Preparing data for ENM/SDM

Species and climate data

Data types

- Species occurrence (0/1; absences/presence) data. Usually a `data.frame`.
- Environmental (climatic) data. Usually a `SpatRaster`.

Species data

Species occurrence data

Podarcis muralis (Laurenti, 1768) from GBIF: https://doi.org/10.15468/dl.x74f4b.
Filters:

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

Figure 1: The common wall lizard *Podarcis muralis*.

Species occurrence data

Load GBIF data into R.

```
library(terra)

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

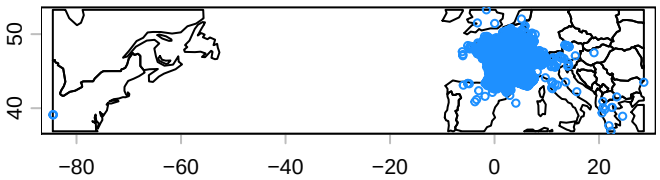
> **Note**
>
> `sep = "\t"` specifies that the separator of the columns is a `TAB`, which is the standard used by GBIF.

This data frame has many columns that we do not need.

Drop duplicates

Keep only long/lat columns and drop duplicate coordinates.

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



Warning

This is an European species.

George Rau, a boy [...] returned from a family vacation to northern Italy.

Check for coordinate issues

The package `CoordinateCleaner` performs several quality checks on GBIF data and flags potential inaccuracies.

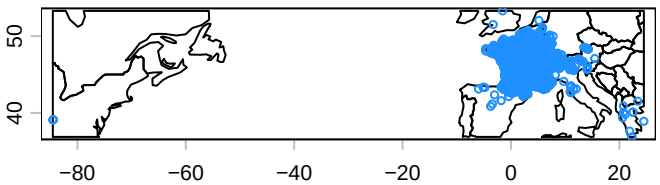
```
library(CoordinateCleaner)

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/FALSE`.

Remove coordinates with issues

Retain only GBIF records that have `.summary = TRUE`.

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

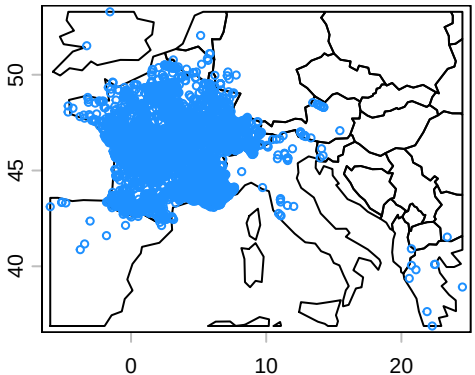


There are still points in the USA, which we want to remove manually.

Remove coordinates manually

We can remove inaccuracies manually.

```
gbif <- gbif[gbif$decimalLongitude >= -20, ]
```



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

Pseudo-absences

- Generally, we need both presences and absences of species for ENM.
- We need to generate some *pseudo-absences*, i.e. simulated absences, and add them to the data frame.
- We do not want absences in the same location (grid cell) of presences.

Pseudo-absences

Define the sampling region.

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

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

Pseudo-absences

Rasterize GBIF data to a 0 (at least one record) 1 (no records) layer.

```
# 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)
```

Pseudo-absences

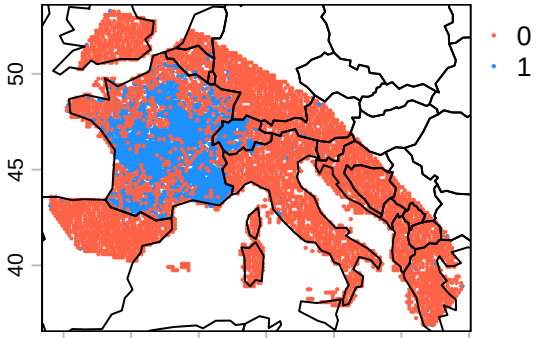
Sample within the area excluding cells with at least one presence.

```
# 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 = (
  values = FALSE       # we do not care about the values of the grid templa
)
```

Finalize species occurrence data

Stitch the two SpatVector together.

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

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



Climate data

Climate data

- WorldClim bioclimatic variables.
- Many others are available, but WorldClim is easy to start with.
- Bioclimatic variables are derived temperature and precipitation variables that have the strongest influence on species.
- A list of all of them can be found at https://www.worldclim.org/data/bioclim.html.

Climate data

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
)
ff <- ff[!grepl("MPI", ff)]

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

```
class       : SpatRaster
size        : 1080, 2160, 8  (nrow, ncol, nlyr)
resolution  : 0.1666667, 0.1666667  (x, y)
```

Extract climate

Extract the values of climate at the species occurrence locations using p.

```
d <- extract(climate, p, ID = FALSE, cell = 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.

Assign species occurrences

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

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

Drop duplicates

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

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

# drop the `cell` column
d <- d[, -which(names(d) == "cell")]
```

Balance absences and presences

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

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

```
   0    1
5016 1644
```

```
# subsample
n <- table(d$occ)[["1"]]
index_pres <- which(d$occ == 1)
index_abs <- which(d$occ == 0)
d <- d[c(index_pres, sample(index_abs, n)), ]
table(d$occ) # balanced
```

```
   0    1
1644 1644
```

Workflow

Occurrence data

1. Download GBIF data.
2. Filter and clean GBIF data.
3. Sample absences (if needed).

Climate data

1. Download climate data.
2. Extract values for occurrence data.
3. Drop duplicates.

Occurrence + climate data $\rightarrow$ ENM.