

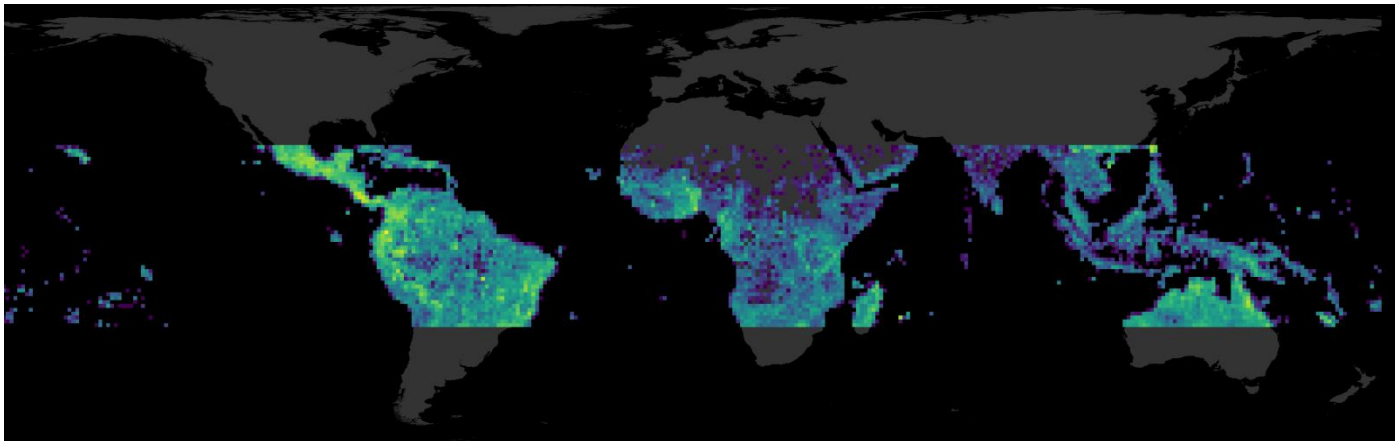


UNIVERSITY OF
GOTHENBURG

The Antonelli Lab

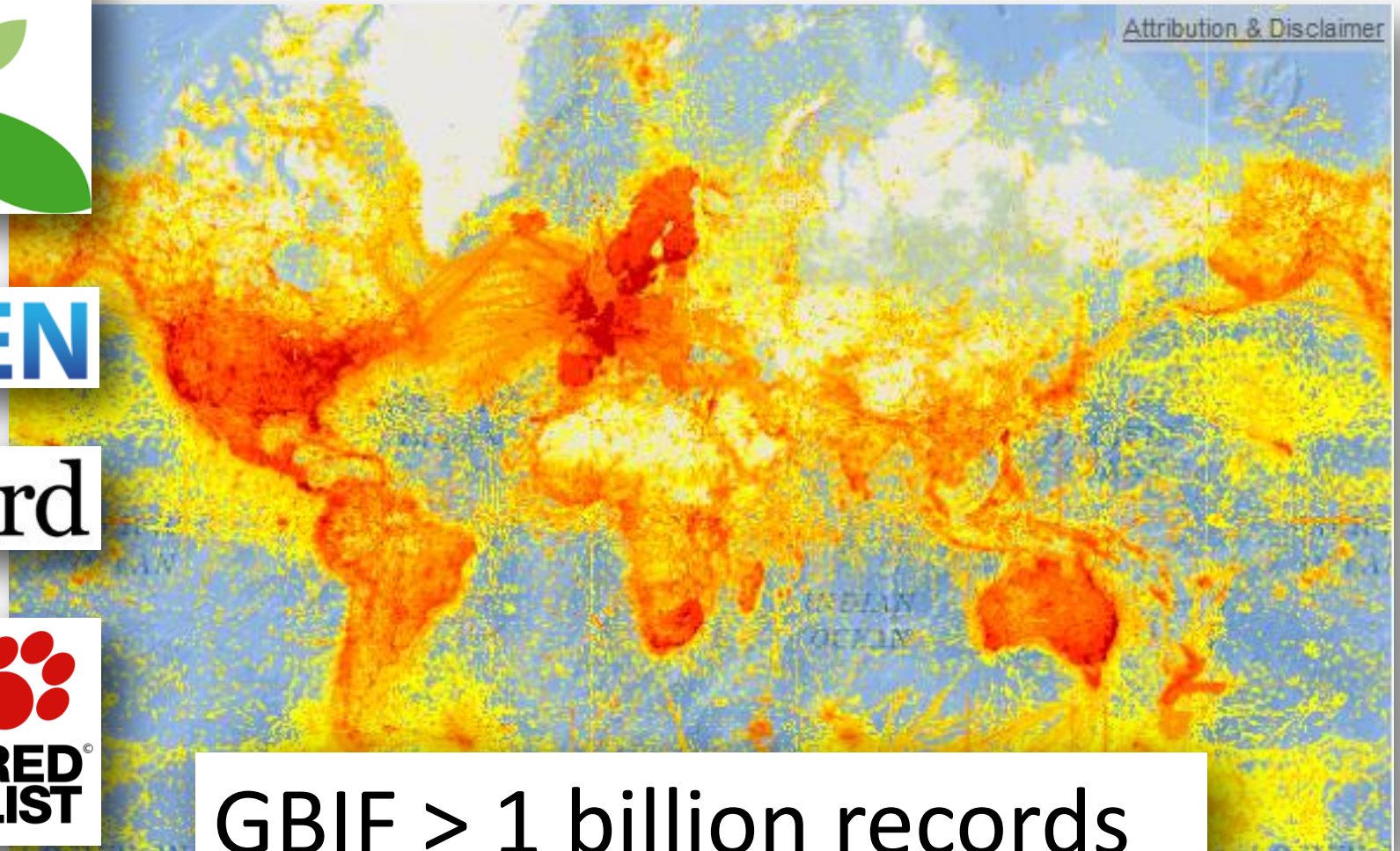
Evolution and biogeography with focus on the Neotropics

Biodiversity Data in Ecology and Biogeography



Alexandre Antonelli & Alexander Zizka

Species distribution data – a revolution



GBIF > 1 billion records

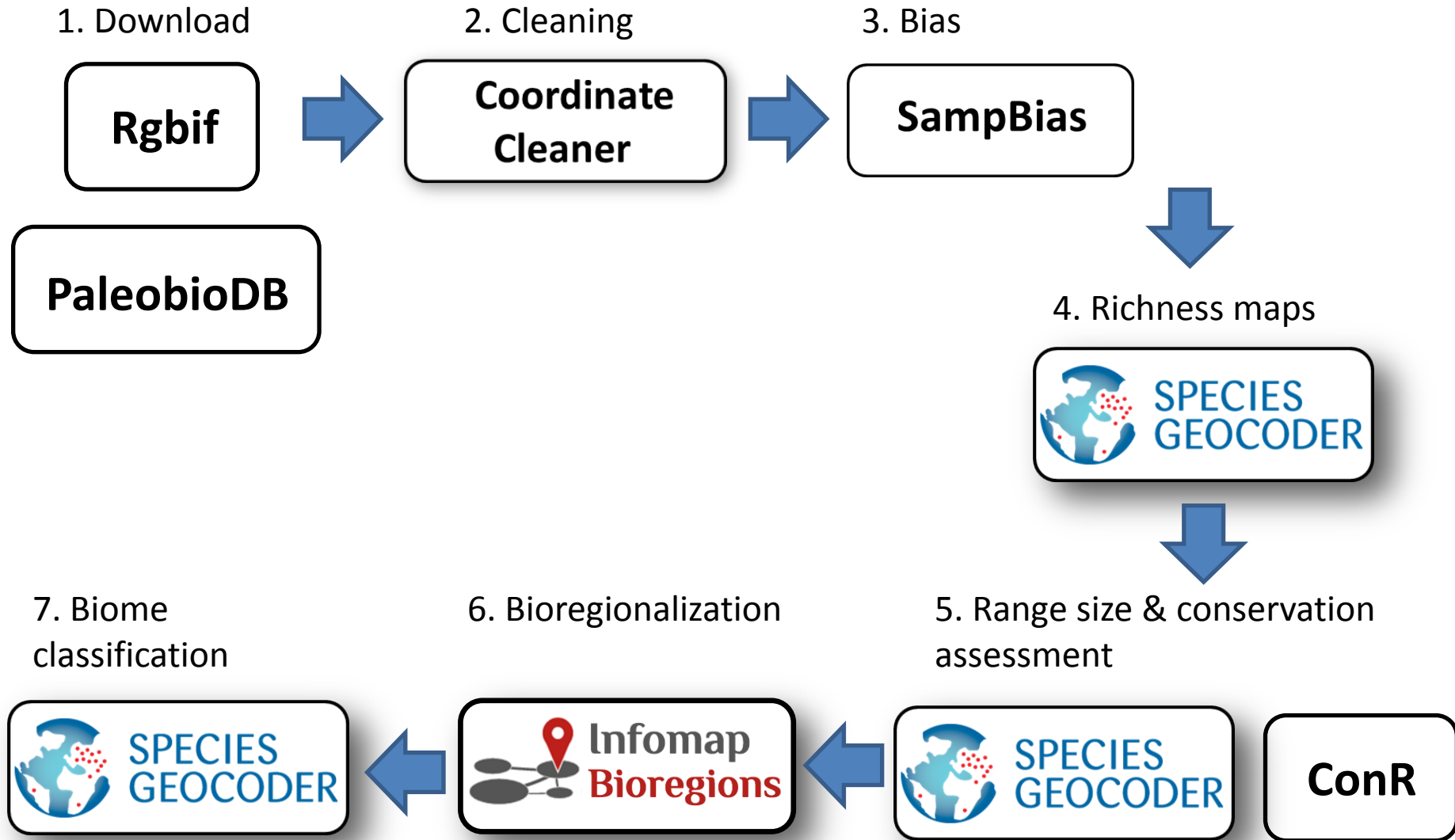
Fantastic!

- How can we use these data in biogeography and ecology?

How can we use these data in biogeography and ecology?

- Data quality
- Sampling effort

Analysis pipeline



Exercises

- 1. Downloading geographic occurrence data from GBIF **(R)**
- 2. Combine with data from the field & cleaning **(R)**
- 3. Quantifying sampling bias **(R + GUI)**
- 4. Species richness maps **(R)**
- 5. Range size and conservation assessment **(R)**
- 6. Bioregionalization **(GUI)**
- 7. Biome classification **(R)**

1. Download - Rgbif

Rgbif

- A programmatic interface to the Web Service methods provided by the Global Biodiversity Information Facility
- includes functions for searching for taxonomic names, retrieving information on data providers, getting species occurrence records, getting counts of occurrence records



2. Data cleaning - CoordinateCleaner

A logo for 'Coordinate Cleaner' consisting of the text 'Coordinate Cleaner' in a bold, black, sans-serif font, centered within a white rounded rectangle with a thin black border and a subtle drop shadow.

Coordinate Cleaner

An R-package to identify potentially problematic records based on gazetteers

<https://github.com/azizka/CoordinateCleaner>

2. CoordinateCleaner

Coordinate
Cleaner



2. Data cleaning - Common coordinate errors

Coordinate
Cleaner



2. Data cleaning - Common coordinate errors

**Coordinate
Cleaner**

Invalid or missing



2. Data cleaning - Common coordinate errors

Coordinate
Cleaner

Invalid or missing
Zeros



2. Data cleaning - Common coordinate errors

Coordinate
Cleaner

Invalid or missing
Zeros
Seas



2. Data cleaning - Common coordinate errors

Coordinate
Cleaner

Invalid or missing
Zeros
Seas
Country centroids



2. Data cleaning - Common coordinate errors

Coordinate
Cleaner

Invalid or missing
Zeros
Seas
Country centroids
Capitals



2. Data cleaning - Common coordinate errors

Coordinate
Cleaner

Invalid or missing
Zeros
Seas
Country centroids
Capitals
Institutions



2. Data cleaning - Common coordinate errors

Coordinate
Cleaner

Invalid or missing
Zeros
Seas
Country centroids
Capitals
Institutions
Wrong country



2. Data cleaning - Common coordinate errors

Coordinate
Cleaner

Invalid or missing
Zeros
Seas
Country centroids
Capitals
Institutions
Wrong country
Outliers



2. Data cleaning - Workflow

Coordinate Cleaner

```
flags <- CleanCoordinates(x = dat, lon = "decimallongitude", lat = "decimallatitude",
                          countries = "countryCode",
                          species = "species",
                          countrycheck = T,
                          outliers = T) # most test are on by default
```

```
## running validity test
## running zero coordinate test
## flagged 27 records
## running capitals test
## flagged 5 records
## running centroids test
## flagged 22 records
## running seas test
## flagged 14 records
## running countrycheck test
## flagged 16 records
## running GBIF test
## flagged 0 records
## running institutions test
## flagged 9 records
## flagged 67 of 1332 records, EQ = 0.05
```

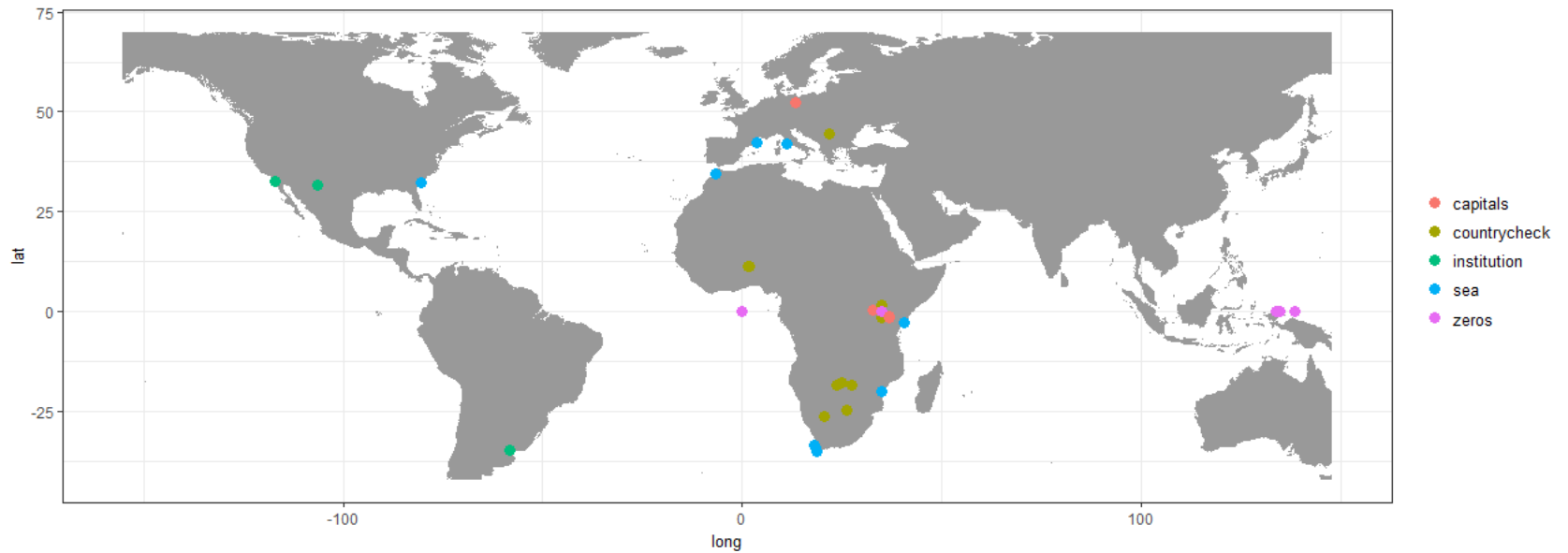
##	decimallongitude	decimallatitude	validity	zeros	capitals	centroids	sea
## 1	1.46994	11.45179	TRUE	TRUE	TRUE	TRUE	TRUE
## 2	1.47035	11.46455	TRUE	TRUE	TRUE	TRUE	TRUE
## 3	1.49126	11.44658	TRUE	TRUE	TRUE	TRUE	TRUE
## 4	1.58874	11.40803	TRUE	TRUE	TRUE	TRUE	TRUE
## 5	1.47939	11.44816	TRUE	TRUE	TRUE	TRUE	TRUE
## 6	1.35556	11.24228	TRUE	TRUE	TRUE	TRUE	TRUE

##	countrycheck	gbif	institution	summary
## 1	TRUE	TRUE	TRUE	TRUE
## 2	FALSE	TRUE	TRUE	FALSE
## 3	TRUE	TRUE	TRUE	TRUE
## 4	FALSE	TRUE	TRUE	FALSE
## 5	TRUE	TRUE	TRUE	TRUE
## 6	TRUE	TRUE	TRUE	TRUE

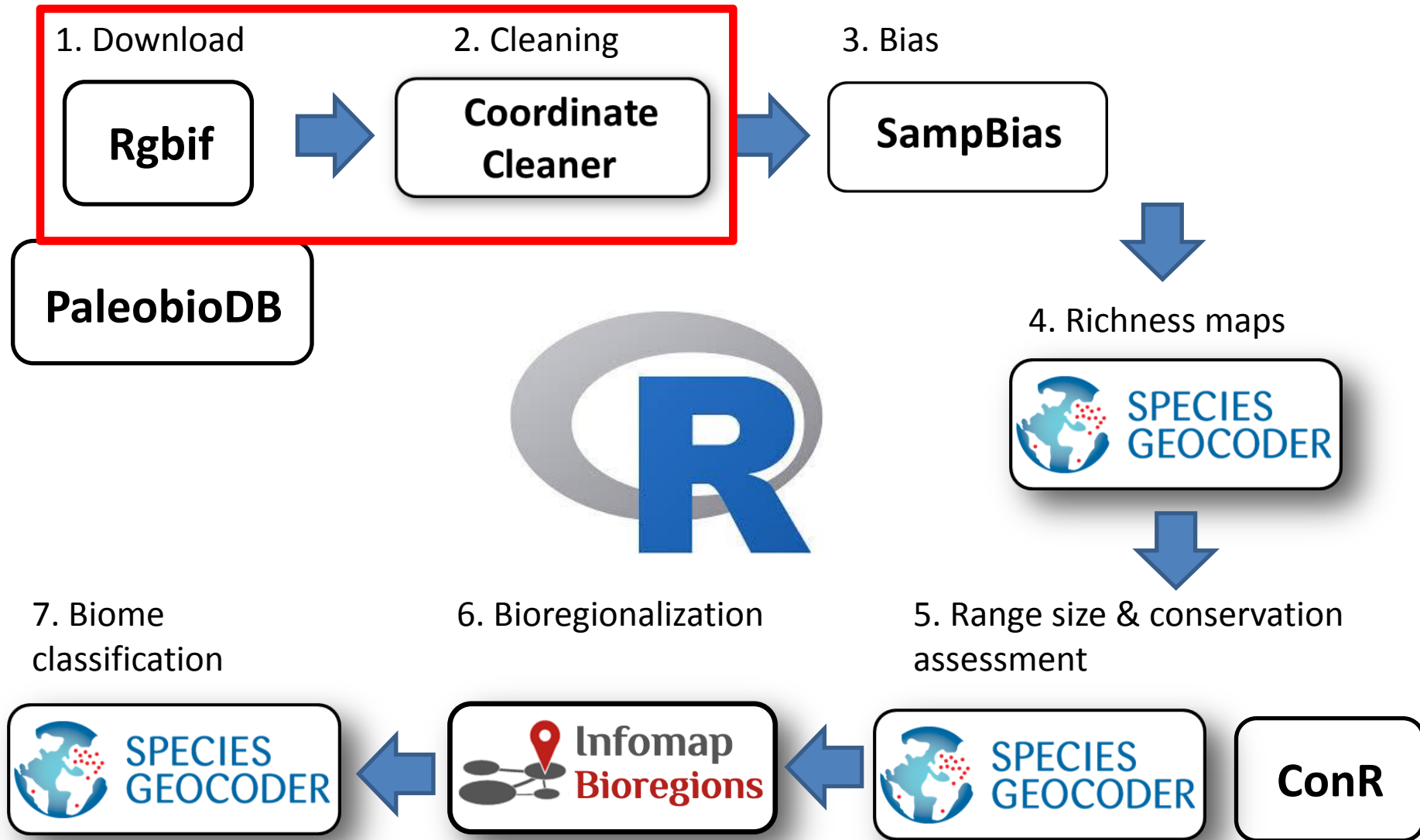
<https://github.com/azizka/speciesgeocodeR>

2. Data cleaning - Workflow

**Coordinate
Cleaner**

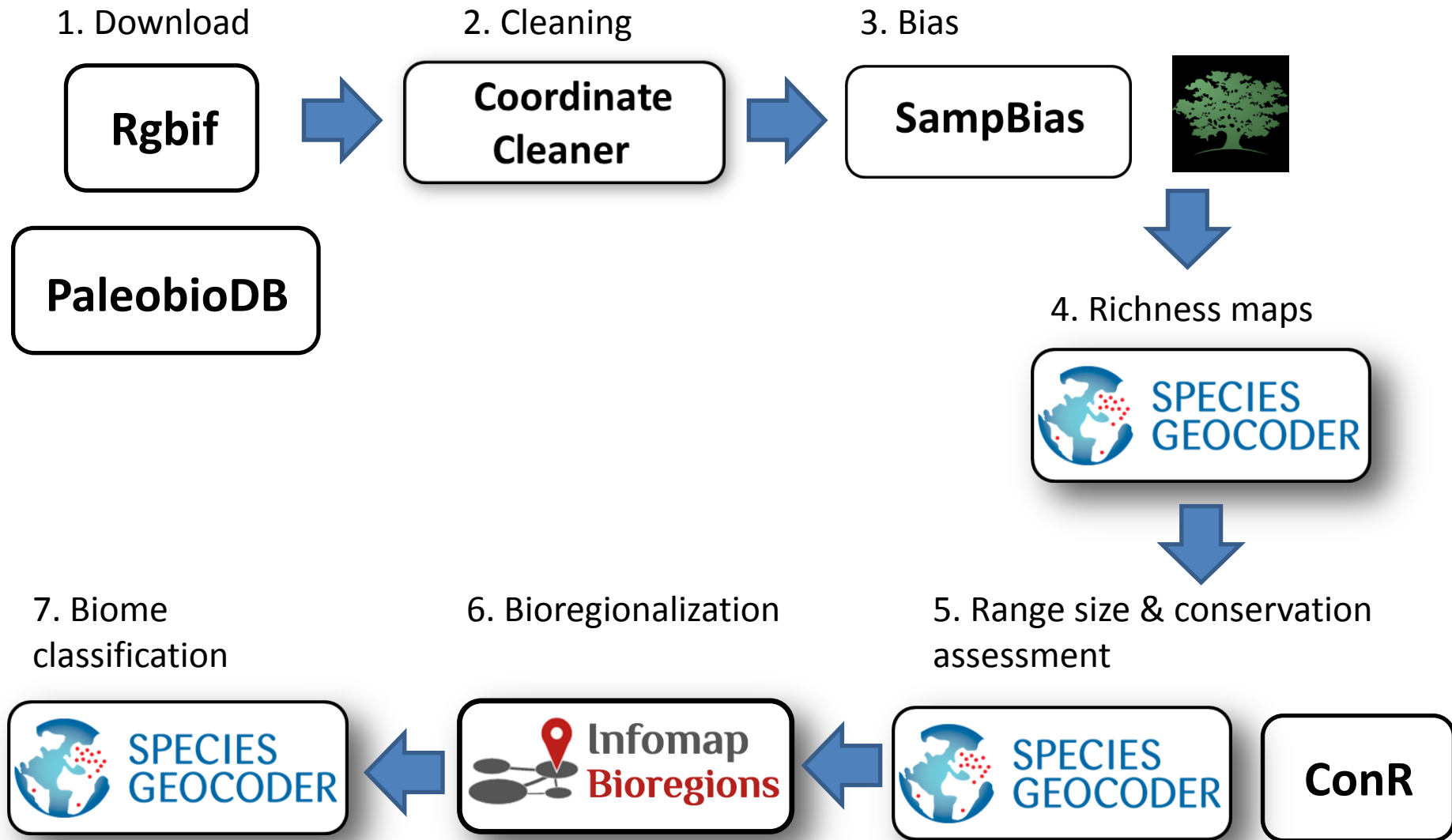


Analysis pipeline



-
- Webpage

Analysis pipeline



3. Bias

SampBias

3. Bias - Background

SampBias

- Relation between anthropogenic geographic features and occurrence records
- Based on gazetteers and frequency distributions of distances

3. Bias - Background

SampBias



3. Bias - Background

SampBias



3. Bias - Background

SampBias

- Roads



3. Bias - background

SampBias

- Roads
- Cities



3. Bias - Background

SampBias

- Roads
- Cities
- Airports



3. Bias - Background

SampBias

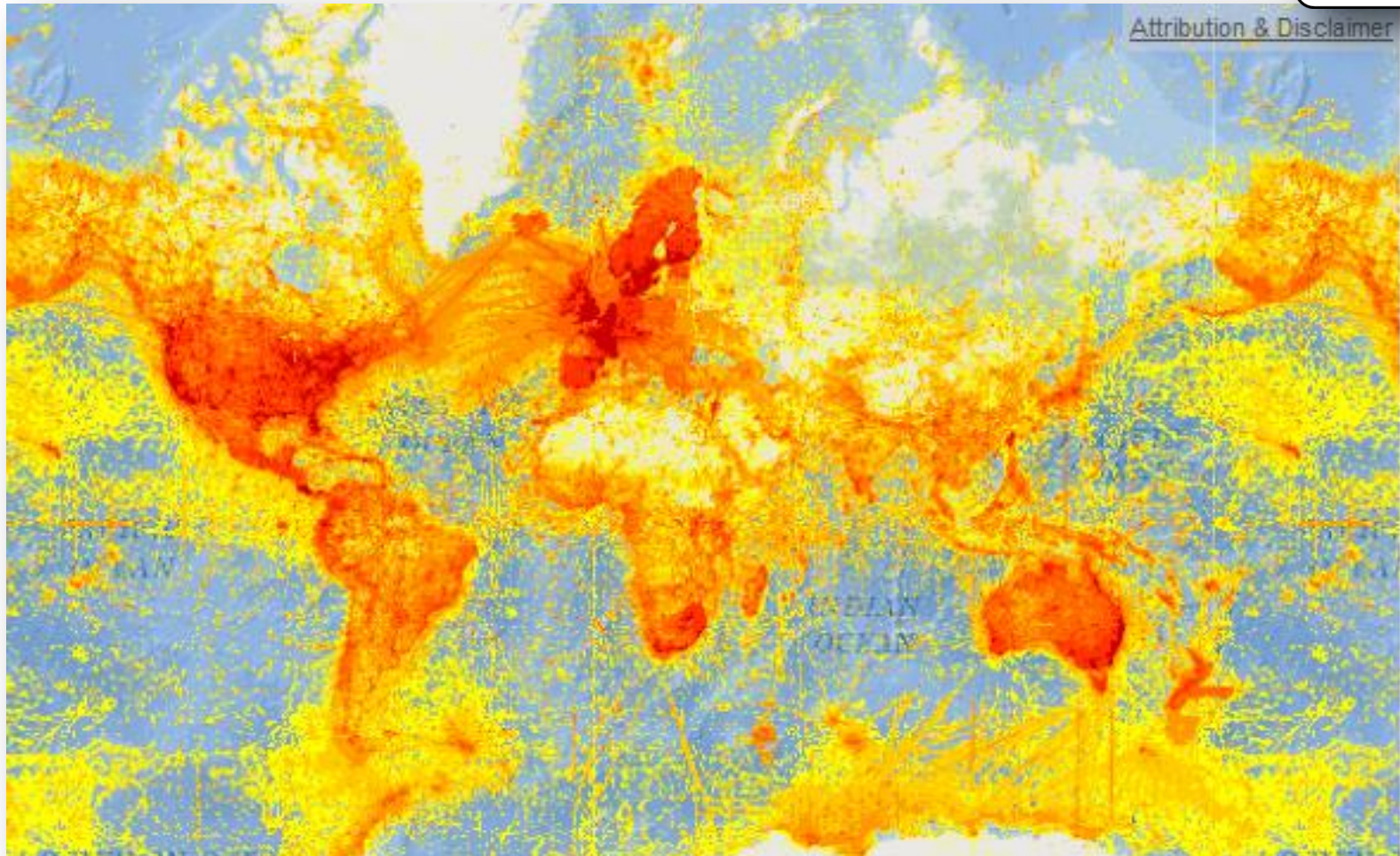
- Roads
- Cities
- Airports
- Rivers

➔ Sampling increases
with accessibility



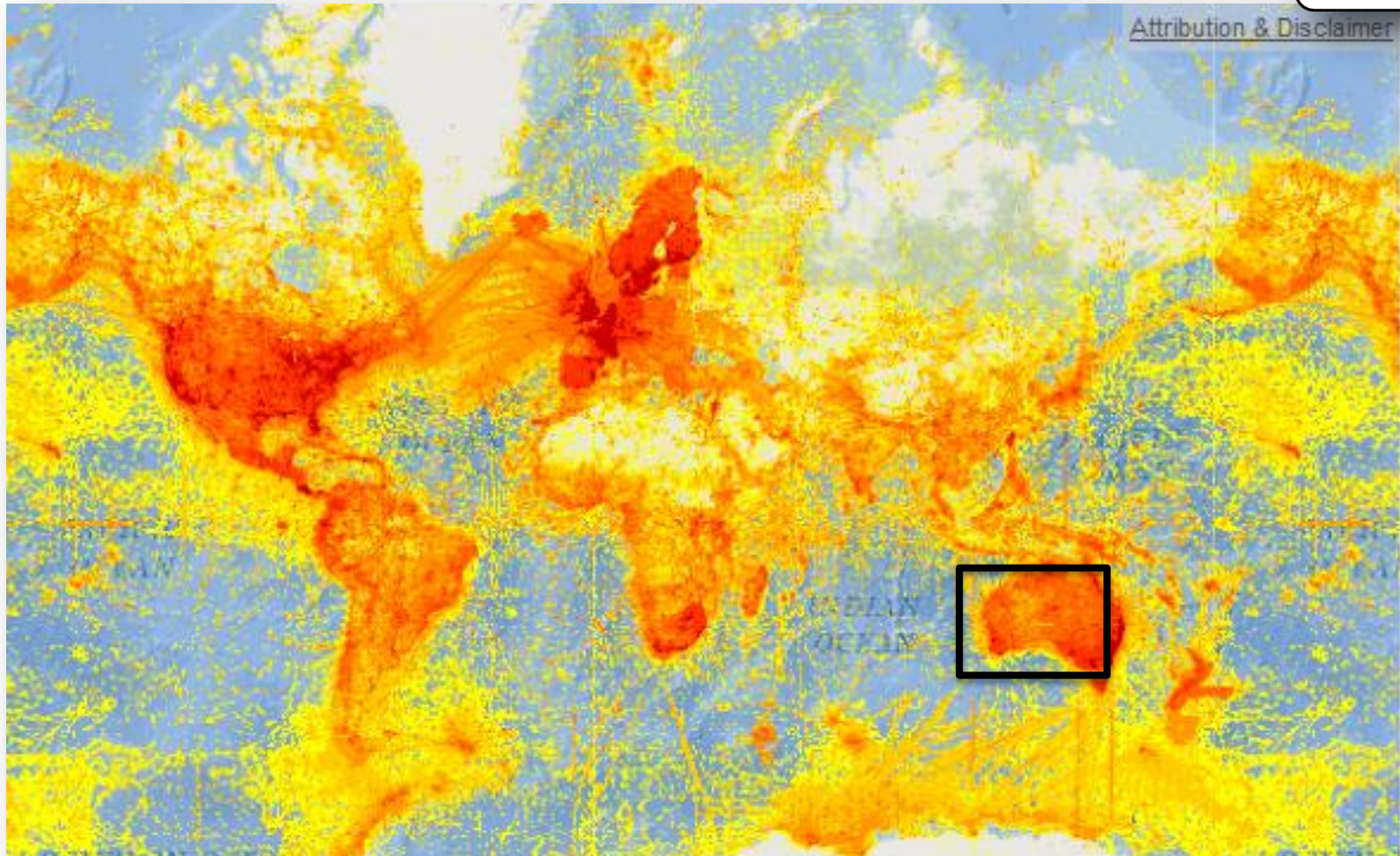
3. Bias - Background

SampBias



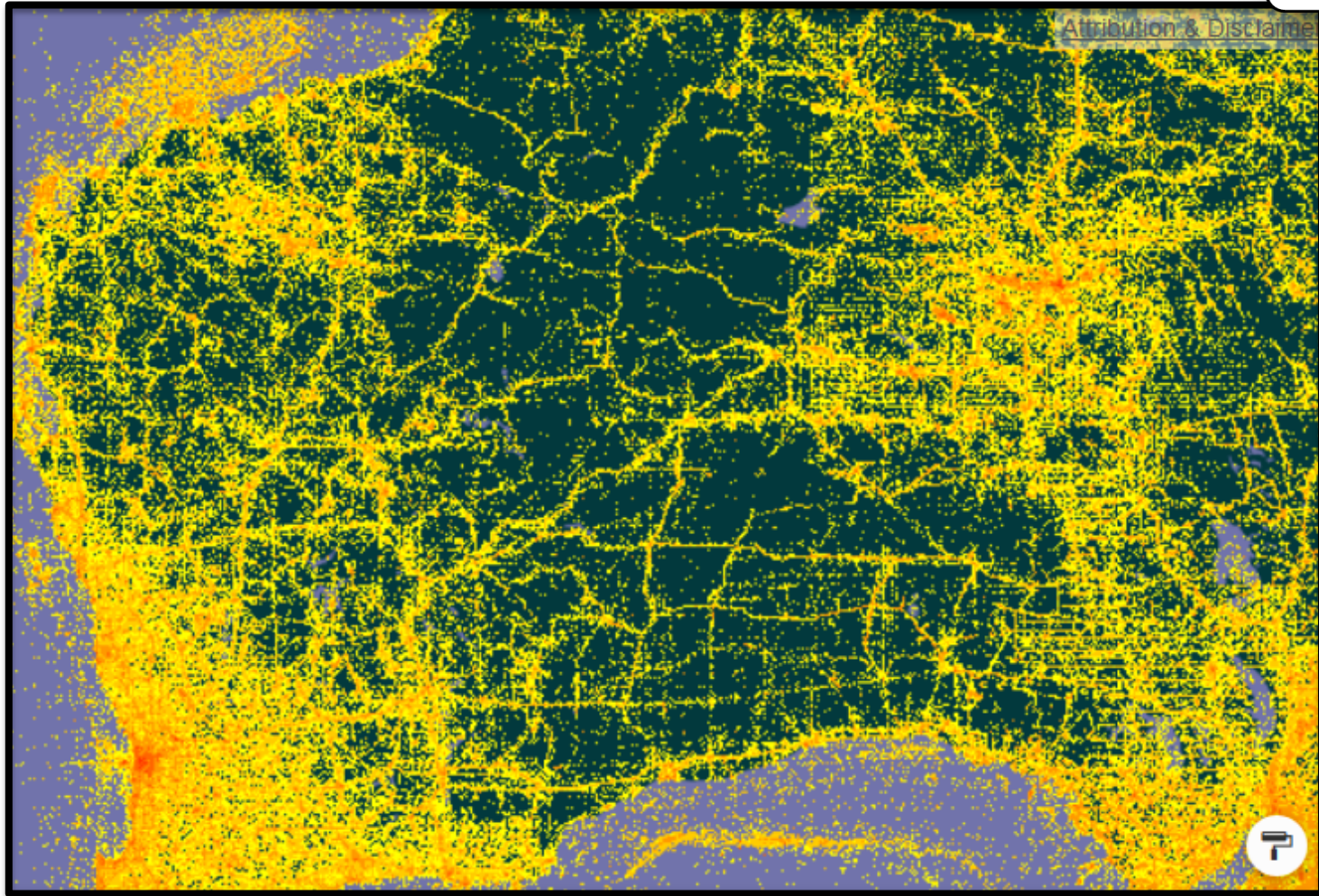
3. Bias - Background

SampBias



3. Bias - Background

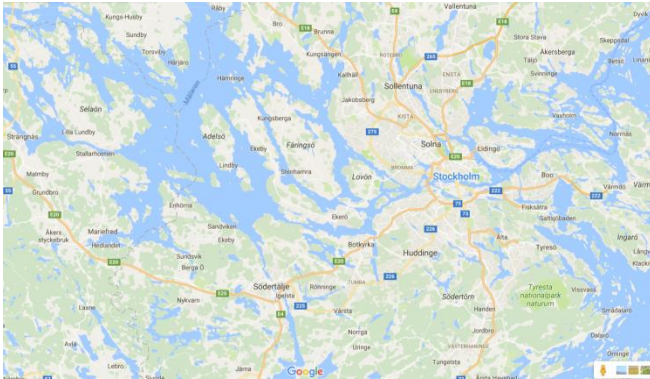
SampBias



3. Bias - How does it work?

SampBias

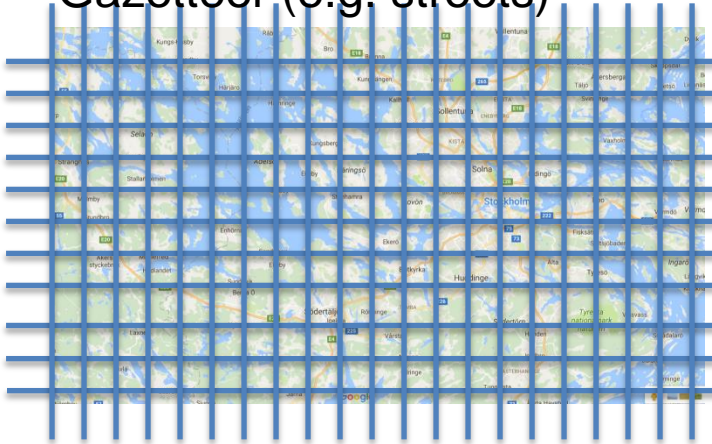
Gazetteer (e.g. streets)



3. Bias - How does it work?

SampBias

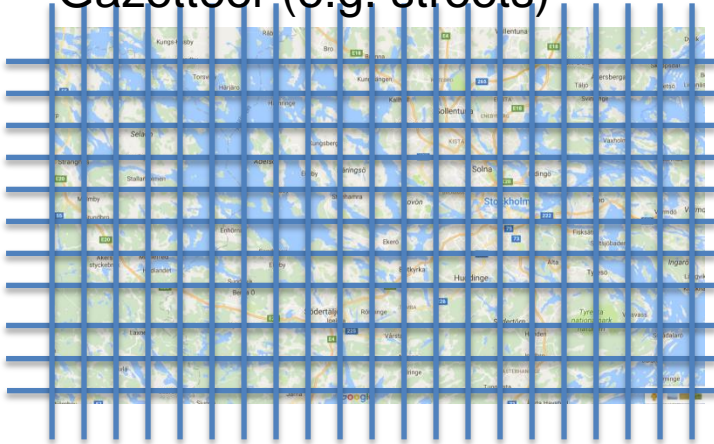
Gazetteer (e.g. streets)



3. Bias - How does it work?

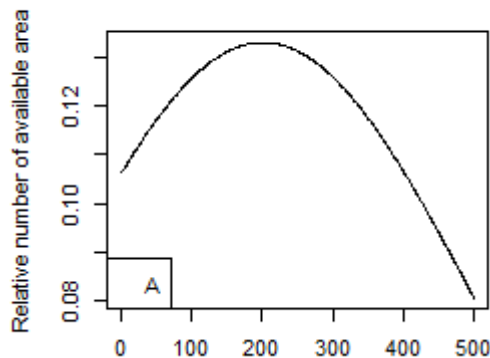
SampBias

Gazetteer (e.g. streets)



Minimum distance

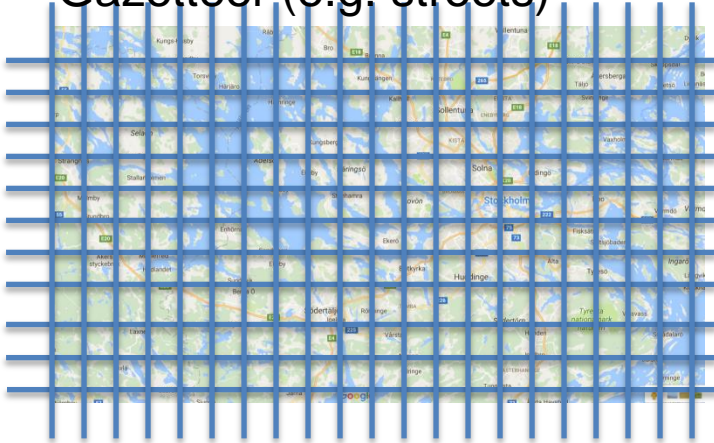
Expected distribution



3. Bias - How does it work?

SampBias

Gazetteer (e.g. streets)

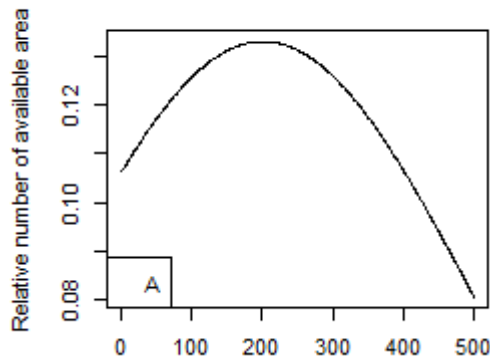


Occurrences



Minimum distance

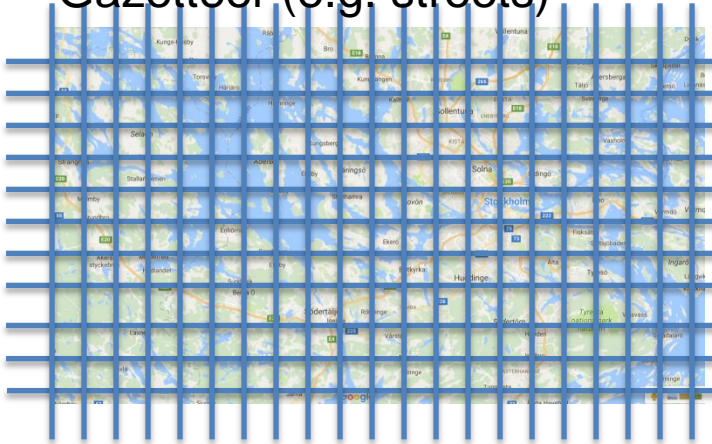
Expected distribution



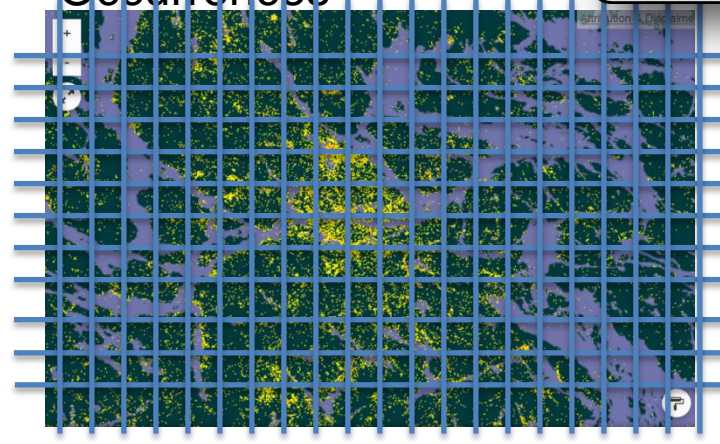
3. Bias - How does it work?

SampBias

Gazetteer (e.g. streets)



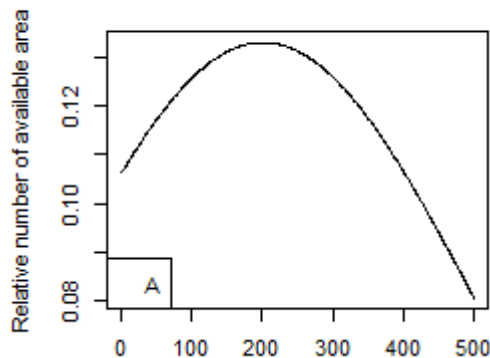
Occurrences



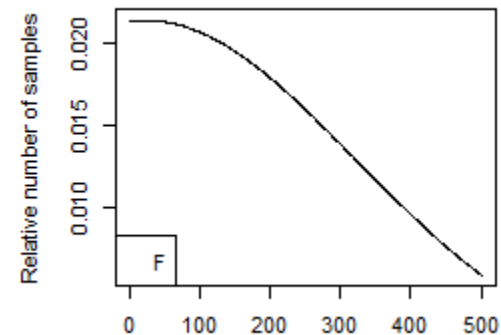
Minimum distance



Expected distribution



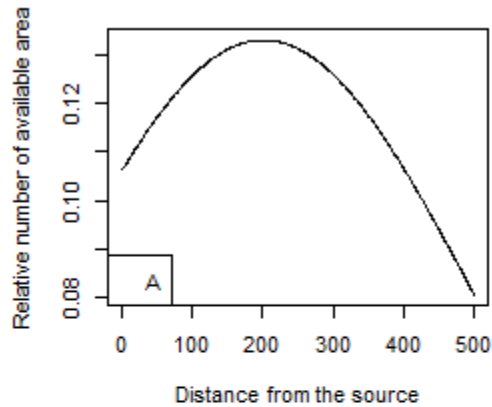
Observed distribution



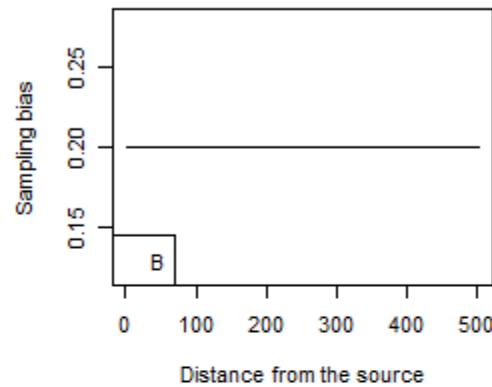
3. Bias - How does it work?

SampBias

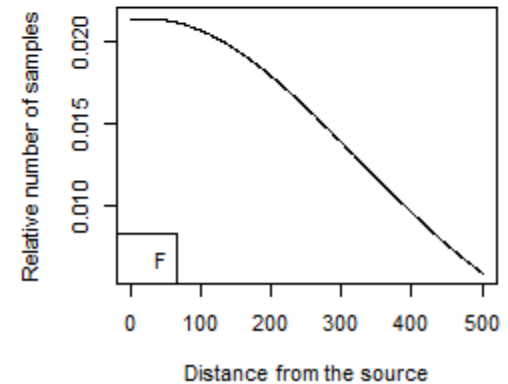
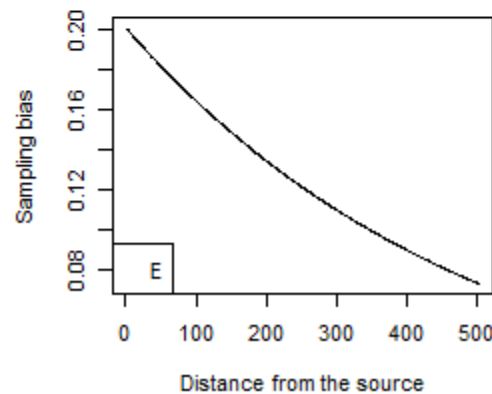
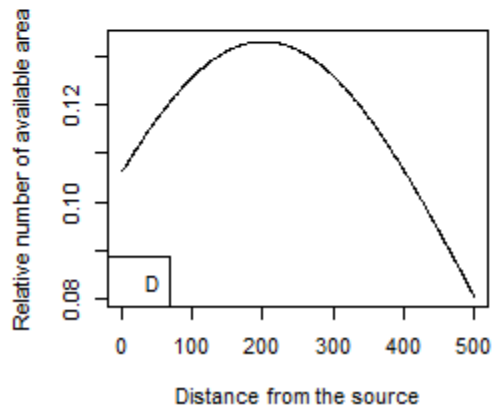
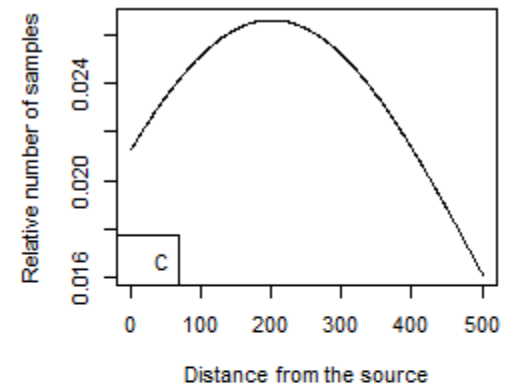
Expected distribution



Effect of distance from bias source

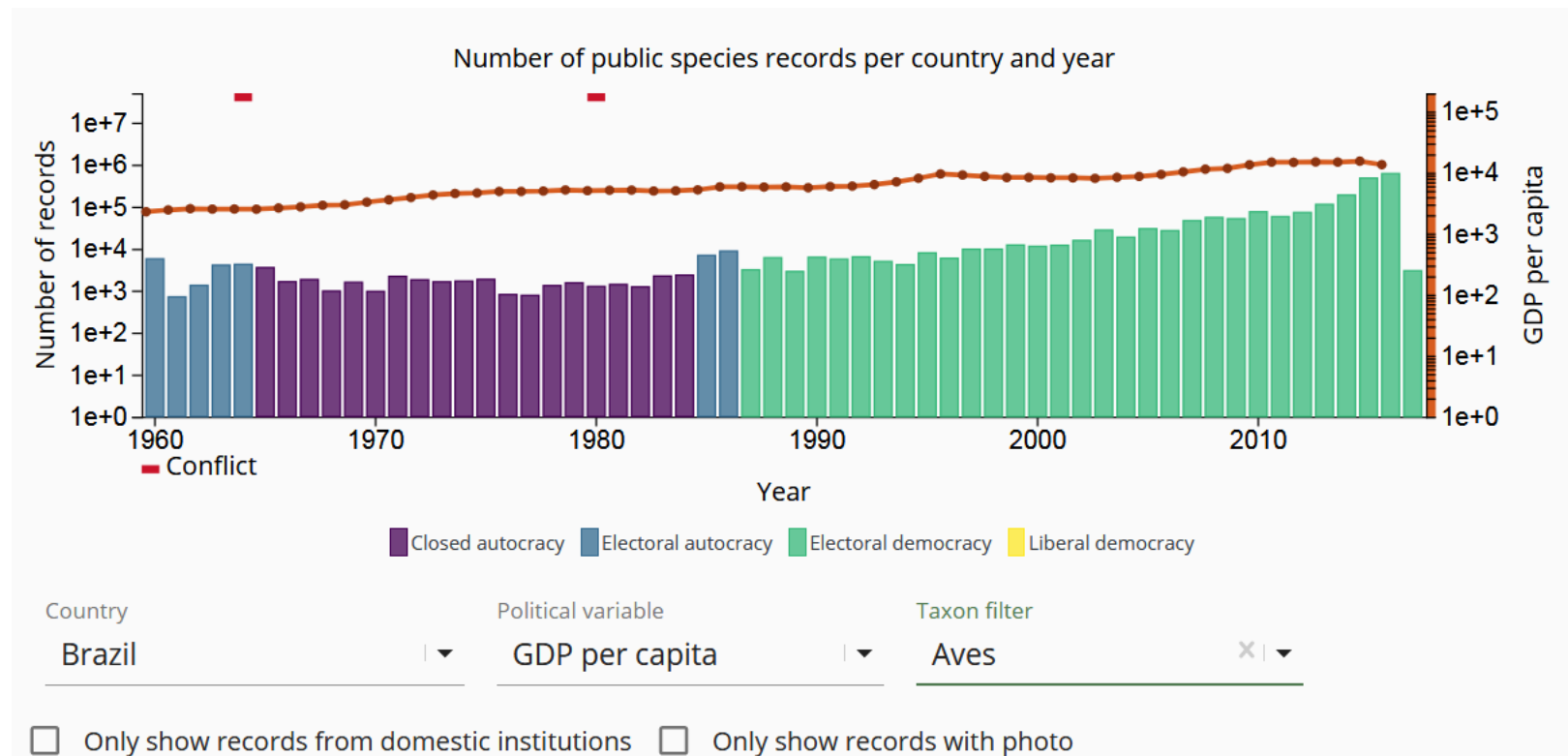


Observed distribution



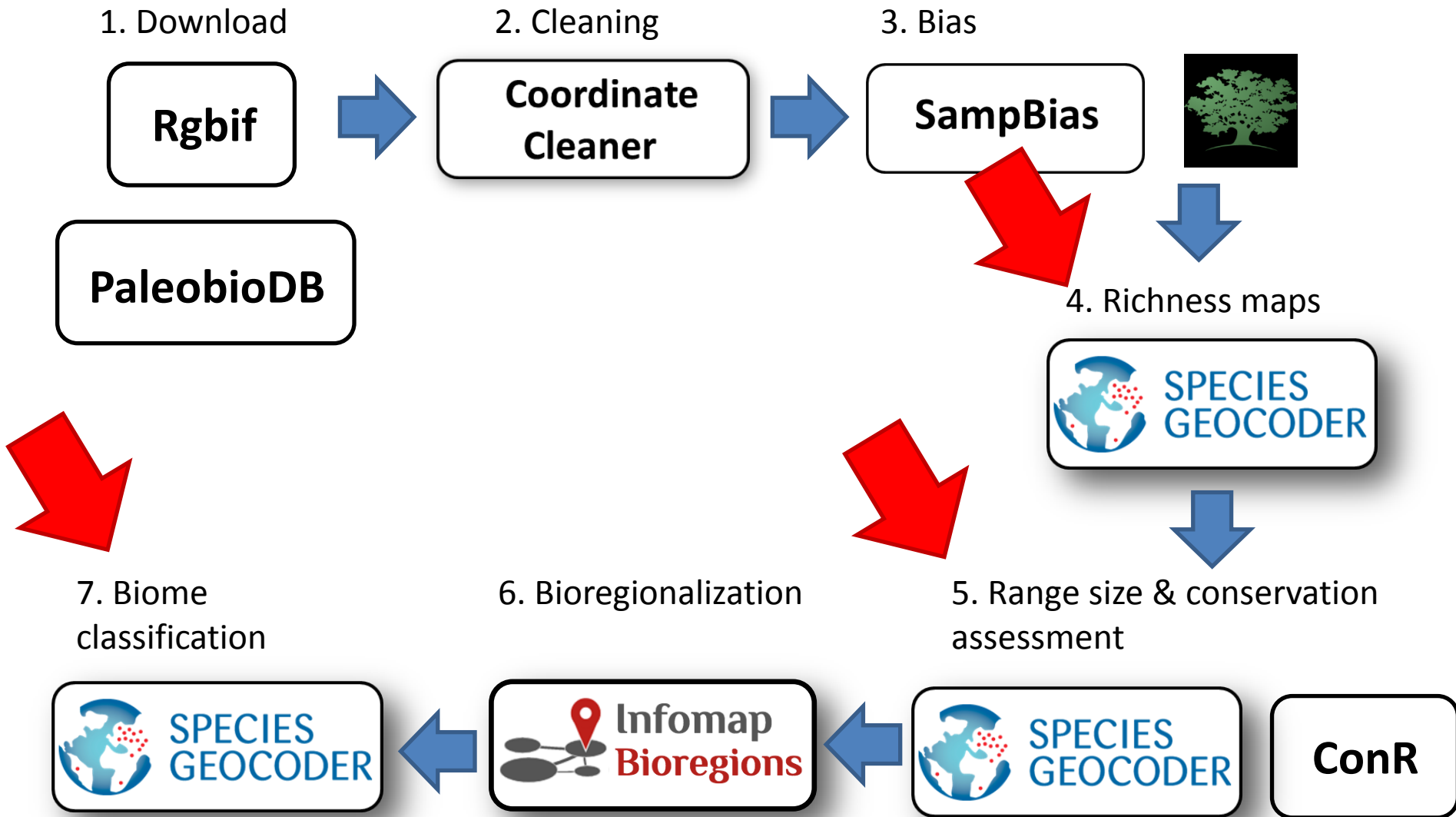
3. Bias - BioDem

- Explore the connection between political systems and biodiversity record collection



<http://bio-dem.surge.sh/>

Analysis pipeline



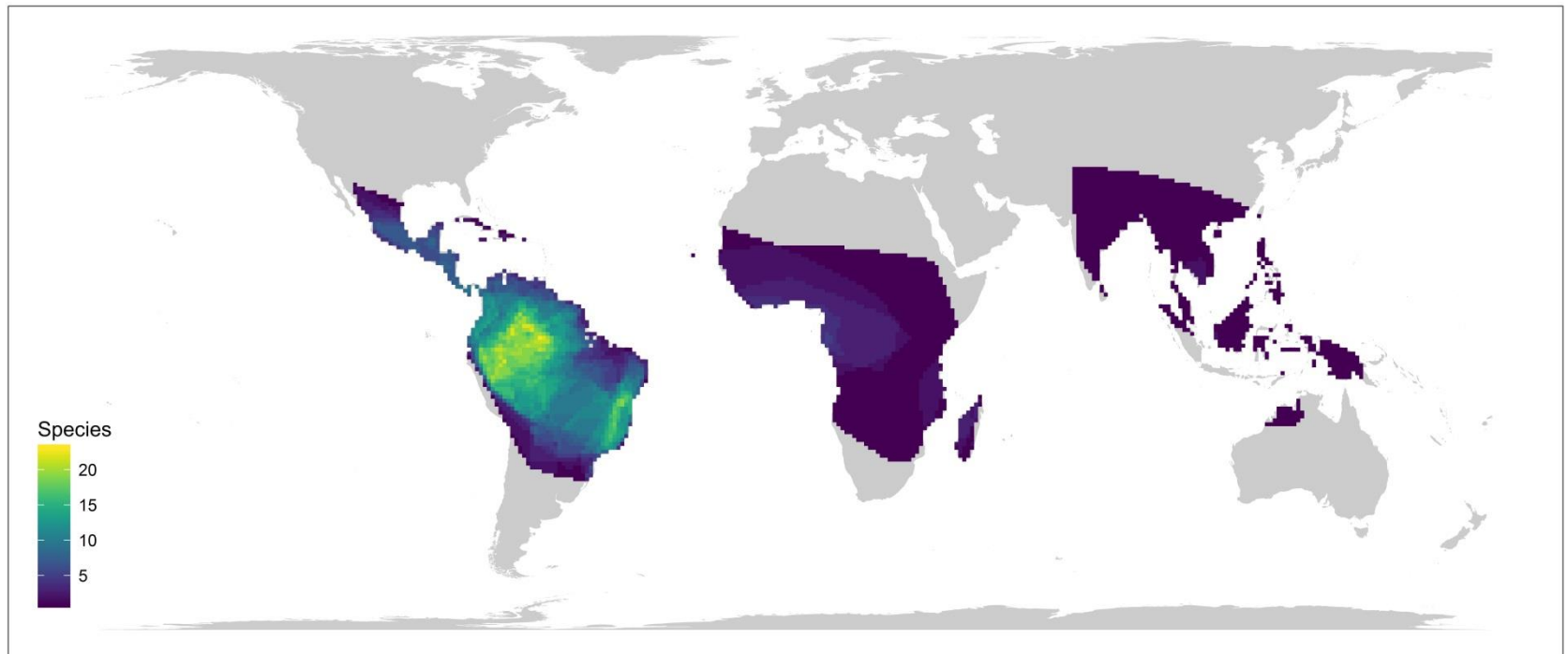
4., 5. & 7. Richness maps, range size and biome classification



4. Species richness maps



- Approximate species ranges
- Visualize species richness patterns



5. Range size - EOO



5. Conservation assessment - ConR

ConR

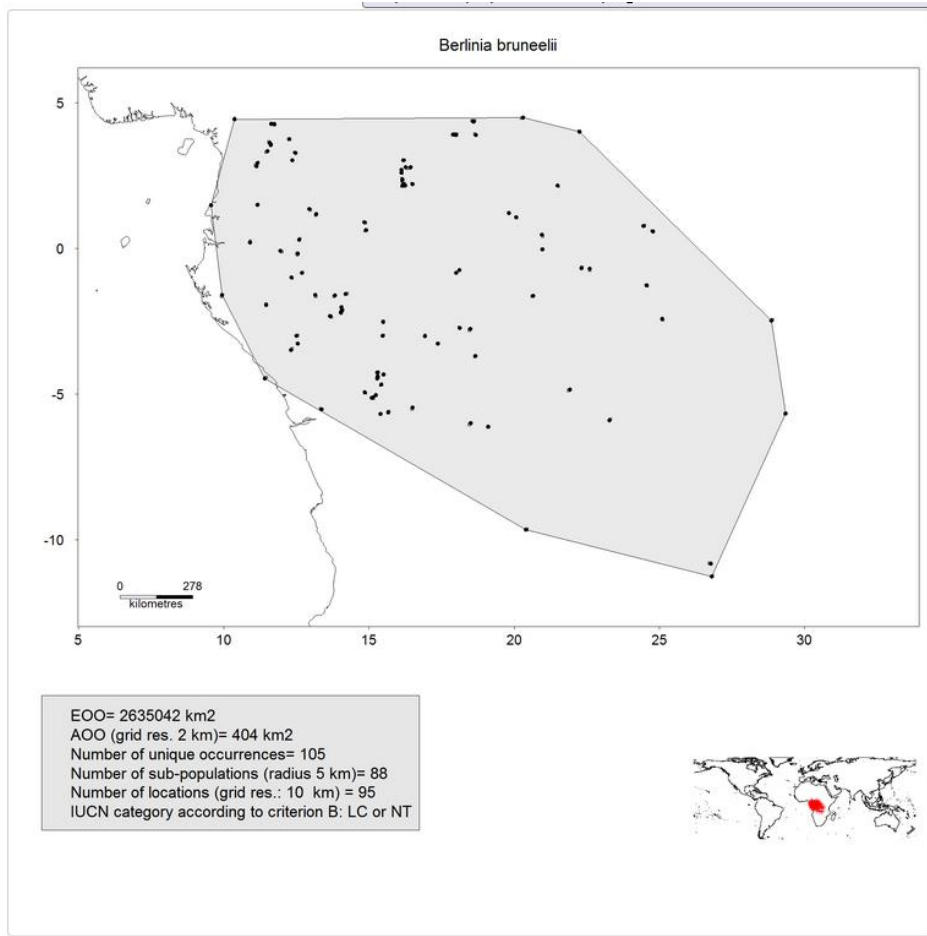
Computation of Parameters Used in Preliminary Assessment of Conservation Status

ddlat	ddlon	tax	higher.tax.rank	coly
-4.46667	11.4167	Berlinia bruneellii	Fabaceae	1827
-5.66667	29.3500	Berlinia bruneellii	Fabaceae	1989
3.88333	18.6833	Berlinia bruneellii	Fabaceae	1980
4.48333	20.3000	Berlinia bruneellii	Fabaceae	1805
-2.76667	18.4833	Berlinia bruneellii	Fabaceae	1788
-1.26667	24.5500	Berlinia bruneellii	Fabaceae	1993

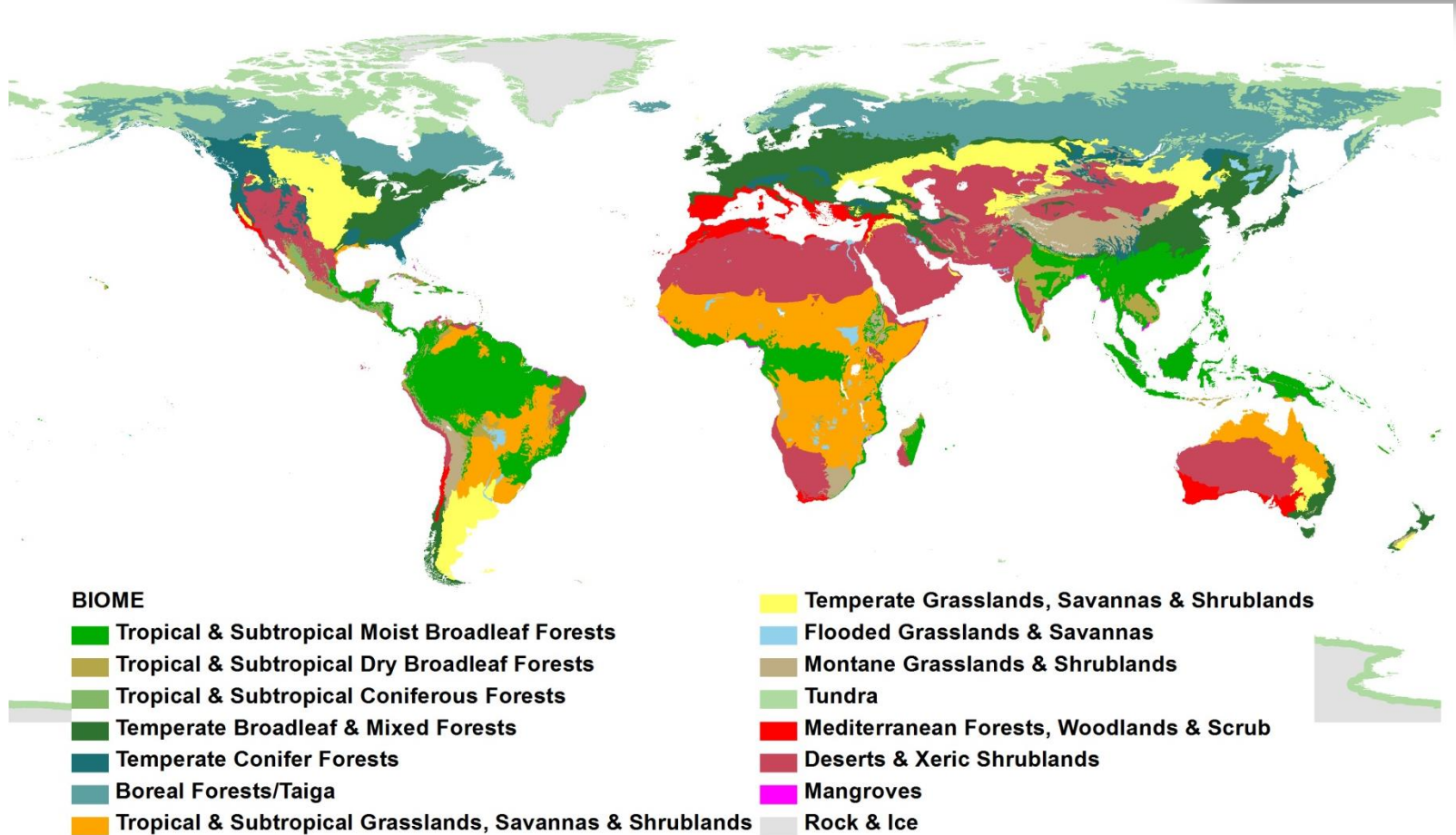
```
IUCN.eval(MyData)
```


5. Conservation assessment - ConR

ConR

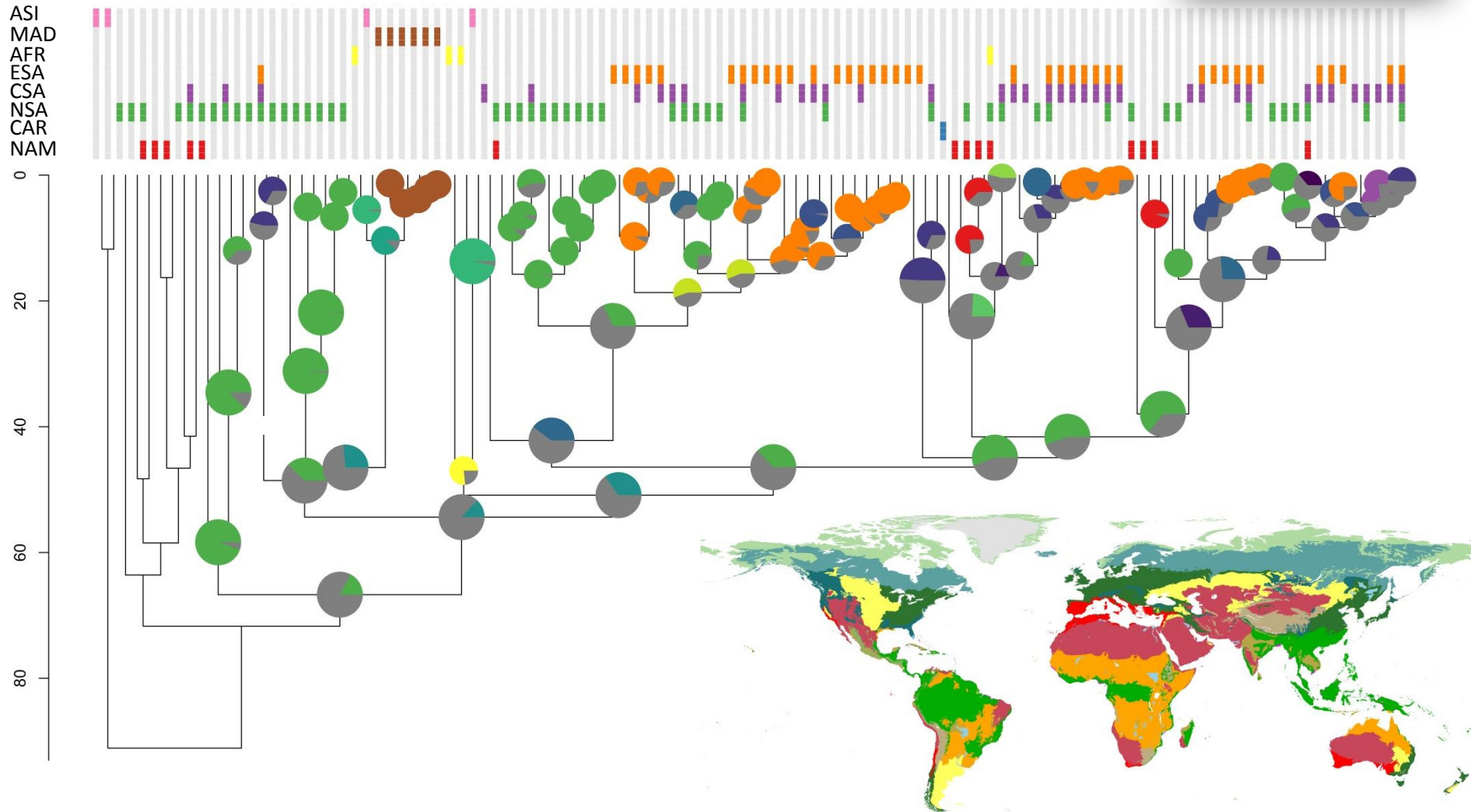


7. Biome classification

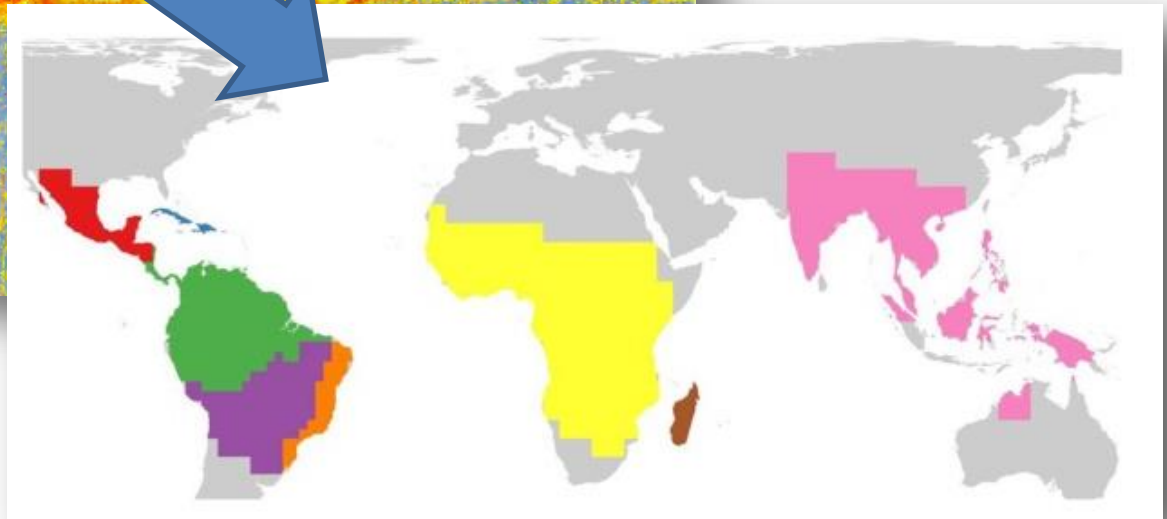
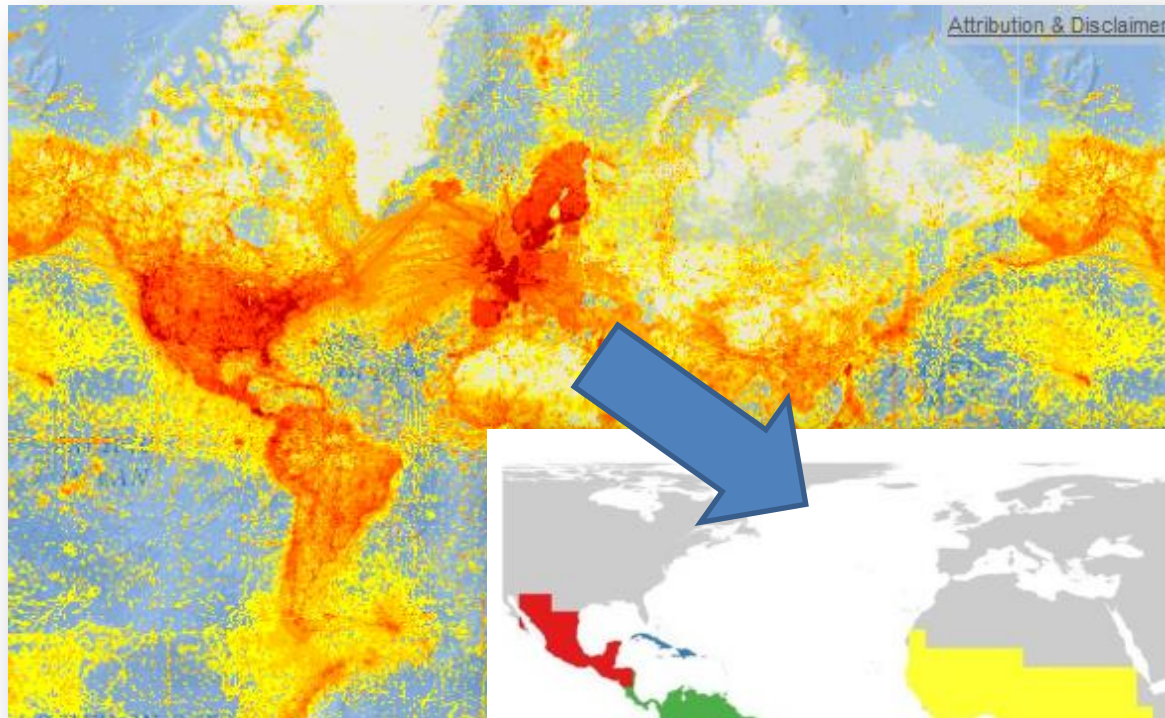


From: Olson et al. (2001) Terrestrial ecoregions of the world: New map of life on earth. Bioscience 51:933-938

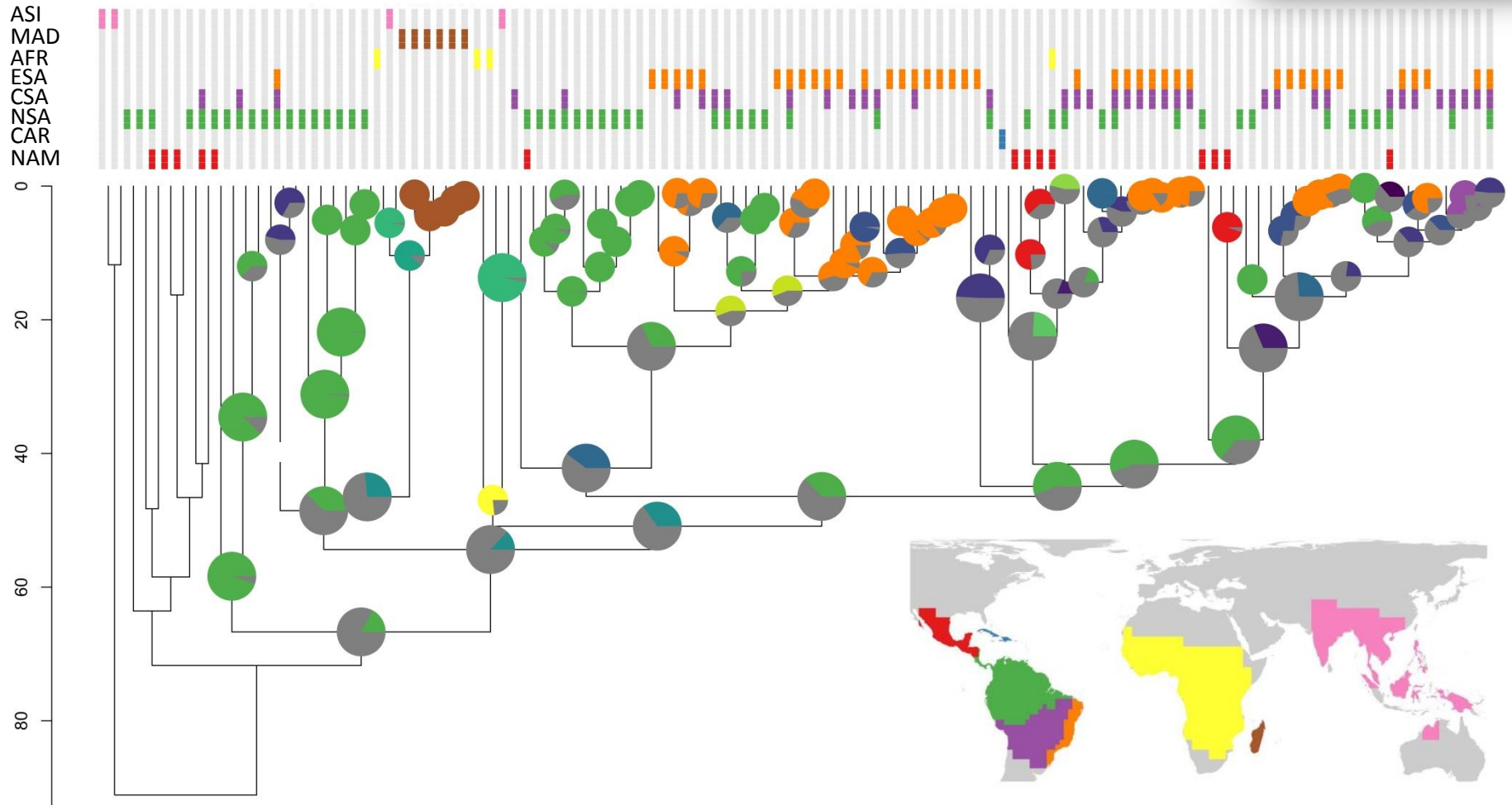
7. Biome classification



6. Bioregionalization



6. Bioregionalization



6. Bioregionalization - How does it work?

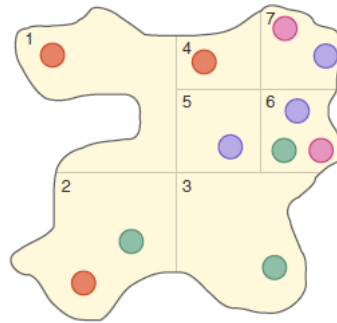


a) Input data

Name	Lat	Long
Species A	6.9	1.0
Species A	6.7	4.7
Species A	1.3	2.8
Species B	2.3	2.9
Species B	1.8	6.4
Species B	4.6	6.6
Species C	4.7	5.3
Species C	5.5	6.8
Species C	6.8	7.6
Species D	7.4	6.5
Species D	4.6	7.4

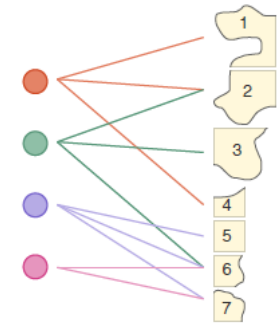
Quadtree
mapping

b) Binned data



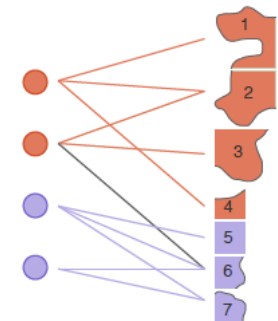
Network
mapping

c) Bipartite network



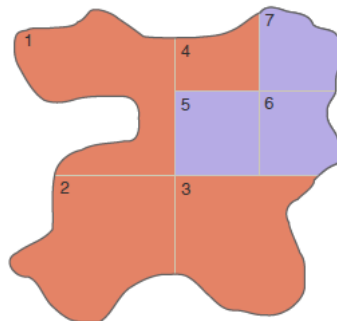
Network
clustering

d) Network clusters



Bioregions

e) Bioregions



Exporting


f) Output data

- svg/png
- csv
- NEXUS
- shapefile
- GeoJSON



Bioregionalization - Workflow





Infomap Bioregions
Interactive mapping of biogeographical regions from species distributions

[Documentation](#)

Data

Load data...

Resolution ?

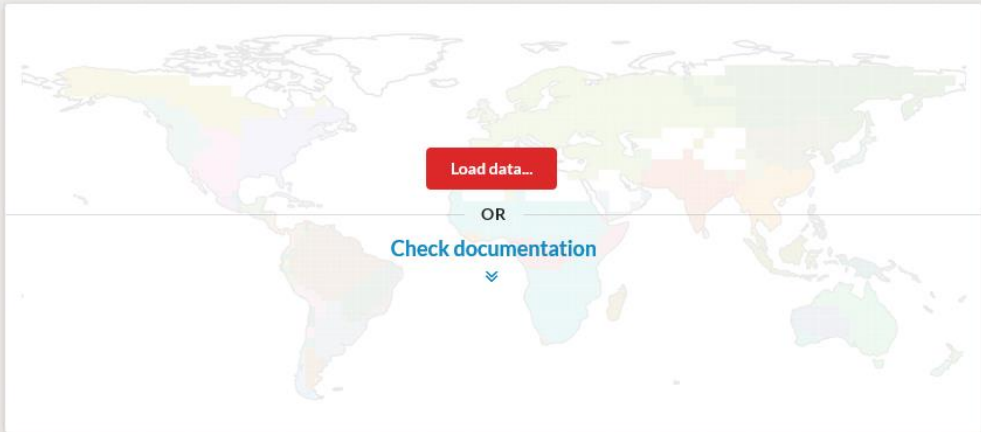
Max cell size: 4°

Min cell size: 1°

Max cell capacity: 100

Min cell capacity: 10


Map



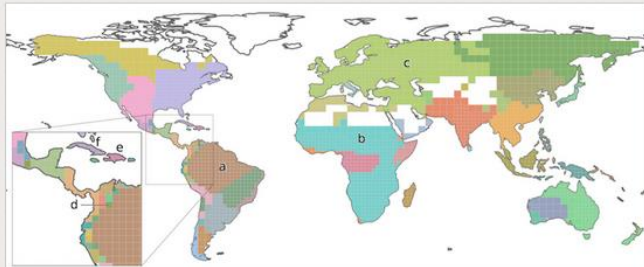
Load data... OR Check documentation

Infomap Bioregions: Interactive mapping of biogeographical regions from species distributions

Daniel Edler, Thais Guedes, Alexander Zizka, Martin Rosvall, and Alexandre Antonelli [pdf], [arXiv:1512.00892]

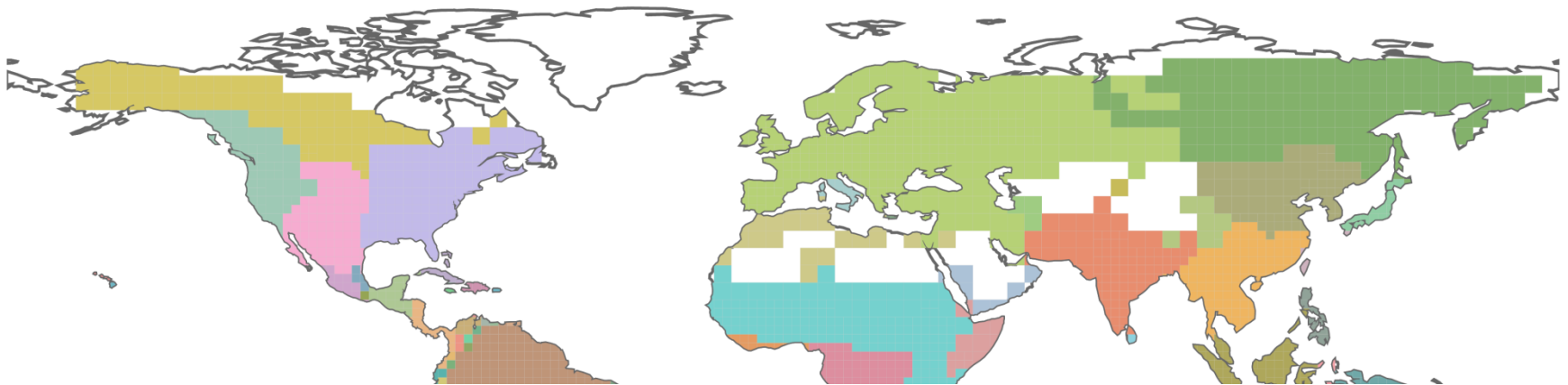


Biogeographical regions reveal how species are spatially grouped and therefore are important units for conservation, historical biogeography, ecology and evolution. Several methods have been developed to identify bioregions based on species distribution data rather than expert opinion. One approach successfully applies network theory to simplify and highlight the underlying structure in species distributions data. However, there are no tools that make this methodology simple and efficient to use. Here we present Infomap Bioregions, an interactive web application that inputs species distribution data and generates bioregion



Location	Records	Species	Cells	Most common species	Most indicative species
(a) South America	42,161	719	167	<i>Trachycephalus venulosus</i> (600) Veined tree frog	<i>Lithobates palmipes</i> (3.3) Amazon River frog
(b) Africa	22,767	652	222	<i>Psephenus saundersi</i> (670)	<i>Blatta orientalis</i> (7.1)

6. Bioregionalization - Output



Location	Records	Species	Cells	Most common species (records)	Most indicative species (score)
(a) South America	42,161	719	167	<i>Trachycephalus venulosus</i> (600) Veined tree frog	<i>Lithobates palmipes</i> (3.3) Amazon River frog
(b) Africa	27,267	553	333	<i>Kassina senegalensis</i> (970) Senegal running frog	<i>Hildebrandtia ornata</i> (2.1) African ornate frog
(c) Eurasia	13,083	103	313	<i>Rana arvalis</i> (1,547) Moor frog	<i>Triturus cristatus</i> (1.3) Northern crested newt
(d) Andes	121	75	1	<i>Pristimantis nervicus</i> (13) —	<i>Pristimantis nervicus</i> (157) —
(e) Hispaniola	181	65	4	<i>Hypsiboas heilprini</i> (28) Los Bracitos tree frog	<i>Osteopilus vastus</i> (73) Hispaniola tree frog
(f) Cuba	214	61	4	<i>Osteopilus septentrionalis</i> (28) Cuban tree frog	<i>Eleutherodactylus varleyi</i> (73) —

Today's schedule

- 8.00-9.00: Finish exercises 1-2
- 9.00-9.30: Zizka's presentation of further analyses and discussion
- 9.30-15.00: Exercises 3-6 on your clade of interest. *(If time allows, additional analyses.)*
- 15.00-17.00: Preparation of slides for tomorrow
- https://github.com/azizka/Biodiversity_Data_from_Field_to_Yield/tree/master/field_data

Project presentation

- 5 minutes, 4-5 slides
 - S1: General information on your clade (#spp/gen, global distribution, a few images)
 - S2: How many records in GBIF & PaleoDB (E1)? How many potentially wrong records in GBIF (E2)?
 - S3: Richness map (E3), biome classification (E7)
 - S4: Bioregionalization (for the larger taxon, e.g. order or family) (E6)
 - S5: Additional analysis if time allows (e.g., conservation status, mapping on a phylogeny, major spatial biases, ... see Tutorials for examples)

Obrigado!



SampBias

**Coordinate
Cleaner**

ConR

Rgbif

<http://antonelli-lab.net/resources.php>

<https://github.com/azizka/CoordinateCleaner>

<https://github.com/azizka/sampbias>