



A small green seedling with two leaves grows out of dark brown soil. The background is blurred, showing more of the same soil and a bright light source from the right.

Trait-based approach in community ecology

Course structure

Theoretical course (2h)

- General introduction
- Community assembly and null model
- Functional diversity indices
- Functional spaces
- Trait standards, data bases and missing data

Practical (4h)

- How to use R ? (~30 min , install R, packages, solving problem version, etc...)
- Ecological data bases (1h, import files, explore data, identify errors/NA, etc...)
- Propose a scientific question (~30 min)
- Propose analyses to answer the question (2h, statistical analyses, figures/tables, R script)

Course structure

Evaluation

- Participation
- Questions

Course material available in github



ID: **AureleToussaint**

Repository: **Master24**
> Code > Download (Zip)



All analyses are made in **R**. The most popular language in ecology.

Other languages are also possible: PyThon, Julia, ...

Course material available in github



Knowing R is **NOT** mandatory but highly recommended

R scripts of Figures/analyses are available in GitHub.

- If you know R, perfect !
- If not, don't panic !

Biodiversity has fascinated humans for long time

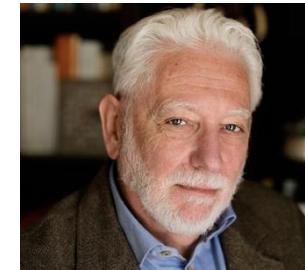
30,000 years ago...



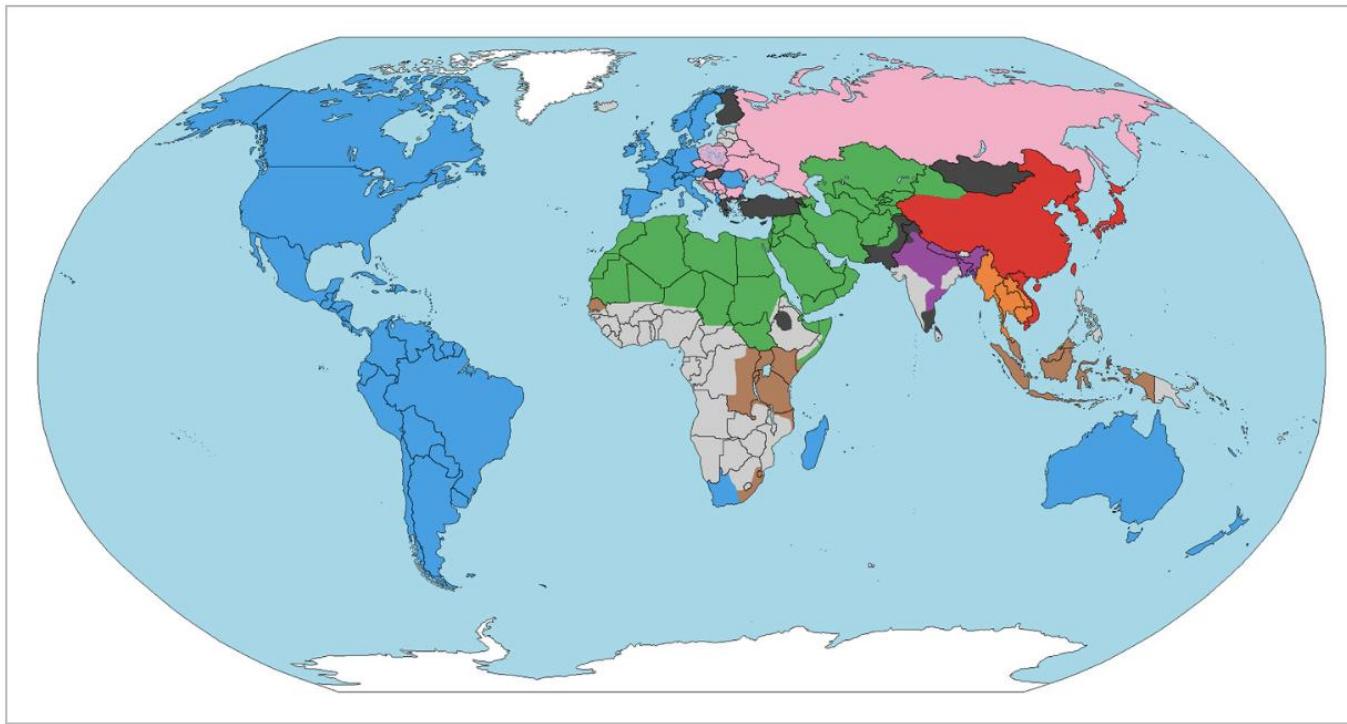
Chauvet-pont-d'arc (Ardeche, France)

Different view of biodiversity across the world

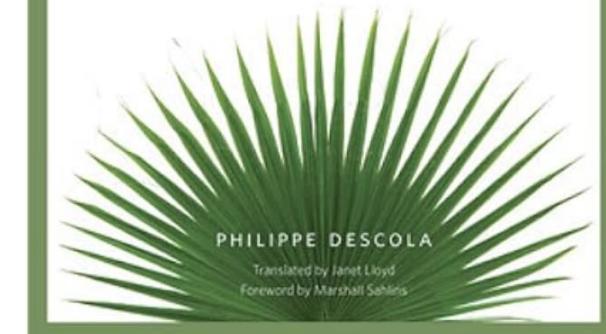
Philippe Descola



"The idea of nature exists in most cultures, so awareness of the diversity of the concepts of nature is essential for nature conservation"

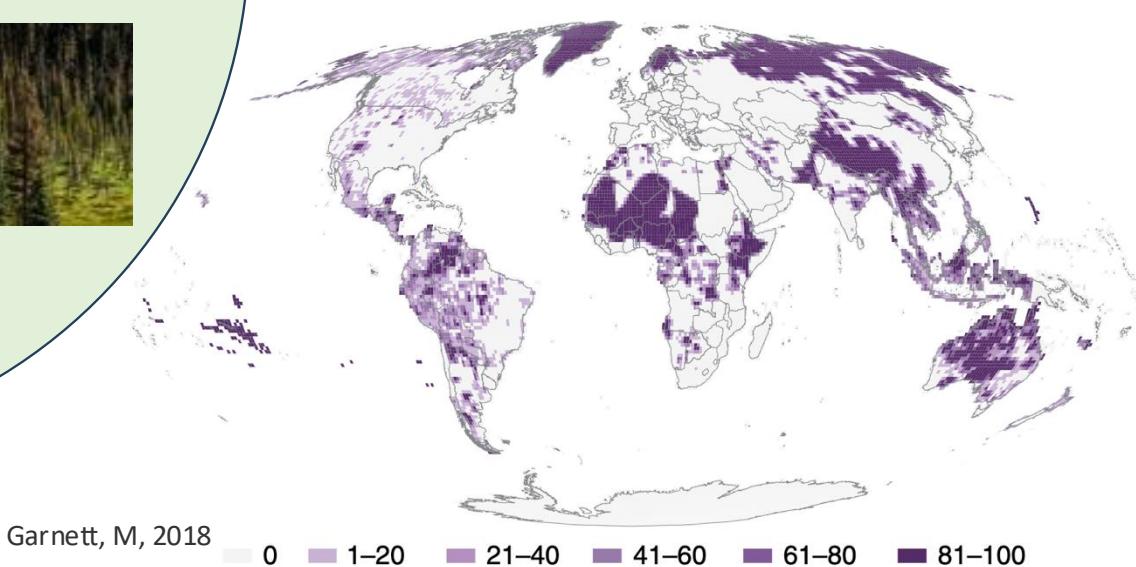
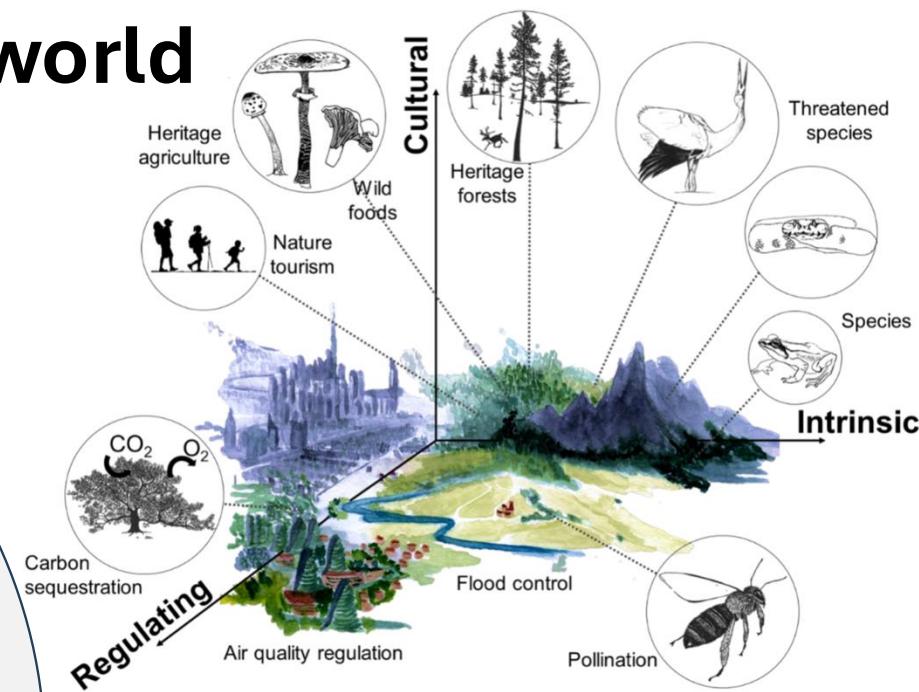
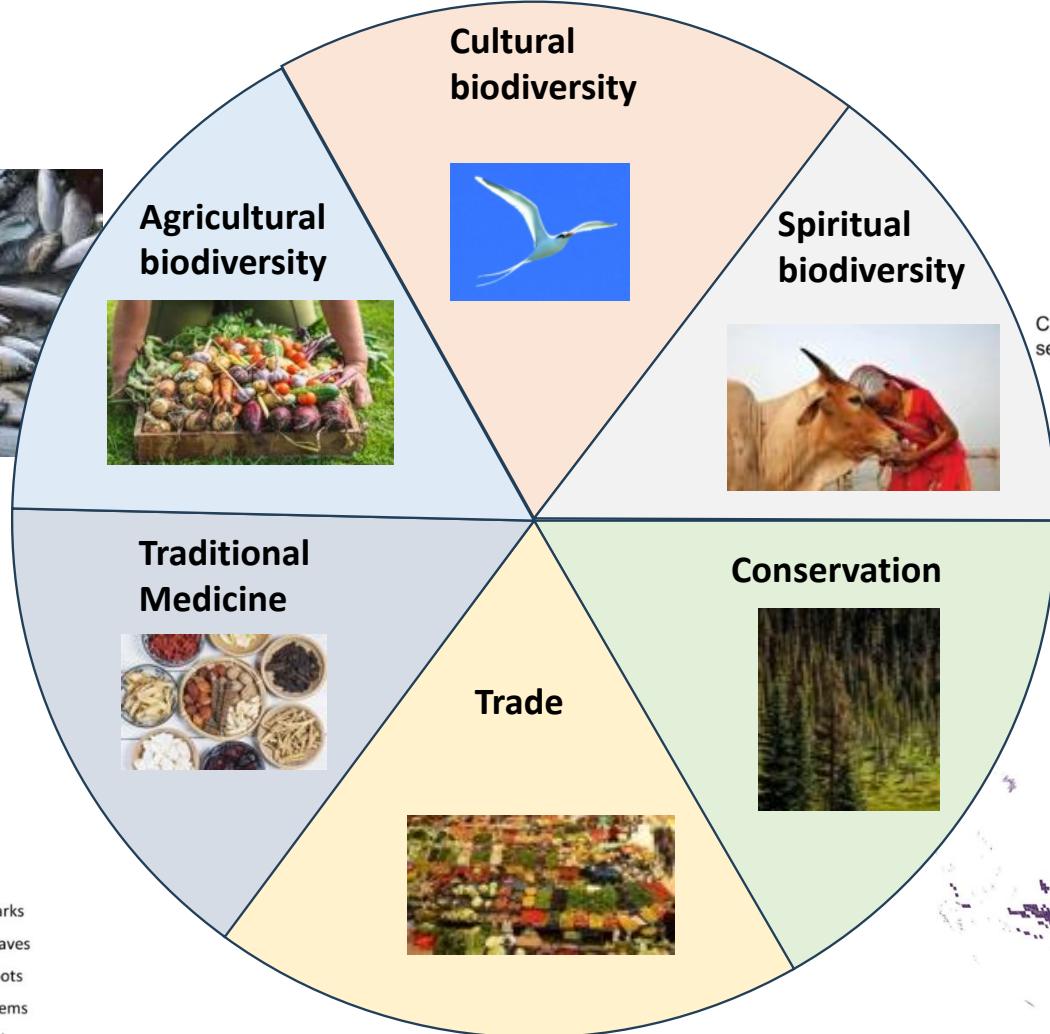


BEYOND
NATURE AND CULTURE



Ducarme, F., Flipo, F. and Couvet, D. **How the diversity of human concepts of nature affects conservation of biodiversity.** *Conservation Biology* (2021).

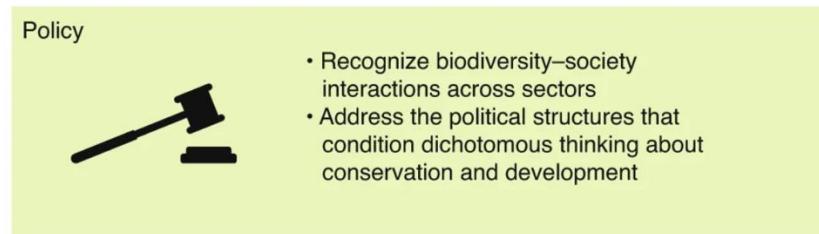
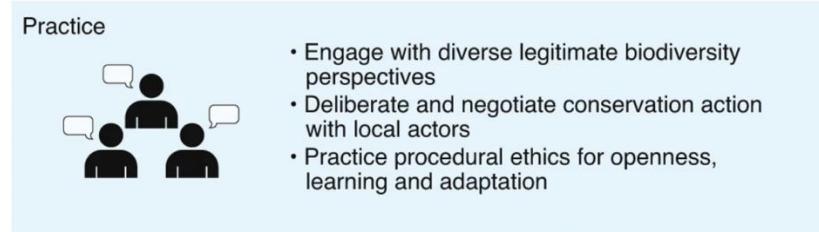
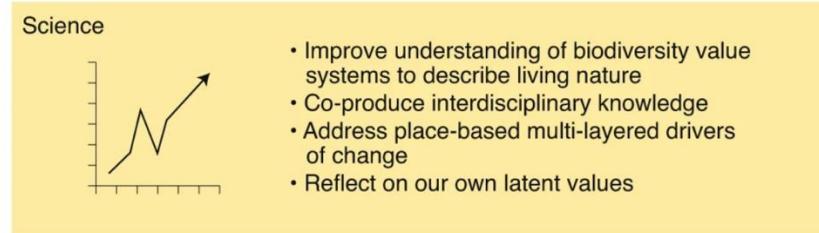
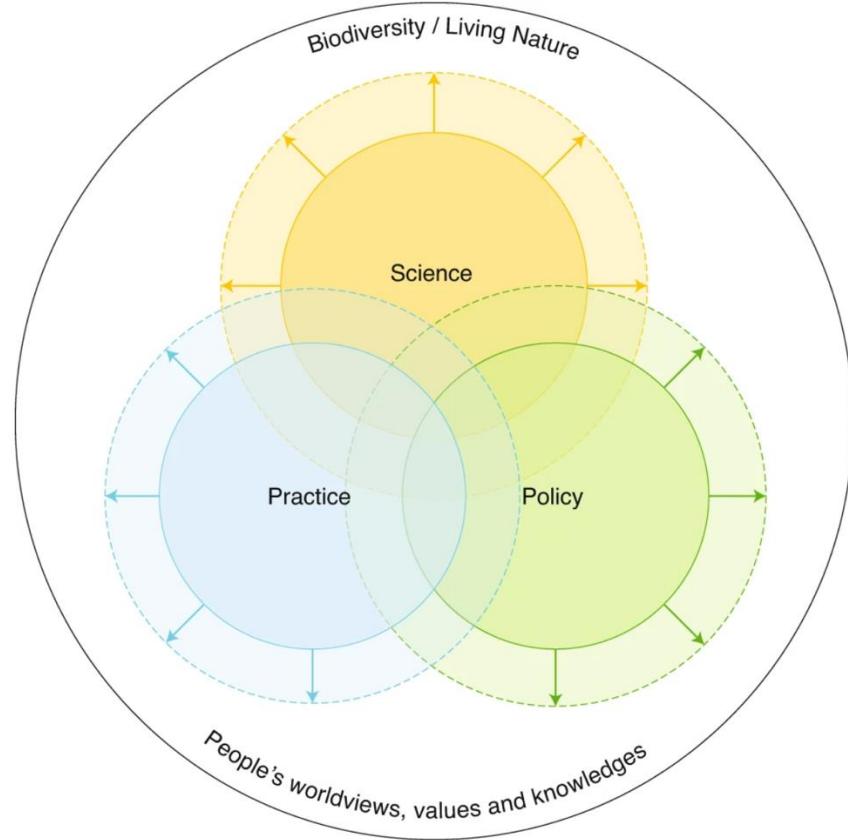
Different view of biodiversity across the world



Challenge of protection of biodiversity • • •

• • • is a challenge of pluralism

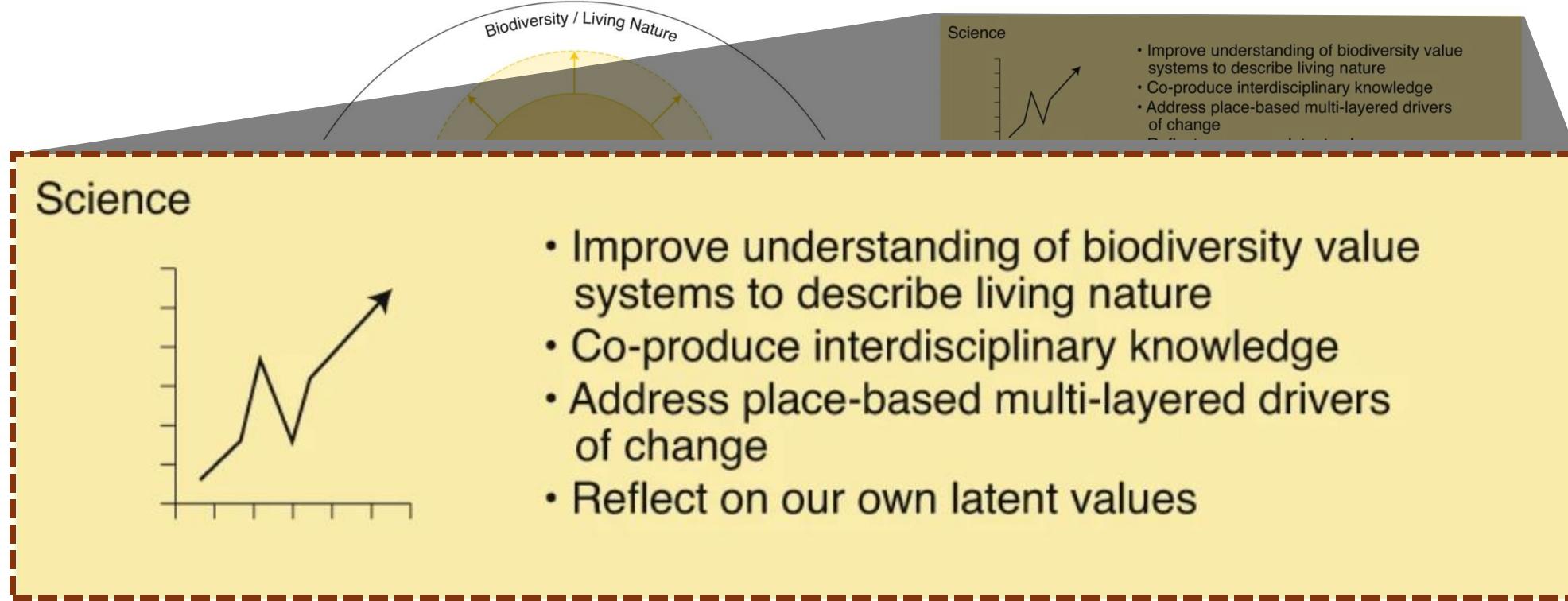
From: [Biodiversity and the challenge of pluralism](#)



Arrows indicate the need for expanding interactions among science, policy and practice to grapple with the plurality of biodiversity/living nature, given people's multiple worldviews, values and knowledge systems.

Challenge of protection of biodiversity

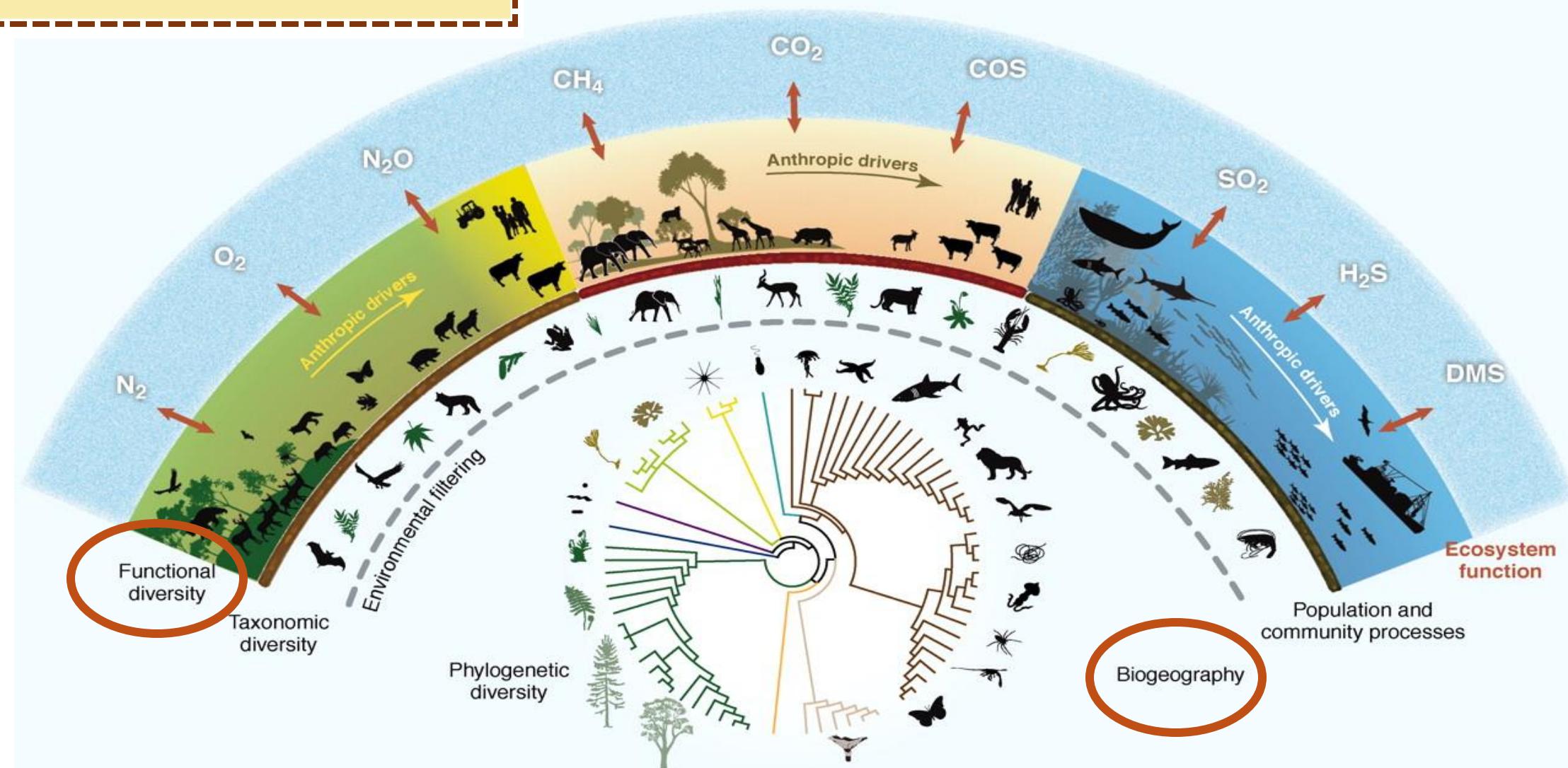
From: [Biodiversity and the challenge of pluralism](#)



people's multiple worldviews, values and knowledge systems.



- Improve understanding of biodiversity value systems to describe living nature
- Co-produce interdisciplinary knowledge
- Address place-based multi-layered drivers of change
- Reflect on our own latent values



Why functional ecology ?

To overcome some of the well-known problems of species-based approaches.

It is possible to:

- Connect community functions such as production to environmental changes via functional traits.
- Address evolutionary processes because evolution selects organisms in a community according to their function and not their taxonomy.
- More suitable than species-based approaches for generalizations across species as they are not tied to taxonomy.
- Benefit from the rapid expansion of trait databases more than species-based approaches, because trait-based approaches are not dependent on species-specific trait information
- Trait databases are especially well developed for plants.

Functional
ecology

Measure the roles or functions that species plays in the community



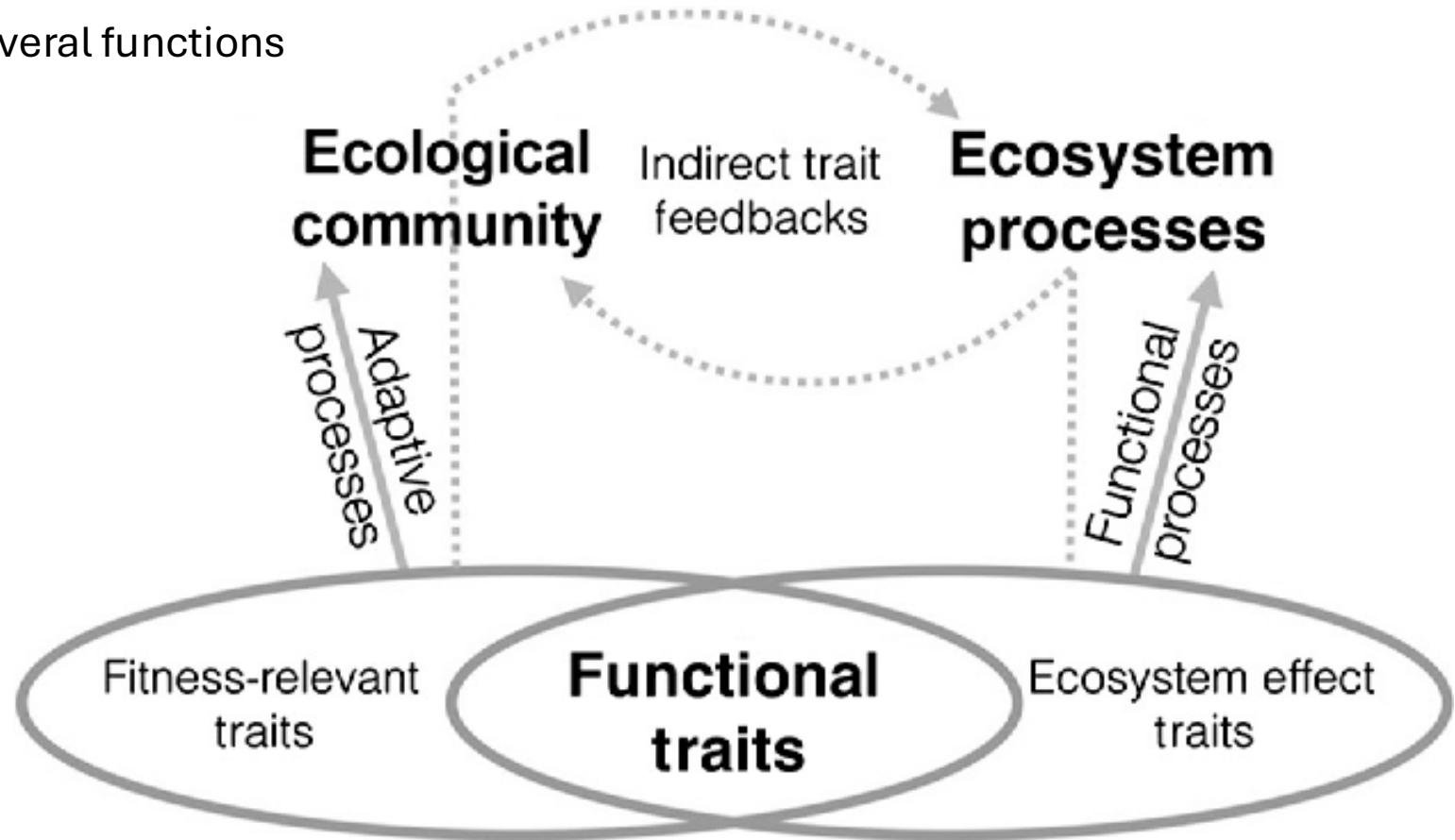
Trait-based approach: describe species through a set of trait

Why functional ecology ?

- Beyond the taxonomic approach

Example: a plant = 1 organism + several functions

- Photosynthesis
- Respiration
- Absorption
- Stockage
-



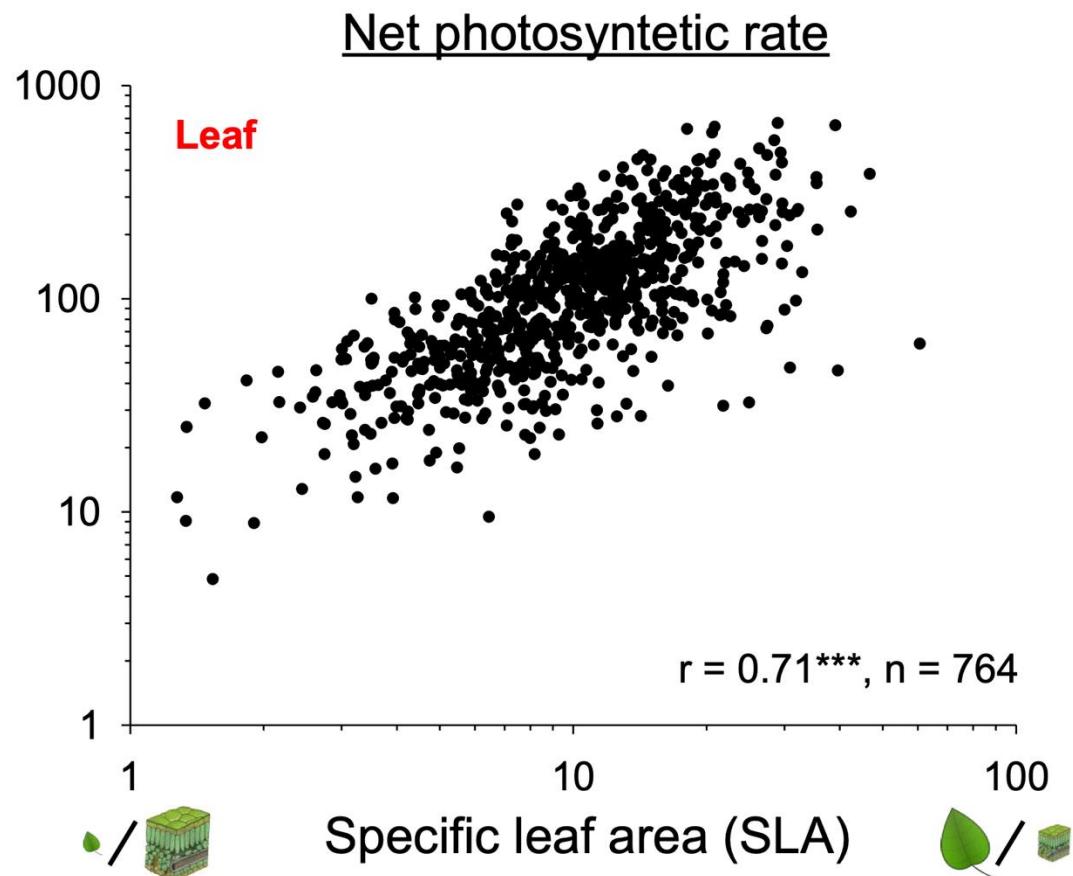
Trait-based approach

There are four requirements for a trait (Lavorel et al., 2007):

- Connected with a function;
- Relatively easy to observe and quantify;
- Possible to measure it in a standardized way across a wide range of species and environmental settings;
- A range of values that is comparable among individuals, species and habitats.

Trait-based approach

- Example: link between photosynthetic rate and SLA



Trait-based approach

Functions

Fecundity
Dispersal
Recruitment

Light interception
Competitive ability

Resource acquisition/growth
Litter decomposition

Absorption (nutrients, water)
Carbon fluxes (exsudation...)
Underground competition



« Functional markers »

Seed mass
Reproductive height
Reproductive phenology

Vegetative height

Traits of living leaves
NIRS spectrum

Root density
Root diameter, length
Root specific area

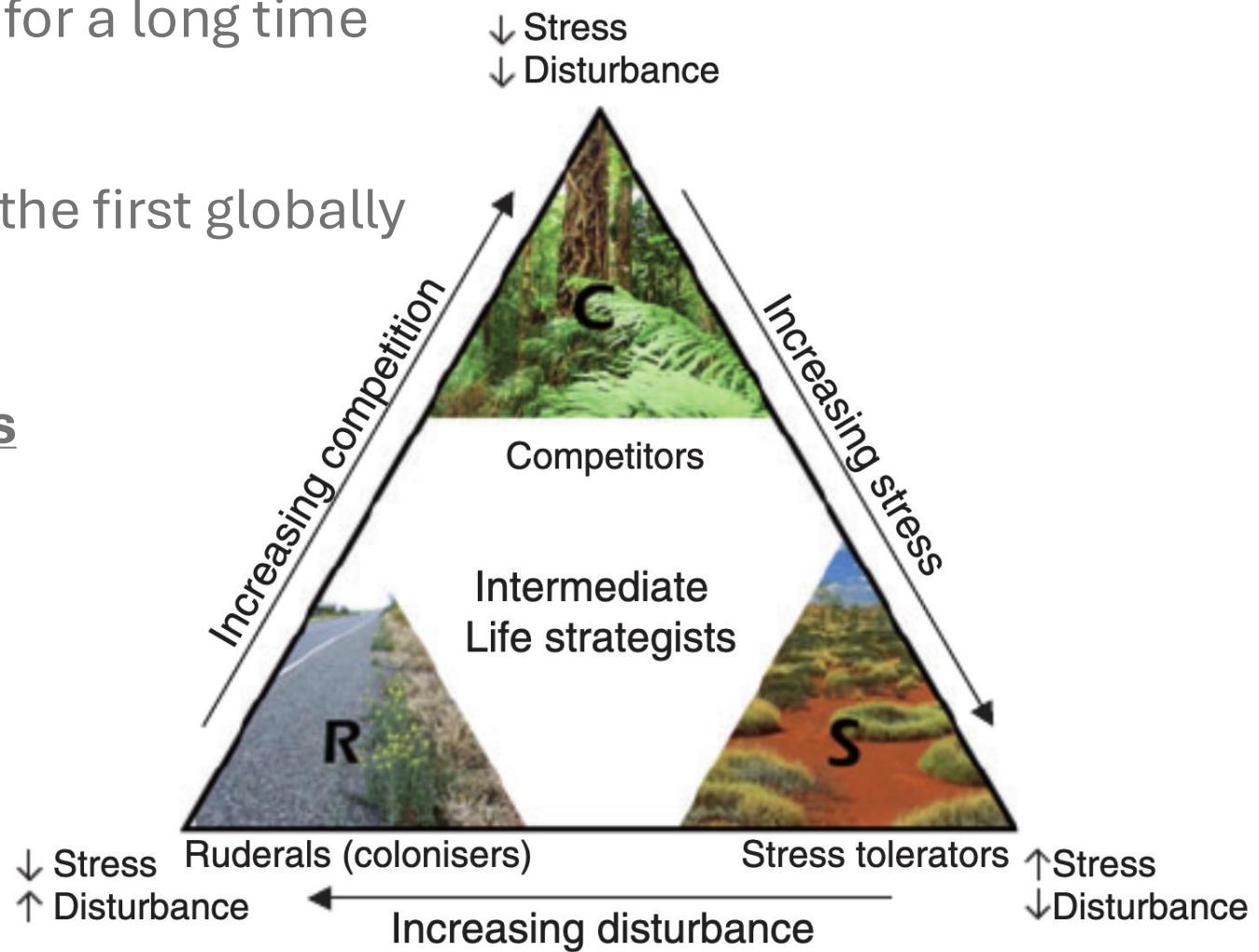
Trait-based approach

Trait-based approaches are an alternative to species-based approaches for functionally linking individual organisms with community structure and dynamics.

Rather than focusing on the species identity of the organism, the focus is on the organism traits, which represent their physiological, morphological, or life-history characteristics.

Historical approach

- Traits have been used in ecology for a long time
- Grime's (1977) CSR triangle was the first globally accepted concept
 - Continuous functional traits



From functional groups...

To classify organisms, a first approach is to group them based on shared morphological features.

-> "boxes"

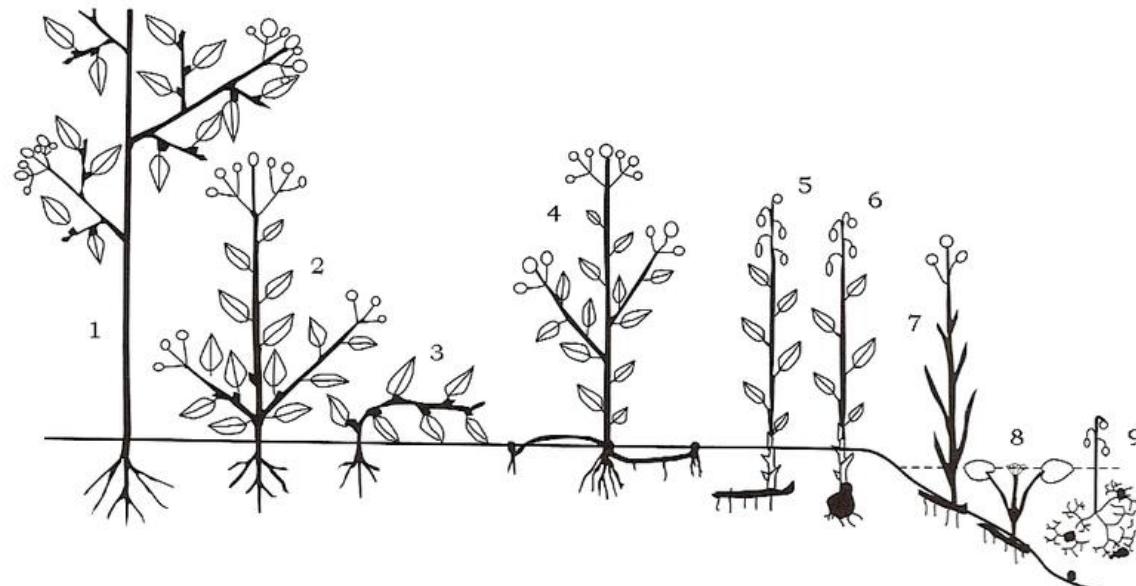
Alexander Von Humboldt (1806)

From functional groups...

To classify organisms, a first approach is to group them based on shared morphological features.

-> "boxes"

Christen C. Raunkier (1934) develop the concept of *plant life-form*



From functional groups...

The concept of trait trade-offs helps to explain why, during speciation and local adaptation; organisms evolve different traits and life strategies.

The r/K selection

... to continuous traits

Functional ecology shifted only much later from functional groups to functional traits and thus from species grouped because they use similar strategies to the similar characteristics underlying those strategies (Yang et al., 2015b).

Trait definitions: know what you talk about

Categorical traits

Nominal traits

Performance traits

Behavioral traits

Traits

Functional traits

Ecological traits

'Hard' traits



Character traits

Morphological traits

Life history traits

Attributes

Ecophysiological traits

Demographic traits

Characteristics

Phenotypic traits

Properties

Effect traits

Biological traits

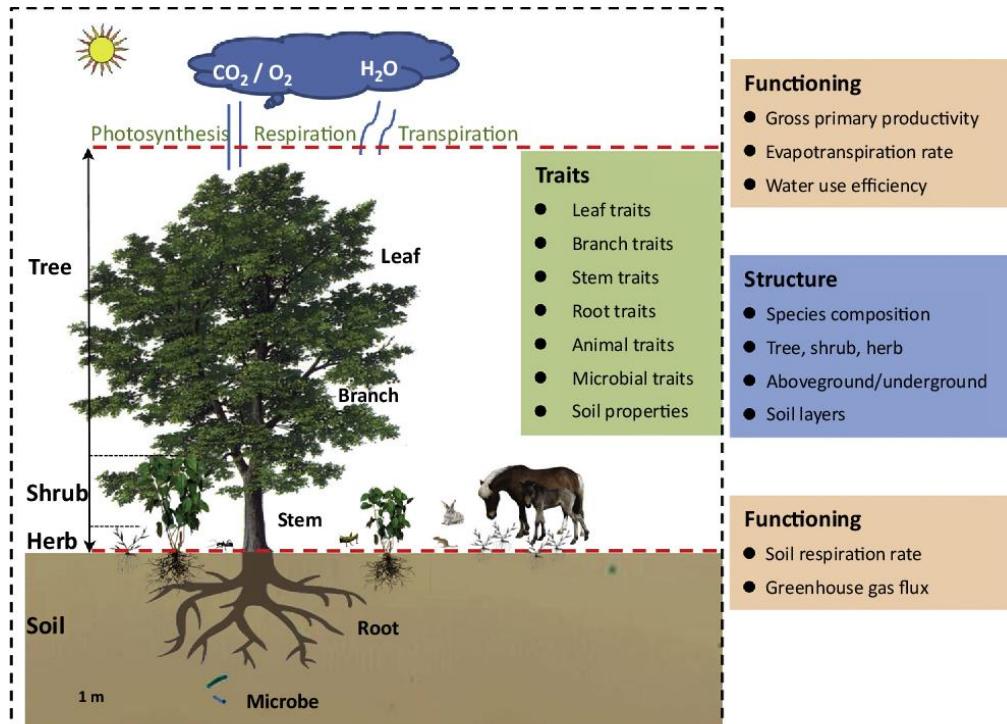
'Soft' traits

Features

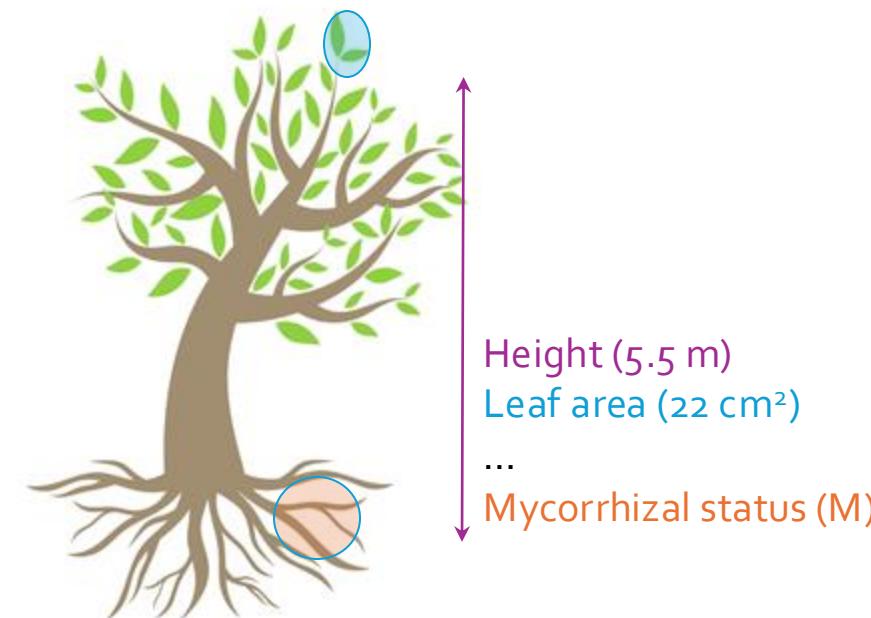
Phenological traits

What is a trait ?

Any morphological, physiological, phenological or behavioural feature measurable at the individual level (cell to whole organism).

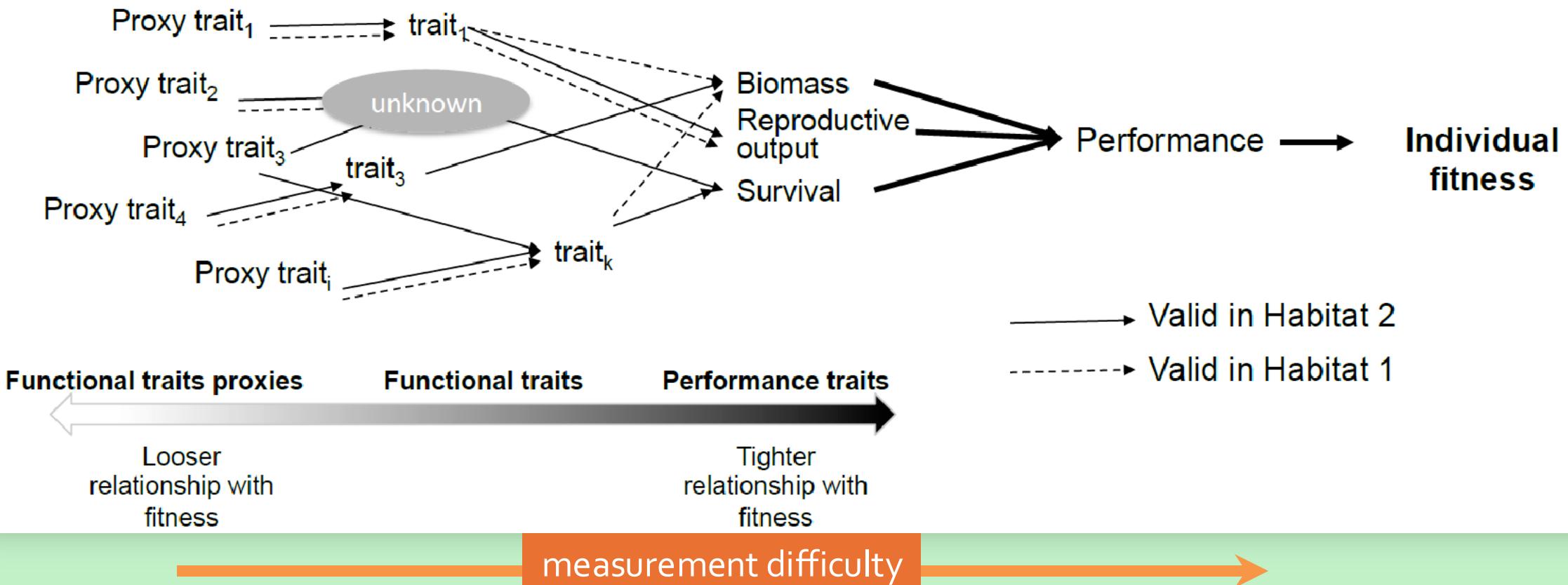


(Violle et al., 2007)

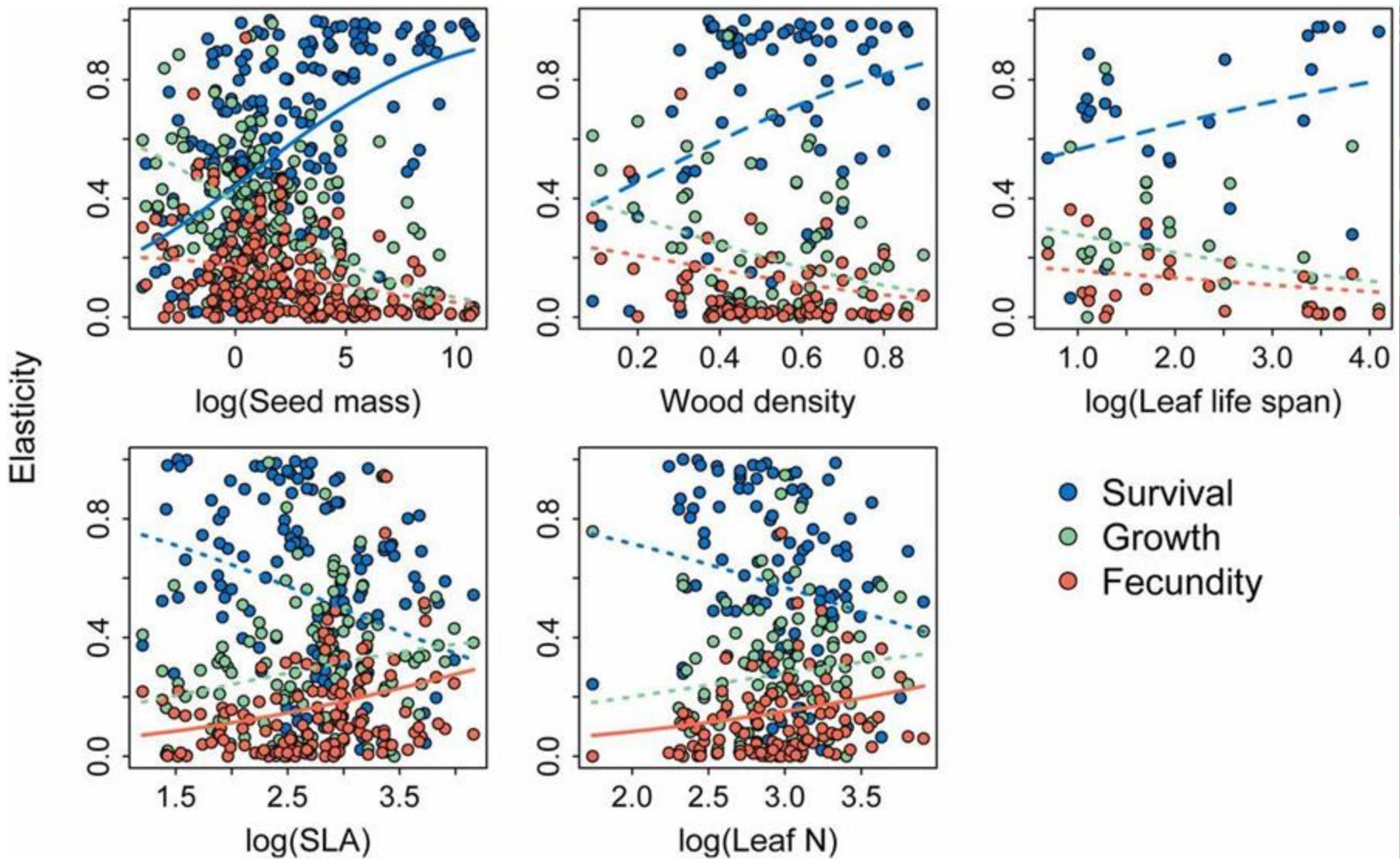


What is a *functional* trait ?

Functional traits are **morphological, physiological and phenological features** that impact fitness indirectly via their effects on individual performance (growth, reproduction, and survival) and interactions with the environment.



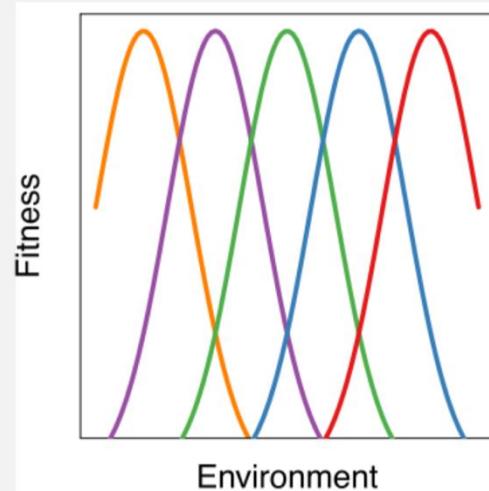
Traits are related to fitness



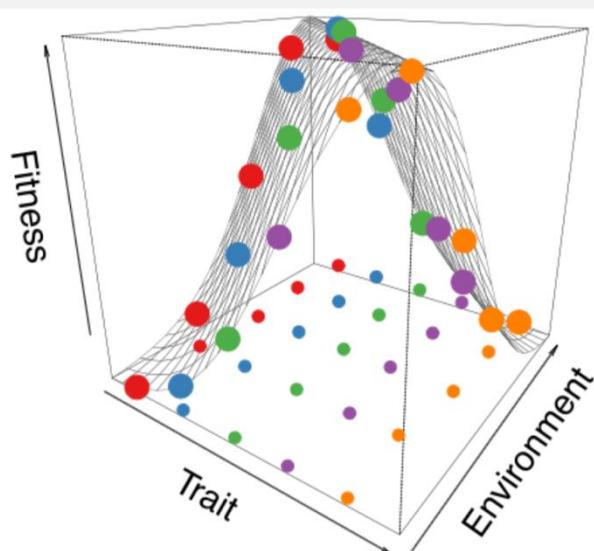
Identify some traits, easy to measure and ecologically relevant

Identify the functional traits that drive population fitness

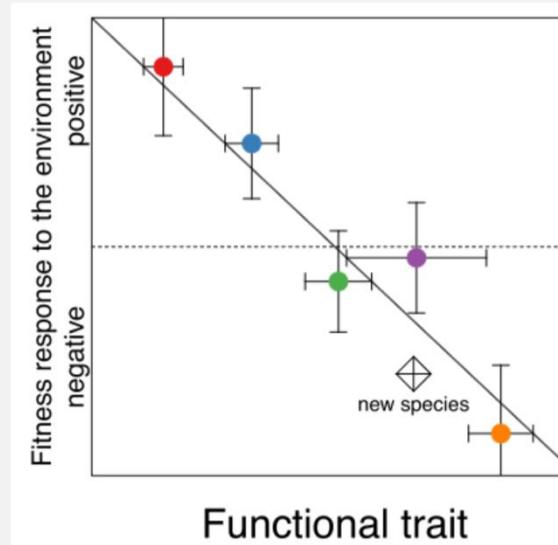
(A) Theory predicts that species are sorted along environmental gradients based on the adaptive value of their functional traits. To test this, measure fitness using methods in Figure 2 across environmental gradients.



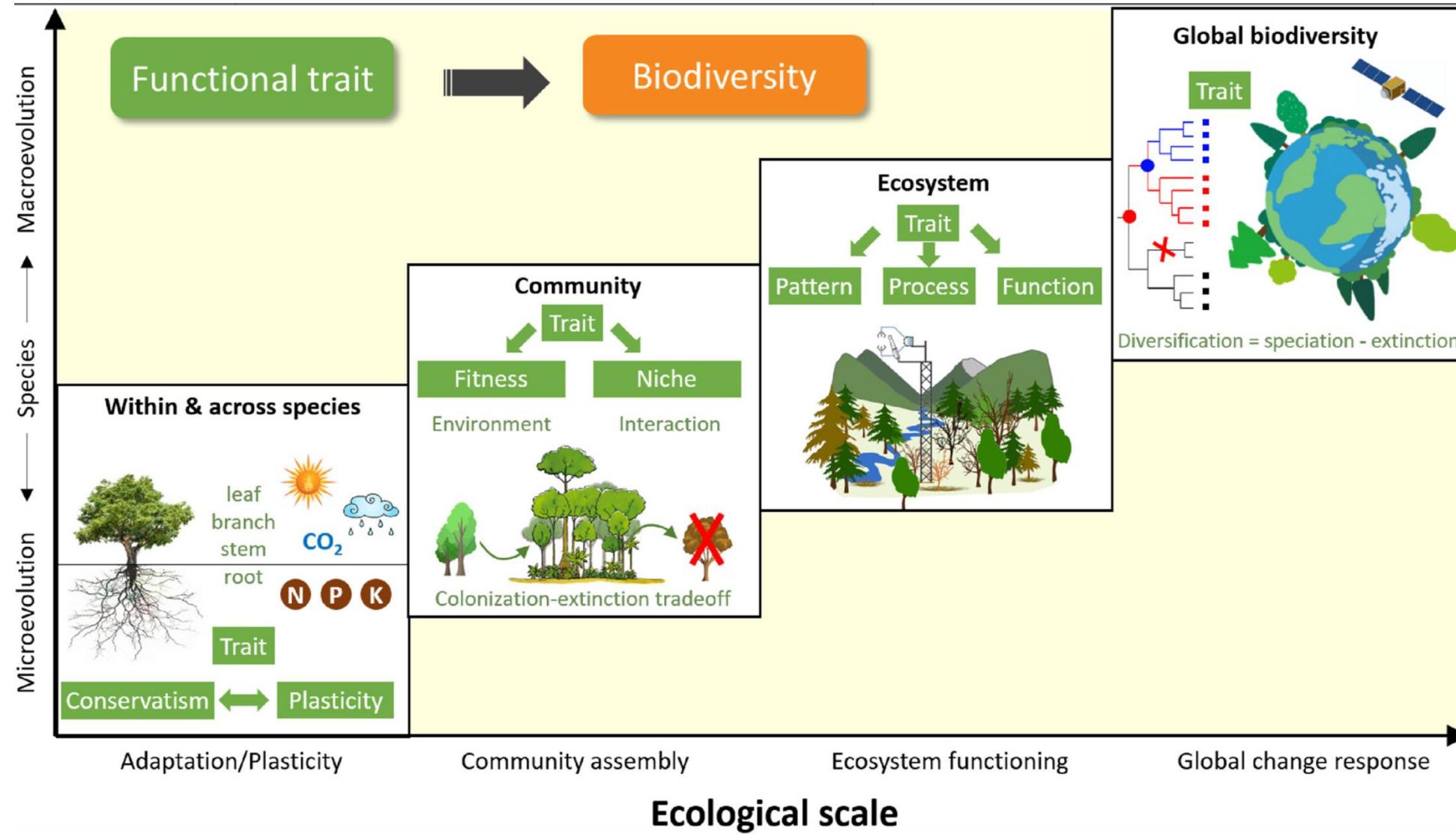
(B) Model fitness (λ) landscapes across multiple populations of coexisting species as a function of an interaction between their traits and the environment.



(C) Use the model to predict how population fitness would respond to a change in environment using their functional traits. A strong test would predict this for a new species outside the original training dataset.



Spatial and temporal scale



Many traits....

Organisms differ in their forms, life-cycles and life strategies.

Those differences can be straightforward or more subtle



Chrysophrys auratus

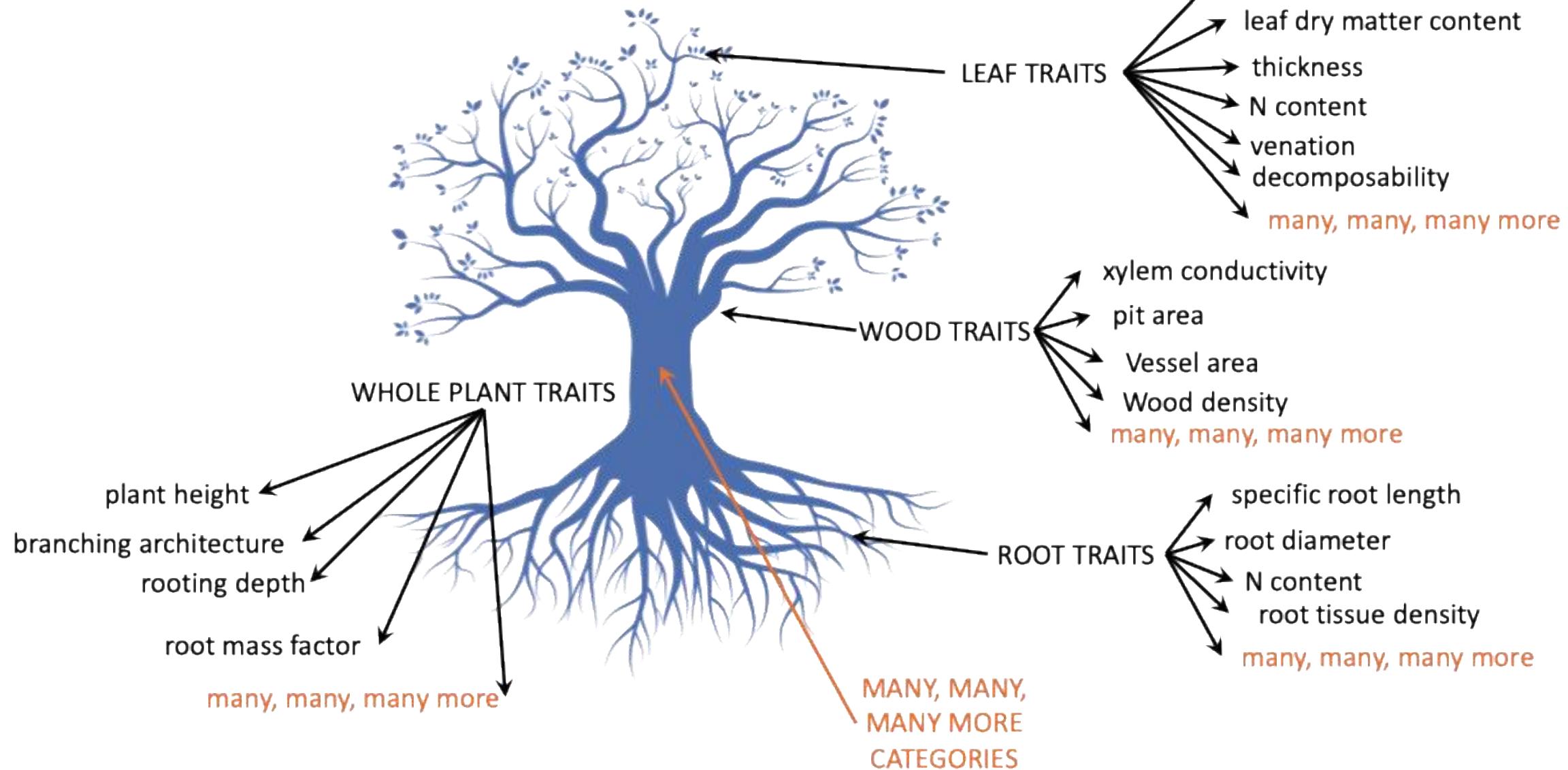


Lethrinus mahsena



Lutjanus rivulatus

Many traits....

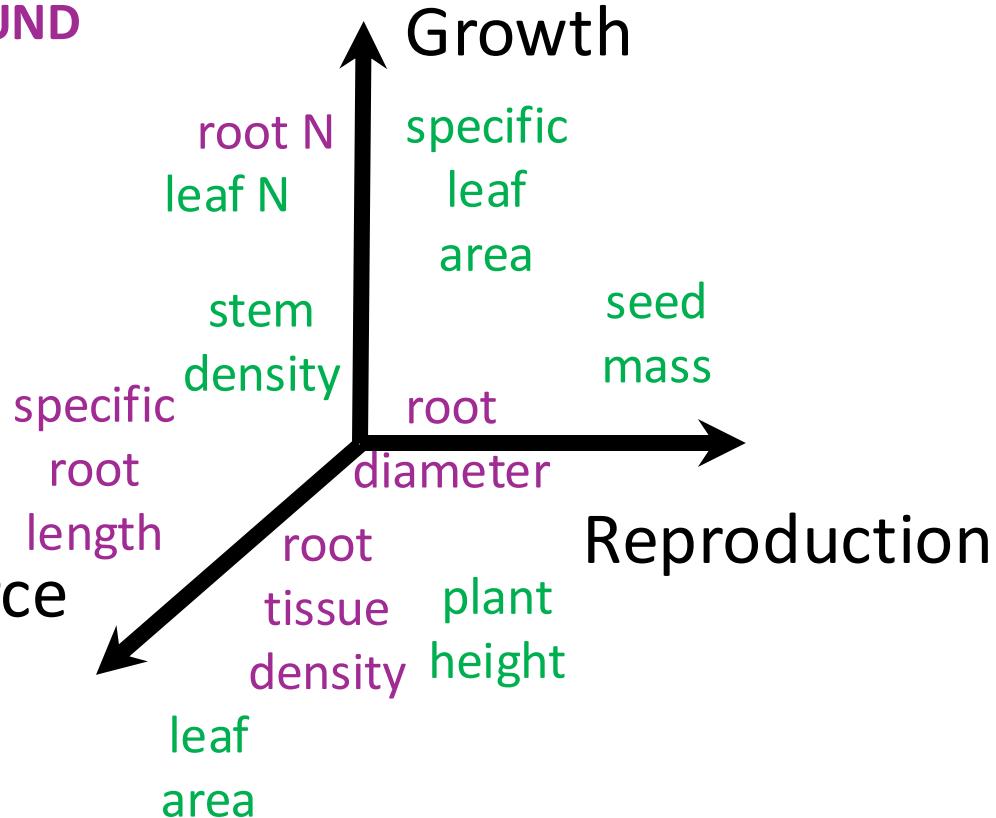


Many traits....

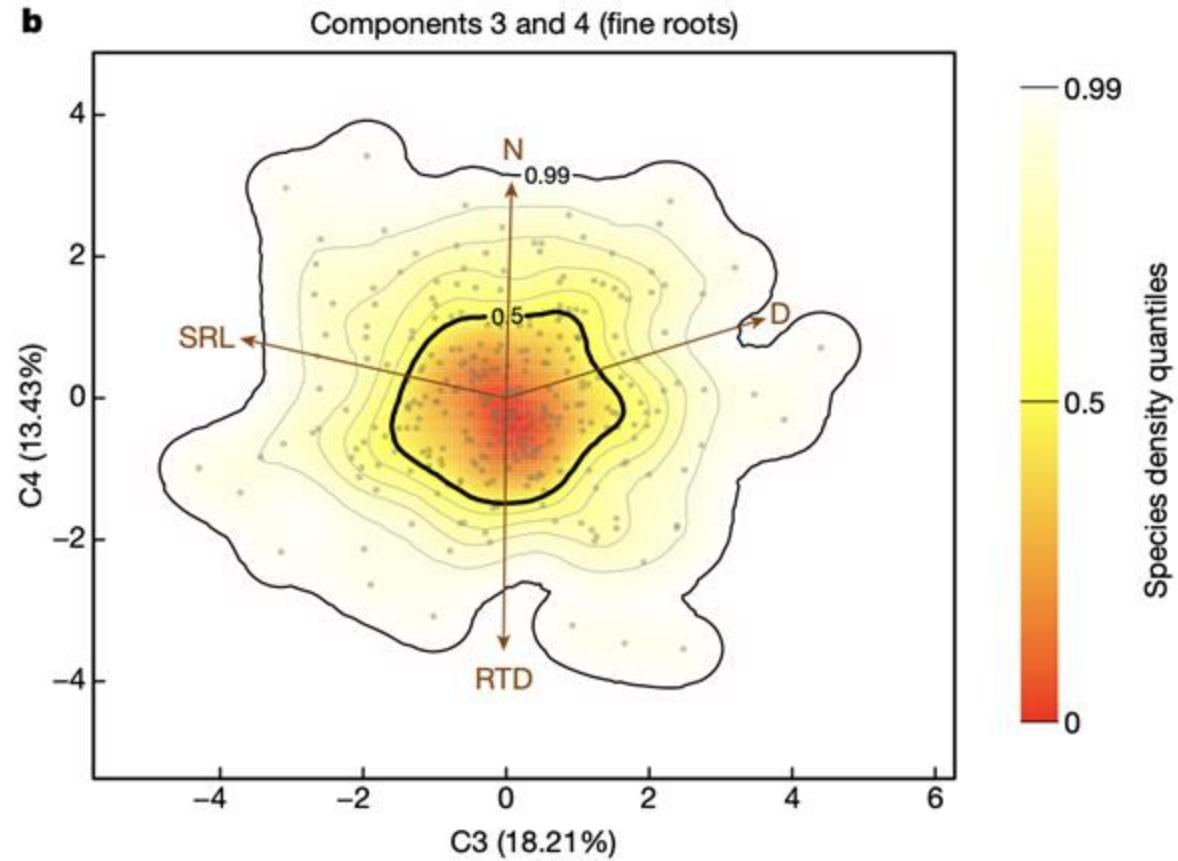
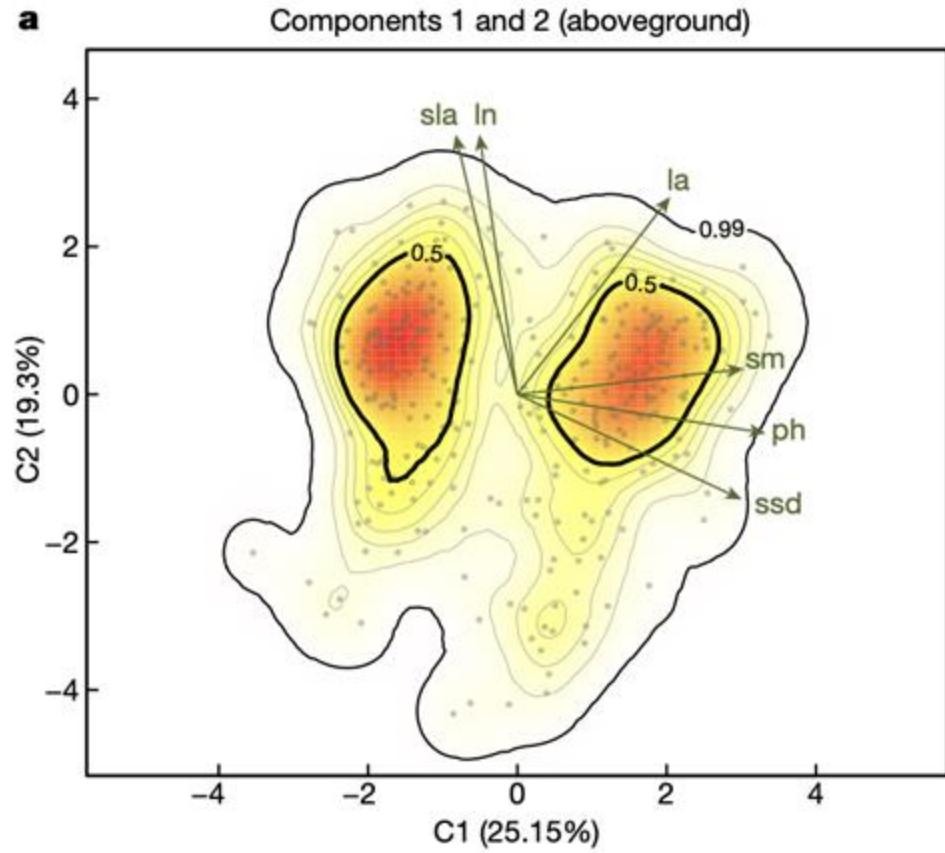


Survival/resource
preemption

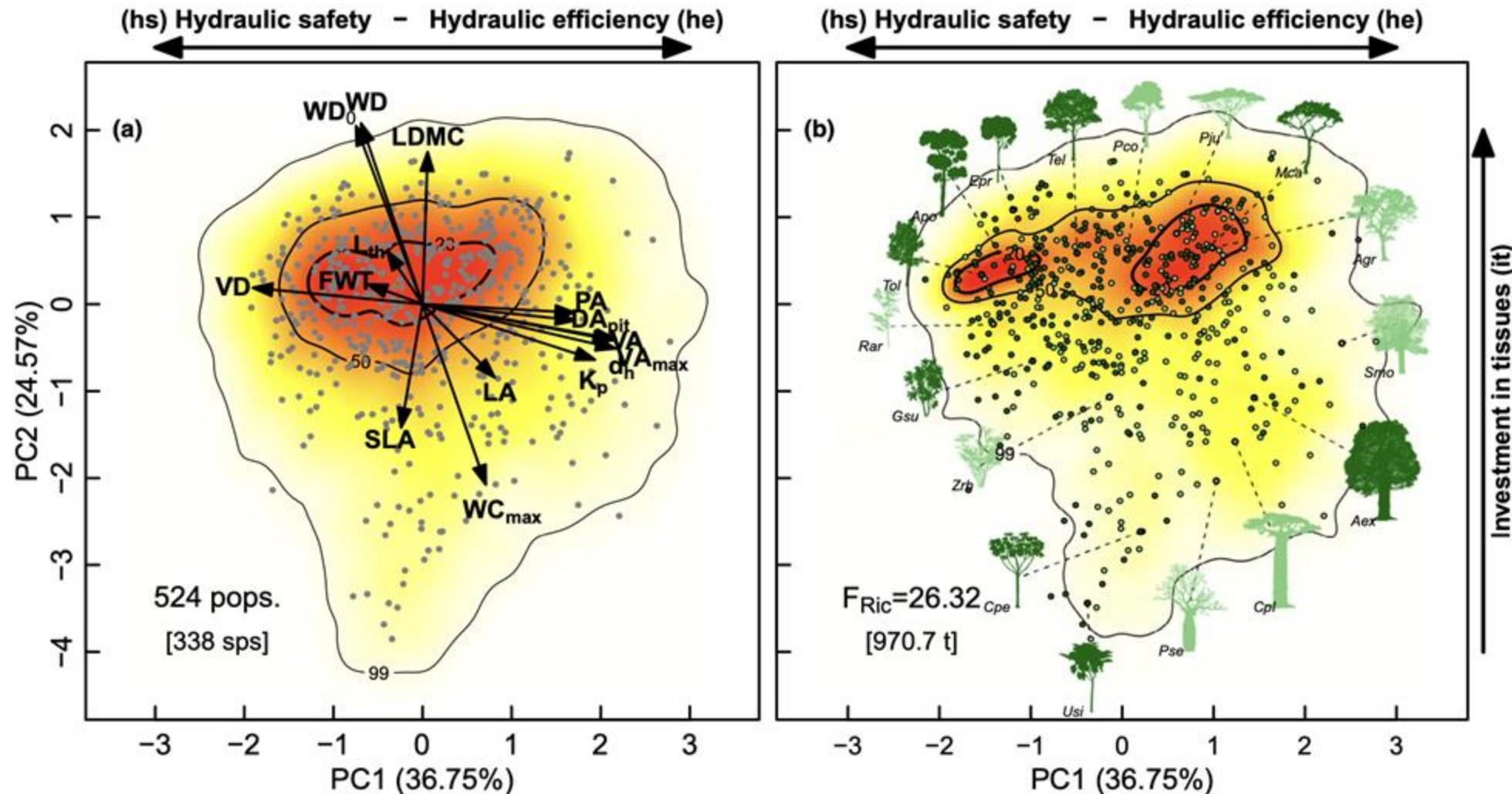
ABOVEGROUND
BELOWGROUND



Many traits....



Many traits....



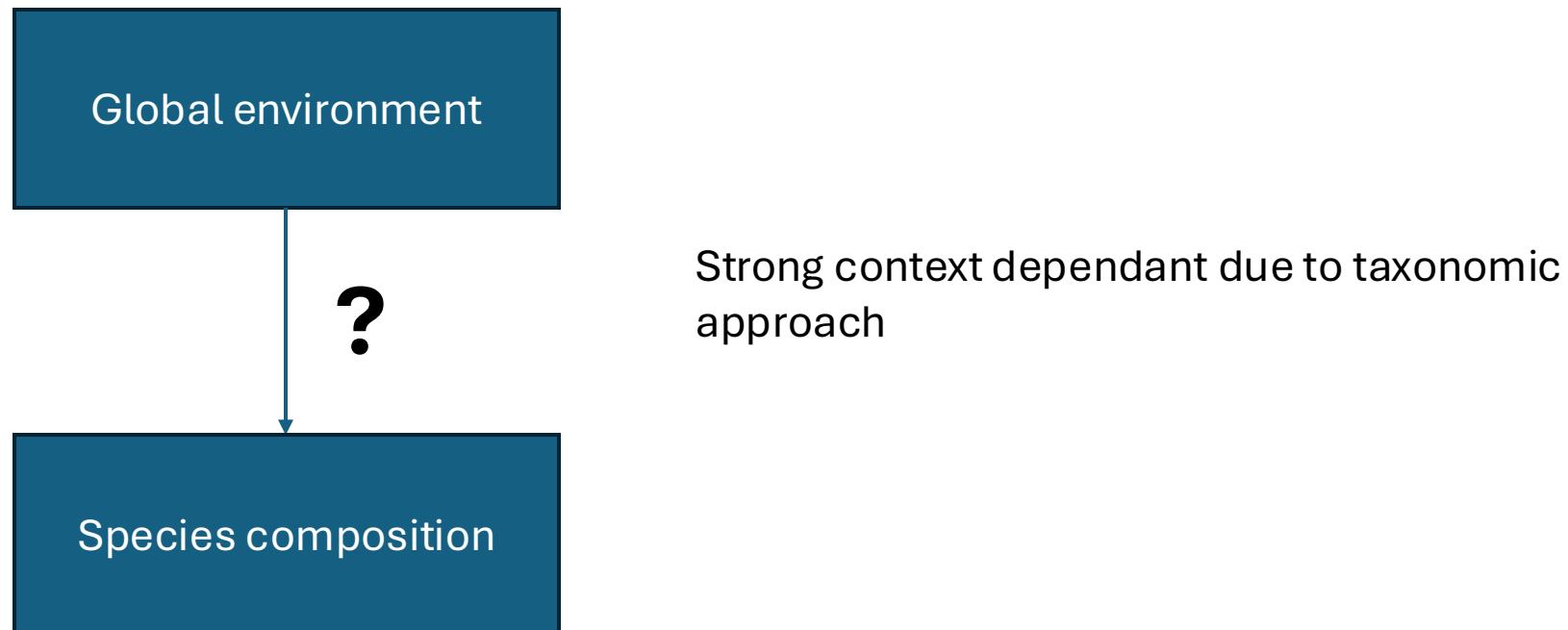
Take-home message

- The last decades have witnessed a shift in ecological research from a focus on species composition and species richness to a focus on the functional traits of species
- Functional traits are any of the characteristics of organisms, generally measurable at the individual level, that affect their fitness. These are called 'response traits'. At the same time, some traits have strong effects on ecosystem functions or other trophic levels, regardless of whether they affect fitness or not. They are called 'effect traits'
- Functional traits can enhance our ability to provide a mechanistic understanding of observed ecological patterns in the field and may facilitate the formulation of generalization of these patterns across species and ecosystems.

Community ecology and traits

General principles in community ecology

- Why do we observe a certain variety of species ?
- Why are some communities more species-rich than others?
- Why are some species present in a particular community but not in others ?



Community ecology and traits

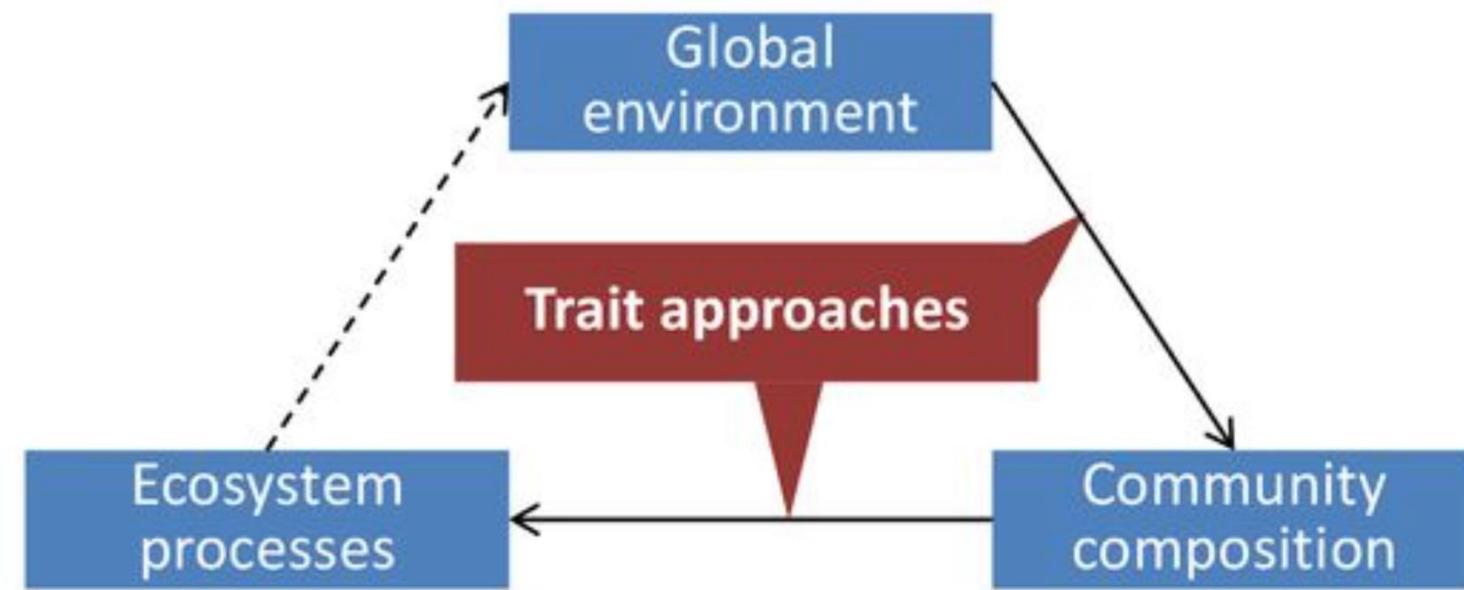
- Central question in community ecology:
 - What processes are responsible for the identity and relative abundances of co-occurring species in local assemblages?
 - What is the relative importance of different ecological processes in structuring communities
- Search for patterns in community structure that may reflect underlying processes
- This understanding was traditionally mediated by species-based approaches.
- More recently, such approaches were complemented by approaches based on traits.
- Trait-based approaches are popular, because they allow the direct connection of organism performance to its functions and to the functions of higher levels of organization such as populations, communities and ecosystems.

Community functional trait structure

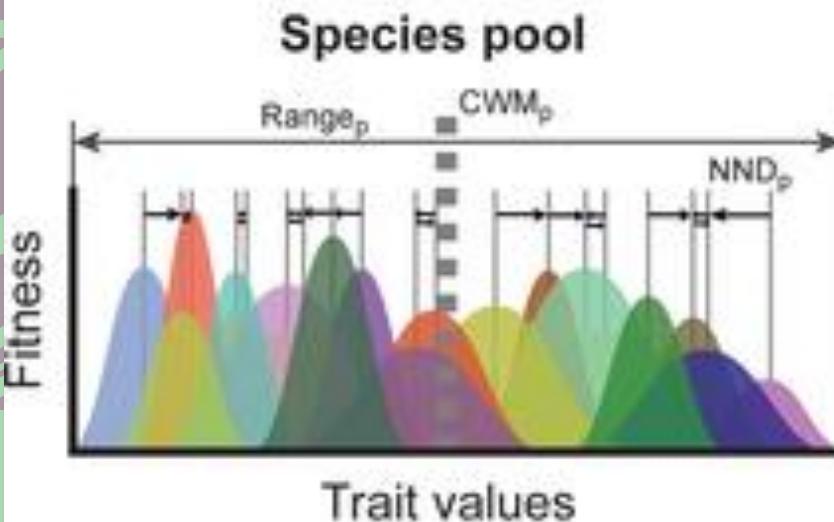
- A biological community is an assemblage of species coexisting at a given time and space
 - Describe from sampling units, including identity, and often abundance, of co-occurring species.
-
- For ease of interpretation, the functional trait information of a biological community is often summarized into a limited number of indices

General principles in community ecology

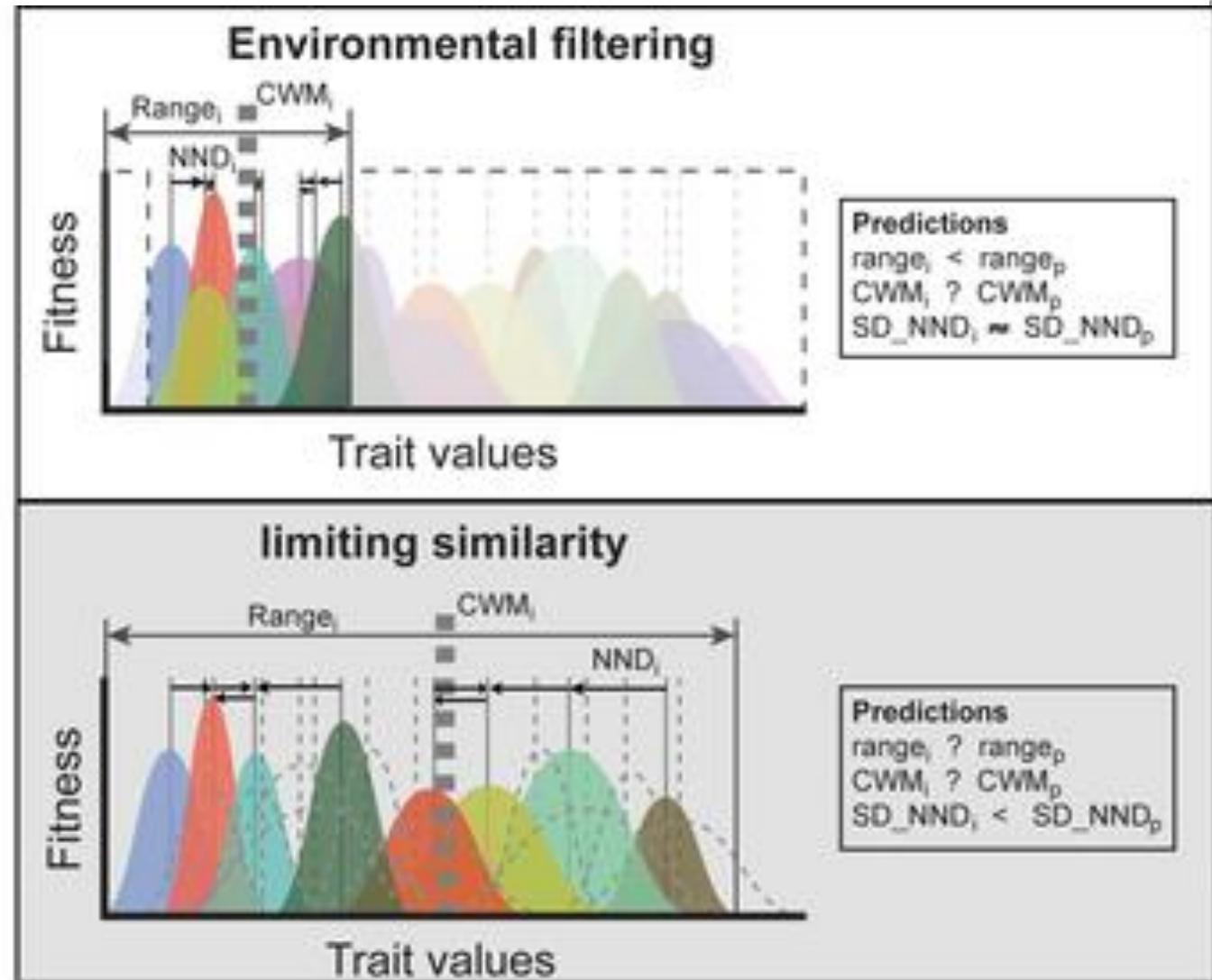
Such questions can be better answer using trait-based approach



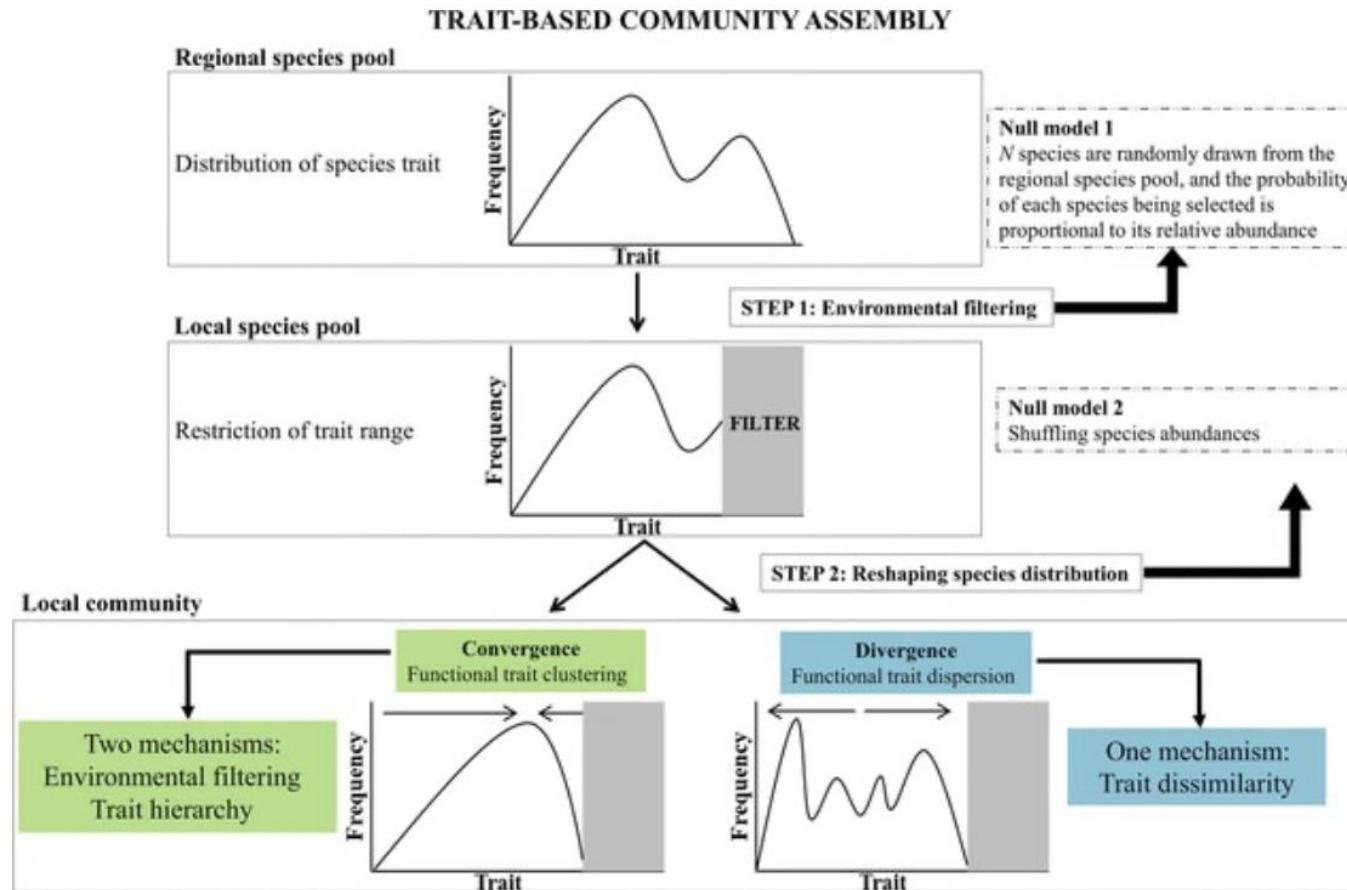
Filtering metaphor



Range = Max. trait value - min. trait value
CWM = Community weighted mean trait value
SD_NND = Standard deviation of nearest neighbor distances (NND) on trait axis

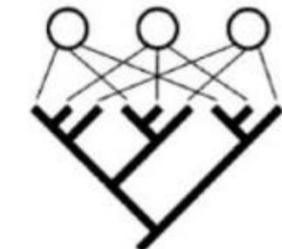
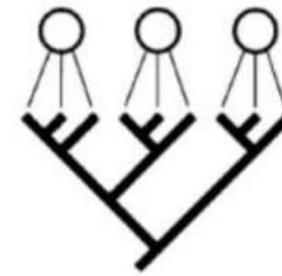


Patterns of community structure



Patterns of community structure

- Functional clustering
 - Co-occurring species are more closely related than expected by chance
- Functional dispersion
 - Co-occurring species are more distantly related than expected by chance
- Random patterns



Functional indices

Functional trait diversity

Similarly, in functional ecology, several indices corresponding to those moments can be used to characterize a community

The functional structure of communities cannot be assessed by a single measure but rather needs a multi-index approach

There are two main families of indices:

- (1) characterizing the dominant traits
- (2) functional differences

Functional trait diversity

Hutchinson : « Why are there so many kinds of species ? »

There is a family of indices intends to quantify how many kinds of species there are in a study unit

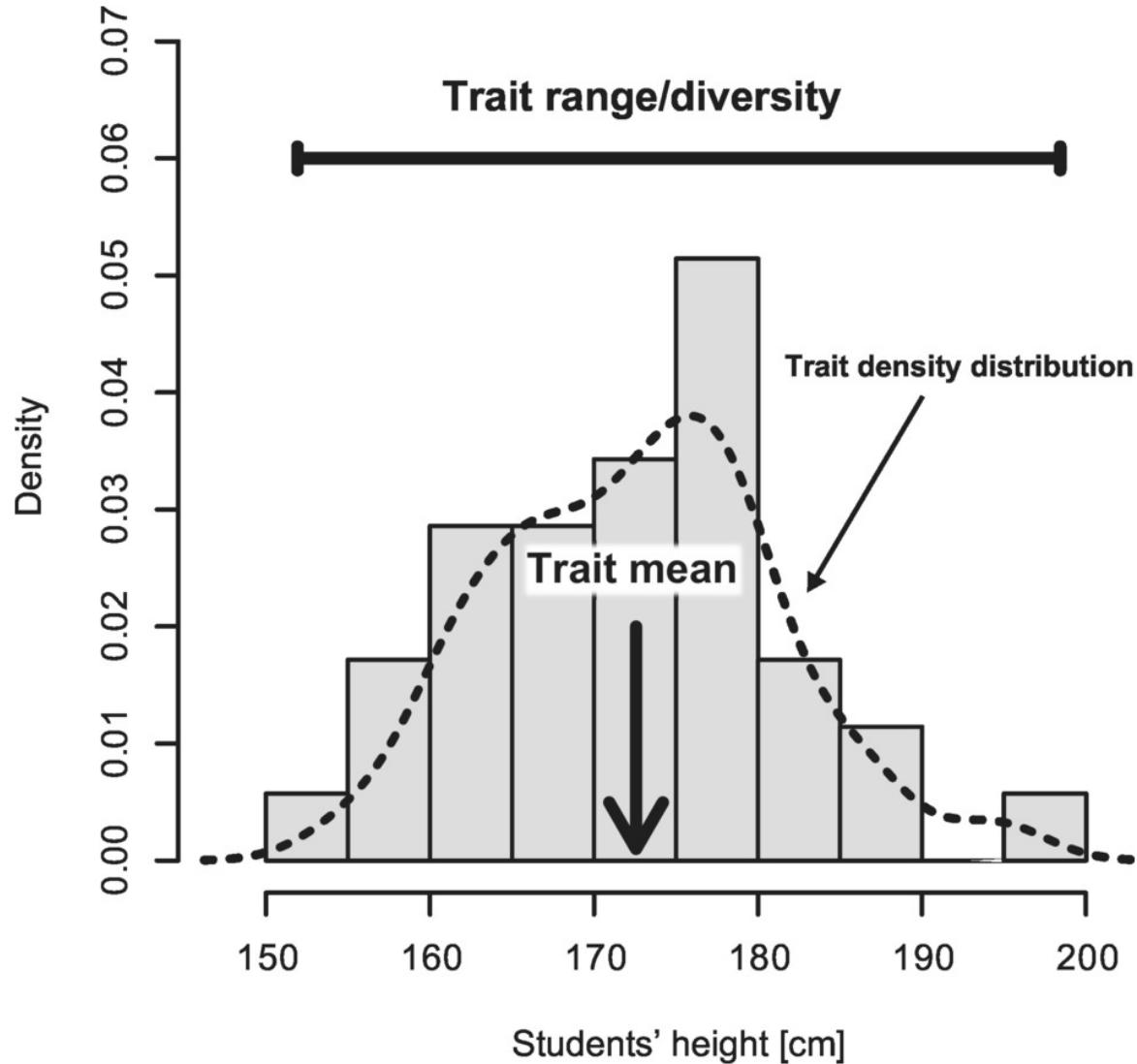
-> it is what we call ***functional trait diversity*** or ***Functional diversity***

- It can be quantify by various indices, called moment in mathematical terms
 - Example: first momment: mean; second moment: variance, etc
 - Similarly, in functional ecology, several indices corresponding to those moments can be used to characterize a community

How to calculate functional diversity ?

- Diversity index :
 - A mathematical measure of species diversity in a community
 - Reveals important information regarding rarity and commonness

Community functional trait structure



- Two most intuitive parameters
 - Trait mean
 - Trait range

Community functional trait structure



```
load("R_script/Data/community.rda")
traits <- read.table("R_script/Data/vas.plant.traits.txt")
# seed weight mg, clonal spread classes, leaf size classes. NB! Many NA values!
head(traits)
```

Trait: seed weight



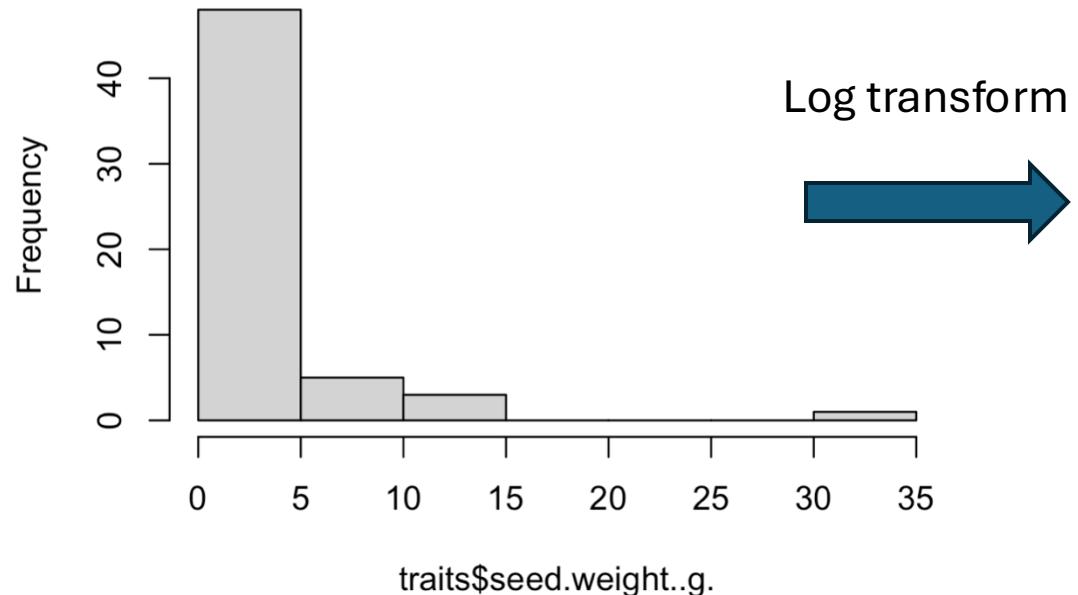
	seed.weight..g.	clonal	leaf
1	6.40	1	NA
2	2.36	1	5
3	4.00	2	4
4	3.16	2	NA
5	NA	1	NA
6	2.56	3	4
.	.	.	.

79 species

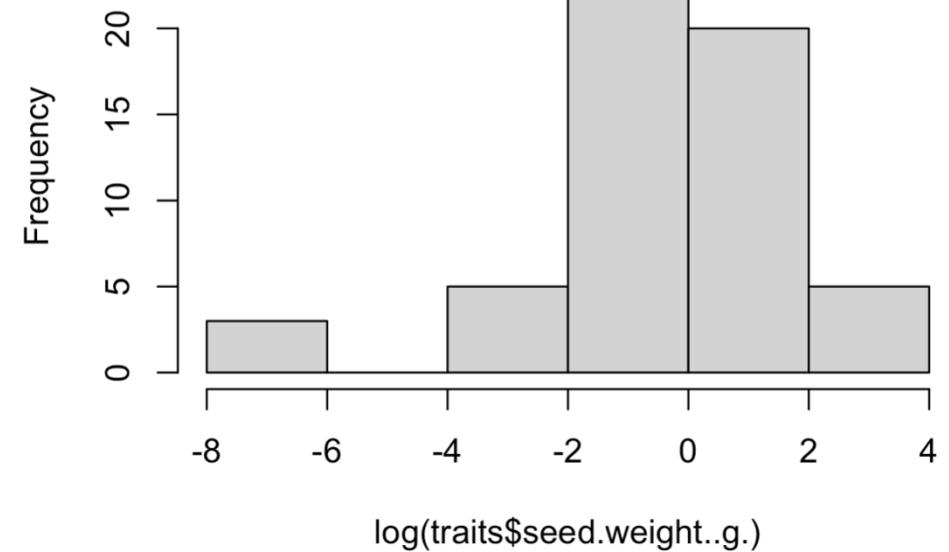
Community functional trait structure

Sometimes, some adjustment are needed

Histogram of traits\$seed.weight..g.

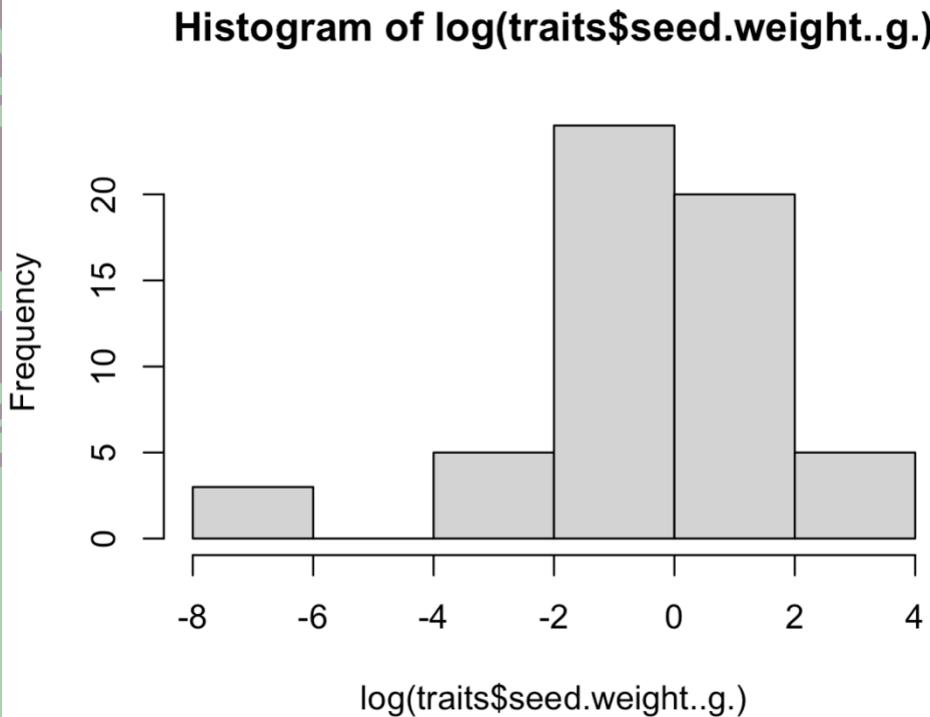


Histogram of log(traits\$seed.weight..g.)



```
hist(trait$seed.weight..g.) # very skewed  
hist(log(trait$seed.weight..g.)) # looks better  
trait$seed.weight..g. <- log(trait$seed.weight..g.)
```

Community functional trait structure



```
> # mean
> mean(traits$seed.weight..g.,na.rm=T) # in the log-scale
[1] -0.3841576
> mean(exp(traits$seed.weight..g.),na.rm=T) # in the original scale
[1] 2.632158
> #range
> range(traits$seed.weight..g.,na.rm=T) # in the log-scale
[1] -6.907755 3.440418
> range(exp(traits$seed.weight..g.),na.rm=T) # in the original scale
[1] 0.001 31.200
> #summary
> summary(traits$seed.weight..g.,na.rm=T) # in the log-scale
   Min. 1st Qu. Median      Mean 3rd Qu.    Max.    NA's
-6.9078 -1.2040 -0.3567 -0.3842  1.0986  3.4404     22
> summary(exp(traits$seed.weight..g.),na.rm=T) # in the original scale
   Min. 1st Qu. Median      Mean 3rd Qu.    Max.    NA's
0.001  0.300  0.700  2.632  3.000  31.200  22
```

Community functional trait structure



```
load("R_script/Data/community.rda")
traits <- read.table("R_script/Data/vas.plant.traits.txt")
# seed weight mg, clonal spread classes, leaf size classes. NB! Many NA values!
head(traits)
```

Trait: seed weight

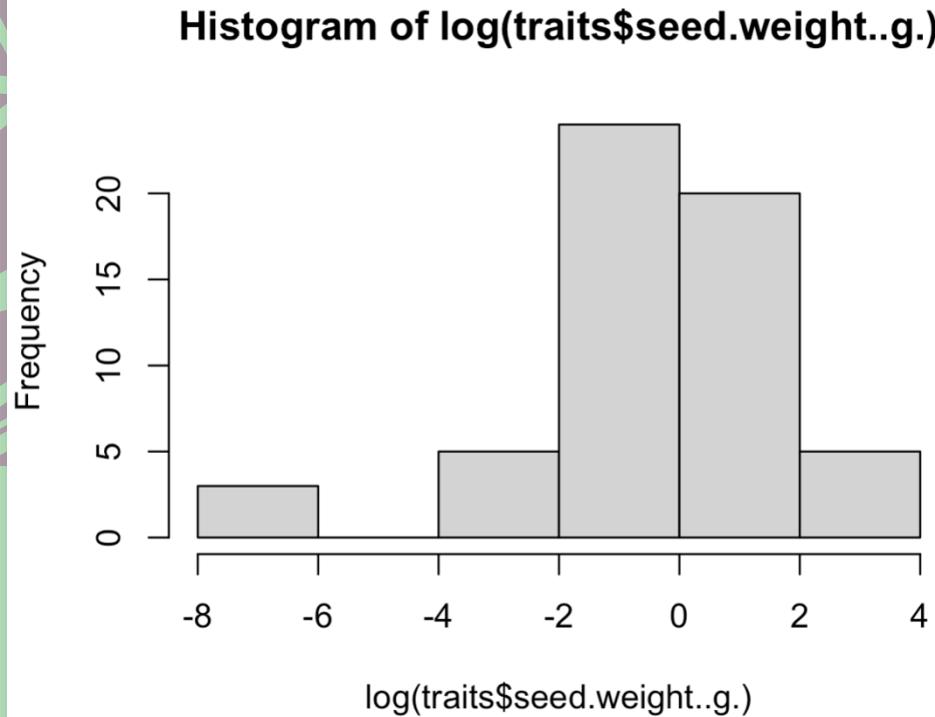
	seed.weight..g.	clonal	leaf
1	6.40	1	NA
2	2.36	1	5
3	4.00	2	4
4	3.16	2	NA
5	NA	1	NA
6	2.56	3	4

Abundance

79 species

Community functional trait structure

Community Weighted Mean



$$CWM = \sum_{i=1}^N p_i x_i$$

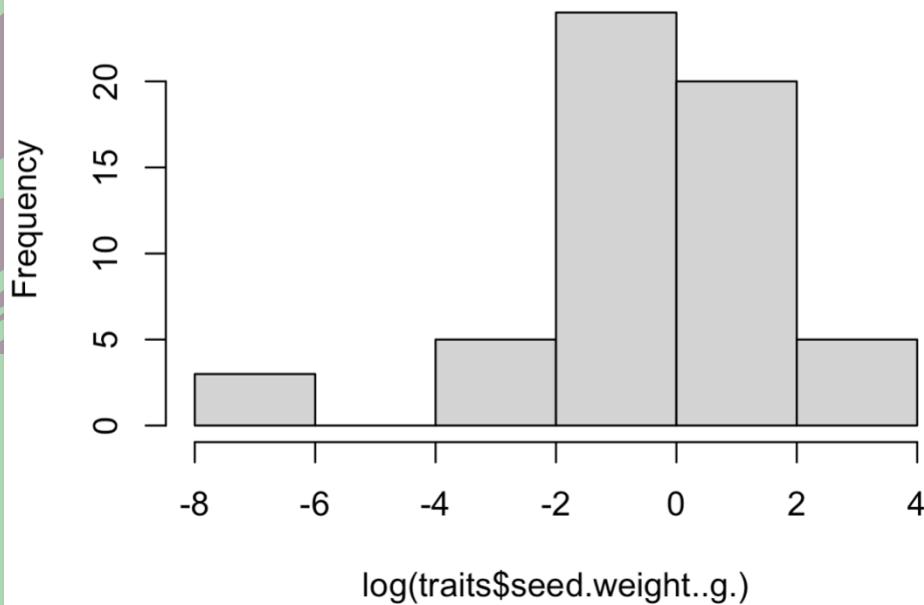
The average trait value of a sample, weighted according to species' abundances. It shows which trait value is the most common.

If our traits have a very skewed distribution (which is generally the case with seed mass), it is recommendable to work with the logarithm, to avoid species with very high values being extremely influential (the mean is sensitive to outliers)

Community functional trait structure

Community Weighted Mean

Histogram of `log(traits$seed.weight..g.)`



$$CWM = \sum_{i=1}^N p_i x_i$$

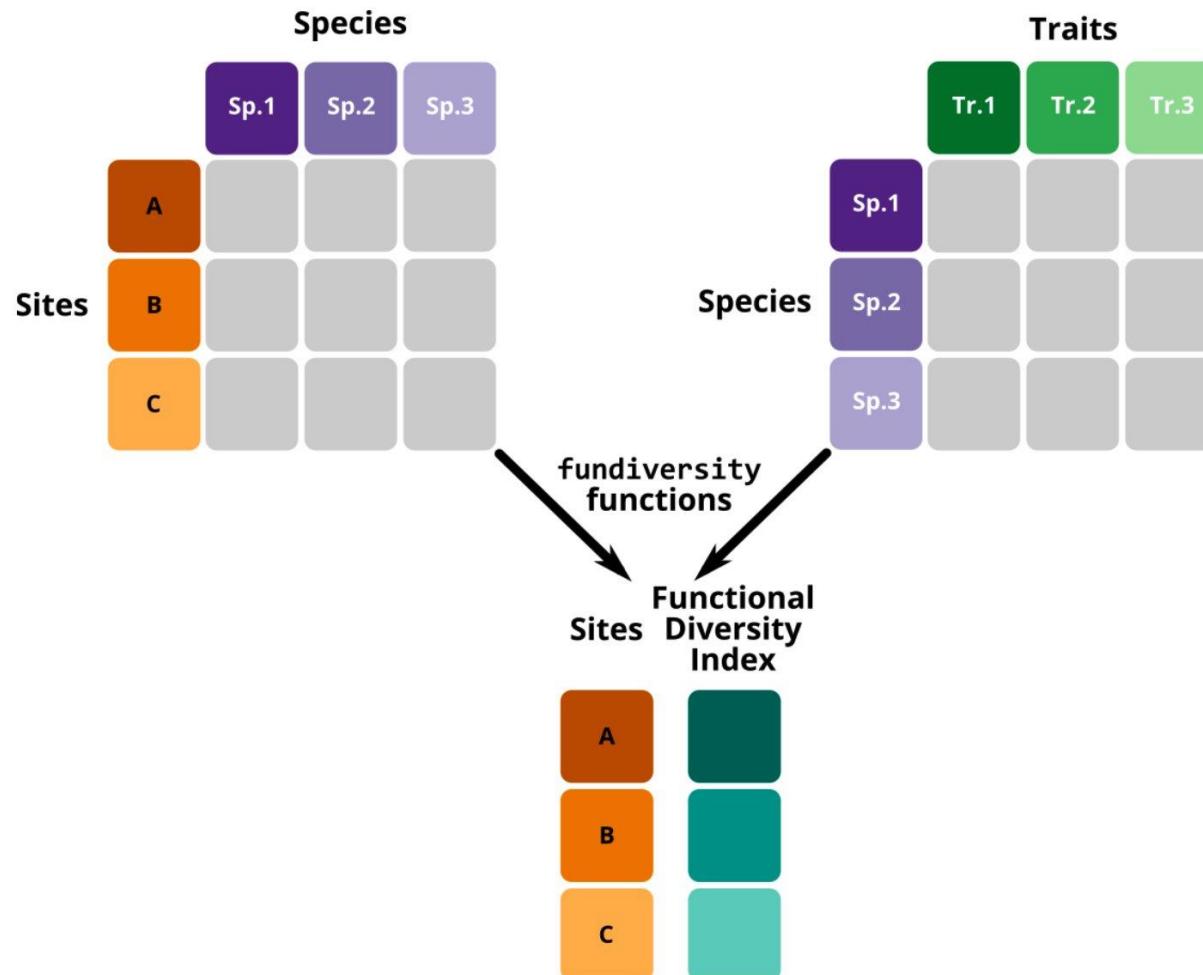
```
# CWM
mean.seed <- numeric() # empty numeric object
for (i in 1:nrow(vas.plants)) {
  mean.seed[i] <- weighted.mean(traits$seed.weight..g.,
                                w = vas.plants[i, ],
                                na.rm = T)
}
```

Community functional trait structure

$CWM = \sum_{i=1}^N p_i x_i$	Sp1	Sp2	Sp3	MEAN
Size of different individuals (cm)	20 25 30 35 40	35 40 45	80	38.9
Mean per species (x_i)	30	40	80	50
<hr/>				SUM
Species relative abundance (p_i)	5/9 = 0.56	3/9 = 0.33	1/9 = 0.11	1
$x_i * p_i$	30*0.55 = 16.7	40*0.33 = 13.3	80*0.11 = 8.9	38.9

Community Weighted Mean (CWM)

Community functional trait structure



Grenié, Matthias, and Hugo Gruson. 2022. "Fundiversity: A Modular R Package to Compute Functional Diversity Indices." EcoEvoRxiv. July 18. doi:10.32942/osf.io/dg7hw.

Community functional trait structure

Matrix sp x sites



```
> head(spxp)
```

	X1nograz.1	X1nograz.2	X1nograz.3	X1nograz.4	X1highgraz.1	X1highgraz.2	X1highgraz.3
Acercamp	0	0	0	0	0	0	0
Achimill	0	0	0	0	0	0	0
Aegigeni	0	0	0	0	0	0	0
Alchhybr	0	0	0	0	0	0	0
Anemhepa	0	0	0	0	0	0	0
Anthmont	0	0	0	0	0	0	0

Need to be transform as **site x species**

Matrix sp x traits

	GrowthForm	LEG	SLA	LF_Th	LF_G	LF_H	LF_hCh	LF_wCh	LF_NP	LF_P
Acercamp	shrub	0	15.7	0	0	0.0	0.0	0	0	1
Achimill	forb	0	14.6	0	0	0.5	0.5	0	0	0
Aegigeni	grass	0	15.2	1	0	0.0	0.0	0	0	0
Alchhybr	forb	0	19.0	0	0	1.0	0.0	0	0	0
Anemhepa	forb	0	12.9	0	0	1.0	0.0	0	0	0
Anthmont	forb	1	13.5	0	0	1.0	0.0	0	0	0

Community functional trait structure

Matrix sites x trait

$$CWM = \sum_{i=1}^N p_i x_i$$

```
> library(FD)
```

```
> resCWM = functcomp(traits, abundance, CWM.type = "all")
```

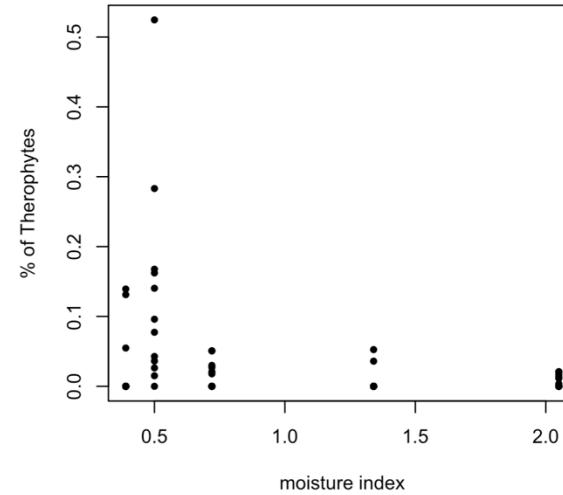
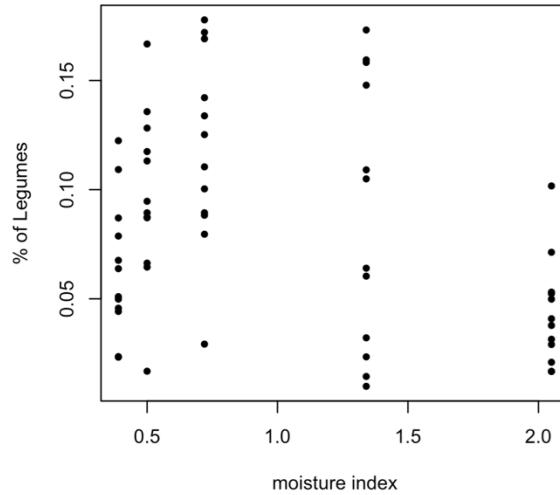
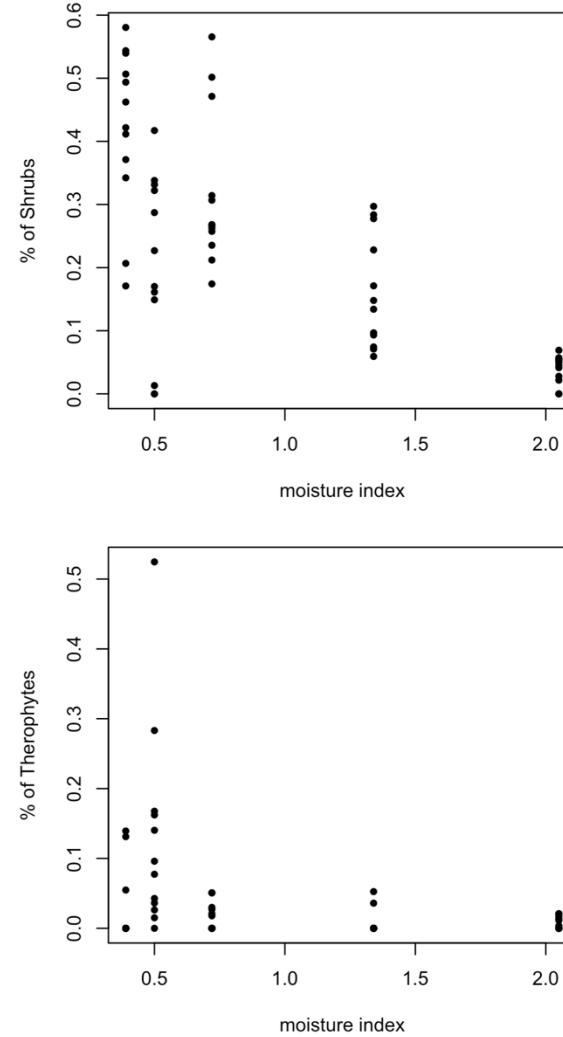
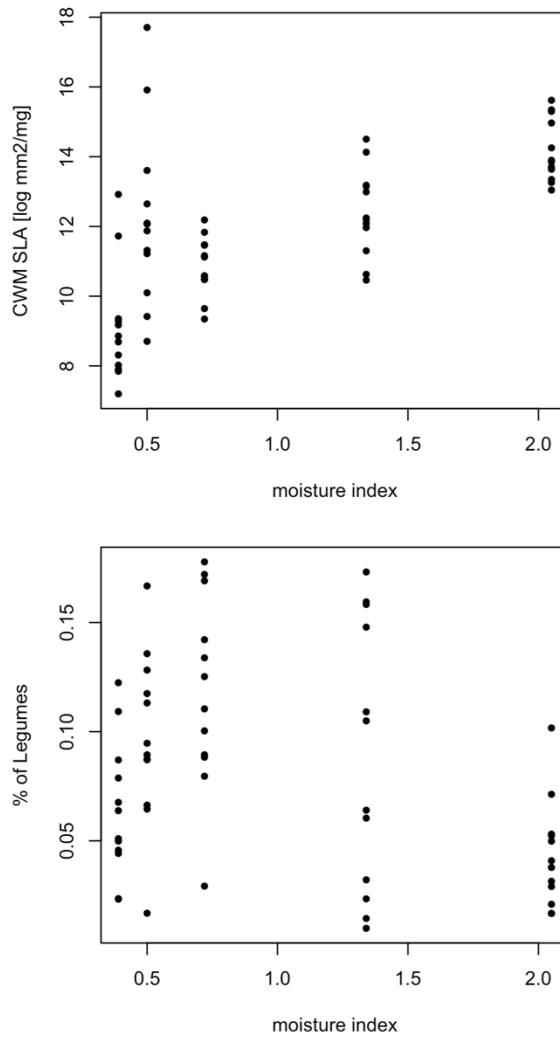
```
> functcomp(spxt, log(t(spxp) + 1), CWM.type = "all")
   GrowthForm_forb GrowthForm_grass GrowthForm_shrub GrowthForm_subshrub    LEG_0    LEG_1      SLA      LF_Th      LF_G      LF_H
X1nograz.1     0.17441466  0.07487008  0.58044233  0.17027294 0.9557956 0.044204387 8.857775 0.00000000 0.00000000 0.17202123
X1nograz.2     0.22658585  0.08545117  0.50653372  0.18142925 0.9501596 0.049840427 9.173906 0.00000000 0.00000000 0.17539752
X1nograz.3     0.14168682  0.13598654  0.46227722  0.26004942 0.8776035 0.122396477 7.903517 0.00000000 0.00000000 0.17354659
X1nograz.4     0.14866320  0.11541070  0.49373162  0.24219449 0.9324006 0.067599403 7.846246 0.00000000 0.00000000 0.15425283
X1highgraz.1   0.23810146  0.06609128  0.42173850  0.27406877 0.9129762 0.087023849 8.687842 0.00000000 0.00000000 0.13218255
X1highgraz.2   0.26870618  0.07414532  0.41154593  0.24560257 0.9764965 0.023503512 9.283435 0.00000000 0.00000000 0.15908503
X1highgraz.3   0.30494757  0.15241911  0.20668052  0.33595280 0.9362010 0.063799041 11.724569 0.13121142 0.00000000 0.21473061
X1highgraz.4   0.17807916  0.15677115  0.17096552  0.49418417 0.8907932 0.109206765 12.918497 0.13929118 0.00000000 0.16268874
X1littlegraz.1 0.17546021  0.09074151  0.53958831  0.19420997 0.9767549 0.023245136 8.312111 0.00000000 0.00000000 0.15599886
X1littlegraz.2 0.19028759  0.00000000  0.54361704  0.26609537 0.9490283 0.050971676 8.021874 0.00000000 0.00000000 0.06925684
X1littlegraz.3 0.07259498  0.18770320  0.34220142  0.39750040 0.9542991 0.045700861 7.198706 0.00000000 0.00000000 0.20398217
X1littlegraz.4 0.14710658  0.13826258  0.37111954  0.34351130 0.9212760 0.078724009 9.352806 0.05477863 0.00000000 0.13826258
X2nograz.1     0.14572270  0.13342045  0.41718924  0.30366761 0.9126012 0.087398816 11.219193 0.00000000 0.00000000 0.27914315
X2nograz.2     0.19496802  0.12825221  0.32215840  0.35462136 0.9053349 0.094665139 10.097614 0.01510614 0.00000000 0.24083971
```

Community functional trait structure

Matrix sites x environment

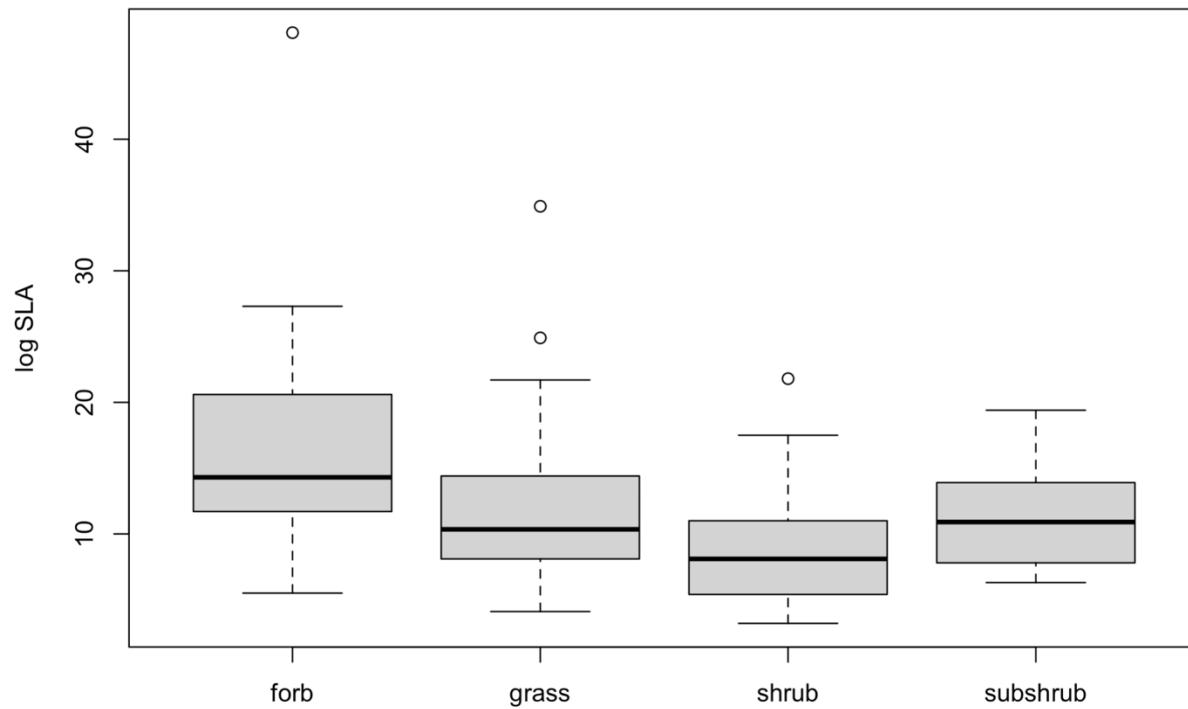
	vegbelt	grazing	moisture.index
1nograz.1	1	0	0.39
1nograz.2	1	0	0.39
1nograz.3	1	0	0.39
1nograz.4	1	0	0.39
1highgraz.1	1	2	0.39
1highgraz.2	1	2	0.39
1highgraz.3	1	2	0.39
1highgraz.4	1	2	0.39
1littlegraz.1	1	1	0.39

Community functional trait structure



- The CWM SLA is increasing with moisture index, likely because of decrease in shrub species with moisture.
- In fact, the different growth forms tend to have different SLA.
- We can test it !

Community functional trait structure

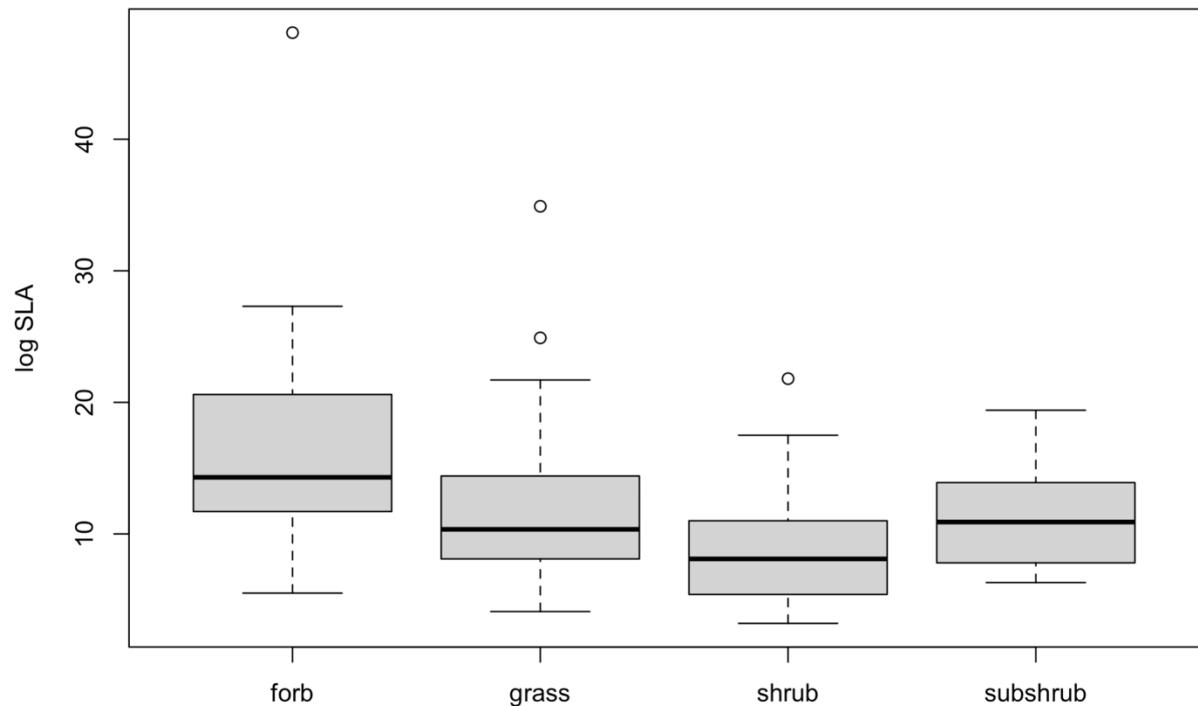


- The CWM SLA is increasing with moisture index, likely because of decrease in shrub species with moisture.
- In fact, the different growth forms tend to have different SLA.
- We can test it !

```
> boxplot(spxt$SLA ~ spxt$GrowthForm, ...)
```

Community functional trait structure

- We can go further by testing the effect of moisture and grazing intensity on the CWM for SLA.



```
> summary(lm(resCWM$SLA ~ moisture.index * grazing, data = envxp))
```

Call:

```
lm(formula = resCWM$SLA ~ moisture.index * grazing, data = envxp)
```

Residuals:

Min	1Q	Median	3Q	Max
-3.1564	-1.0146	0.0383	0.7592	5.8350

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	7.5733	0.6290	12.040	< 2e-16 ***
moisture.index	3.5435	0.5347	6.627	1.43e-08 ***
grazing	1.8867	0.4872	3.872	0.000284 ***
moisture.index:grazing	-1.2485	0.4142	-3.014	0.003867 **

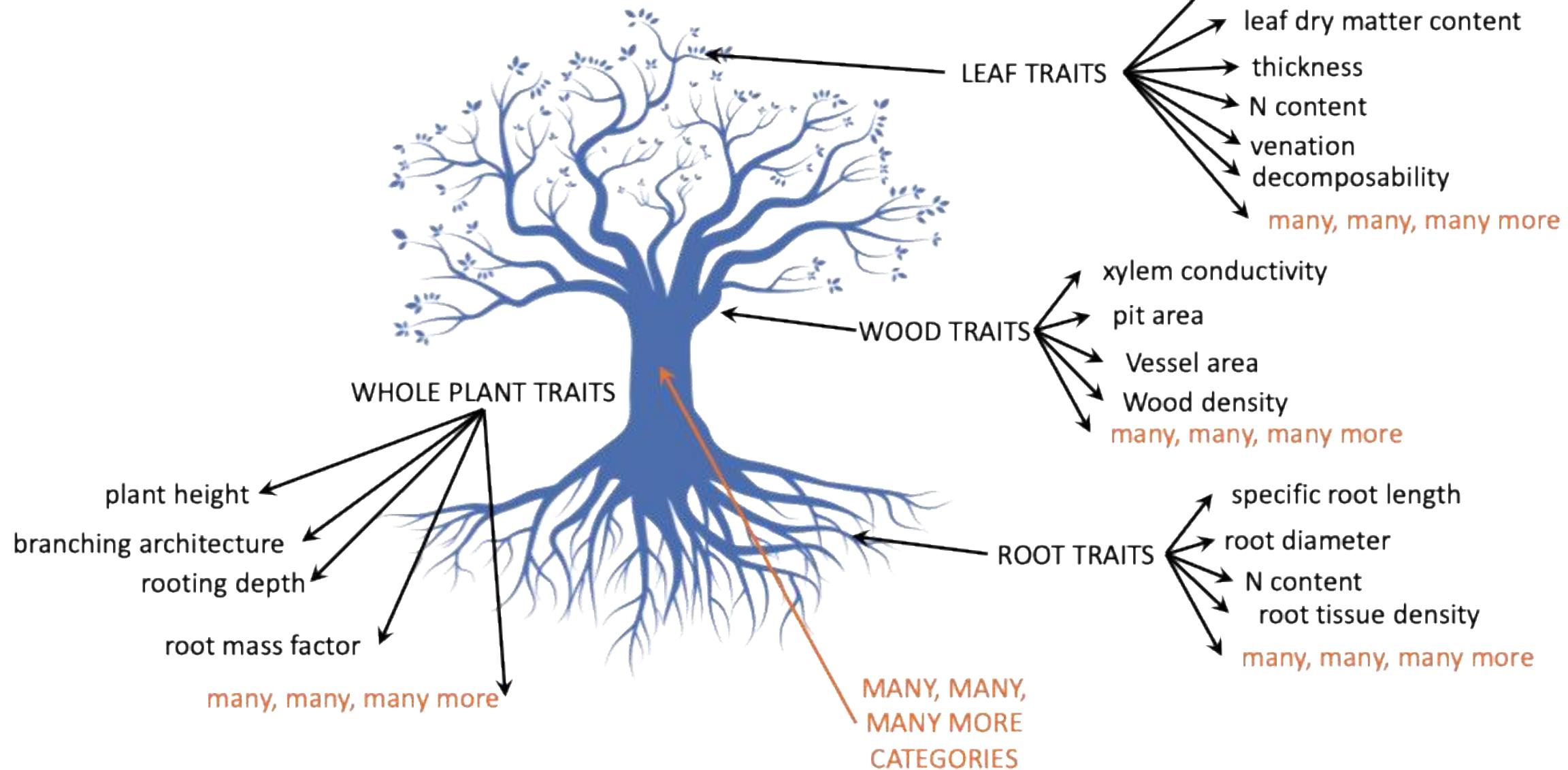
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.623 on 56 degrees of freedom

Multiple R-squared: 0.5227, Adjusted R-squared: 0.4971

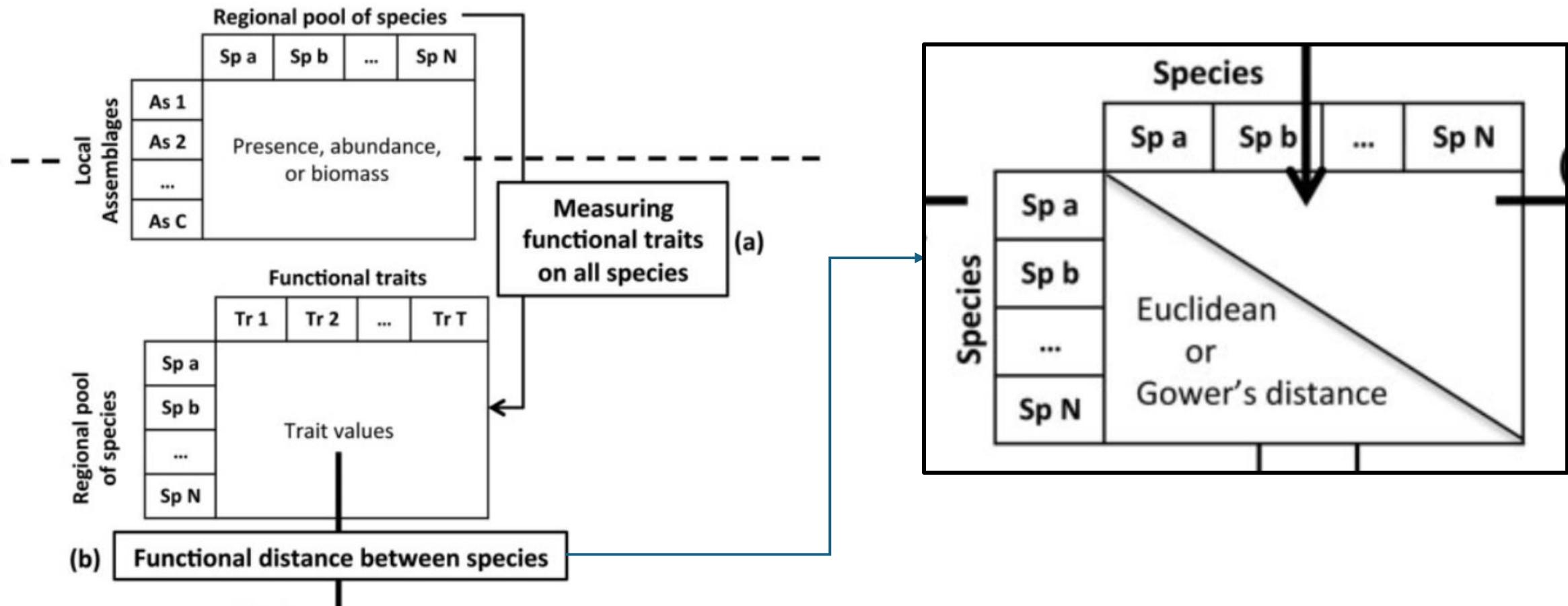
F-statistic: 20.44 on 3 and 56 DF, p-value: 4.509e-09

Many traits....



How to work with several traits?

Step 1. Compute functional distance between species



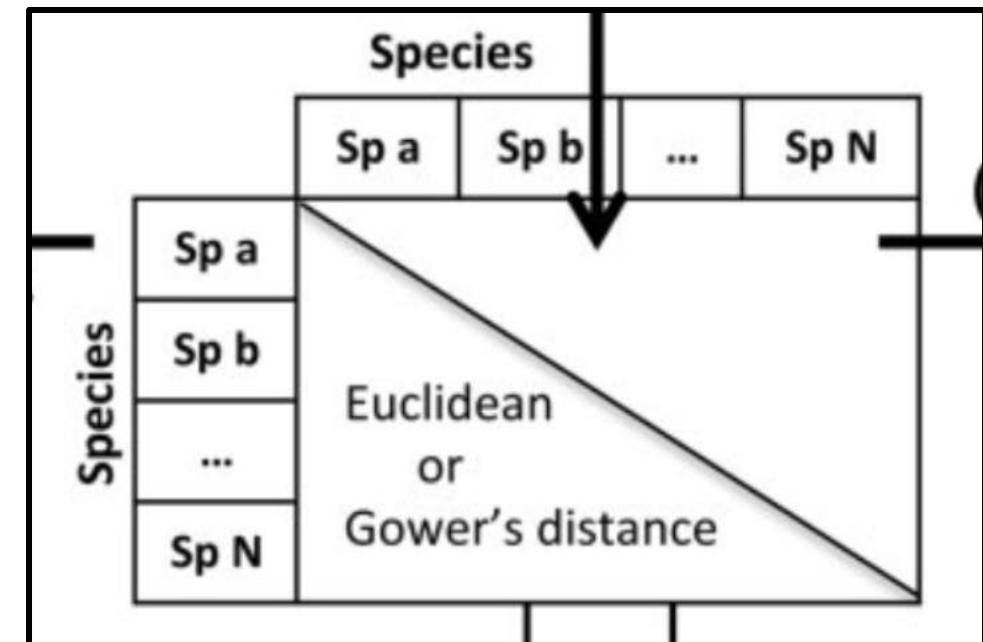
How to work with several traits?

Step 1. Compute functional distance between species



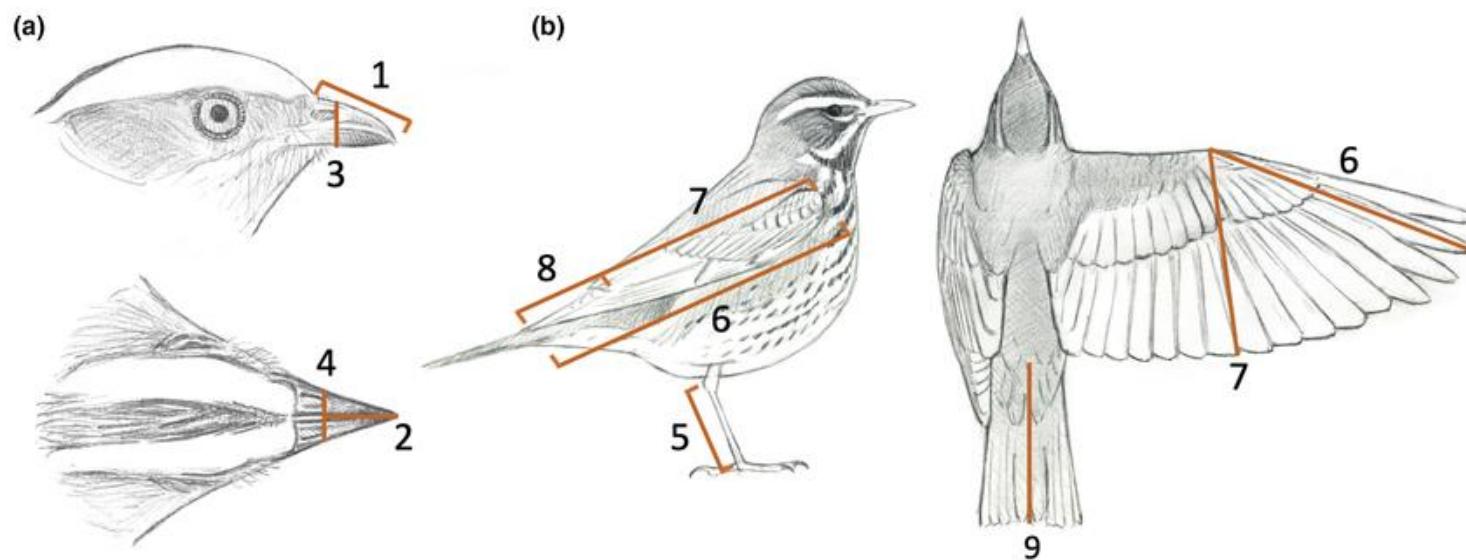
All traits are considered

- *Trait selection*
Which? Why?
- *Trait weight*
Log ? Scale?
- *Trait type*
Continuous? Binomial? Categorical?



How to work with several traits?

AVONET : a database of morphological traits of birds



How to work with several traits?

- Problem when considering trait by trait:
 - Difficult to link a traits (e.g., wing length) to a clear ecological function
 - Correlation between trait
- > Need to consider all traits together to find synthesis axes, representing ecological strategies.

How to work with several traits?

Principal Component Analysis (PCA)

- allows reducing a trait dataset to few independent trait dimensions defined by the inherent relationships between traits.

```
# Run PCA
pca.trait = princomp(imputed.traits, cor = TRUE)

# Building the functional trait space (using the first two PCs)
trait_space_global = funspace(x = pca.trait, PCs = c(1,2), n_divisions = 300)
plot(x = trait_space_global,type = "global",quant.plot = TRUE,arrows = TRUE,arrows.length = 0.9)
```

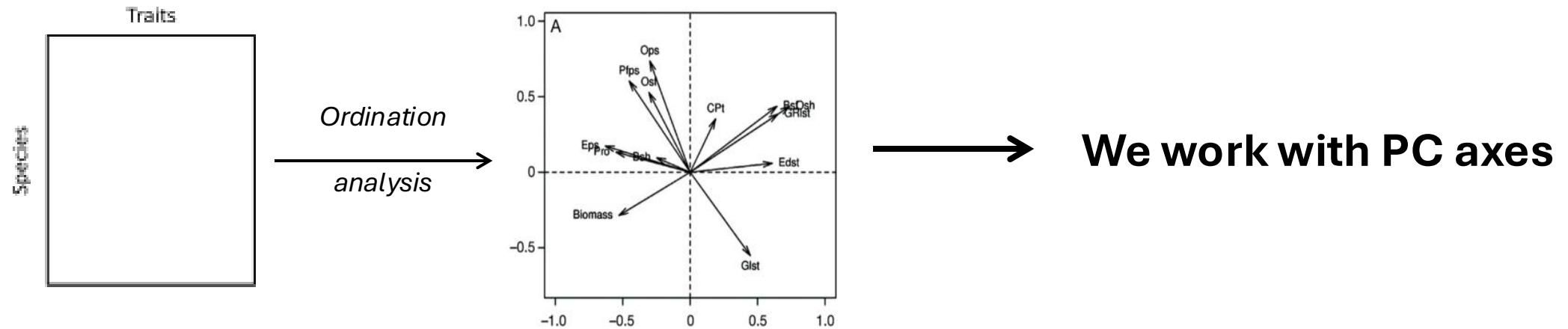
PCA is the most common method, but other methods exist.



PCA works only with continuous data

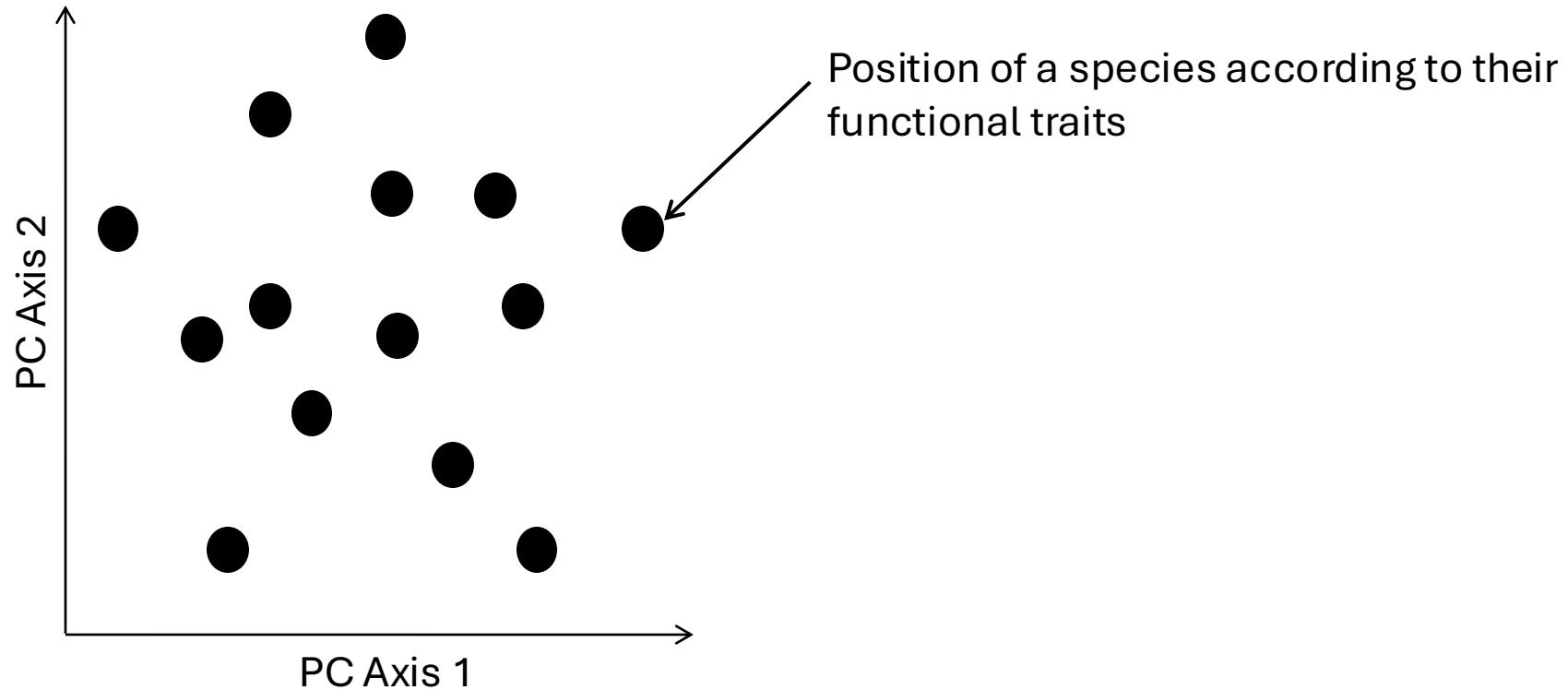
How to work with several traits?

Principal Component Analysis (PCA)

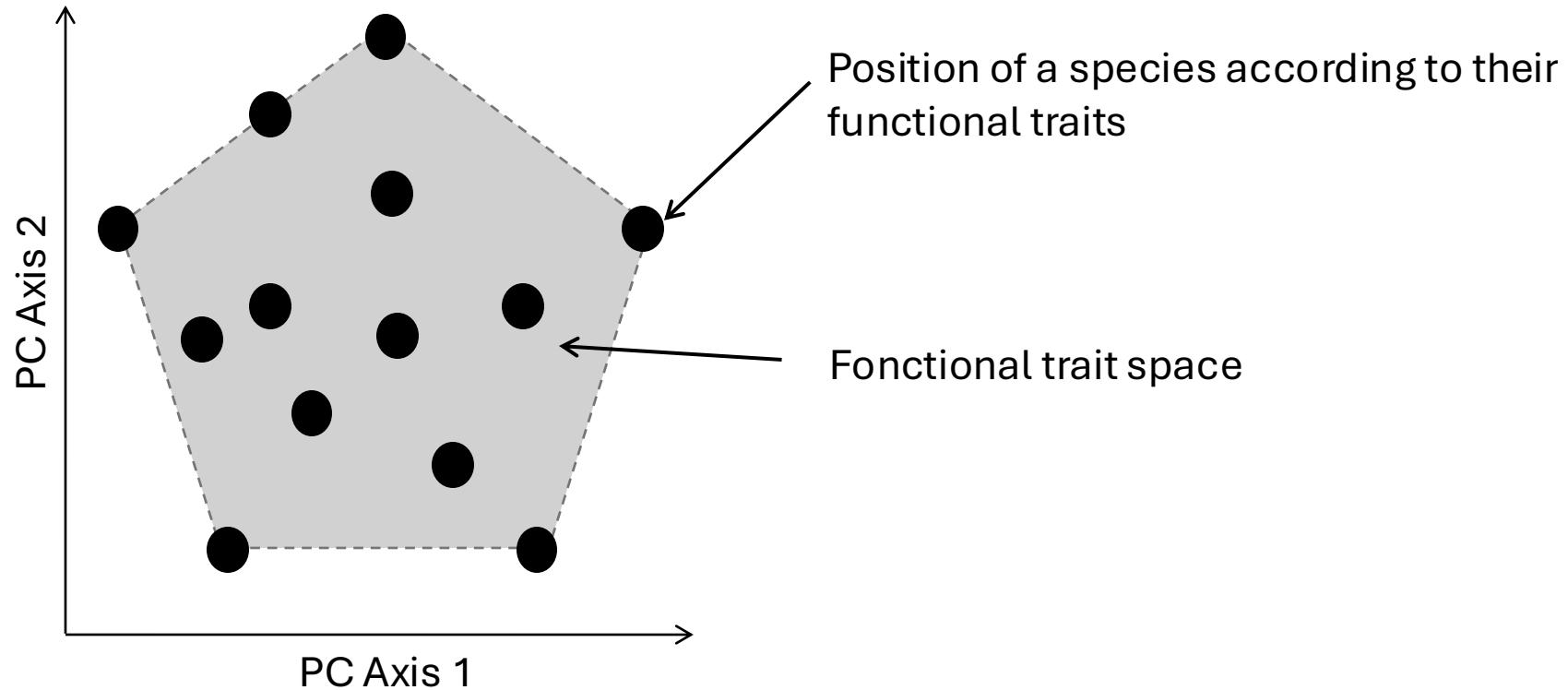


We work with PC axes

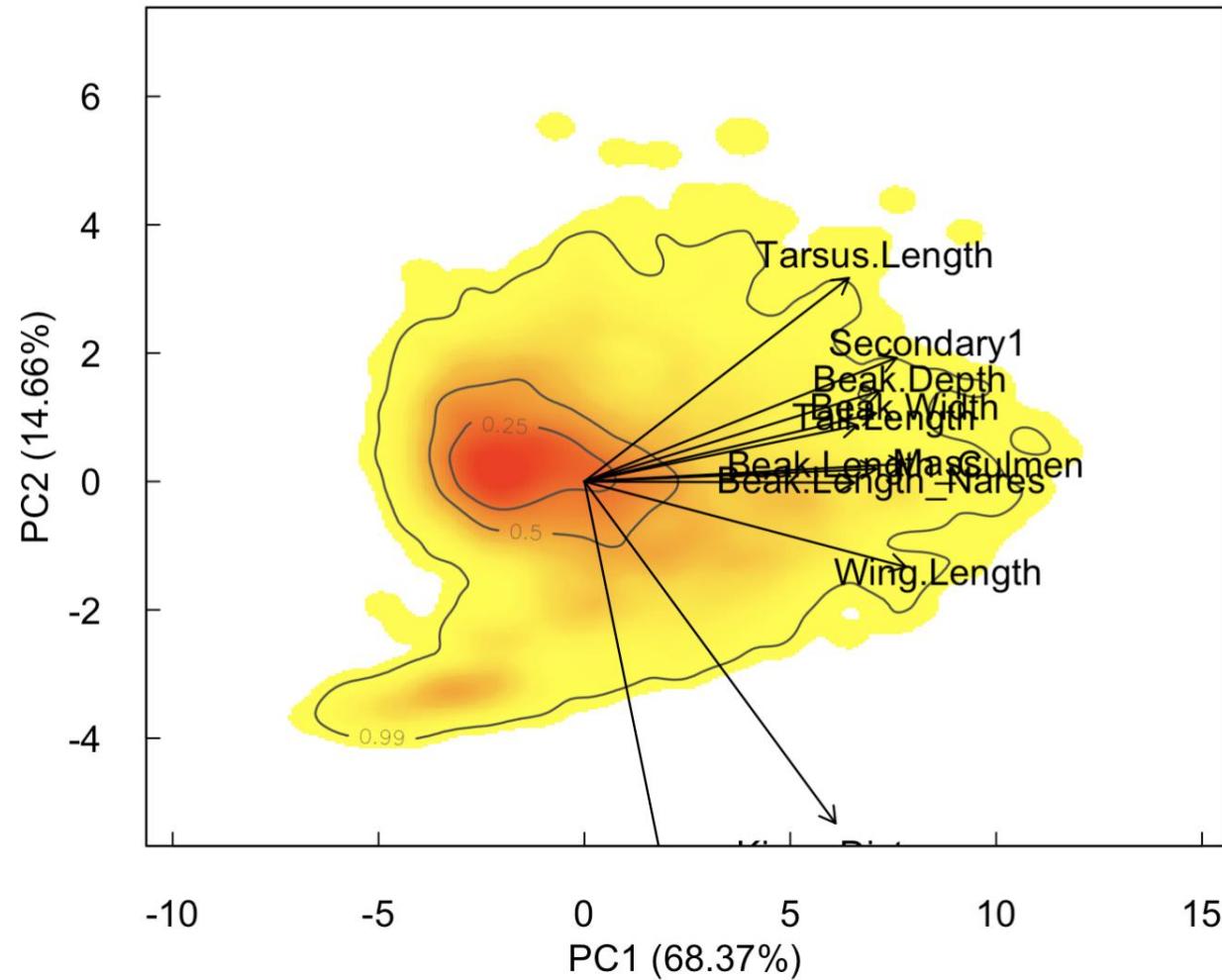
Functional trait space



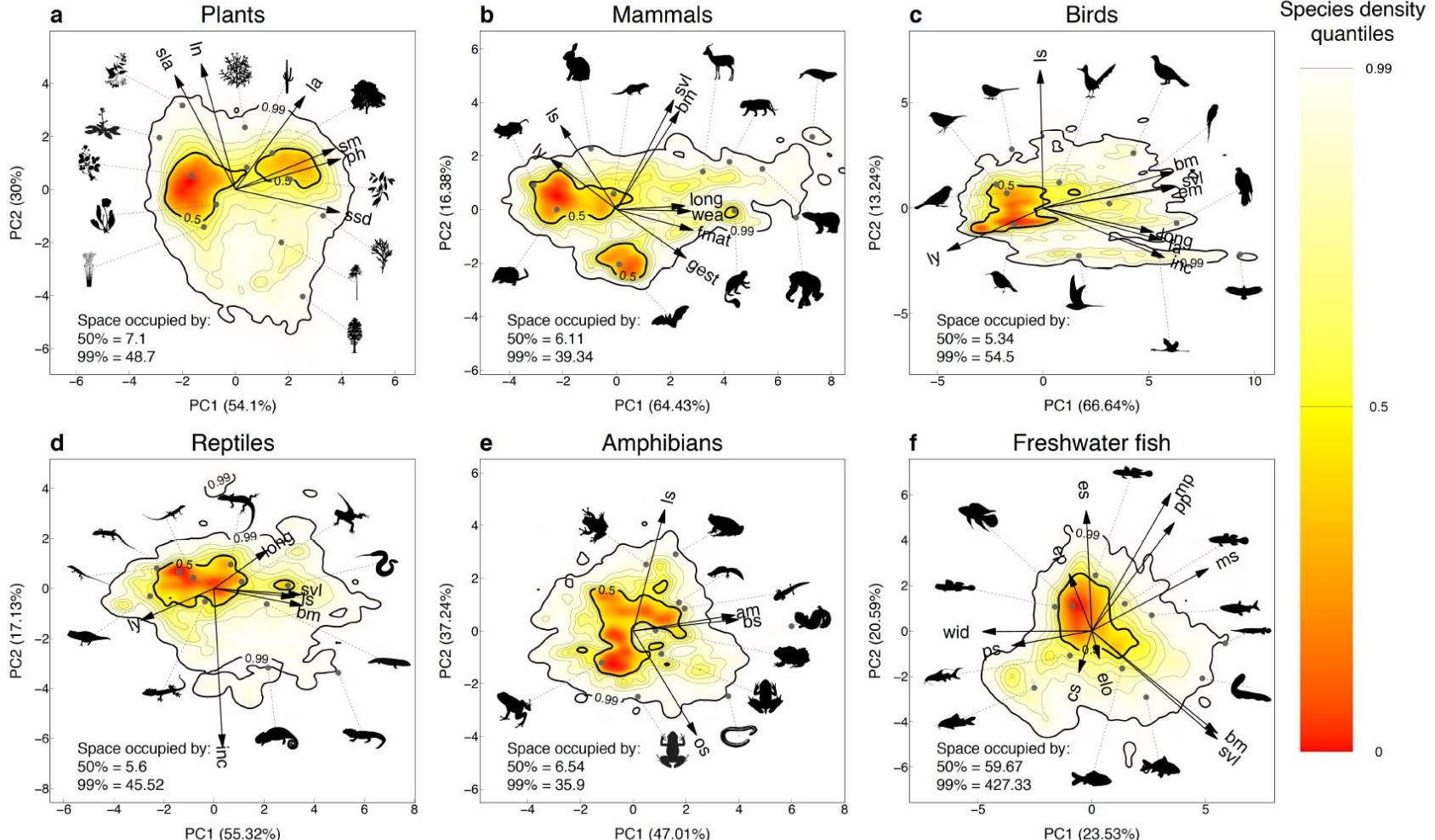
Functional trait space



Functional trait space

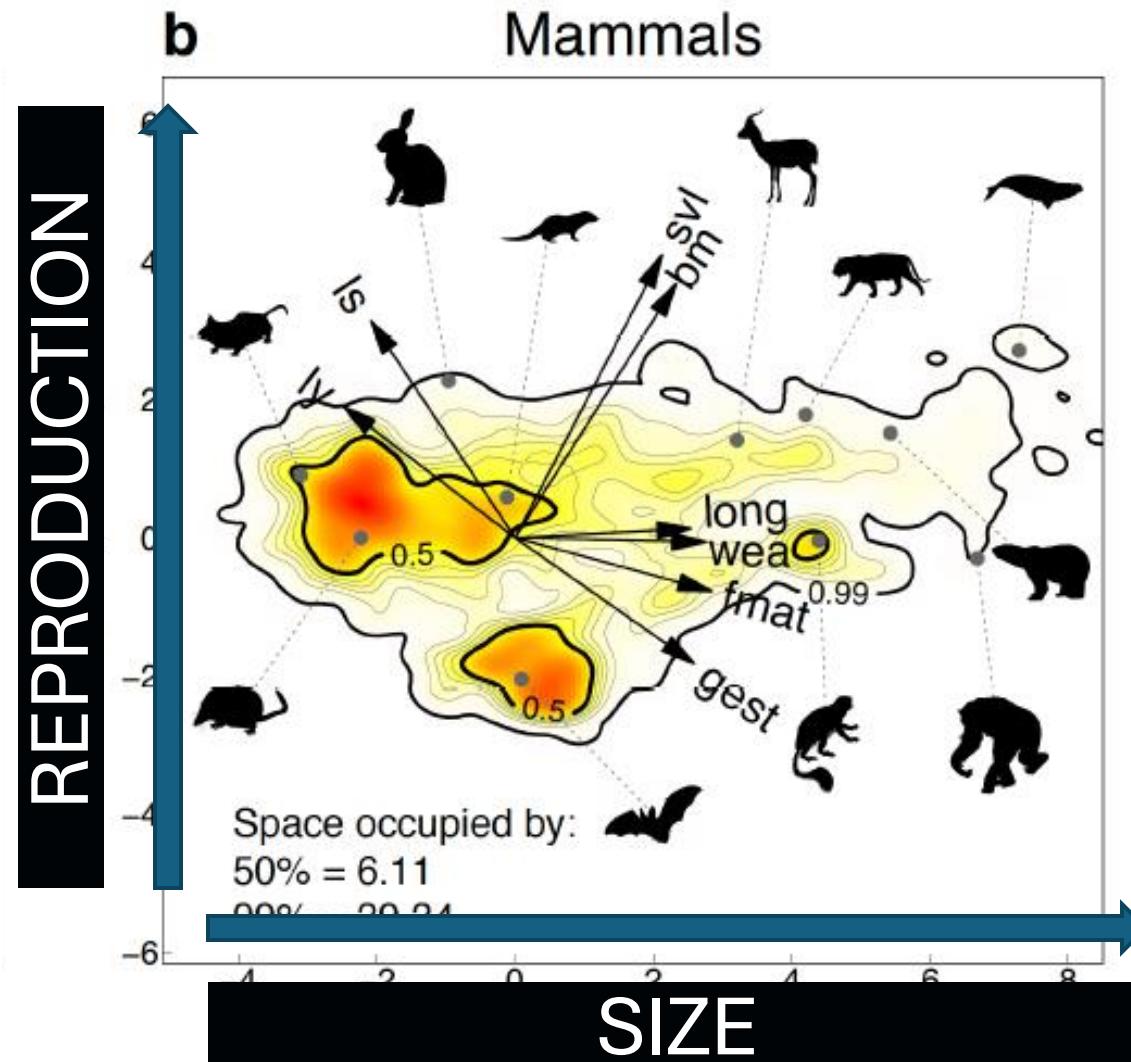


The functional space of vertebrates and plants

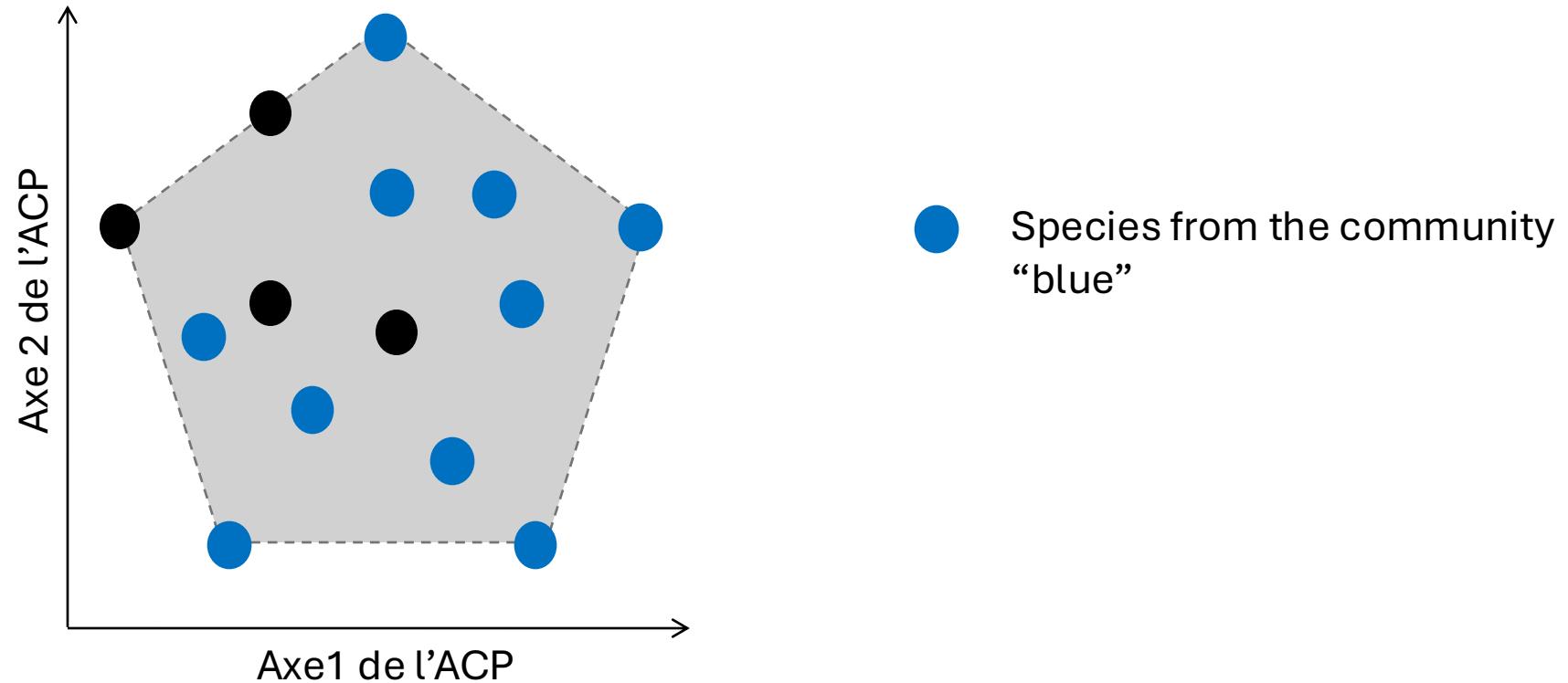


- Few dimensions
- High lumpiness (hotspot)
- Hotspots are close to the extremes (skewed occupation)

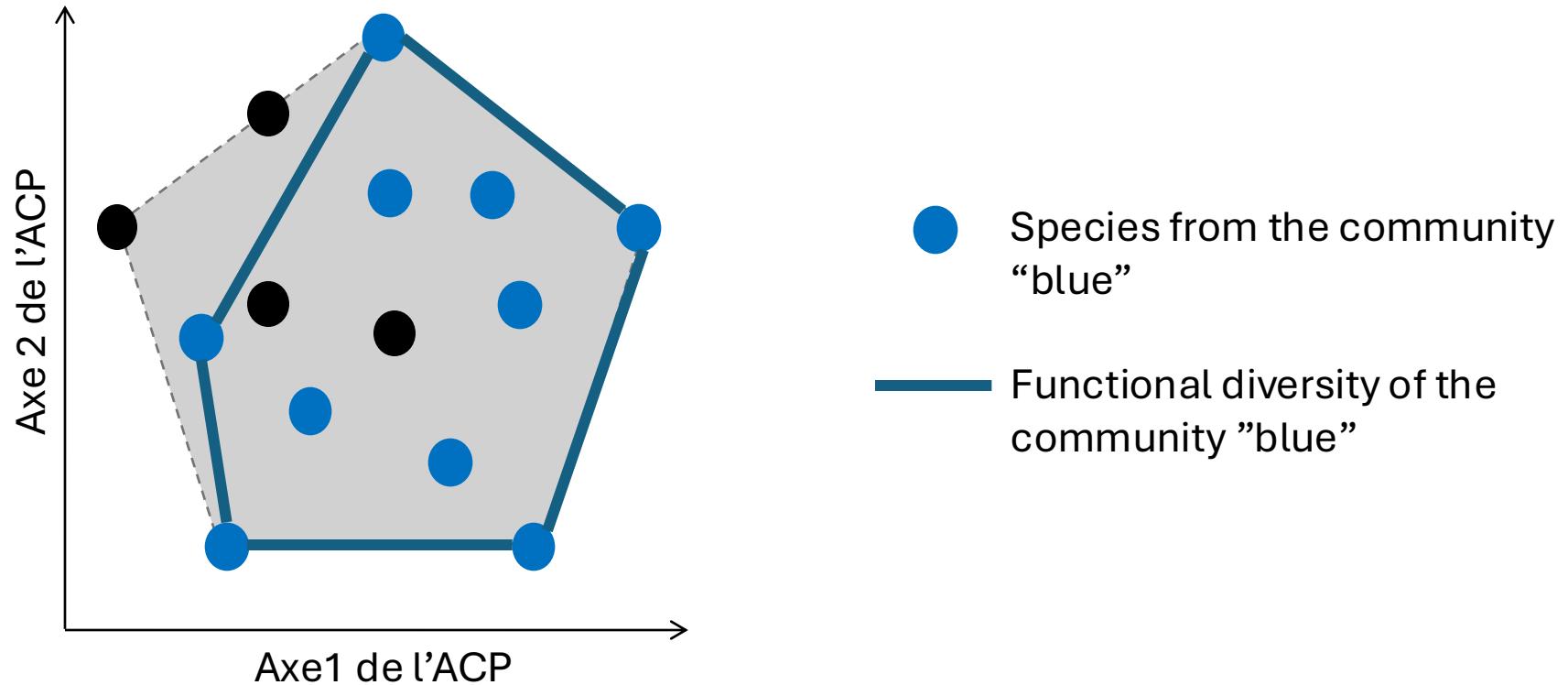
The functional space of vertebrates and plants



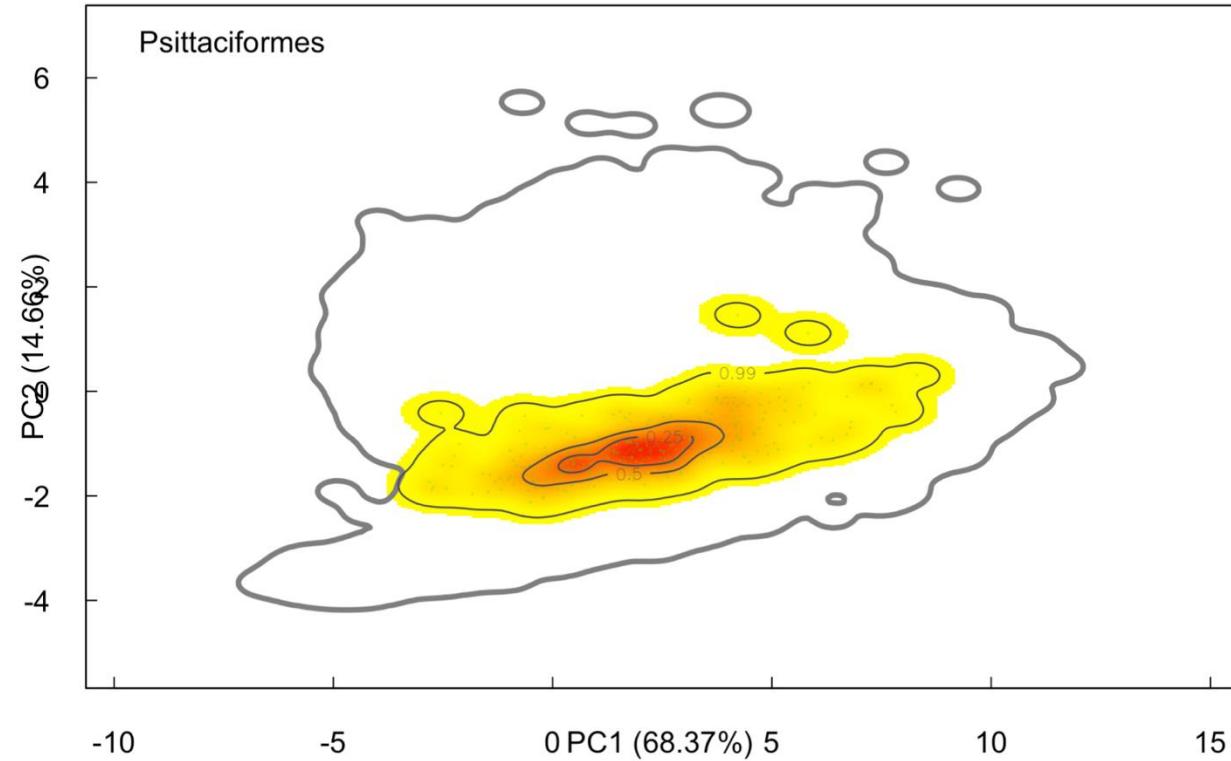
Functional trait space



Functional trait space



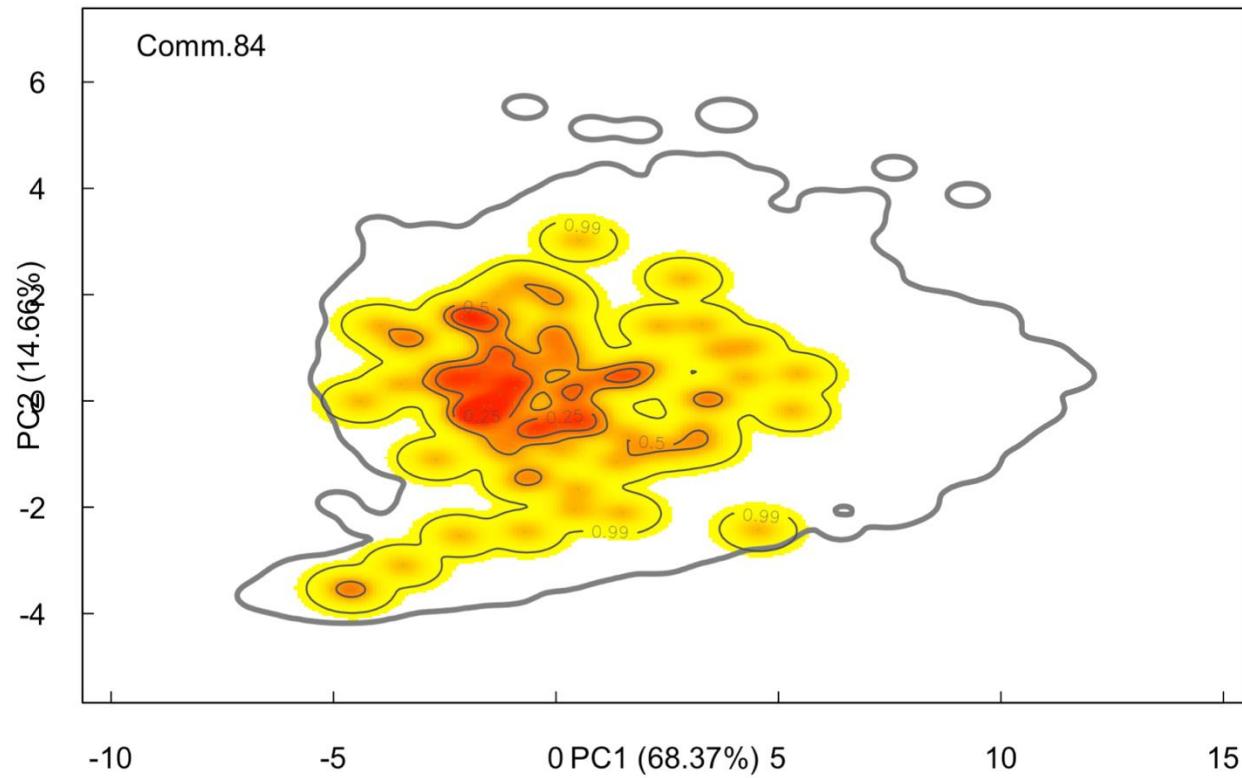
Functional trait space



It is also possible to visualize :

- A group of species. e.g. order

Functional trait space



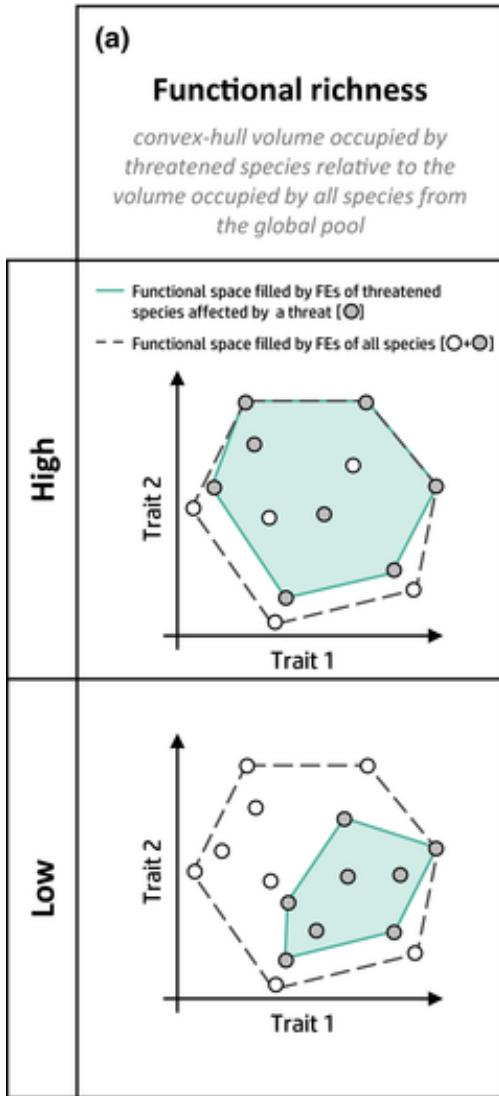
It is also possible to visualize :

- A group of species. e.g. order
- A community.

Species relative abundances (p_i)

	comm. 1	comm. 2	comm. 3	comm. 3.NA
species 1	0.20	0.70	0.00	0.00
species 2	0.20	0.00	0.30	0.33
species 3	0.20	0.07	0.00	0.00
species 4	0.20	0.00	0.20	0.22
species 5	0.20	0.07	0.00	0.00
species 6	0.00	0.00	0.10	0.00
species 7	0.00	0.16	0.40	0.44
Sum	1	1	1	1

How to calculate functional diversity ?

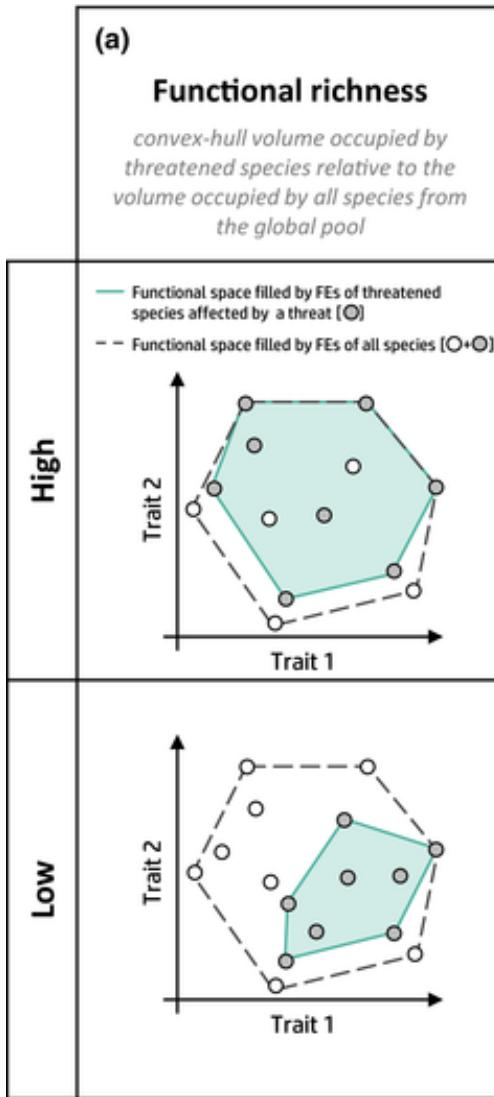


Functional richness

- Range/Volume occupied by the community
- “equivalent” to species richness
- Several method to calculate it:
 - 1st: Convex Hull: most intuitive method

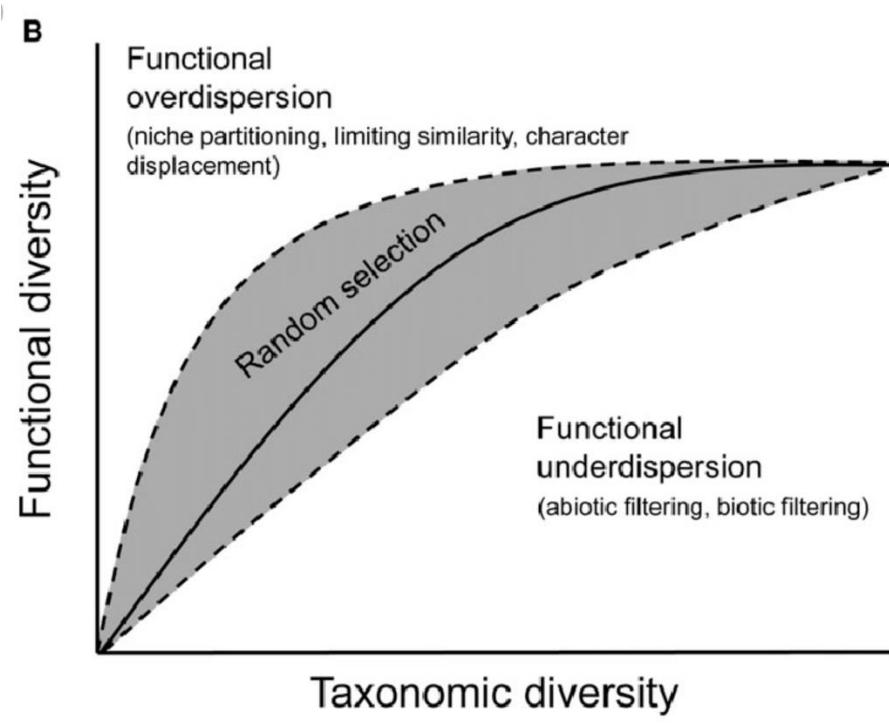
Question related to the amount of trait space occupied by assemblages as well as how it varies in space and time.

Null model



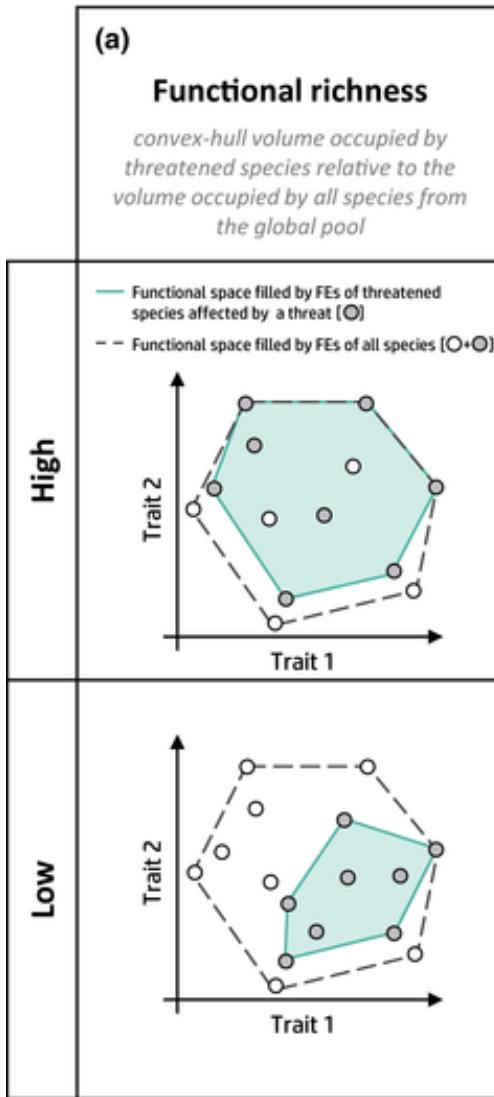
Functional richness

- Expected correlation with species richness



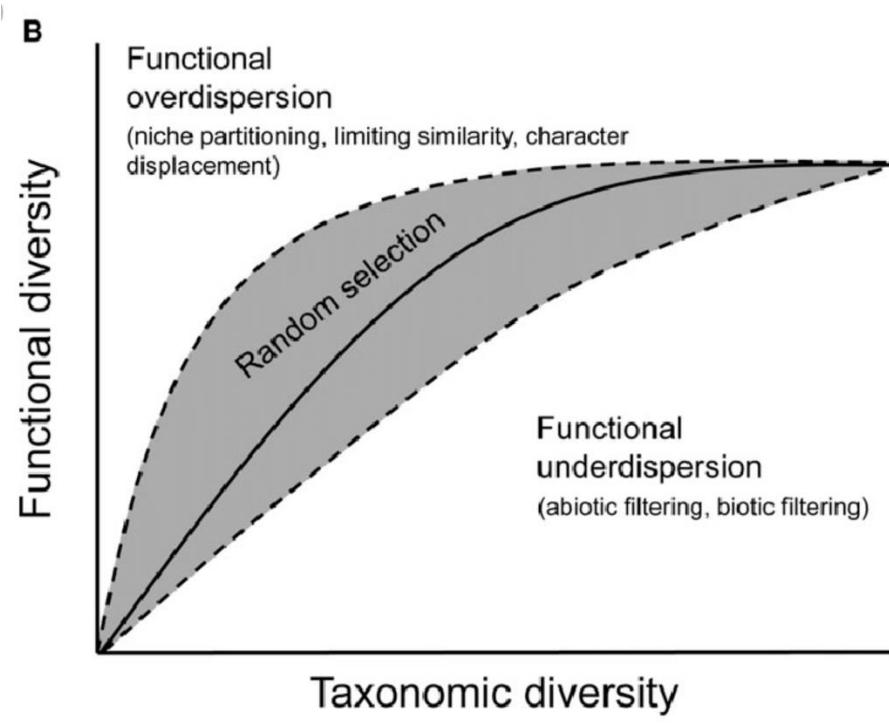
Theoretical relationships between (A) taxonomic diversity and phylogenetic diversity, and (B) taxonomic diversity and functional diversity that are consistent with particular ecological or evolutionary mechanisms or with random selection (Mayfield & Levine 2010, Kluge & Kessler 2011).

Null model



Functional richness

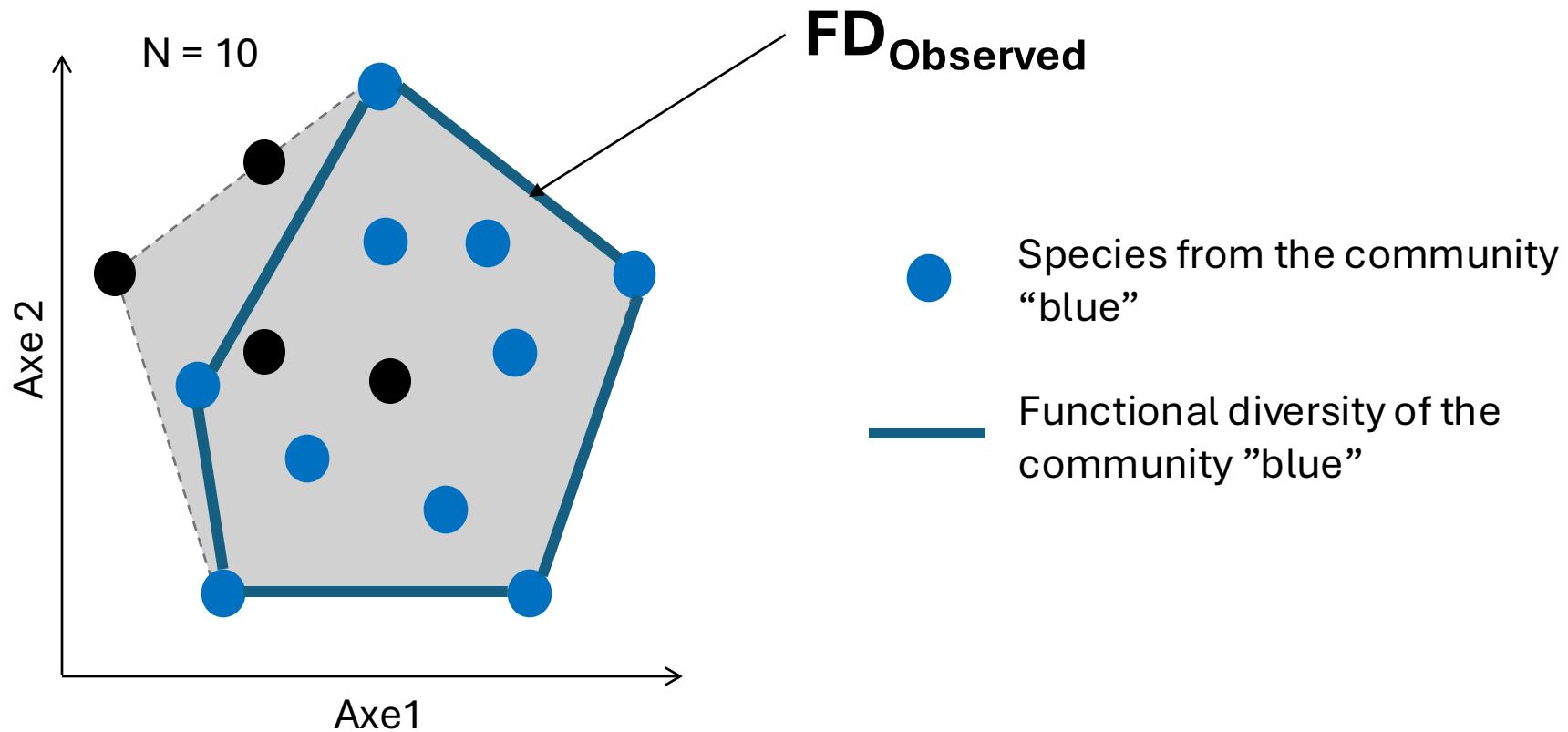
- Expected correlation with species richness



Theoretical relationships between (A) taxonomic diversity and phylogenetic diversity, and (B) taxonomic diversity and functional diversity that are consistent with particular ecological or evolutionary mechanisms or with random selection (Mayfield & Levine 2010, Kluge & Kessler 2011).

Null model

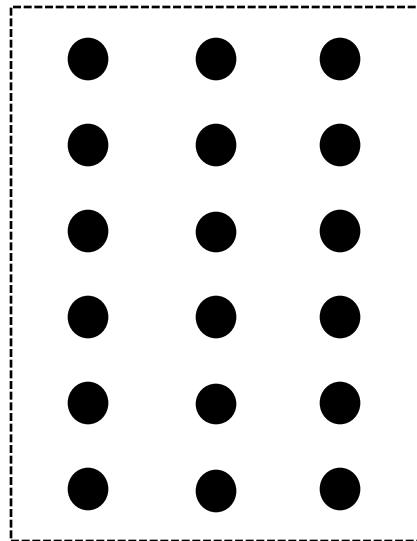
① Observed functional diversity (FD_{Observed})



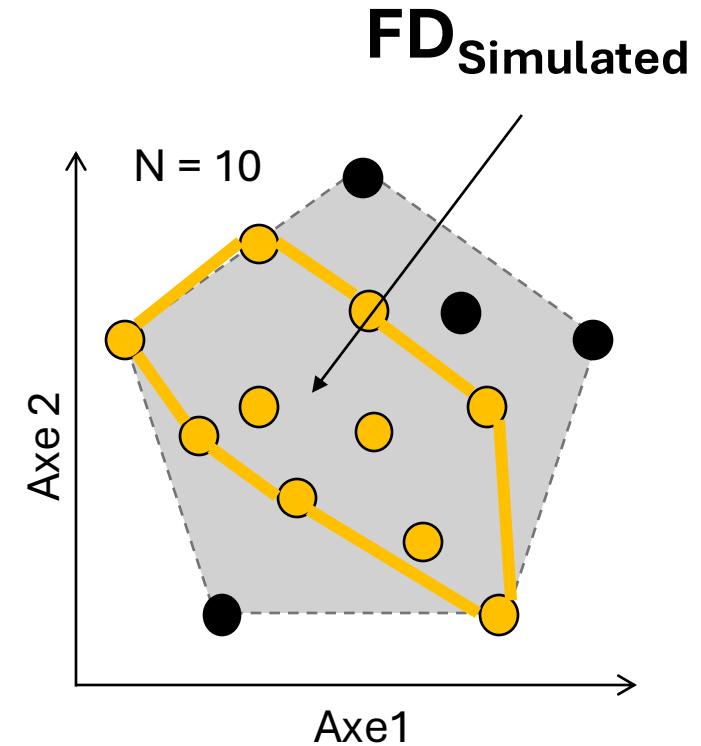
Null model

- ① Observed functional diversity (FD_{Observed})
- ② Simulation of random communities

Species pool

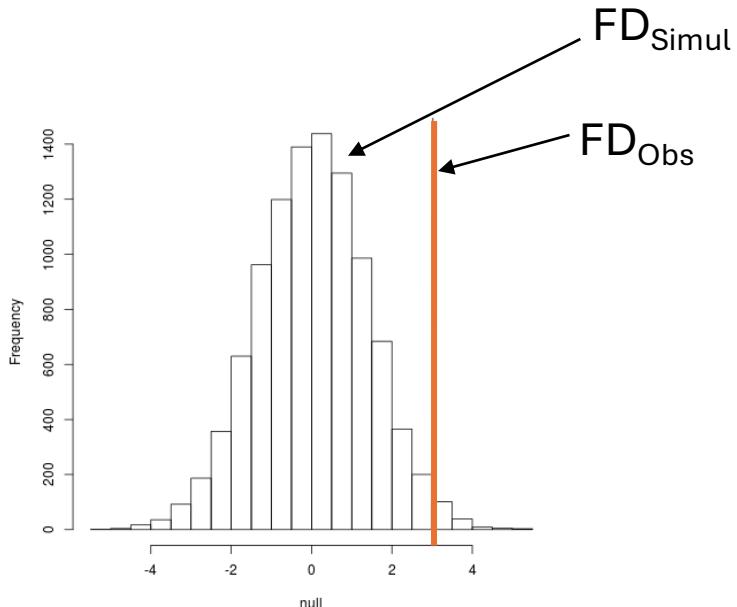


Random sp.



Null model

- ① Observed functional diversity ($FD_{Observed}$)
- ② Simulation of random communities
- ③ Comparaison of the FD_{Simul} et de la FD_{Obs}



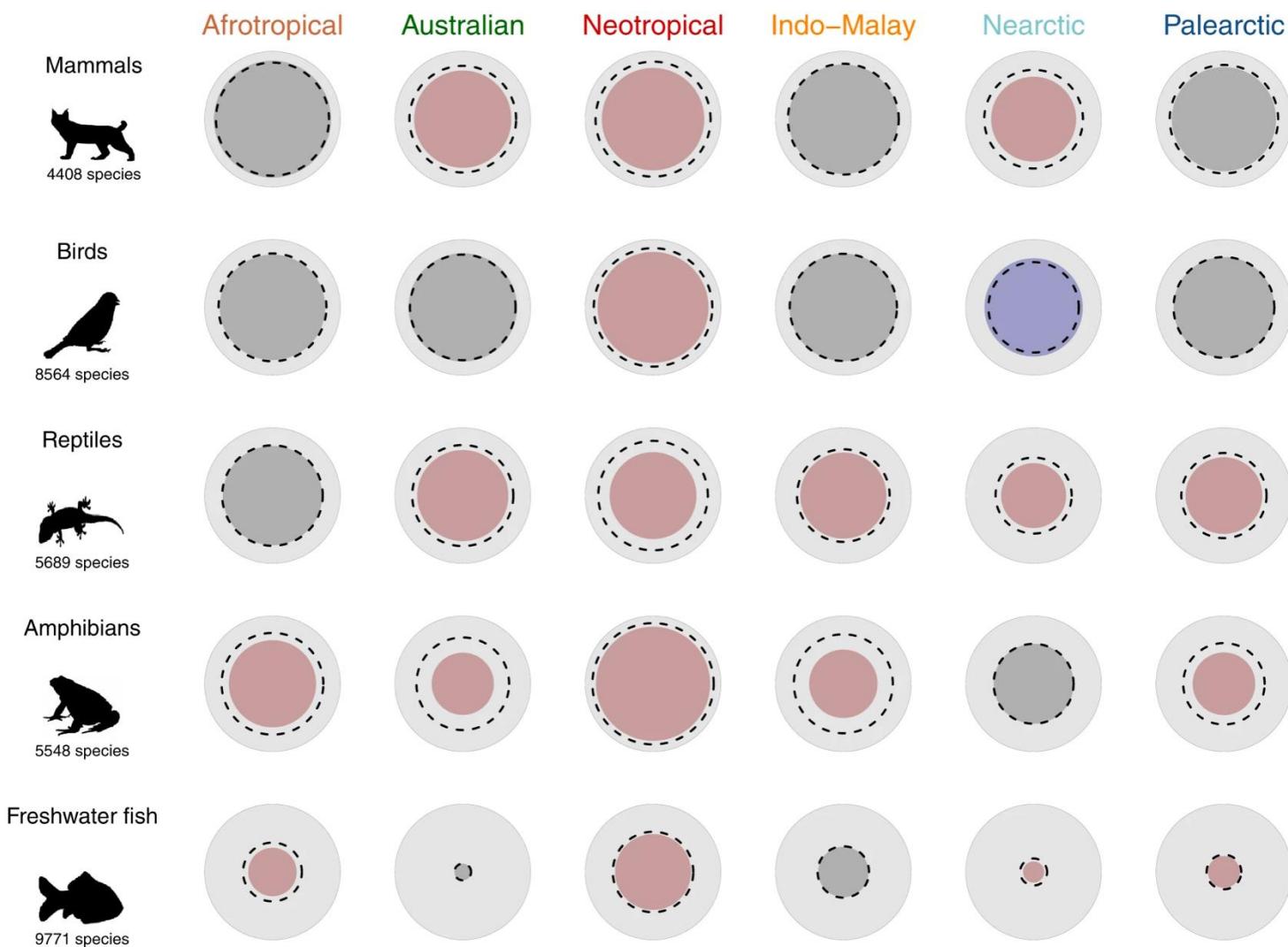
Null model

- ① Observed functional diversity ($FD_{Observed}$)
- ② Simulation of random communities
- ③ **Comparaison** of the FD_{Simul} et de la FD_{Obs}
- ④ Standardized effect size

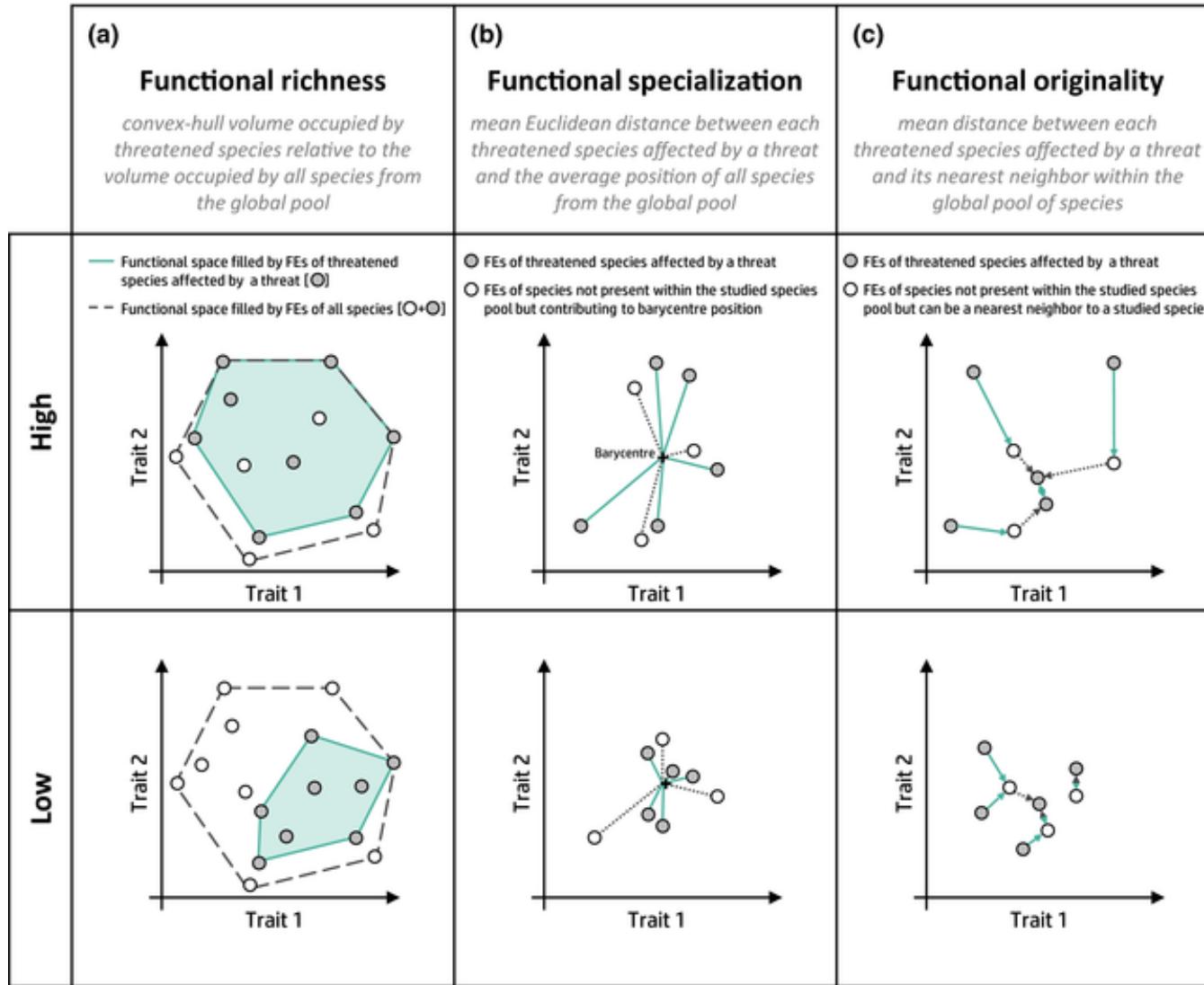
$$SES = (FD_{Obs} - \text{Mean}(FD_{Simul})) / \text{SD}(FD_{Simul})$$

$$p\text{-value} = (\text{No. } FD_{Simul} > FD_{Obs}) / \text{No. } FD_{Simulés}$$

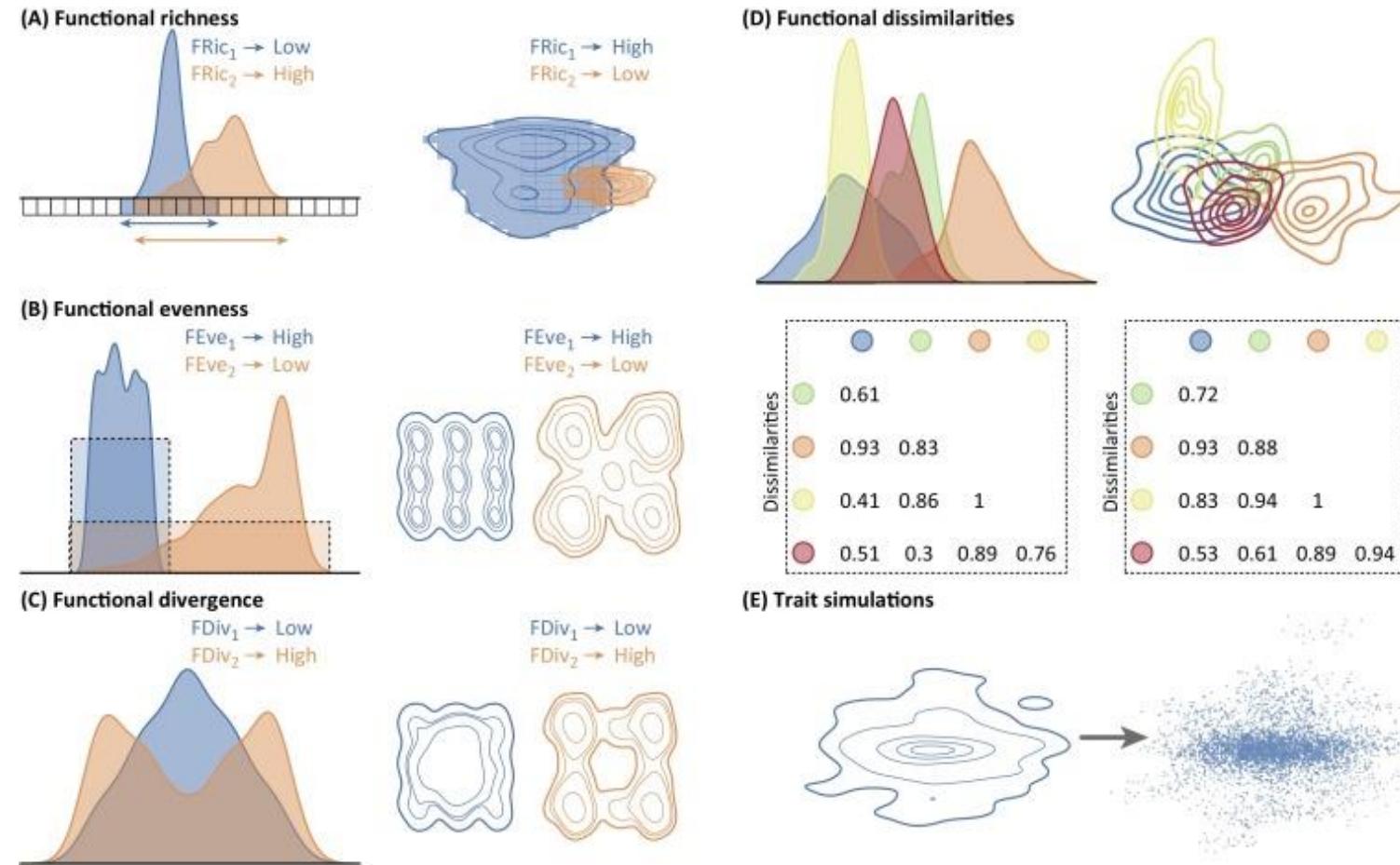
Null model



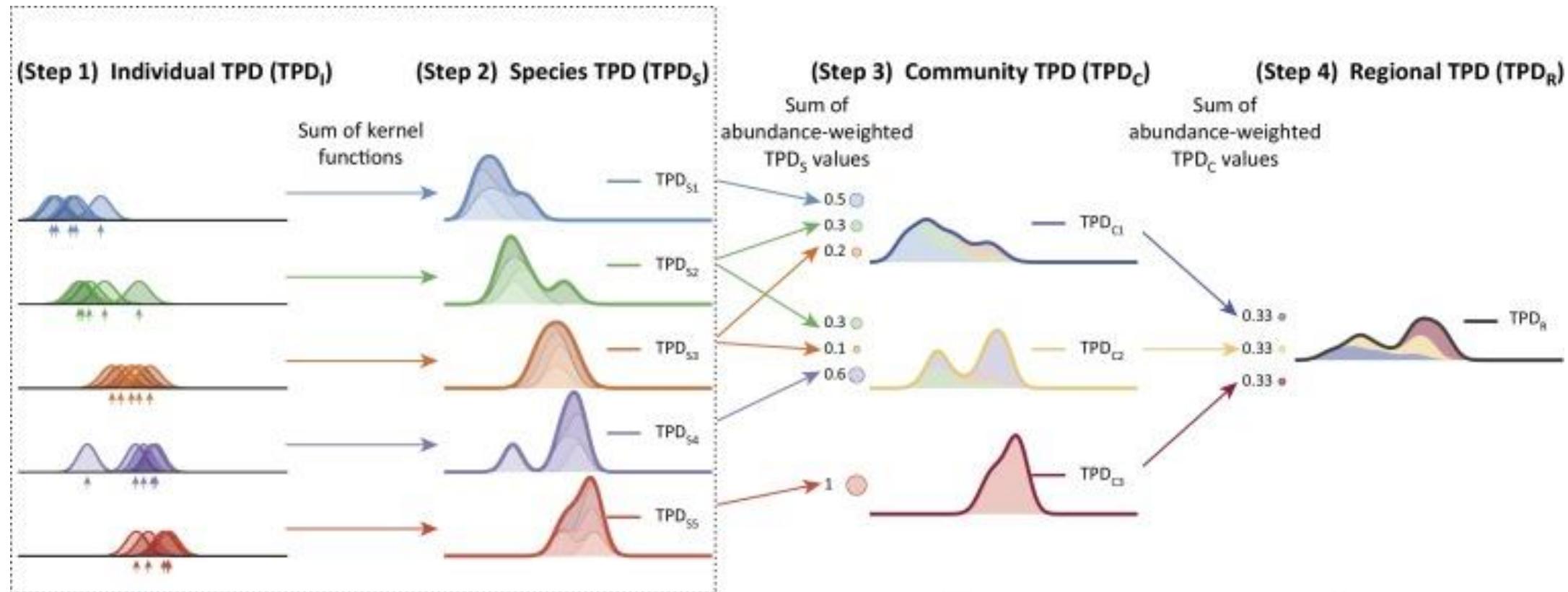
Different facets of functional diversity



Different approaches to calculate FD



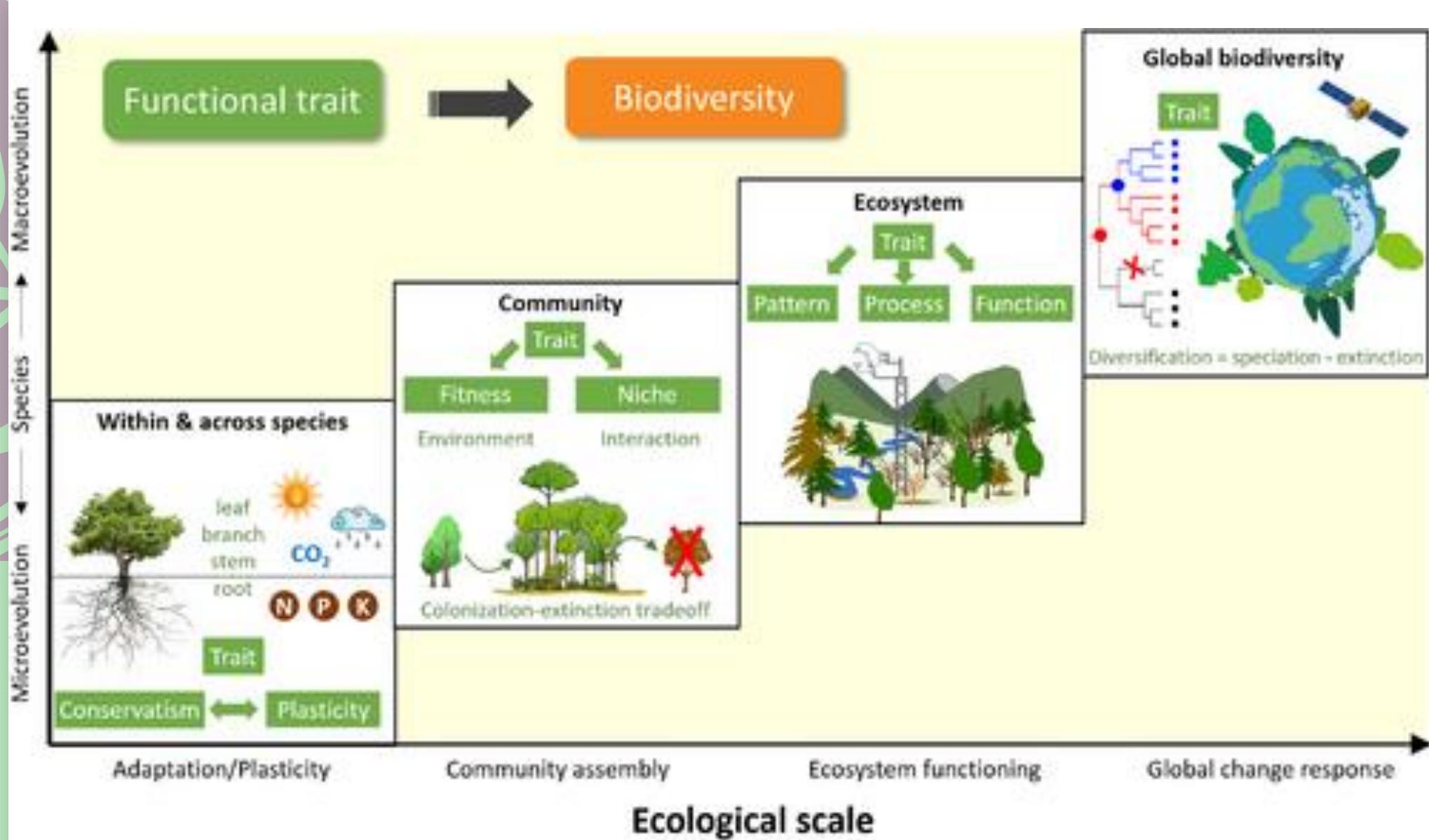
Different approaches to calculate FD



$$TPD_C(x) = \sum_{i=1}^S \text{Abundance}_i \times TPD_{Si}$$

$$TPD_R(x) = \sum_{i=1}^C \text{Abundance}_i \times TPD_{Ci}$$

Application



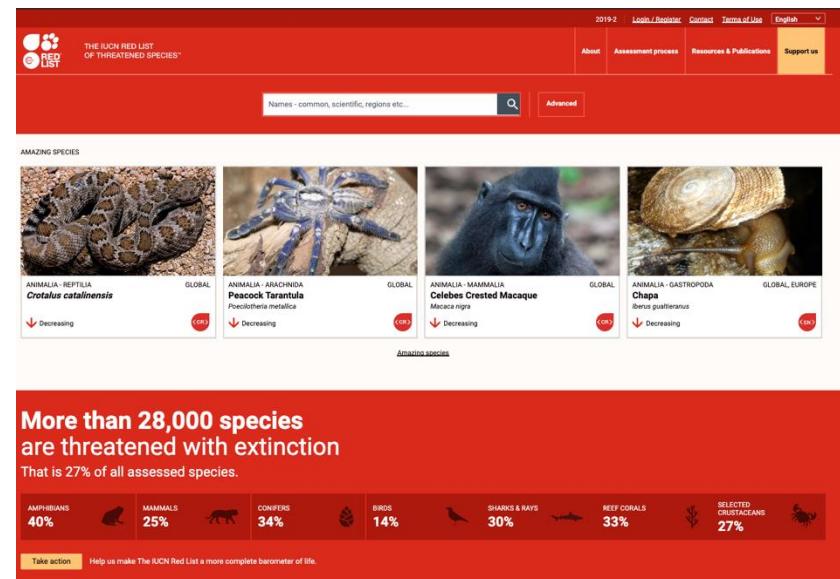
Causes of extinction

Low abundance

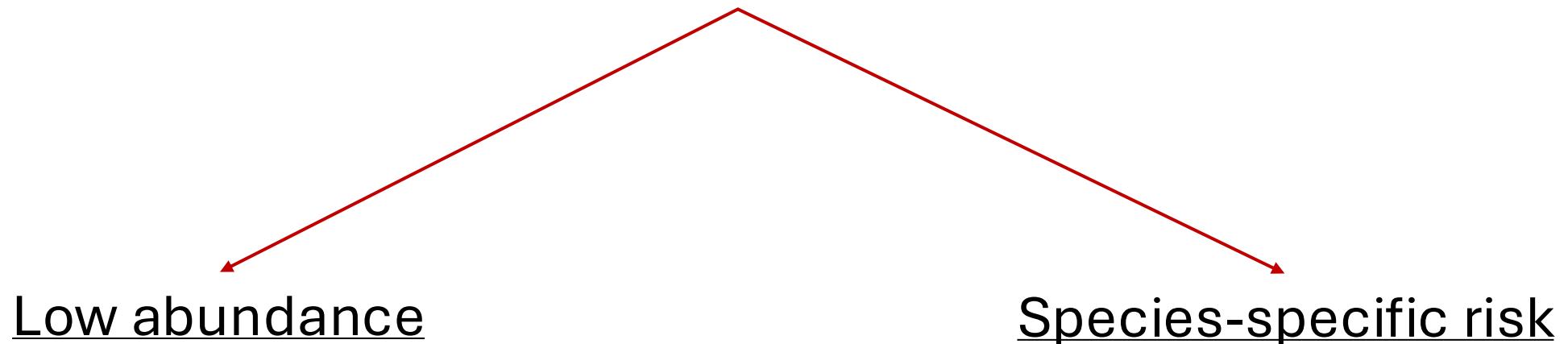
- Isolation
- Allee effect

“Rare species goes extinct first”
(Simberloff, 1986)

Species conservation strategies



Causes of extinction



- Isolation
- Allee effect

“Rare species goes extinct first”
(Simberloff, 1986)

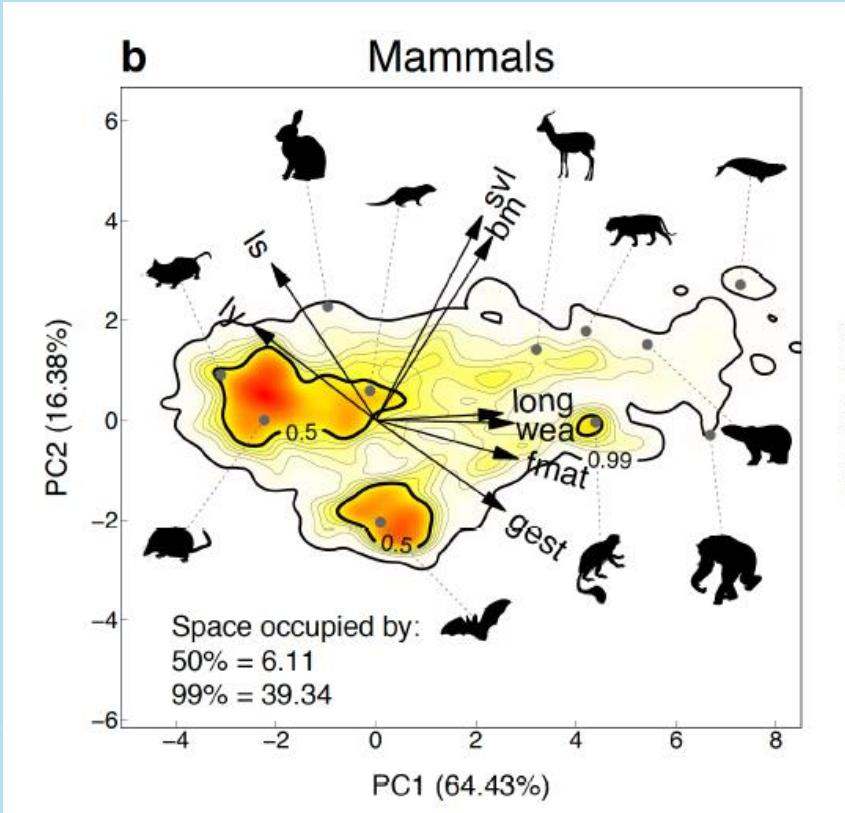
- Traits
- Phylogenetic

*Can we predict which species are
under threat based on traits ?
Phylogeny ?*

Payne et al. Science 2016

Include threatened species

Traits

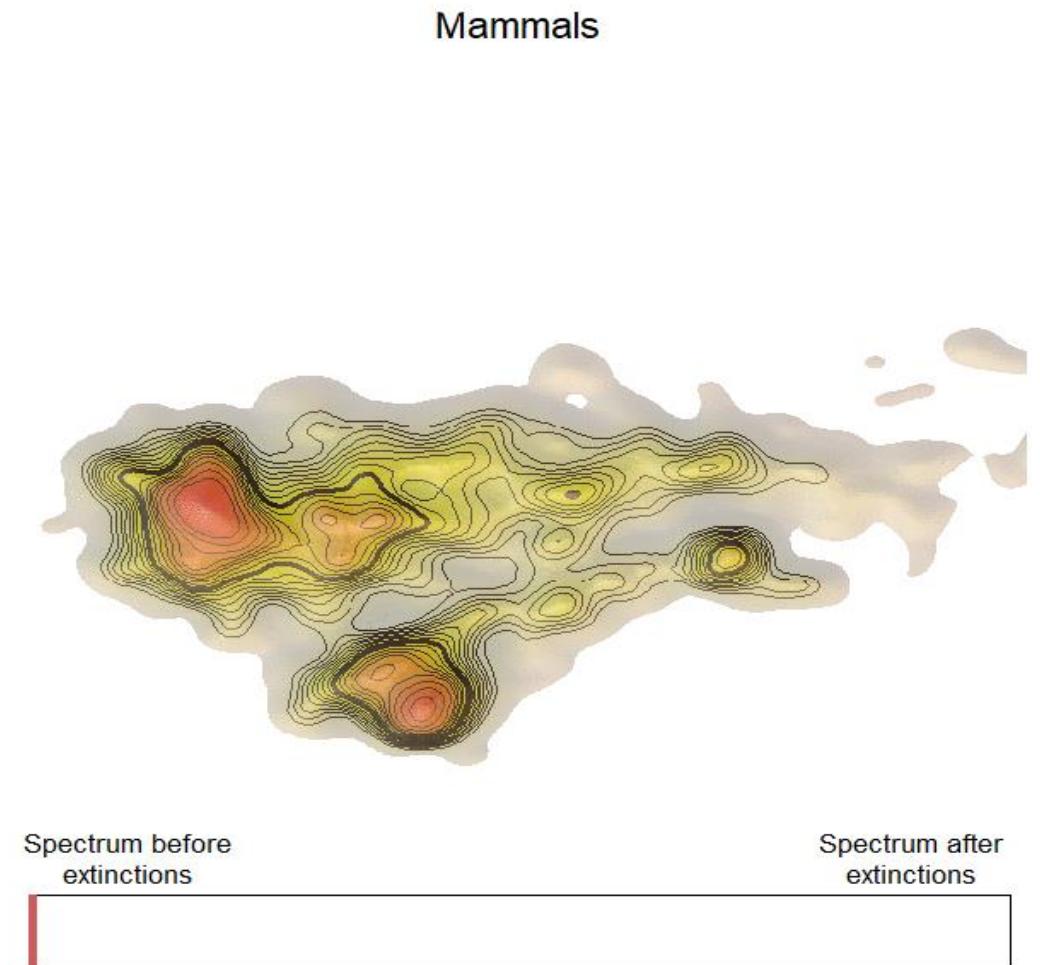
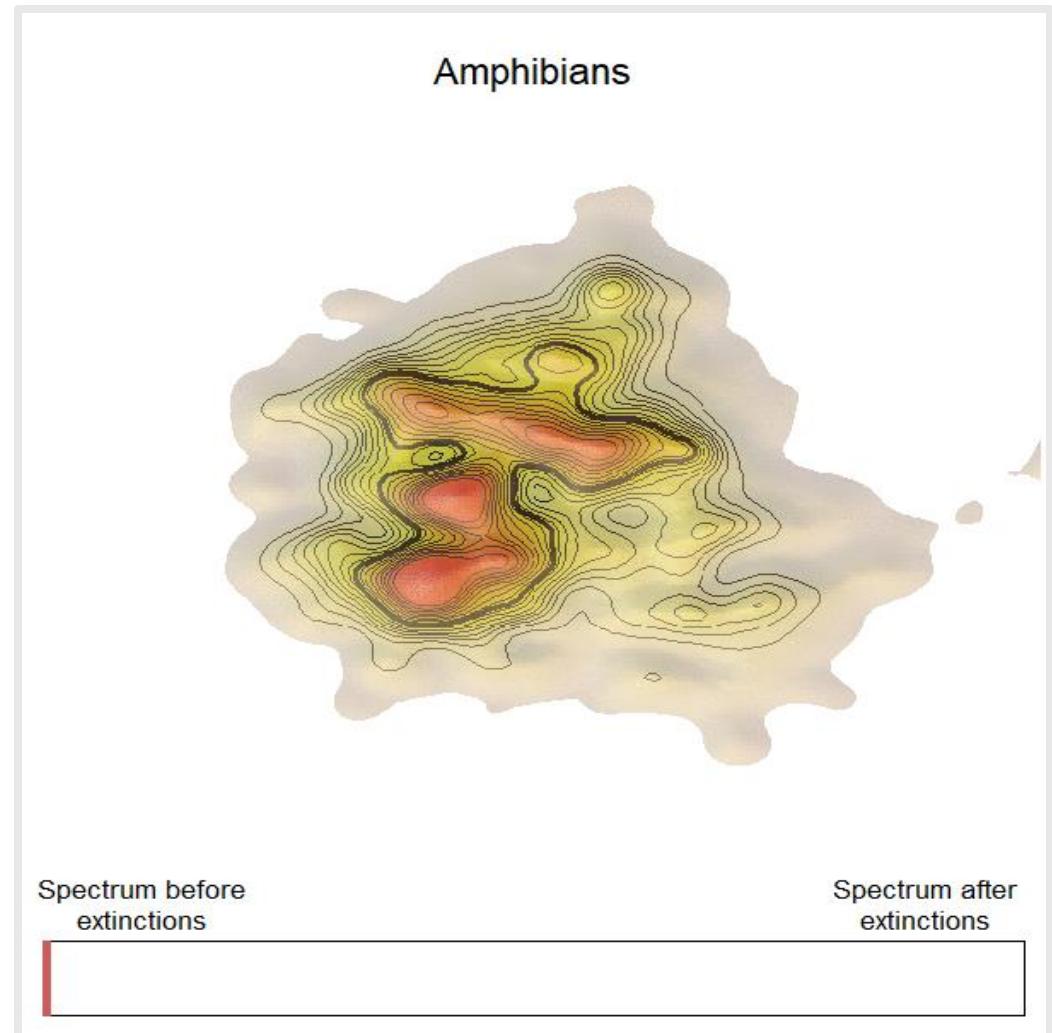


IUCN Red List

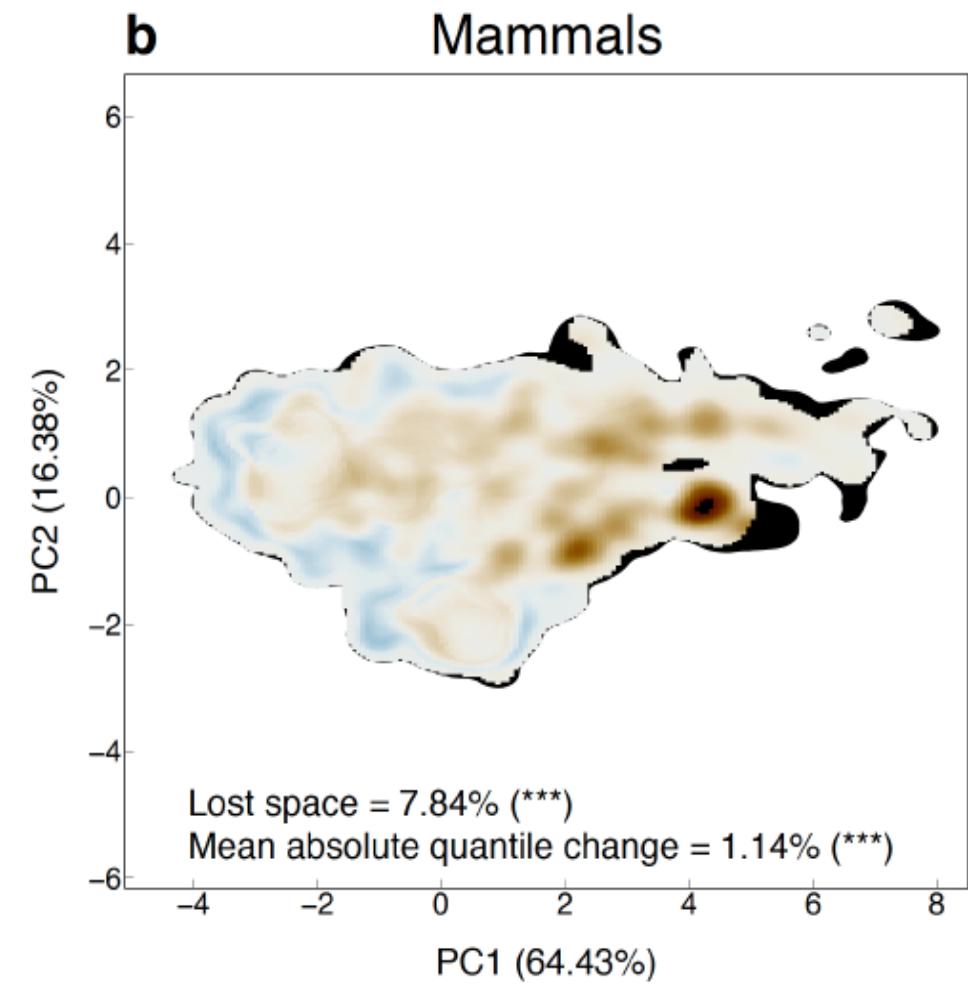
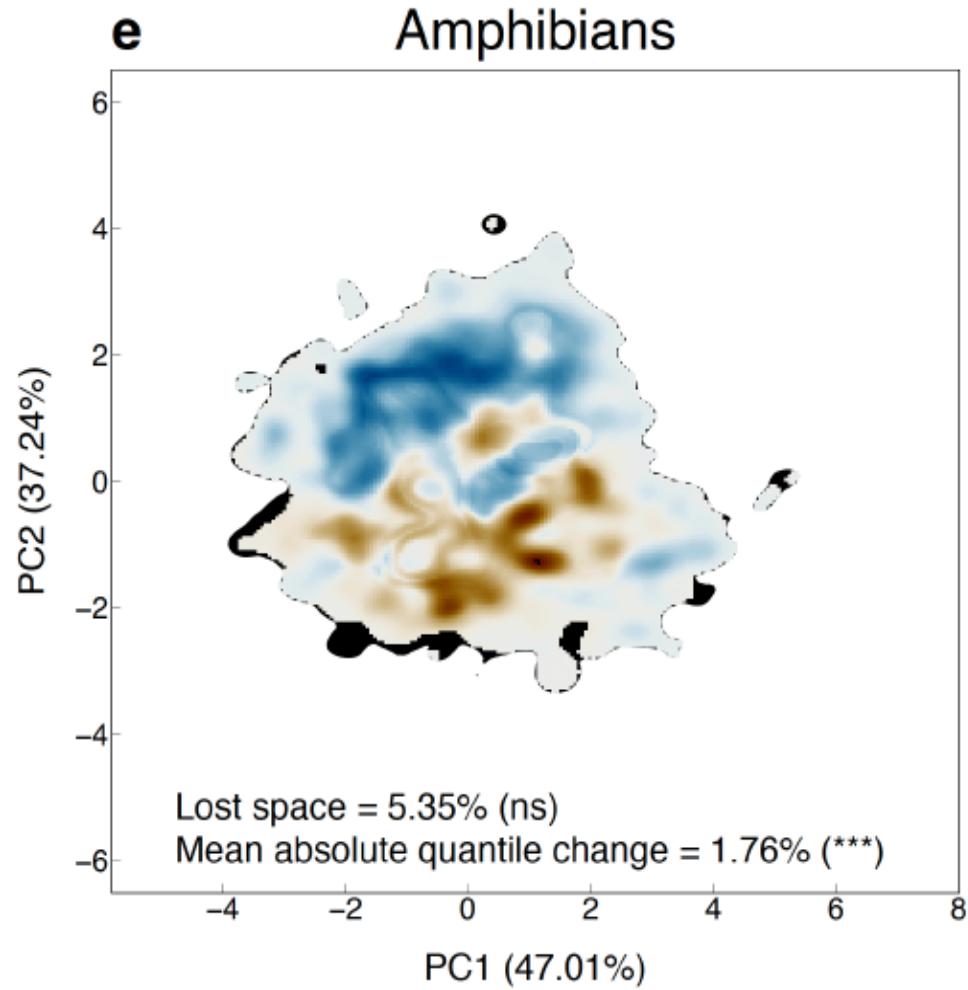


CR - EN - VU

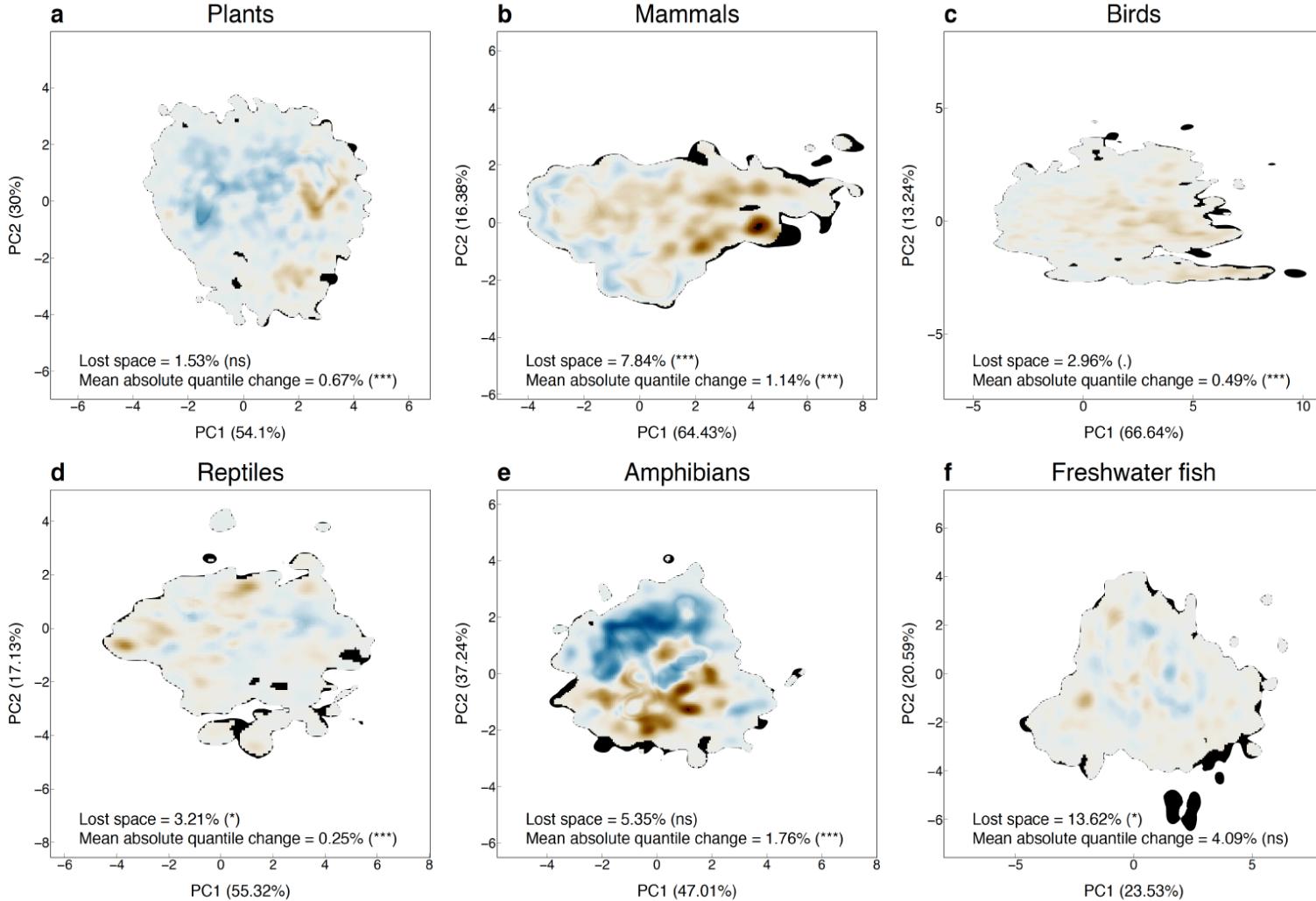
Global spectra of 6 terrestrial groups



Global spectra of 6 terrestrial groups



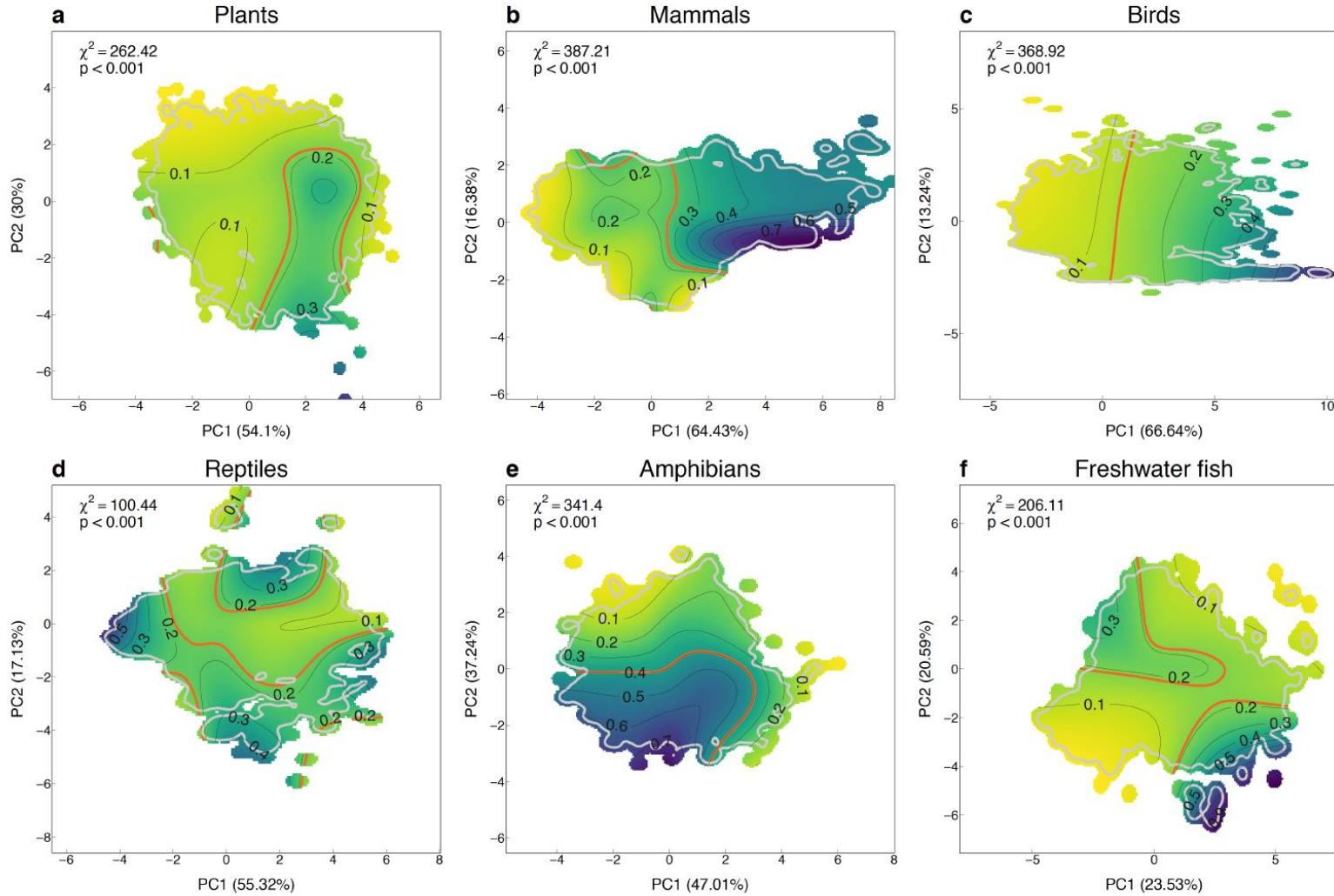
Global spectra of 6 terrestrial groups



Changes in functional spectra

- Reduced lost space (1 – 13%)
- Erosion within spectra
- **Large reorganization of the functional space**

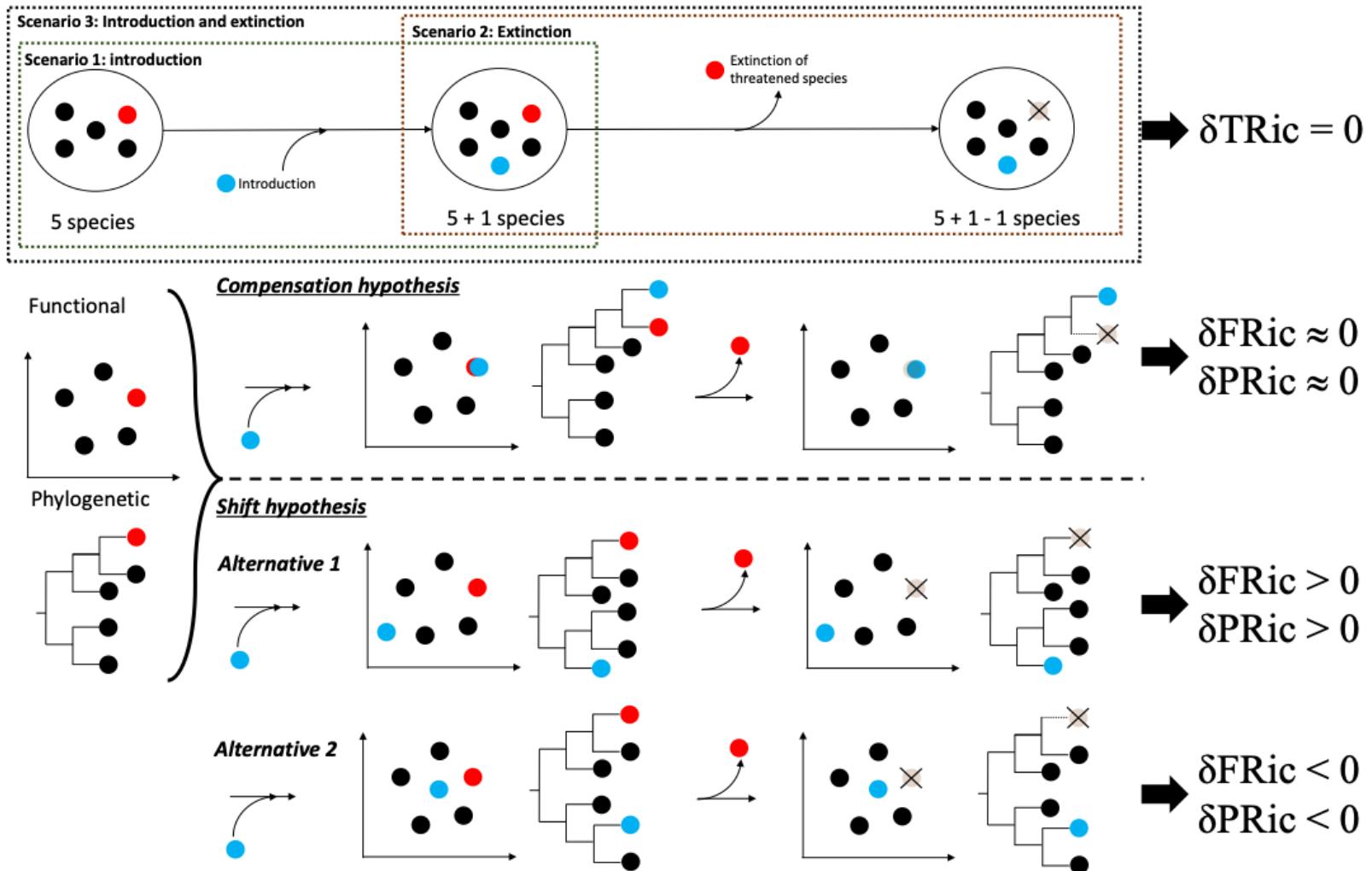
Global spectra of 6 terrestrial groups



Threatened species

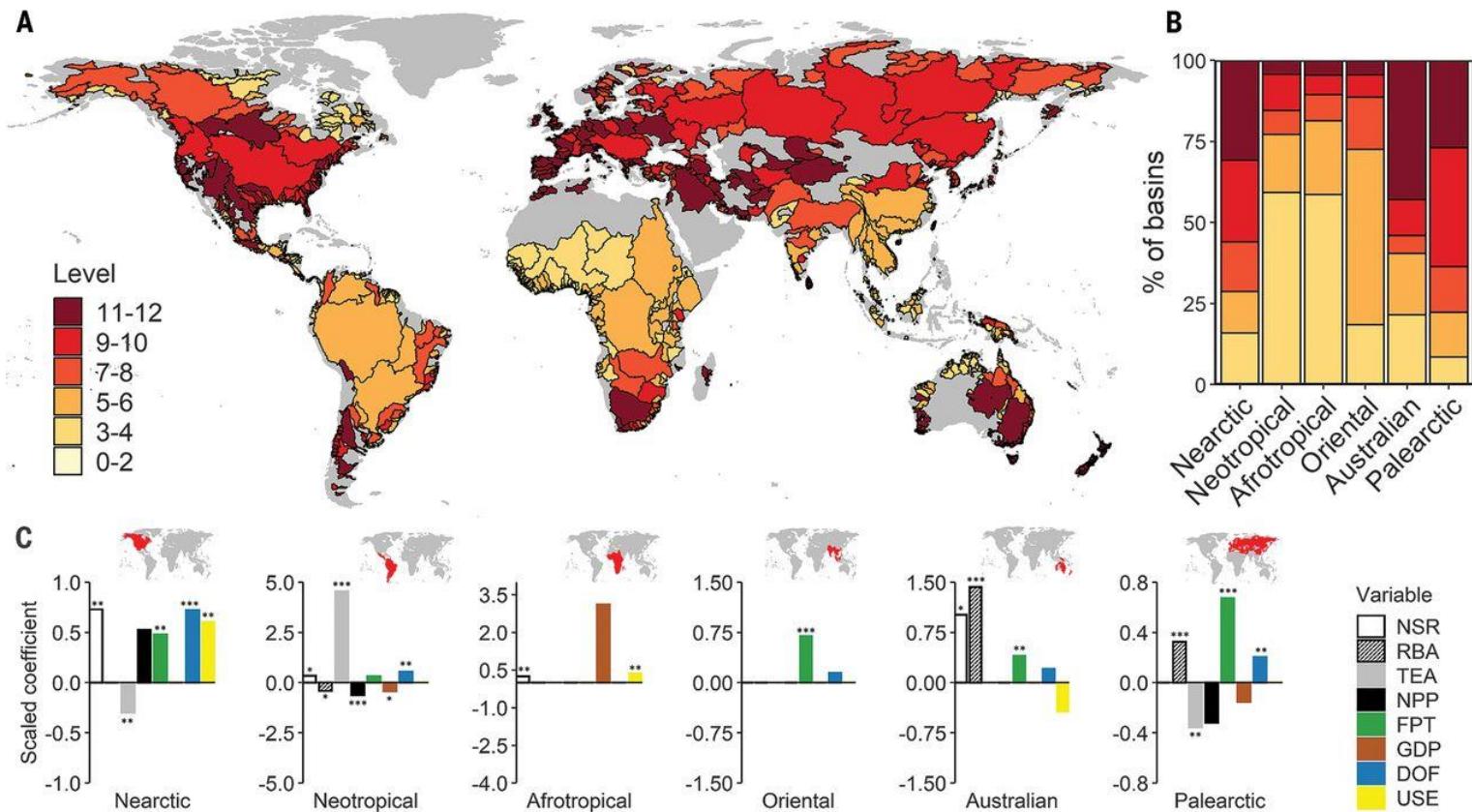
- Large
- “Slow” pace of life
- Low fecundity
- Up to 8x difference in threat risk
- High variability

Introduction/extinction

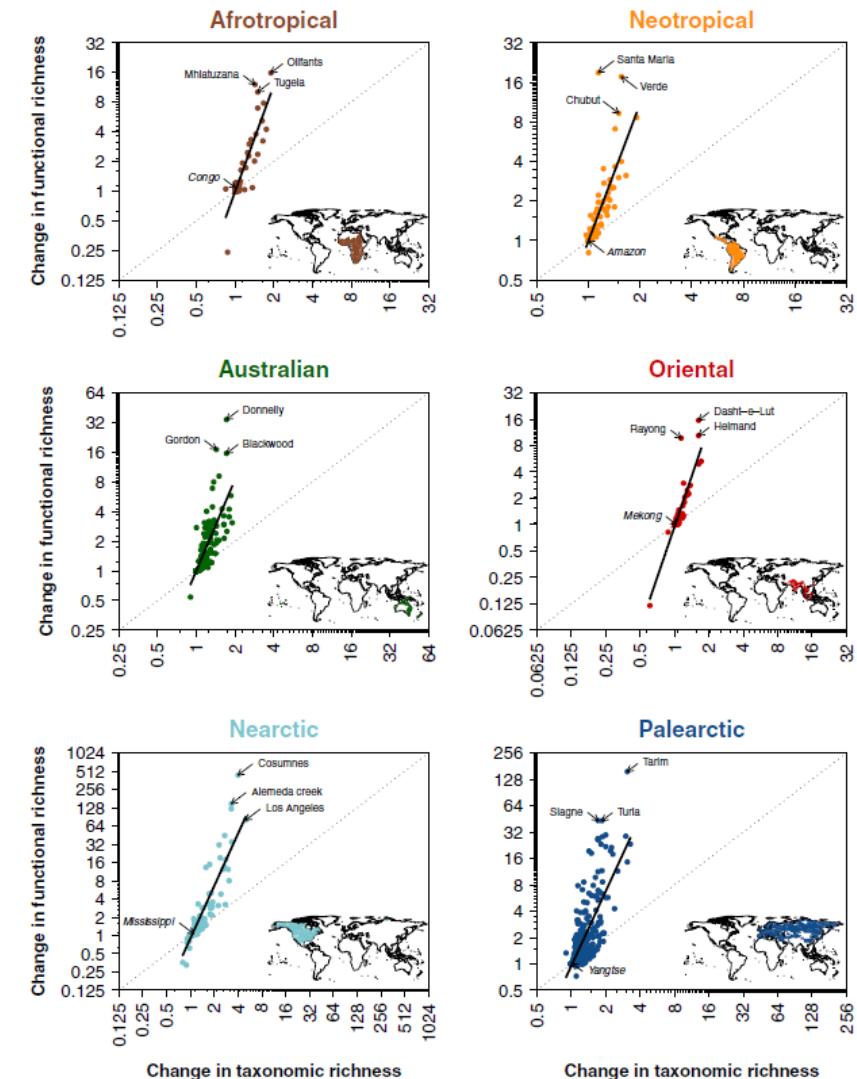


Introduction/extinction

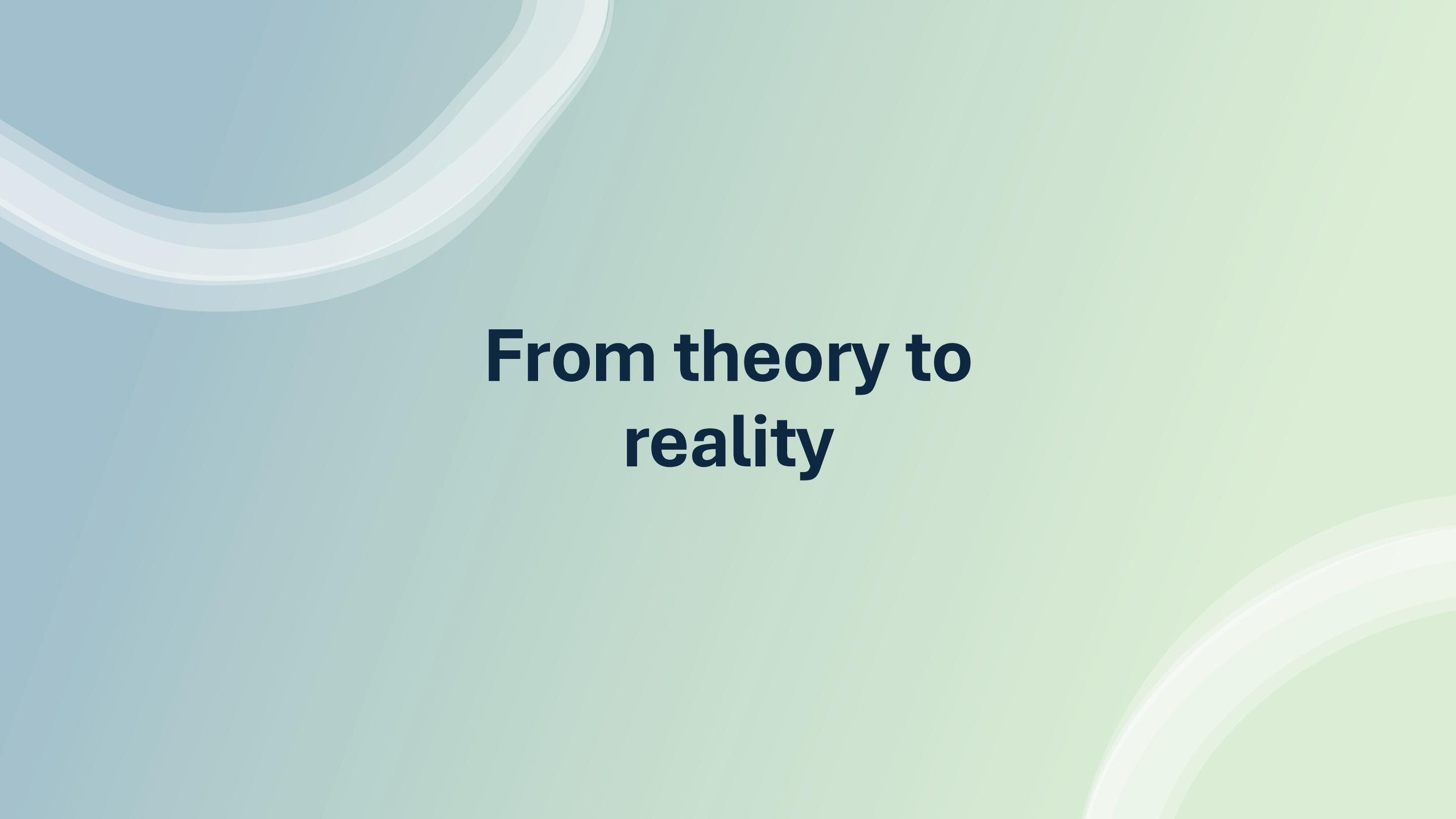
Non-native species are functional distinct than native species



Su et al. 2021



Toussaint et al.
2018



**From theory to
reality**

The reality is much more complex....

Although current trait-based approaches have several benefits, they also have some shortcomings not present in species-based approaches.

The choice of appropriate functional traits and their trade-offs with other traits given that a great diversity of traits are available (Funk et al., 2017).

Furthermore, traits differ intraspecifically but these differences are often neglected (Violle et al., 2012; Bolnick et al., 2011).

Existing trait databases are usually of limited use when it comes to species interactions, intraspecific trait variation and variable environmental settings (Funk et al., 2017).

In addition, the theoretical assumptions of trait-based studies are not always supported by experimental data (Suding and Goldstein, 2008).

3 groups



- Small scale communities
- Environmental gradient
- Large scale assemblages
- Threatened species
- Regional assemblages
- Intra-specific variability

TASK

- Describe the databases
- Develop a scientific question
- Propose analyses to respond to the question

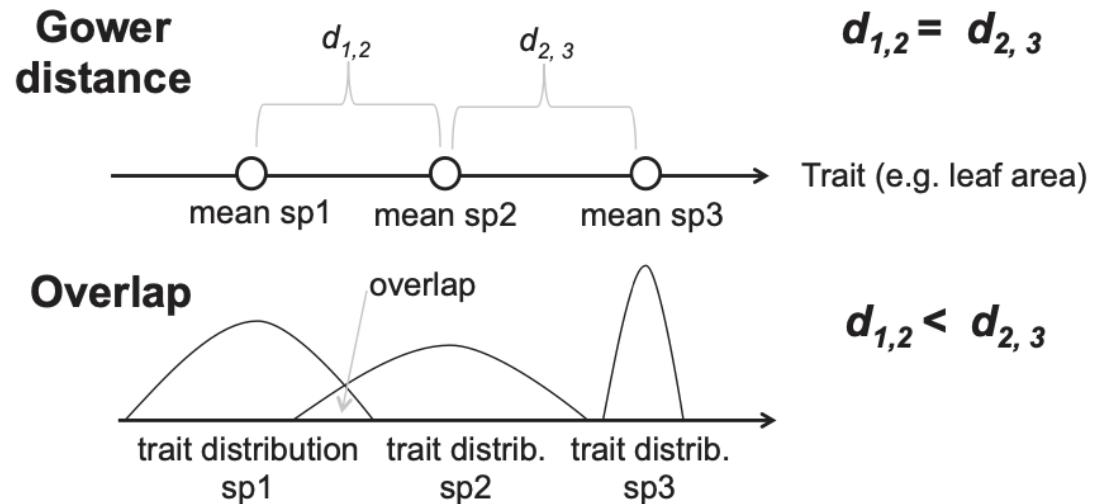
Fish: Intra specific variability



Species are the fundamental unit in biology and ecology;

Functional traits across species, or interspecific trait variability, have been widely used;

Mean trait values capture the majority of species features

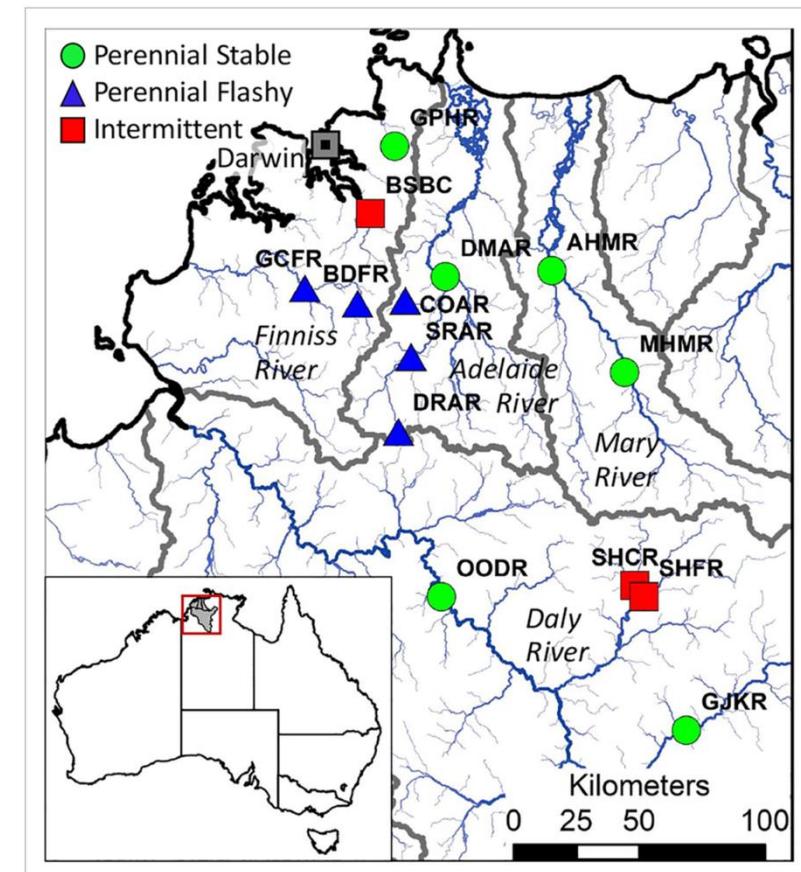


Fish: Intra specific variability



However, few studies have measured the intraspecific variability

- Long/Difficult to measure for a lot of species
- 15 common species (11 families in 5 orders), demonstrating a range of different life-history strategies that vary relative to different environmental regimes
- a maximum of 20 individuals on each sampling occasion at each site.



Fish: Intra specific variability



Ratio



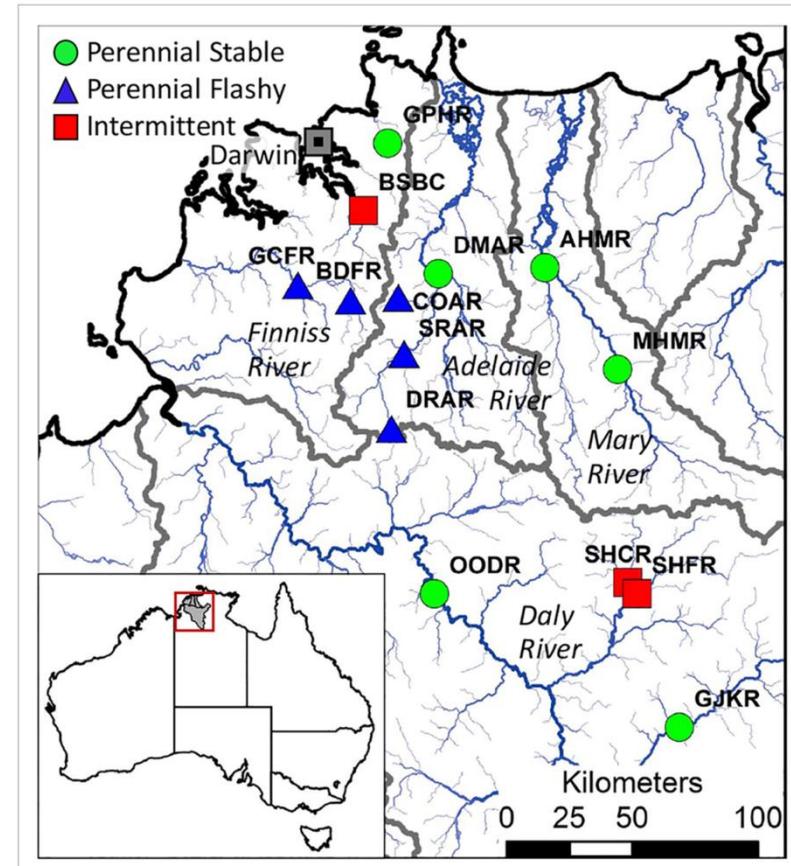
Code	Name	Protocol for measurement
Bl	Body length	Standard length (snout-to-caudal fin basis)
Bd	Body depth	Maximum body depth
Hd	Head depth	Head depth at the vertical of eye
CPd	Caudal peduncle depth	Minimum depth of the caudal peduncle
CFd	Caudal fin depth	Maximum depth of the caudal fin
Ed	Eye diameter	Vertical diameter of the eye
Eh	Eye height	Vertical distance between the center of the eye and the bottom of the body
Mh	Mouth height	Vertical distance from the top of the mouth to the bottom of the body
PFl	Pectoral fin length	Length of the longest ray of the pectoral fin
Md	Mouth depth	Vertical distance between the upper and lower maxilla of open mouth
Mw	Mouth width	Horizontal distance between the left and right ends of open mouth

Code	Trait name	Formula	Potential link with fish functions
EL	Body elongation	Bd / Bl	Hydrodynamism
EP	Eye vertical position	Eh / Bd	Position of fish and/or of its prey in the water column
ES	Relative eye size	Ed / Bl	Visual acuity
MP	Mouth vertical position	Mh / Bd	Feeding position in the water column
GS	Gape size	(Md × Mw) / (Bl ²)	Size of mouth and variety of prey items
GSh	Gape shape	Md / Mw	Size of mouth and variety of prey items
BS	Body lateral shape	Hd / Bd	Hydrodynamism and head size
PFL	Pectoral fin length	PFl / Bl	Pectoral fin used for swimming
CPT	Caudal peduncle throttling	CFd / CPd	Caudal propulsion efficiency through a reduction in drag

Intra specific variability



row.number	BD	PFL	throt	ED	EP	GS	GSh	MP	BS	Site1	species	group
1	0.429	0.205	2.822222	0.090	0.5827506	0.012472821	0.9248619	0.4358974	0.4592075	GCFR	AMNPER	Peren_flashier
2	0.430	0.205	2.600000	0.104	0.5372093	0.007549545	1.4473684	0.4116279	0.5116279	GCFR	AMNPER	Peren_flashier
3	0.390	0.197	2.713178	0.095	0.5692308	0.009251159	0.9302326	0.4205128	0.5102564	GCFR	AMNPER	Peren_flashier
4	0.421	0.209	2.297872	0.102	0.5249406	0.008404255	1.5666667	0.3634204	0.4964371	GCFR	AMNPER	Peren_flashier
5	0.415	0.202	1.823944	0.101	0.5204819	0.007240065	1.7652174	0.3253012	0.4915663	GCFR	AMNPER	Peren_flashier
6	0.412	0.197	2.562044	0.083	0.5995146	0.007082824	1.0435435	0.4708738	0.5169903	GCFR	AMNPER	Peren_flashier
7	0.386	0.184	2.180451	0.079	0.5336788	0.008645333	1.2240664	0.3937824	0.4715026	GCFR	AMNPER	Peren_flashier
8	0.416	0.209	2.592857	0.091	0.5288462	0.009045454	1.2636139	0.3437500	0.4831731	GCFR	AMNPER	Peren_flashier
9	0.417	0.206	2.592857	0.097	0.5371703	0.005403826	1.2616633	0.3597122	0.4892086	BDFR	AMNPER	Peren_flashier
10	0.421	0.195	2.780303	0.085	0.4370546	0.005695635	1.1475694	0.2707838	0.4608076	BDFR	AMNPER	Peren_flashier
11	0.410	0.205	2.364341	0.091	0.4682927	0.007210197	1.1072027	0.2707317	0.4756098	BDFR	AMNPER	Peren_flashier
12	0.407	0.202	2.305970	0.091	0.5110565	0.005991116	1.7500000	0.3538084	0.4963145	BDFR	AMNPER	Peren_flashier
13	0.428	0.222	2.551471	0.096	0.4532710	0.006614876	2.3793103	0.2616822	0.4789720	BDFR	AMNPER	Peren_flashier
14	0.421	0.229	3.000000	0.092	0.4988124	0.004595160	1.1208791	0.2969121	0.4750594	BDFR	AMNPER	Peren_flashier
15	0.417	0.222	2.666667	0.067	0.4700240	0.005606308	1.1538462	0.2781775	0.4364508	BDFR	AMNPER	Peren_flashier
16	0.391	0.212	2.375000	0.082	0.4936061	0.004991830	1.2506596	0.3375959	0.4961637	BDFR	AMNPER	Peren_flashier
17	0.392	0.176	2.563380	0.088	0.4362245	0.004501745	1.0101523	0.2372449	0.4872449	BDFR	AMNPER	Peren_flashier
18	0.410	0.171	2.632353	0.092	0.4951220	0.005616327	1.1944444	0.3268293	0.5195122	BDFR	AMNPER	Peren_flashier



Mammals: Imputation values



- Six life-history traits
- IUCN Threatened species

- NA: values not measured
- Remove sp.
 - Impute values

	female_maturity_d	litter_or_clutch_size_n	litters_or_clutches_per_y	adult_body_mass_g	maximum_longevity_y	gestation_d	weaning_d
Amblysomus_corriae	NA	1.930	2.000	64.800	1.000000	NA	NA
Amblysomus_hottentotus	NA	1.930	2.000	64.800	1.000000	NA	NA
Amblysomus_hottentotus	NA	1.930	2.000	64.800	1.000000	NA	NA
Amblysomus_robustus	NA	1.930	2.000	64.800	1.000000	NA	NA
Amblysomus_septentrionalis	NA	1.930	2.000	64.800	1.000000	NA	NA
Calcochloris_obtusirostris	NA	2.000	NA	24.050	NA	NA	NA
Carpitalpa_arendsi	NA	NA	NA	52.340	NA	NA	NA
Chlorotalpa_duthieae	NA	2.000	NA	31.340	NA	NA	NA
Chlorotalpa_sclateri	NA	2.000	NA	38.300	NA	NA	NA
Chrysochloris_asiatica	NA	3.120	NA	36.930	2.408333	NA	75.26000
Chrysochloris_stuhlmanni	NA	0.960	NA	47.780	NA	NA	73.40500
Chrysochloris_visagiei	NA	3.120	NA	36.720	2.408333	NA	75.26000
Chrysopalax_trevelyani	NA	1.410	1.000	434.040	4.000000	115.00000	NA

Mammals: Imputation values



Plants: Environmental variables



- Traits related to plant strategy for resource capture and allocation: SLA, vegetative plant height and seed mass.

▲	UTM_X	UTM_Y	Species	Plot	Cover	METPOLcov	LDMC(g/g)	LDMCstd	AREA(cm2)	AREAstd	SLA(cm2/g)	SLAstd
1	266654	2138394	ANDVIR	2012	0.0200	0.000	0.430	0.037	2.535282	0.302	242.3569	27.422
2	270444	2138782	ANDVIR	2026	0.1000	0.320	0.408	0.014	3.294391	0.162	236.7441	12.857
3	267456	2140371	ANDVIR	2030	0.0050	0.130	0.413	0.025	3.742567	0.731	269.7484	15.605
4	273367	2140273	ANDVIR	2053	0.0050	0.070	0.347	0.015	3.141388	0.771	130.1414	37.194
5	274006	2139901	ANDVIR	2054	0.0500	0.150	0.342	0.023	3.552421	0.731	172.6345	29.342
6	267290	2140451	ANDVIR	2076	0.0100	0.090	0.445	0.058	3.809685	0.438	265.9530	22.536
7	271015	2137926	ANDVIR	2077	0.2400	0.000	0.402	0.023	3.029507	0.152	238.1656	8.379
8	270637	2137440	ANDVIR	2078	0.0800	0.080	0.407	0.023	3.576748	0.337	215.1350	15.445
9	270480	2138110	ANDVIR	2191	0.0500	0.135	0.420	0.034	3.067920	0.192	218.0938	24.530
10	271101	2137237	ANDVIR	2194	0.0500	0.100	0.407	0.021	3.117939	0.199	240.4982	15.645
11	265607	2137309	ANDVIR	2208	0.0200	0.000	0.456	0.062	2.764275	0.165	208.4263	10.783
12	265326	2137638	ANDVIR	2209	0.0050	0.000	0.415	0.016	3.252385	0.233	218.8700	10.928
13	266924	2137621	ANDVIR	2211	0.0300	0.005	0.447	0.025	3.254602	0.321	211.1129	12.873
14	267836	2137886	ANDVIR	2212	0.0050	0.000	0.436	0.019	3.005378	0.109	188.2369	9.752
15	266654	2138394	BULCAP	2012	0.0050	0.000	0.417	0.211	0.670000	0.198	154.3060	16.723
16	270444	2138782	BULCAP	2026	0.0050	0.320	0.444	0.036	0.825000	0.181	169.0110	30.305
17	271015	2137926	BULCAP	2077	0.0050	0.000	0.622	0.101	0.888000	0.326	123.6970	11.788

Trait selection



Most important methodological decisions are the selection of particular traits:

- the number of traits
- the type of traits
- whether traits should be analysed separately or combined

Trait selection is crucial as it will have a strong impact on the outcome of trait-based studies

Trait selection

Recommend to stating hypotheses and expectation about the causal link between candidate traits and focal environmental gradients, stress factors or ecological processes of interest

A three-step hypotheses-based approach (Brousseau et al. 2018)

1. Define the stressor and/or ecosystem process under study. It determines the potential functional traits under selection that relates to the fitness of individuals.

- if your hypothesis on the relationship between the traits and the stressor is sharp, then it is easier to select which trait you need.
-> strong trait-value-environment linkage.

GIVE EXAMPLE

- if you test how species effect ecosystems, then trait selection should focus on the impact effects traits have on the ecosystem process under consideration.

GIVE EXAMPLE

Trait selection

2. Pragmatic step: Get information on candidate traits selected in the step 1. However, those traits can be either not available for the species, or laborious to measure for many species.

Also, we might end up with a list of potentially interesting traits which are correlated.

Be realistic and try to get trait information which is both relevant and feasible.

3. Trait selection

Finally we compile a list of traits

How many traits/dimension ?

Defining how many traits are needed to answer an ecological question is a tricky task.

1 approach/ Studying the effect of single trait.

However traits do not act in isolation and single traits do not act independently of each other

2 Combined effect of traits/