

Preparing data for ENM/SDM

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Species occurrence data

We selected and downloaded the occurrence data for the species *Podarcis muralis* (Laurenti, 1768) from GBIF: <https://doi.org/10.15468/dl.x74f4b>. I specified already some filters in the query from GBIF, namely:

- The coordinate uncertainty of the records must be $\leq 5km$.
- The year of the record must be ≥ 1970 and ≤ 2000 .

The first filter removes records with high uncertainty, relatively to the spatial resolution of the climatic data we will use (ca. 12km). The second filter removes records outside the range of the climatic data we will use.

We load this data in R.

```
library(terra)

gbif <- read.csv("../data/0002051-260120142942310.csv", sep = "\t")
```

Note

`sep = "\t"` specifies that the separator of the columns is a TAB, which is the standard used by GBIF.

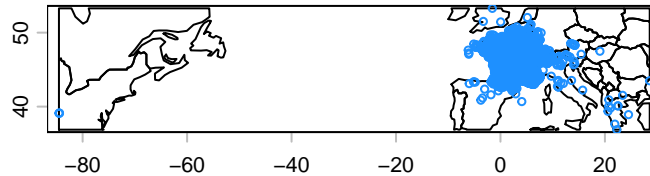
This data frame has many columns that we do not need. We retain only the longitude and latitude columns and drop duplicate coordinates.

```
gbif <- gbif[, c("decimalLongitude", "decimalLatitude")]
gbif <- unique(gbif)

# load countries polygons
# this is from rnatrualearth package, which is required by CoordinateCleaner
```

```
country <- vect(rnaturalearth::countries110)

# plot gbif records
plot(crop(country, gbif))
points(gbif, cex = .5, col = "dodgerblue")
```



GBIF data is known to have inaccuracies and should always be checked for coordinate errors. For example, sometimes the reported coordinates are not where the species was found, but of the museum where the specimen is stored. The package `CoordinateCleaner` performs several quality checks on GBIF data and flags potential inaccuracies.

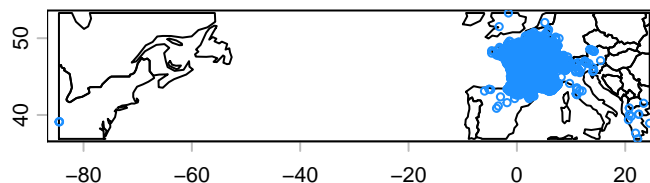
```
library(CoordinateCleaner)

flags <- clean_coordinates(
  gbif,
  species = NULL,
  tests = c("capitals", "centroids", "equal", "gbif", "institutions", "seas", "zeros")
)
```

The data frame `flags` contains the column `.summary` with value `TRUE` if all tests did not find inaccuracies and `FALSE` if that data record failed at least one test. We use this to retain only GBIF records that have `.summary = TRUE`.

```
gbif <- gbif[flags$.summary, ]

plot(crop(country, gbif))
points(gbif, cex = .5, col = "dodgerblue")
```

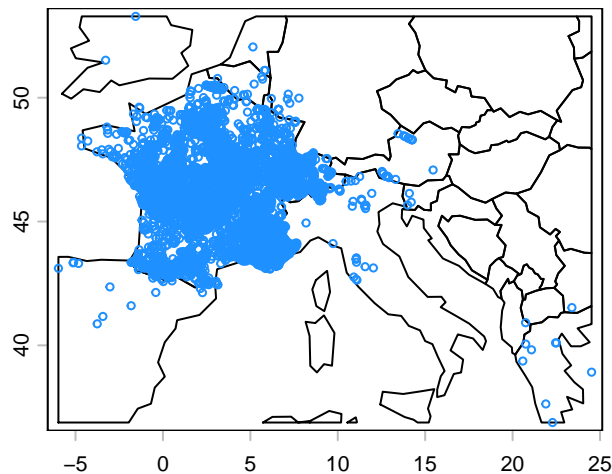


There are still points in the USA, which we want to remove manually.

i Note

The Wikipedia page of this species clarifies why there are detection in North America: *It is referred to locally in the Cincinnati/Northern Kentucky area as the “Lazarus lizard”, as it was introduced to the area around 1950 by George Rau, a boy whose family owned the Lazarus department store chain (Lazarus has since been absorbed into Macy). After he returned from a family vacation to northern Italy, he released about 10 of the reptiles near his Cincinnati home.*

```
gbif <- gbif[gbif$decimalLongitude >= -20, ]  
  
plot(crop(country, gbif))  
points(gbif, cex = .5, col = "dodgerblue")
```



We have now a data frame of cleaned occurrences from GBIF.

Pseudo-absences

To be able to model the niche and the distribution of the species, we need also absences. We thus need to generate some *pseudo-absences*, i.e. simulated absences, and add them to the data frame. There are several ways to generate absences, but here we will focus only one one: randomly sampling the geographic area within the polygon inscribing all known occurrences. In doing so, however, we do not want to sample an absence in the same grid cell of a presence.

The code below show how to generate pseudo-absences following this approach.

```

# data frame as SpatVector
gbif <- vect(
  gbif,
  geom = c("decimalLongitude", "decimalLatitude"),
  crs = "EPSG:4326"
)

# (convex) hull inscribing all known occurrences
hull <- convHull(gbif)

# load one climate layer as template of the grid cell
grid <- rast("../data/wc2.1_10m_bio_1.tif") |> crop(hull)

# create a raster with
# - 0 if there is a gbif record in that cell
# - 1 if not
# - NA for sea cells
r <- rasterize(gbif, grid, fun = \(x) 0, background = 1)
r[is.na(grid)] <- NA

# remove areas outside the polygon inscribing all GBIF records
r <- mask(r, hull)

# sample absences
abs <- spatSample(
  r,
  length(gbif),      # n(abs) = n(pres)
  as.points = TRUE,  # return a SpatVector
  method = "weights", # trick to remove cells with a record (weight = r = 0)
  values = FALSE      # we do not care about the values of the grid template
)

```

We can now stitch the two SpatVector together.

```

gbif$occ <- 1 # presence
abs$occ <- 0 # absence

# combine into one SpatVector
p <- rbind(gbif, abs)

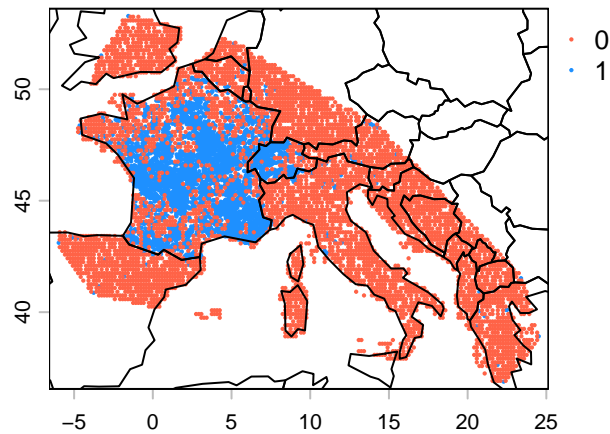
plot(
  p,

```

```

"occ",                                # color by `occ`
col = c("tomato", "dodgerblue"), # color palette
cex = 0.3,
fun = \( ) lines(country)            # outline of countries
)

```



We can now use the `SpatVector p` to extract climatic variables.

Climate data

In this course, we always use the WorldClim bioclimatic variables to model the niche of species. Bioclimatic variables are derived from temperature and precipitation data and are considered to have the strongest influence on the distribution of species. A list of all of them can be found at <https://www.worldclim.org/data/bioclim.html>.

Load eight bioclimatic variables.

```

# list of files of bioclimatic variables
ff <- list.files(
  "../data",          # where the files are
  pattern = "wc2.1", # wc = WorldClim
  full.names = TRUE   # full path
)

# load them into memory
climate <- rast(ff)
climate

```

```

class      : SpatRaster
size       : 1080, 2160, 8  (nrow, ncol, nlyr)
resolution : 0.1666667, 0.1666667  (x, y)
extent     : -180, 180, -90, 90  (xmin, xmax, ymin, ymax)
coord. ref.: lon/lat WGS 84 (EPSG:4326)
sources    : wc2.1_10m_bio_1.tif
              wc2.1_10m_bio_12.tif
              wc2.1_10m_bio_13.tif
              ... and 5 more sources
names      : wc2.1~bio_1, wc2.1~io_12, wc2.1~io_13, wc2.1~io_14, wc2.1~io_15, wc2.1~bio_4,
min values  :   -54.72435,           0,           0,           0,           0.0000,           0.000,
max values  :    30.98764,        11191,        2381,         484,        229.0017,        2363.846,

```

Using `p`, we extract the values of the grid cells of `climate` for the occurrence data.

```
d <- extract(climate, p, ID = FALSE, cell = TRUE, xy = TRUE)
```

Tip

`cell = TRUE` return also the ID of the cell of the raster where the records are found. This is useful to keep only one record per grid cell.

We assign the occurrence status (presence/absence) to this data frame.

```
d$occ <- p$occ
```

Then, drop duplicate records, i.e. multiple records for the same grid cell.

```

# drop rows with duplicated cells
d <- d[!duplicated(d$cell), ]

head(d)

```

	wc2.1_10m_bio_1	wc2.1_10m_bio_12	wc2.1_10m_bio_13	wc2.1_10m_bio_14		
1	14.709969	510	60	20		
2	11.454646	775	89	44		
3	8.854438	933	106	60		
4	10.599990	633	61	44		
5	10.302510	632	58	45		
6	2.760979	549	68	27		
	wc2.1_10m_bio_15	wc2.1_10m_bio_4	wc2.1_10m_bio_5	wc2.1_10m_bio_6	cell	occ

1	25.683231	686.3660	32.04650	2.11375	620998	1
2	21.440331	589.9808	25.82825	-0.33375	621014	1
3	18.089415	578.0707	22.92975	-2.12900	618853	1
4	9.118695	567.0883	23.99325	0.50650	538936	1
5	8.751935	560.5479	23.76875	0.34775	534618	1
6	30.307224	617.9191	15.89150	-8.37175	562745	1

Finally, make sure to have more or less the same number of presences and absences.

```
table(d$occ) # not balanced
```

```

      0      1
5016 1644
```

```

n <- table(d$occ)[["1"]]
index_pres <- which(d$occ == 1)
index_abs <- which(d$occ == 0)

# subsample
d <- d[c(index_pres, sample(index_abs, n)), ]

table(d$occ) # balanced
```

```

      0      1
1644 1644
```

```
write.csv(d, "../data/occurrences.csv", row.names = FALSE)
```

We have now a data frame obtained from GBIF that is ready to be used for ENM/SDM.