How to compute a Habitat Suitability map without absence data? Use the Ecological Niche Factor Analysis (ENFA) !

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(1) Habitat Suitability (HS) maps are commonly built on **presence/absence** data, but the latter are most generally **unavailable** or **unreliable**.

HS maps are basically computed by **fitting** some statistical or numerical **model** on environmental data and species distribution data.

Classical methods (e.g. logistic regression, discriminant analysis, GLM, etc.) need both species presence and absence data; presences attest a good habitat and absences attest a bad habitat.

An "absence" (=lack of observation) may have three causes:
1° the species is present but was **not detected** => **FALSE ABSENCE**
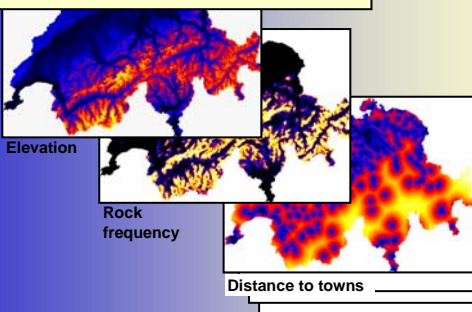2° the habitat is suitable, but the species is **not yet/no more present** => **FALSE ABSENCE**
3° the habitat is actually **not suitable** => **TRUE ABSENCE**

(2) Ecogeographical variables (EGV)

The EGV describe **environmental**, **topographical** and **anthropic** parameters of the study area.

Elevation

Rock frequency

Distance to towns

(3) Presence data

Only presence data are needed. This makes ENFA particularly robust to the quality of data.

(4) Ecological Niche Factor Analysis (ENFA): Marginality and Specialisation

The ENFA's principle is to compare EGV **distribution** for the presence data set (**species distribution**) to that of the whole area (**global distribution**).

Like the Principal Component Analysis, the ENFA summarises many EGV into a few **uncorrelated factors** retaining most of the information. But here, the factors have an **ecological meaning**.

(5) HS map computing

The species distribution on the factors allows to compute a HS index for any set of EGV values and thus to draw the HS map.

Specialisation factor

Global distribution

Species distribution

Marginality factor

Biomapper
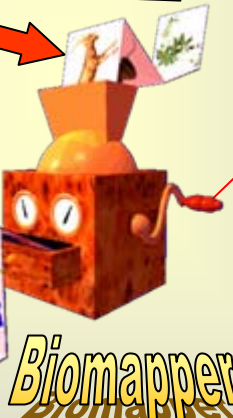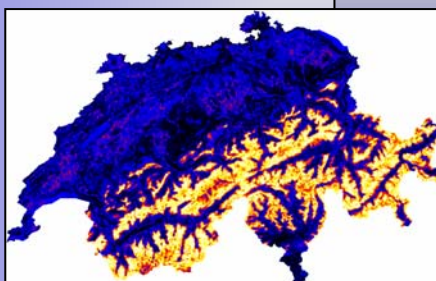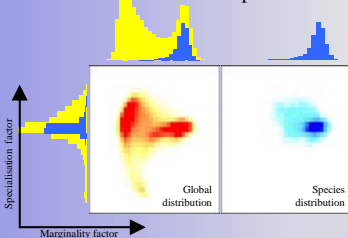
4a. Marginality Factor

It is the direction on which the species niche differs most from the available conditions in the global area.

It is computed by drawing a straight line between the centroids of the global- (yellow) and the species (blue) distribution.
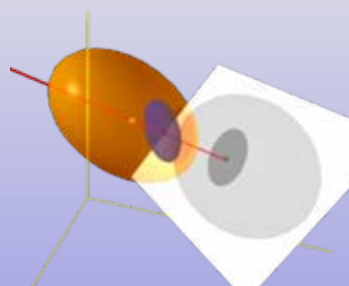
4b. Specialisation Factors

Once the marginality has been removed, a specialisation factor can be extracted by computing the direction that maximises the ratio of the variance of the global distribution (yellow) to that of the species distribution (blue).

It is then removed and this procedure is repeated until all the information has been extracted. At the end, most of it is accounted for by a few of the first factors and only those will then be used.

Min species variance

Max global variance

Specialisation factor
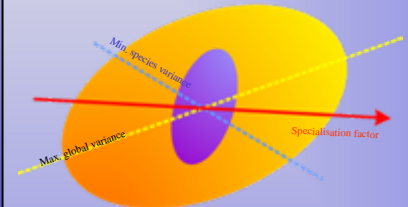
(6) Download Biomapper

The software package **Biomapper** encompasses ENFA and many tools needed to prepare and explore the EGV maps, as well as evaluate the HS map. It is freely available at the following URL:

www.unil.ch/biomapper/