# Biological data: Primary biodiversity data

# What primary biodiversity data are?

# Where do they come from?

# Are they complex?









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Primary biodiversity data should answer 4 questions:

- 1. What was collected / observed (the name of the organism)?
- 2. Where was it collected / observed (locality, geo-referenced or not)?
- 3. When was it collected / observed?
- 4. By whom was it collected / observed?

While normally observations made in the field do contain these 4 information alone, even if sometimes completed by some notes on the site, natural history collections specimens often contain a wealth of other information. While modelling the climatic niche of an organism, we need coordinates of occurrence points. However, when we are trying to define the systematic position of a taxon, many other information could be relevant.

Biological collections are the source of PBD, and include:

- Collections of living organisms
- Natural history collections
- Botanical or zoological observations

Especially in the second case, they a an important source of **falsifiable information**.

A statement is **falsifiable** if some observation can prove it to be false.

The concept was introduced by Karl Popper in his book *The Logic of Scientific Discovery*, in 1934, as the cornerstone of his view of science as critical rationalism.

Specimens stored in natural history collections are falsifiable, in the sense that any hypothesis made on then can be proven false. This is doable by viewing, or physically accessing specimens.

Thus, the relevance of storing specimens when doing any research, from molecular phylogeny (in which specimens are stored in NHM collections, and sequences are stored in online data banks) to taxonomy (in which specimens, especially type specimens, which are the voucher of a new taxon name, are stored in NHM collections).

In the case of primary biodiversity data, accessing a specimen could allow especially the falsification of the name (i.e., one can verify whether the identification made by previous researchers is correct). However, other data can potentially be falsified as well, even if the process is often indirect. Is an observation falsifiable?

Yes. No. Maybe.

It can be potentially falsified indirectly, and directly.

Indirectly, one can check whether the observation falls into the known range of a species. If yes, it could be classified as correct. However.... If one reports a seagull, inside the known range of the species, while observing a blackbird, the observation is incorrect, even if, by indirect falsification, it could be classified as correct.

Directly, one can go in the field and check whether the observation is correct, i.e. whether the reported organism is present in that very location.

However, if the observation is old (months, years...), depending on the lifespan, and phenology of an organism, falsification could not be possible. Plus, if the observed organism is an animal, it could have moved, thus not be present in that very location, even if the observation was actually correct.

Furthermore, even if one goes in the field, and observes the reported organism in the same location, can it be stated that the observation was correct?

### **Insight: PBD falsifiability**

Let's make a simple example.

I go in the field, and report a seagull.

I am not an ornithologist, thus I mistake a blackbird for a seagull.

After a little time, one is willing to model the distribution of seagulls in Trieste, and wants to check my observation.

In the field, in the location I reported, he observes a seagull. Thus, he states that my observation was correct.

But it was not.....

Plus, even if me and the one ho verifies the observation observe the same organism, was it the same individual?





# Big problem: To be used, data should exist in the digital domain....

GBIF	www.gbif.org
Map of Life	https://mol.org/
LifeMapper	lifemapper.org/
IUCN Red List	www.iucnredlist.org/
HerpNET	herpnet.org/
MaNIS	vertnet.org/
OBIS	www.iobis.org/
AmphibiaWeb	http://amphibiaweb.org/
ORNIS	http://ornisnet.org
Bird Life	www.birdlife.org/
Atlas Flora Europaea	www.luomus.fi/en/
	database-atlas-florae-europaeae/
BIEN	http://bien.nceas.ucsb.edu/bien/
REMIB	www.conabio.gob.mx/remib_ingles/
	doctos/remibnodosdb.html?
SpeciesLink	http://splink.cria.org.br/
	GBIF Map of Life LifeMapper IUCN Red List HerpNET MaNIS OBIS AmphibiaWeb ORNIS Bird Life Atlas Flora Europaea BIEN REMIB SpeciesLink



Occurrence records 1.403.571.225

Datasets 51.736 Publishing institutions 1.587

Peer-reviewed papers using data 4.362



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43 VOTING PARTICIPANTS 15 ASSOCIATE COUNTRY PARTICIPANTS 38 OTHER ASSOCIATE PARTICIPANTS 1.293 PUBLISHERS

### The GBIF - some figures [at 2021/03/16, 5:52 pm]:

1.662.149.688 occurrence records

57.008 datasets

1.655 publishing institutions

5.579 peer reviewed papers using GBIF data



#### Complete species occurrence records accessible through GBIF over time



#### Complete observation records accessible through GBIF over time



#### Complete specimen records accessible through GBIF over time

Observation records are the most complete, since they often are natively in the digital domain, especially when they come from citizen science activities.

Basis of record	^
Observation	19.653.975
Machine observation	11.912.825
Human observation	1.105.925.840
Material sample	25.326.297
Literature	219.987
Preserved specimen	166.087.620
Fossil specimen	9.029.568
Living specimen	1.637.949
Unknown	17.147.671

Furthermore, when they are not, their digitization is often far easier that for natural history collection specimens.

Just to give you an idea of the relevance of *citizen science* as far as GBIF data are concerned.....



### 50% of occurrence records on GBIF are citizen science observations





However....

#### There are > 8 000 000 seagull occurrence records



Larus argentatus subsp. argenteus by G.Droege via Botanic Garden and Botanical Museum Berlin-Dahlem. Photo licensed under CC BY-SA 3.0

#### Top insect is the red admiral butterfly 200k records



Vanessa atalanta by W.-H. Kusber via BoBO - Botanic Garden and Botanical Museum Berlin-Dahlem. Observations. Photo licensed under CC BY-SA 4.0

#### Top mammal is the roe deer 140k records



Capreolus capreolus by Trine Brevig via the Norwegian Species Observation Service. Photo licensed under CC BY 4.0

#### Top plant is the common nettle 100k records



Urtica diolca subsp. diolca by Peter de Lange via iNaturalist. No copyright.

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# GBiF data: should we trust them (human observations especially)?

# Yes.

# No.

# Maybe...

# Examples of biases due to low quality, or poor PBD

In a paper of 2015, Medone et al. Described the possible switch in climatic niche for two insects of the family Triatominae, which are vectors for the parasite *Trypanosoma cruzi*, which is a relevant disease in South America.

The authors, starting from expert accessed distributional maps, derived a great amount of georeferenced occurrence points for the two species, and developed maps of current and future (2050) distribution, with the aim of understanding which areas will be more affected by disease after the impact of foreseen climate changes.



Figure 1. Climatic suitability changes from current to 2050 conditions for (a) & profess and (b) T. infestance. Colours indicate climatic suitability transitions between the three main suitability categories (low, medium and high). (Online sension in colour.)



Figure 3. Current dimatic suitability (base map green to red/grey to black colours) and predicted number of new human cases of *R. cutal* infection (current: black bar, 2050; blue/grey bar) in Argentina. Provinces were numerated (white dride on the map) to fadilitate the identification on the pie charts (number preceding name). Pie charts indicate the 'relative contribution' (%) of each province to the total number of new predicted cases over all high transmission dsk provinces. Upper pie thart: current conditions; lower pie chart: 2050; conditions. (Chine version in colour.)



Figure 7. Current dimatic suitability (base map green to red/grey to black colours) and predicted number of new cases of *in. auxi* human infection (current: black bar, 2050; blue/grey bar) in Venezuela. States were numerated (white circle on the map) to fadilitate the identification on the pie charts (number preceding name). Fie charts indicate the 'relative contribution' (%) of each province to the total number of new predicted cases over all high transmission risk states. Upper pie chart, current conditions, lower pie chart, 2050 conditions. (Online version in colour.)

It is obvious that the presence points obtained by the authors are "pseudo-presences".

Since they derive from maps depicting not the **area of occupancy** of the two species, but the **extent of occurrence**, they hardly can be used for making assumptions on the actual distribution of a taxon.

Furthermore, deriving considerations on the possible spread of parasitic infections on the basis of such data is far more than a long shot.

To highlight this issue, together with the importance of correct identification of each specimen (or observation), Lozier et al., in 2009, made an interesting exercise modelling the niche of a crypto-species, the Sasquatch, in western North America.

They collected all the data of sightings of the "animal" and of its footprints, geo-referenced them *a posteriori* with the highest degree of confidence as possible, and produced models for present and future distribution as an effect of climate change.

Furthermore, they compared the models with those of the black bear, animal which often is misidentified as Sasquatch.





Figure 1 Map of Bigfoot encounters from Washington, Oregon and California used in the analyses. Points represent visual/auditory detection, and foot symbols represent coordinates where footprint data were available. Shading indicates topography, with lighter values representing lower elevations.

Figure 2 Predicted distributions of Bigfoot constructed from all available encounter data using MAXENT (a) for the present climate and (b) under a possible climatechange scenario involving a doubling of atmospheric CO2 levels. Results are presented for logistic probabilities of occurrence ranging continuously from low (white) to high (black). Differences between (a) and (b) are shown in (c), with whiter values reflecting a decline in logistic probability of occurrence under climate change, darker values reflecting a gain, and grey reflecting no change. A predicted distribution of Ursus americanus in western North America under a present-day climate is also shown (d). White points indicate sampling localities in California, Cregon and Washington taken from GBIF (n = 113 for training, 28 for testing; comparewith Fig. 1) used for the maxent model with shading as in (a) and (b); black points indicate additional known records not included in the model.



The authors were not willing to criticize the use of ENMs as a whole, but to evidence that data quality can badly affect the results and their interpretation.

In particular, they evidenced that:

- careful scrutiny of specimen records should be encouraged
- assessing specimens should be done whenever possible (taxonomic impediment)
- identifications should be made by expert taxonomists (taxonomic impediment), and specimens identified by taxonomists should be preferred when available (specimens > observations)
- all efforts should be made to ensure taxonomic accuracy when digitizing specimen data (taxonomic impediment)

As a conclusion, they state that today more than in the past well trained taxonomists are fundamental.

An interesting study by Romero et al., 2014, describe the effect of changing taxonomy on two newt species, *Triturus pygmaeus* and *T. marmoratus*, both known to occur in Spain. The two were considered a unique species, but are now treated as separate species thanks to DNA evidences.

It is interesting to notice how the models are affected by a separate treatment vs. the modelling of the two as a single taxon.

It is especially evident that the rarer taxon changes in suitability in consequence of climate changes is badly underestimated by the second approach.



Triturus pygmaeus



Triturus marmoratus



Figure 1 The study area in the European context. Current distributions of *Triturus pygmaeus* and *T. marmoratus* represented in 10 km  $\times$  10 km UTM cells within the study area of mainland Spain (data from Pleguezuelos *et al.*, 2004).



**Figure 2** Favourability in mainland Spain predicted for (a) *Triturus pygmaeus* and (b) *T. marmoratus*, as separate species, and (c) for both *Triturus* taxa as belonging to the same species, respectively, according to each climate model and for each time period – ranging from 0 (low favourability) to 1 (high favourability). Increment (I) and maintenance (M) values are shown at the lower right corner of each map.



**Figure 3** Discrepancy values (difference between favourability predicted for both *Triturus* taxa as belonging to the same species and favourability predicted for the combination of *T. pygmaeus* and *T. marmoratus* as separate species) in mainland Spain according to each climate model and for each time period. When favourability was maximum for the *Triturus* spp. and minimum for the combination of the species, discrepancy was +1 (shown in red); in the opposite case, discrepancy was -1 (shown in blue). Total discrepancies (sum of all absolute discrepancy values, TD) are shown at the lower right corner of each map.

In this case, is evident that an incorrect taxonomic delimitation of one or more taxa can badly influence the results of a model, together with the interpretation of the results.

This is particularly relevant when these results have a consequence in conservation practices.

Amphibians are seen as possibly the most endangered group because of human activities. Developing incorrect conservation practices following misleading models, generated by incorrect taxonomic knowledge (**taxonomic impediment**), could play a major role in the future loss of biodiversity, especially in extremely vulnerable groups.

An interesting approach to data cleaning of datasets, and in particular for datasets obtained by the GBIF, is depicted by Smith et al., 2016.

In the paper, the authors used GenBank data to develop a niche model of the lichen *Usnea longissima*. Once developed, the model has been compared with the data obtained from the GBIF for the same taxon.

The comparison evidence a huge number of incorrect records from the GBIF dataset, from ca. 600 to more than 3000, depending on the limits set in the model. In particular, it has been evidenced that all the occurrences of *U. longissima* from the southern hemisphere are incorrect, and derived from misidentifications, since the tropical area is a strong ecological barrier for the species.

There is anyway a further issue: even if an occurrence point is falling in the predicted area, it does not mean that it is a correct occurrence record. The principle of accepting records which fall inside the known distribution of a taxon can lead to overestimation of populations size, or, as an example, to an underestimation of local varieties in comparison with nominal species, or most common varieties.



Fig 2. Best fitting MexEnt model for Usnea longissima based on 1477 sequenced samples corresponding to 160 localities from Rolstad et al. (2013), indicated by shaded areas ranging from pale blue-green to red. Bright blue areas indicate range of predicted absence. Map is overlayed by occurrence records from GBIF (white dots), and those falling outside the predicted range are marked with red circles. One dot may include more than one GBIF record (S1 Table).

# However....

# ...even with their limits and issues, PDB are the base on which we build SDMs.

Thus, what is required are tools for quality control, and a lot of work to select properly the data we aim at using.

# How to obtain PBD

There are three way to obtain PBD:

- 1. Go in the field and collect them
- 2. Find and prepare an existing dataset
- 3. Get them from an online repository

The third is obviously the simplest, since downloading data from the GBIF is a quick operation, which could be done by a web browser, or directly in R.

However, when downloading PBD from the GBIF, one intrinsically accepts to trust them, since there is no way (but for NHM specimens) to actually falsify them. This is normally done by many researchers every day, all over the world. It can be a relevant issue, but it is often overlooked. Plus, by citing the dataset, each inference made on the data is falsifiable, thus providing a sort of "alibi", an implicit warning sign, stating something like: "*Ehi, we obtain this, but if you want to check, you can anytime. Do not use our results without checking please*". Problem is, these warnings are often "written" in veeeeery small characters. The consequence is that often results of many researches are accepted in scientific journals without an adequate review, and maybe used as a baseline for other researches, or worse, for relevant decision making on the management of ecosystems. In any case, however, the GBIF - as well as other online data aggregators - remains a fundamental resource for modern research.

Dataset can be obtained from the GBIF in two ways A) by a web browser B) directly from R

By mean of a web browser it is simpler to set all the relevant filters, and especially do delimit the survey area, by simply drawing a polygon on a map (see later). However, at the very end, the two processes produces the same result as far as data are concerned.

This is not true for DOI and persistence of the downloaded dataset, which could not be assured by downloading data through R.



Occurrence records 1.403.573.093

Datasets 51.760 Publishing institutions
1.587

Peer-reviewed papers using data 4.362



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Basis of record	×	Asplenium radicans L.	Brazil	25.28, 50.0W	2020 January	
Location	~	Hypoxylon cercidicola (Berk. & M.A.Curtis e	Austria	48.4N, 16.2E	2020 January	
Year	~	Hemitrichia intorta (Lister) Lister	Austria	48.2N, 16.4E	2020 January	
Month	~	Melithreptus gularis (Gould, 1837)	Australia	35.DS, 138.6E	2020 January	
Dataset	~	Melithraptus gularis (Gould, 1837)	Australia	35.0S, 138.6E	2020 January	
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Media type	~	Macroderma gigas (Dobson, 1880)	Australia	26.4\$, 131.7E	2020 January	
Publisher	~	Dasycerous cristicauda (Krefft, 1867)	Australia	30.55, 131.8E	2020 January	
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Direct download from R is possible by mean of several different functions, included in different packages.

We will use the function *gbif* of the library *dismo* 

We will also perform some data cleaning, and especially: A) remove records with no data in the latitude or longitude fields B) remove duplicate records

We will also store a *comma separated value* (csv) file in the working directory, containing the data which are normally necessary to run an algorithm, i.e. longitude and latitude

# Let's switch to R