25)
```



```
> # take a smallish sample of the background training data
> va <- data.frame(back_train[sample(nrow(back_train), 100), ])
> vorm <- voronoiHull(p=pres_train, a=va)
> e <- evaluate(vorm, p=pres_test, a=backg_test, tr=quantile(ds, c(1:50/50)))
> e
```

```
class      : ModelEvaluation
n presences : 4439
n absences  : 38600
AUC         : 0.499987
cor         : -0.0001095032
max TPR+TNR at : 6.537932e-07
```

```
> 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)
```





# Part IV

## Additional topics

## Chapter 13

# Model transfer in space and time

13.1 Transfer in space

13.2 Transfer in time: climate change

# Chapter 14

## To do list

You can ignore this chapter, it is the authors' to-do list.

There are many sophistications that are required by the realities that (a) there are multiple end uses of models, and (b) there are numerous issues with ecological data that mean that the assumptions of the standard methods don't hold. Could include:

- spatial autocorrelation
- imperfect detection
- mixed models (for nested data, hierarchical stuff)
- Bayesian methods
- resource selection functions
- measures of niche overlap, linked to thoughts about niche conservatism
- link to phylogeography
- additional predictors including remote sensing variables, thinking about

extremes

- species that don't "mix" with grids – freshwater systems etc.
- quantile regression
- model selection literature (AIC etc etc)
- multispecies modeling: Mars, gdm
- SDMTTools
- Model averaging
- See the BIOMOD for on multi-model inference.

- Dealing with uncertainty using uncertainty field in georeferences. How to target the "important" uncertainties (will vary with the application), an example of partial plots with standard errors, and predicting the upper and lower bounds; the idea of testing sensitivity to decisions made in the modeling process (including dropping out points etc etc).

# Part V

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