



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

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# 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 during lecture
  - Group work
- **Question:**
  - Documents analyses (Figures, Tables)
  - Ecological interpretation (15 – 30 min, at the end of the day)

# C.V.

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- Functional ecology, macroecology
- Vertebrates, plants
- Threatened/invasive species
- Large databases, R programming



# Course material available in github



ID: **AureleToussaint**

Repository: **Master2**  
**> 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 !

# **General introduction**

# Biodiversity has fascinated humans for long time

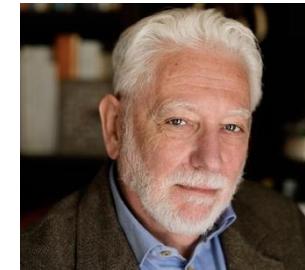
30,000 years ago...



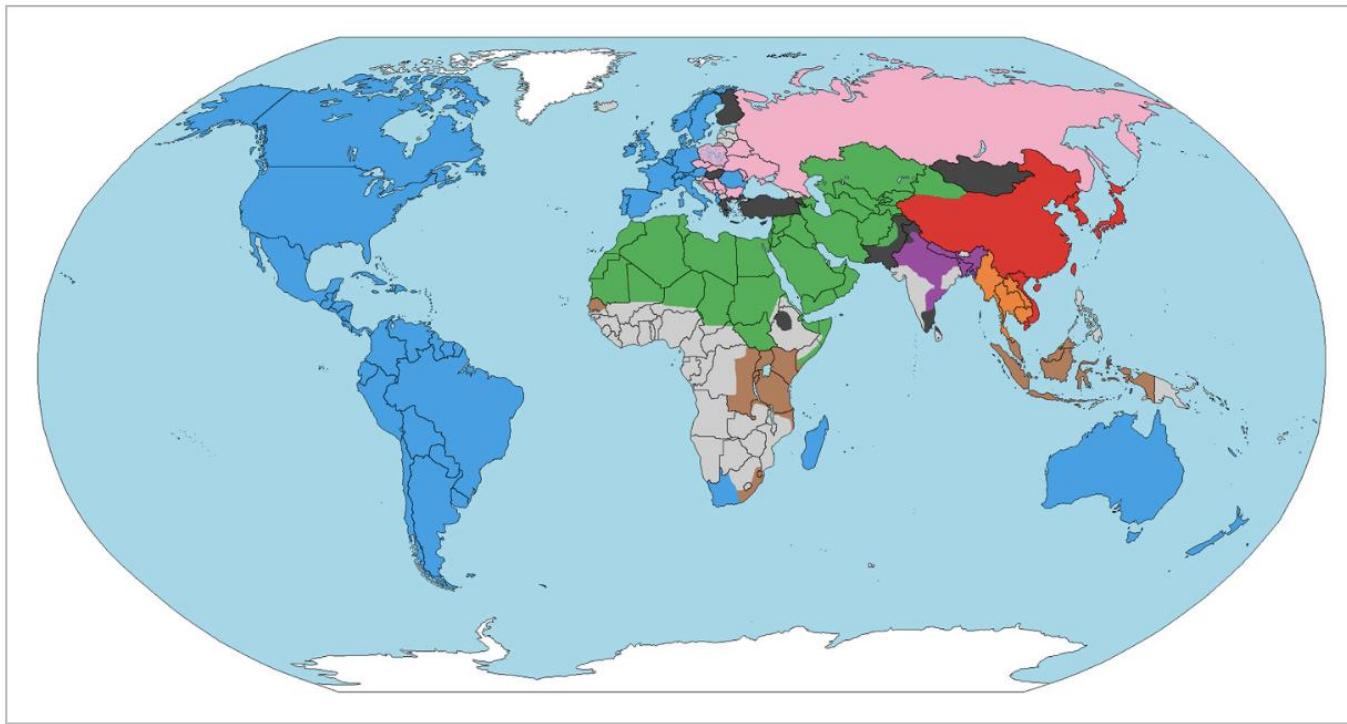
Chauvet-pont-d'arcs (Ardeche, France)

# Different view of biodiversity across the world

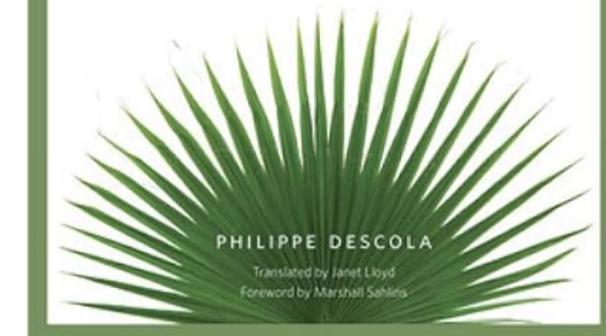
Philippe Descola



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

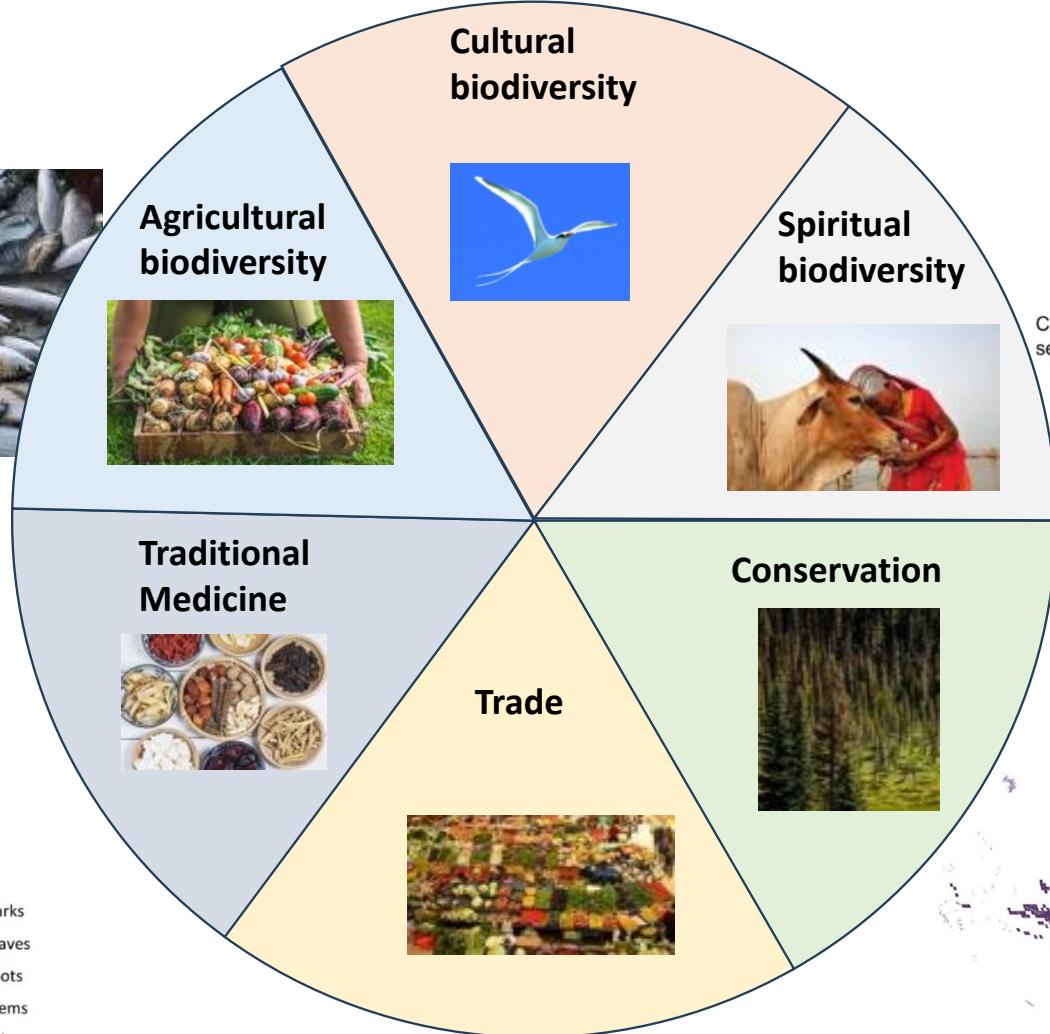


BEYOND  
NATURE AND CULTURE

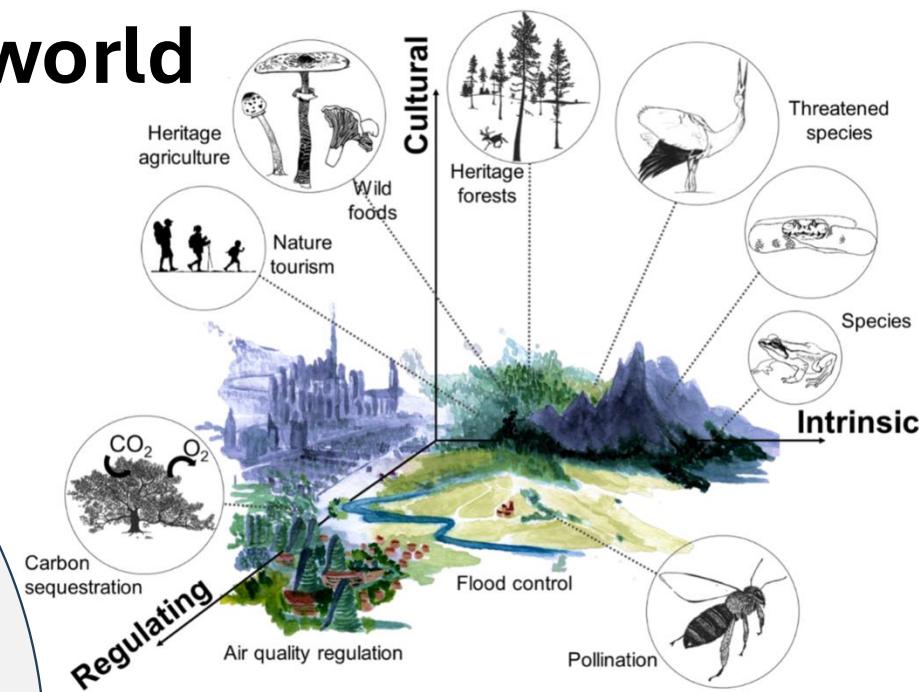


Ducarme, F., Flipo, F. and Couvet, D. **How the diversity of human concepts of nature affects conservation of biodiversity.** *Conservation Biology* (2021).

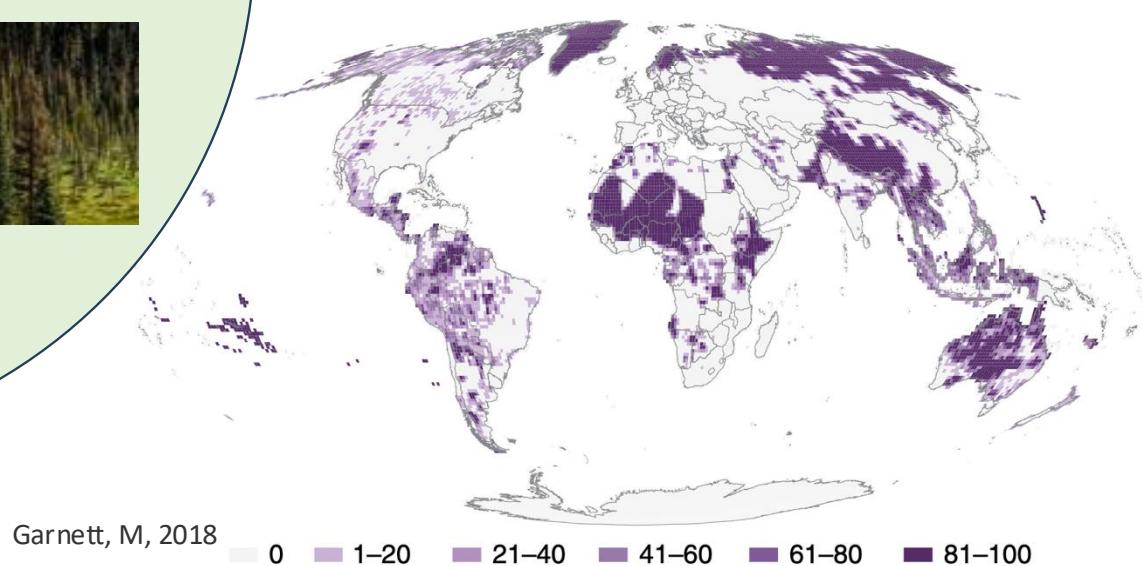
# Different view of biodiversity across the world



Eshete, M, 2021



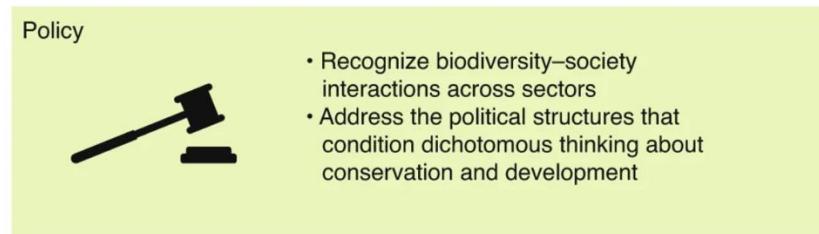
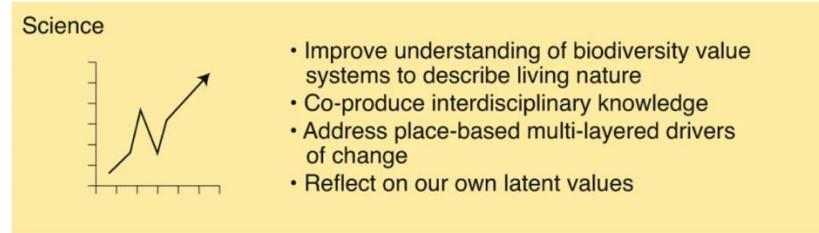
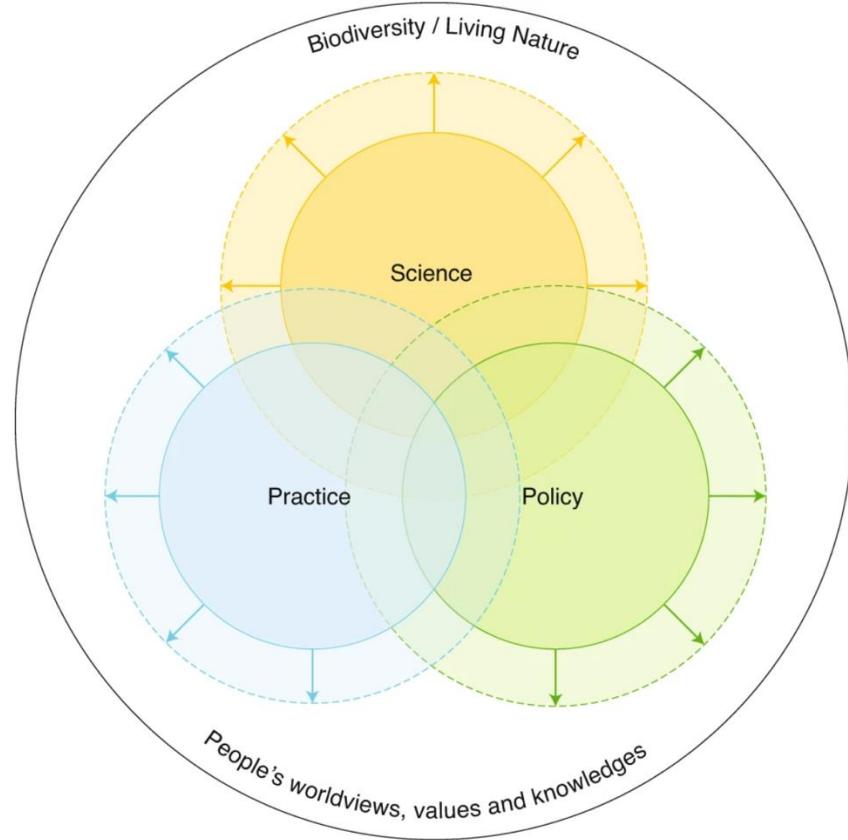
O'Connor et al., 2021



# Challenge of protection of biodiversity • • •

• • • is a challenge of pluralism

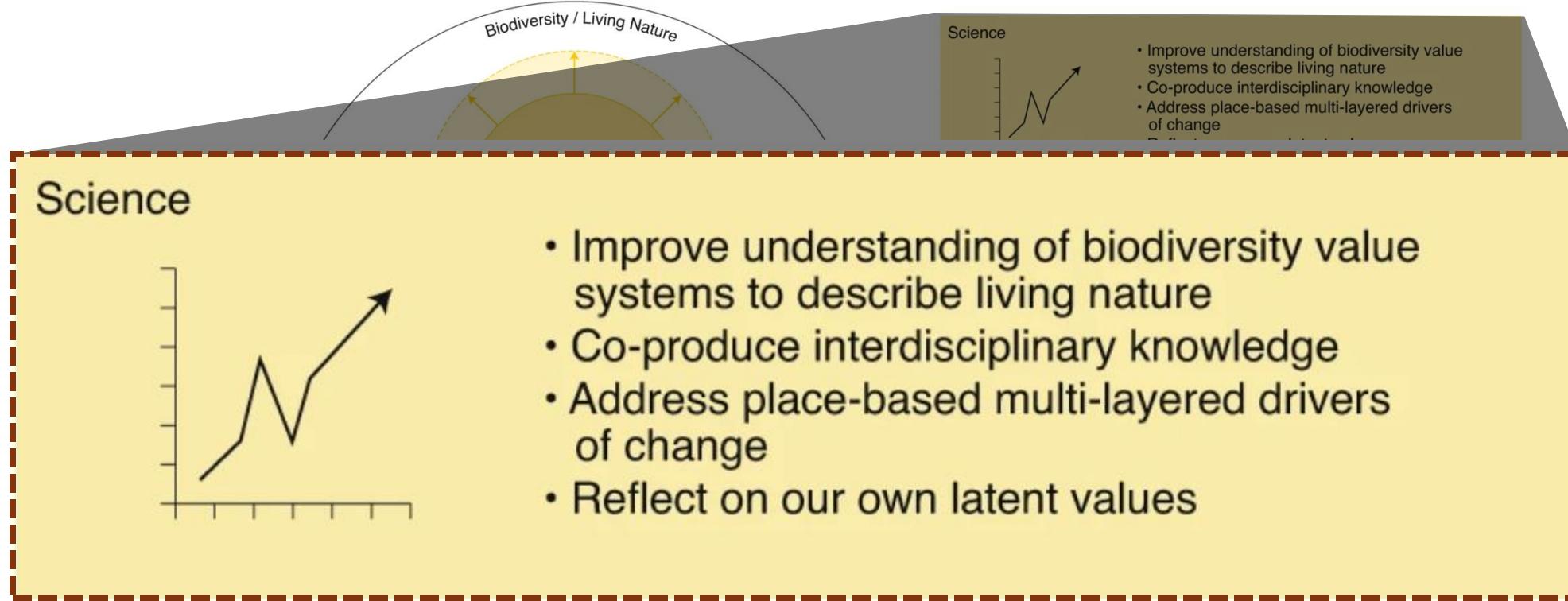
From: [Biodiversity and the challenge of pluralism](#)



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

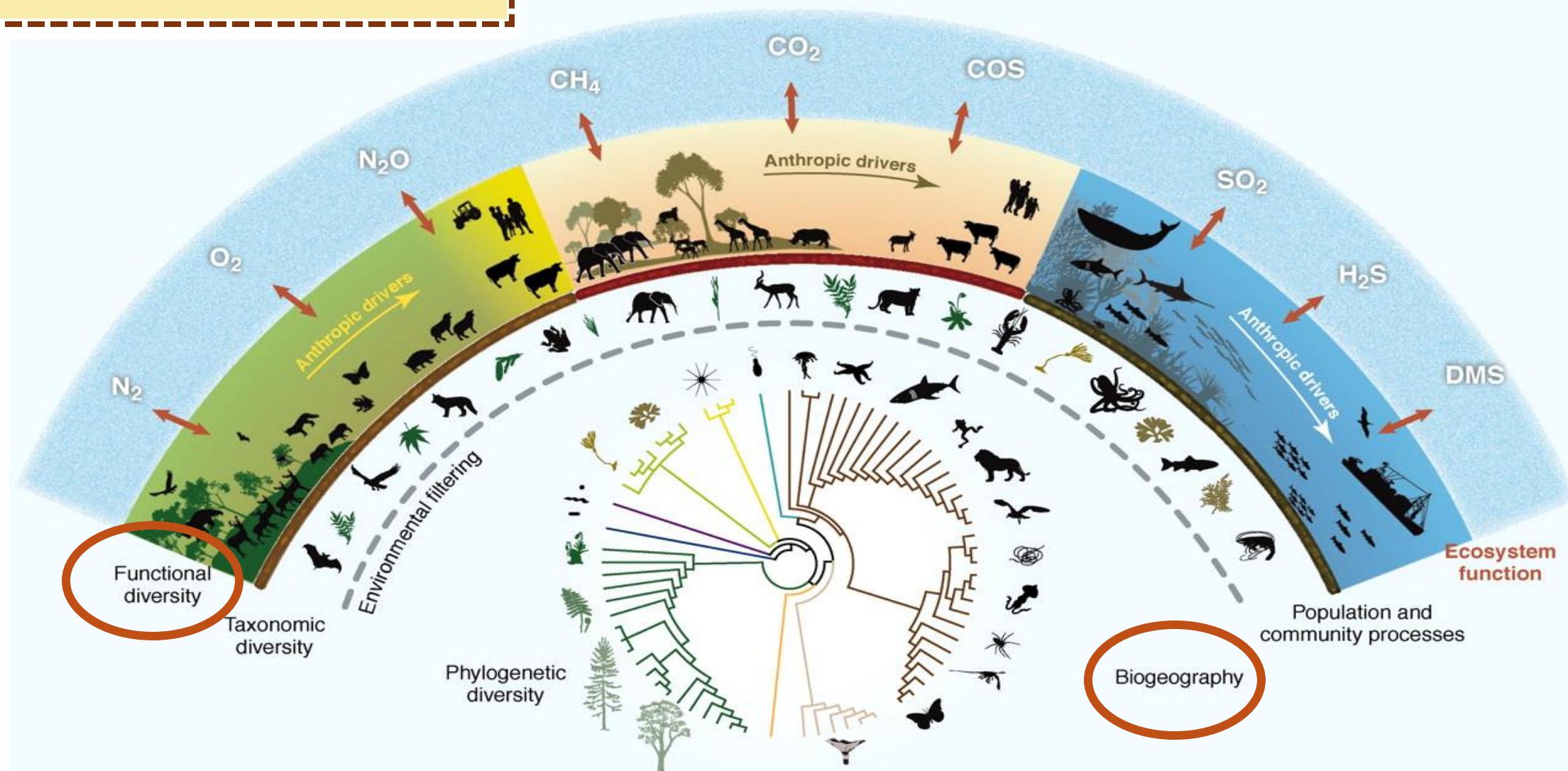
From: [Biodiversity and the challenge of pluralism](#)



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



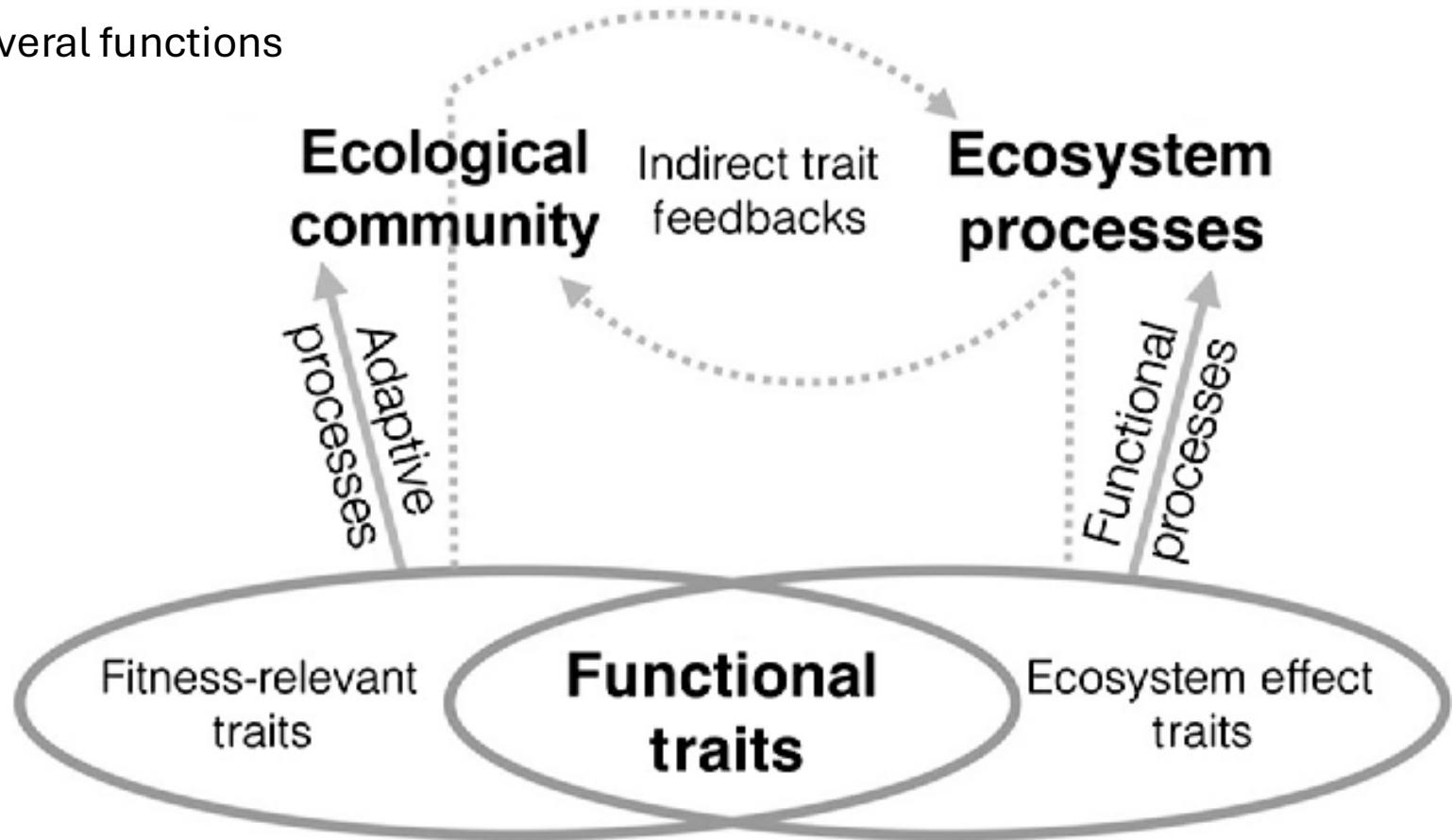
**Trait-based approach:** describe species through a set of trait

# Why functional ecology ?

- Beyond the taxonomic approach

Example: a plant = 1 organism + several functions

- Photosynthesis
- Respiration
- Absorption
- Stockage
- ....

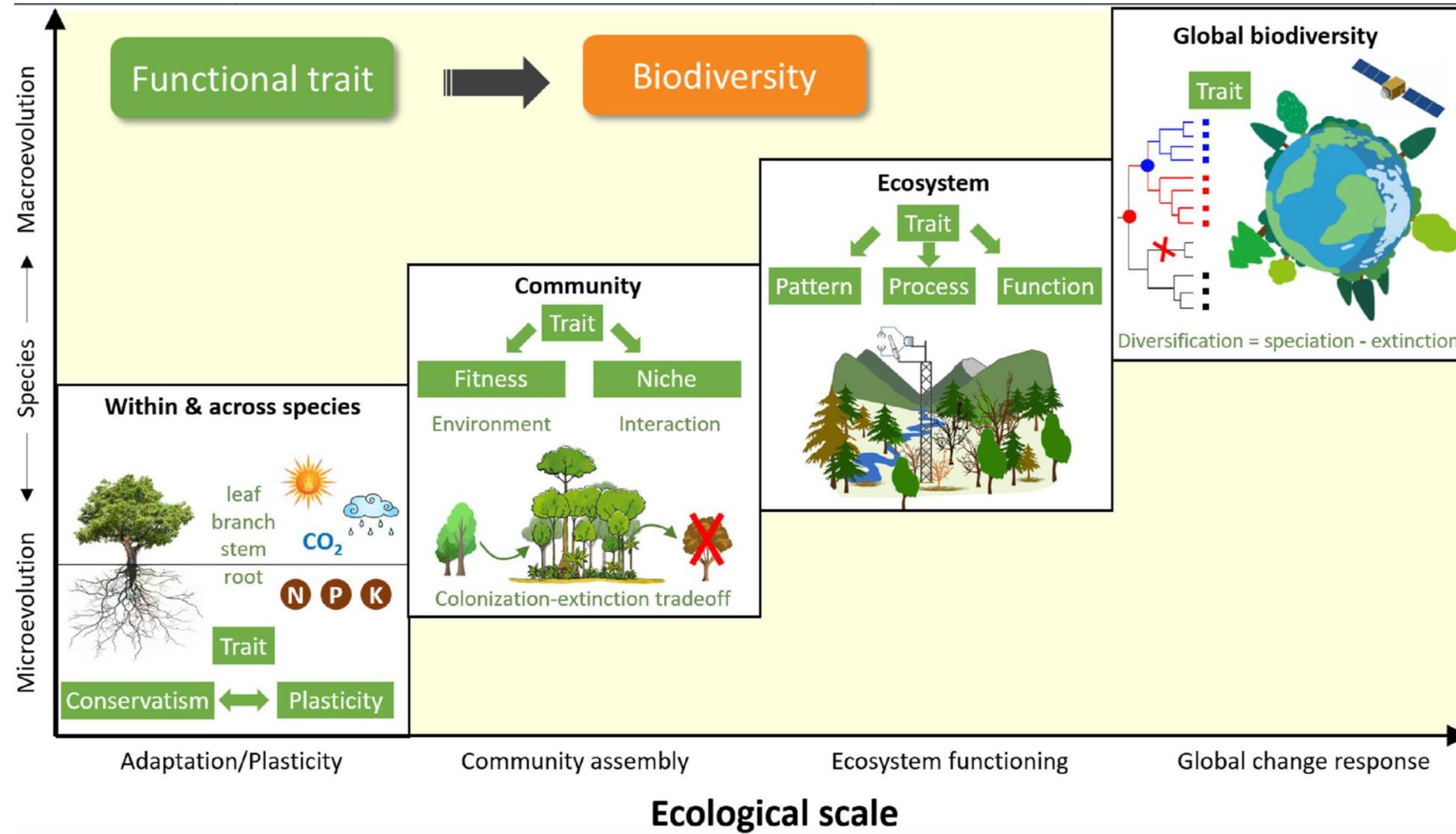


# Trait-based approach

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.

# Spatial and temporal scale

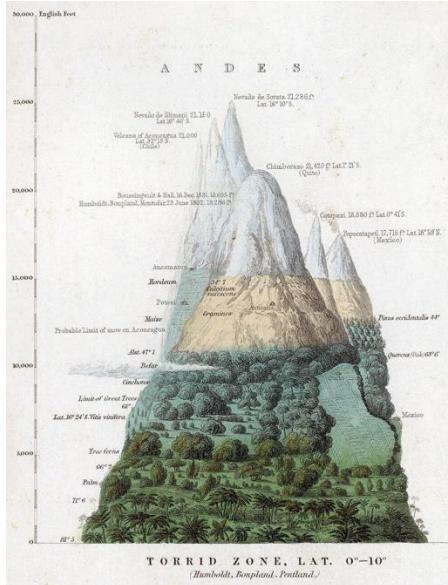
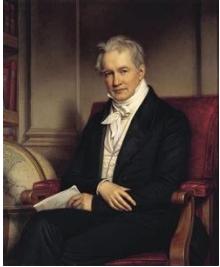


# Historical approach

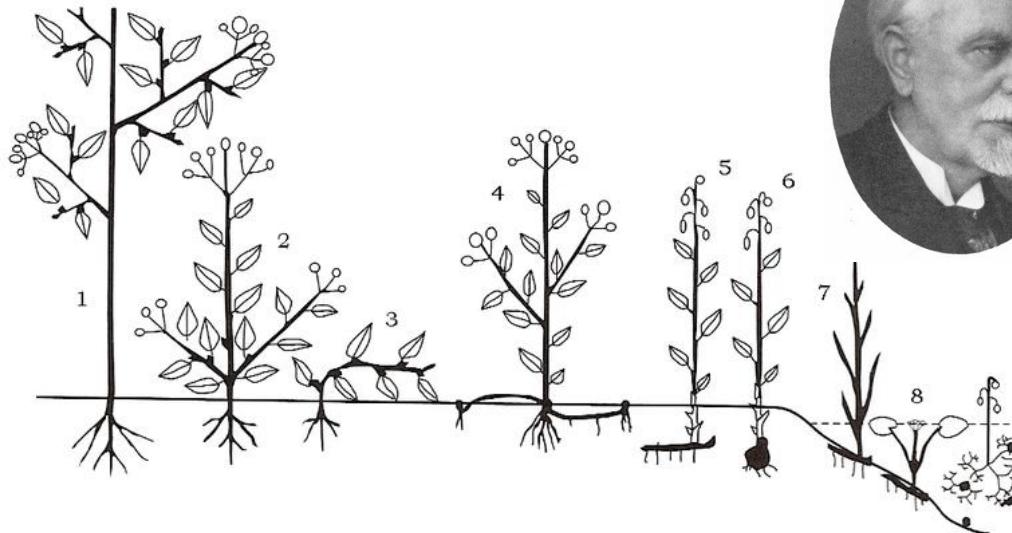
- Traits have been used in ecology for a long time

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

## Alexander Von Humboldt (1806)



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



# From functional groups...

## The r/K selection

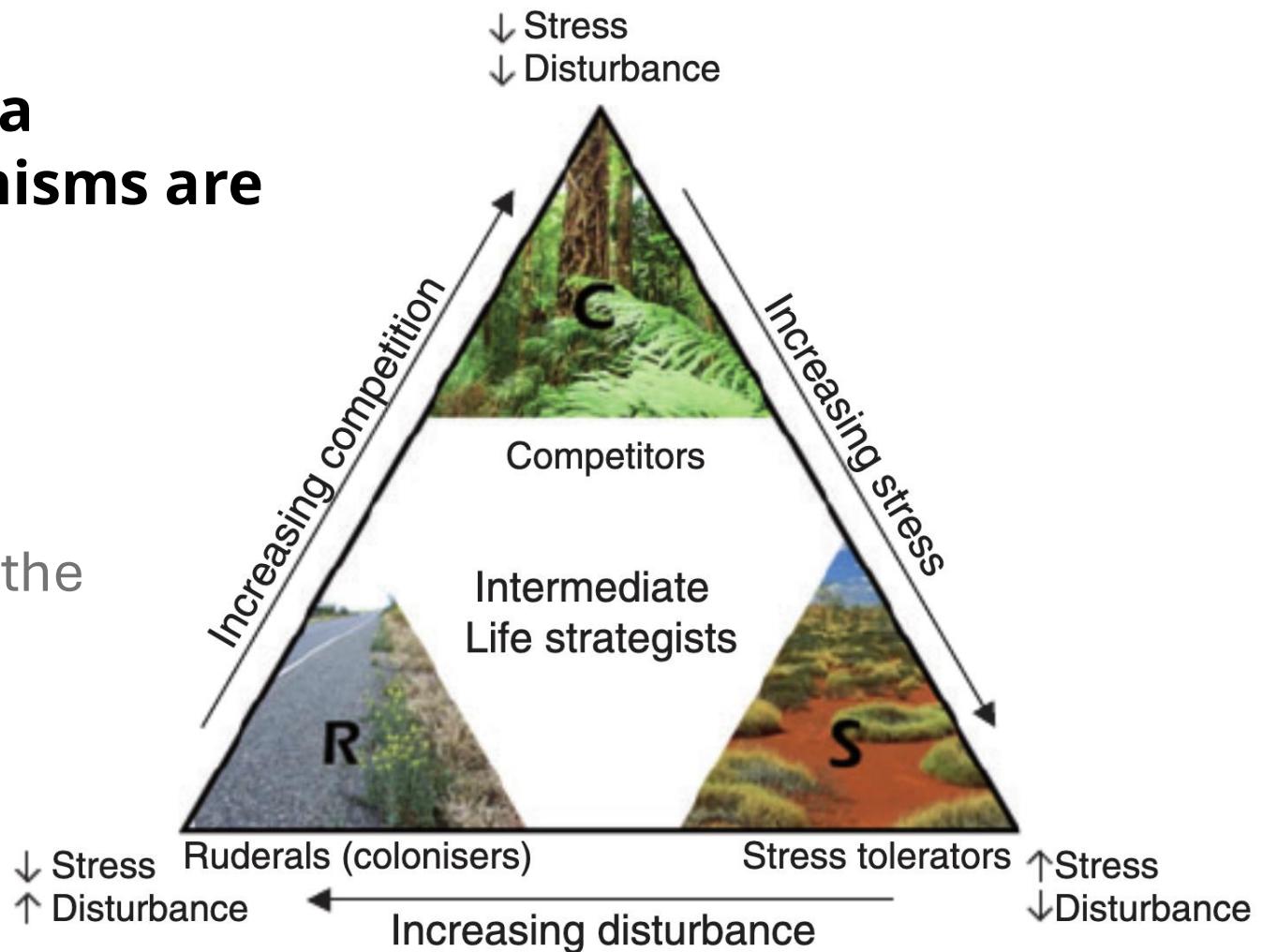
The concept of trait trade-offs helps to explain why, during speciation and local adaptation; organisms evolve different traits and life strategies.

- r – intrinsic rate of increase
  - r-selected species have evolved to put a lot of energy into reproduction and growth
- K – carrying capacity
  - K- selected species have evolved to put a lot of energy into maintenance

# From functional groups...

The r/K selection are ends of a continuum; while most organisms are in between

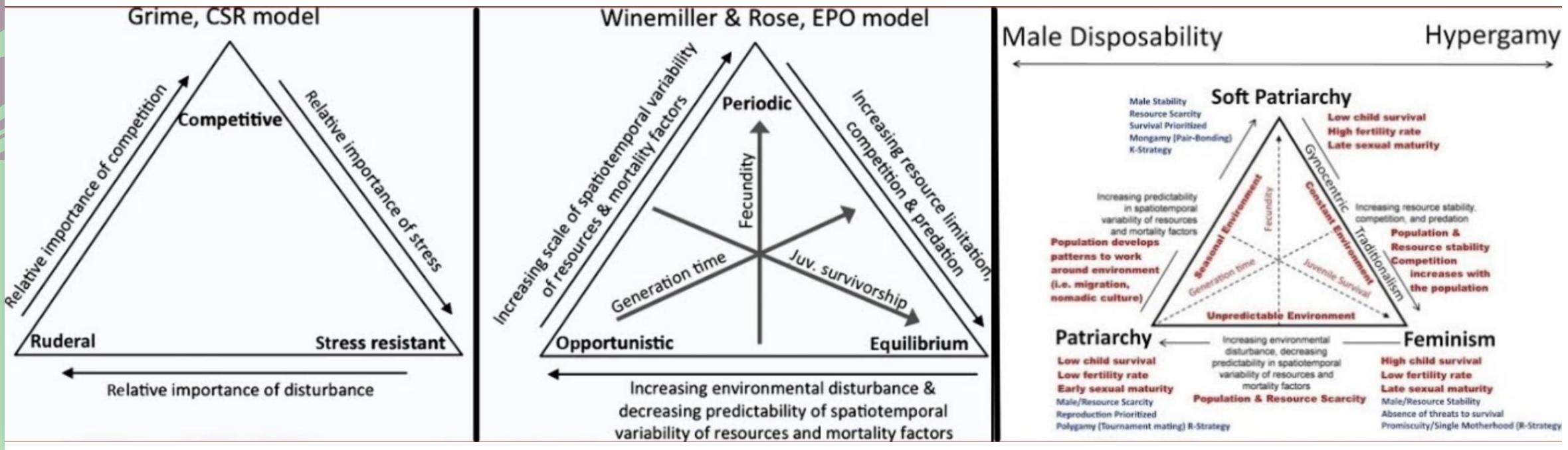
- Grime's (1977) CSR triangle was the first globally accepted concept



# ... 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).

Example: Intersex relations:



# 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

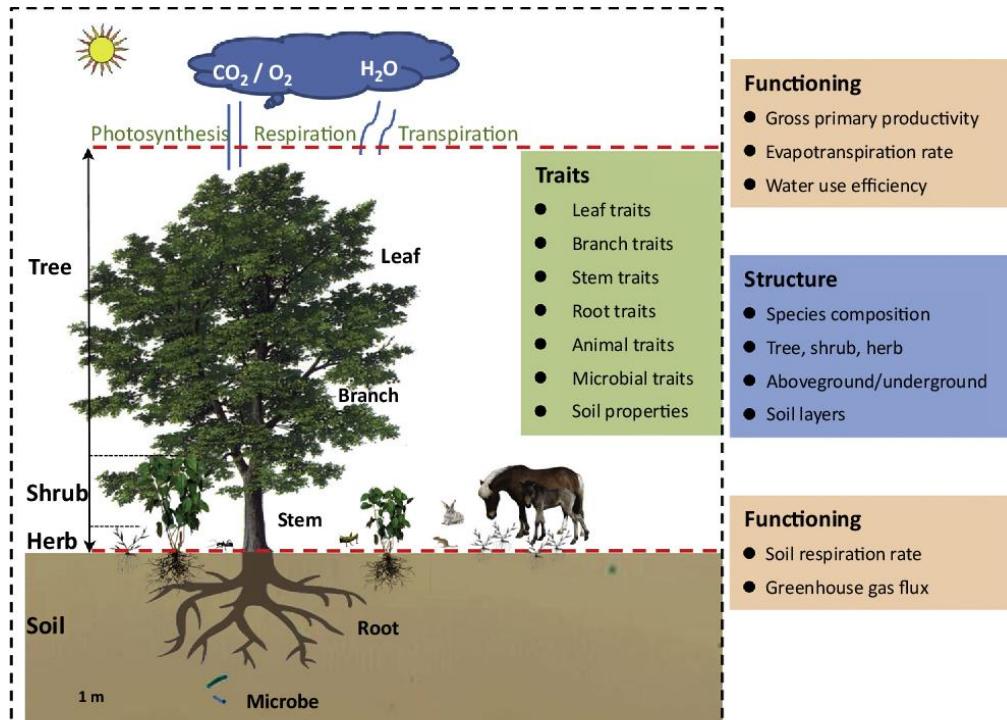
'Soft' traits

Phenological traits

Features

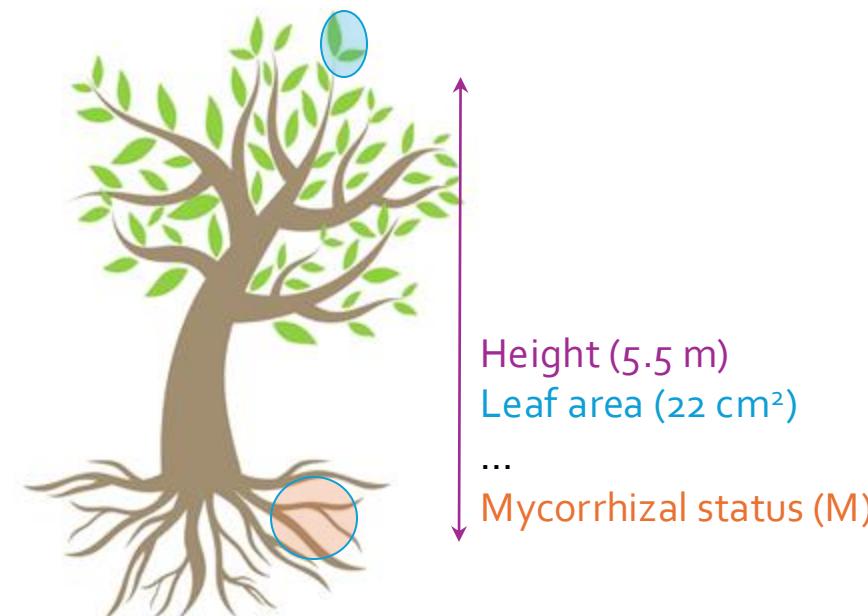
# What is a trait ?

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



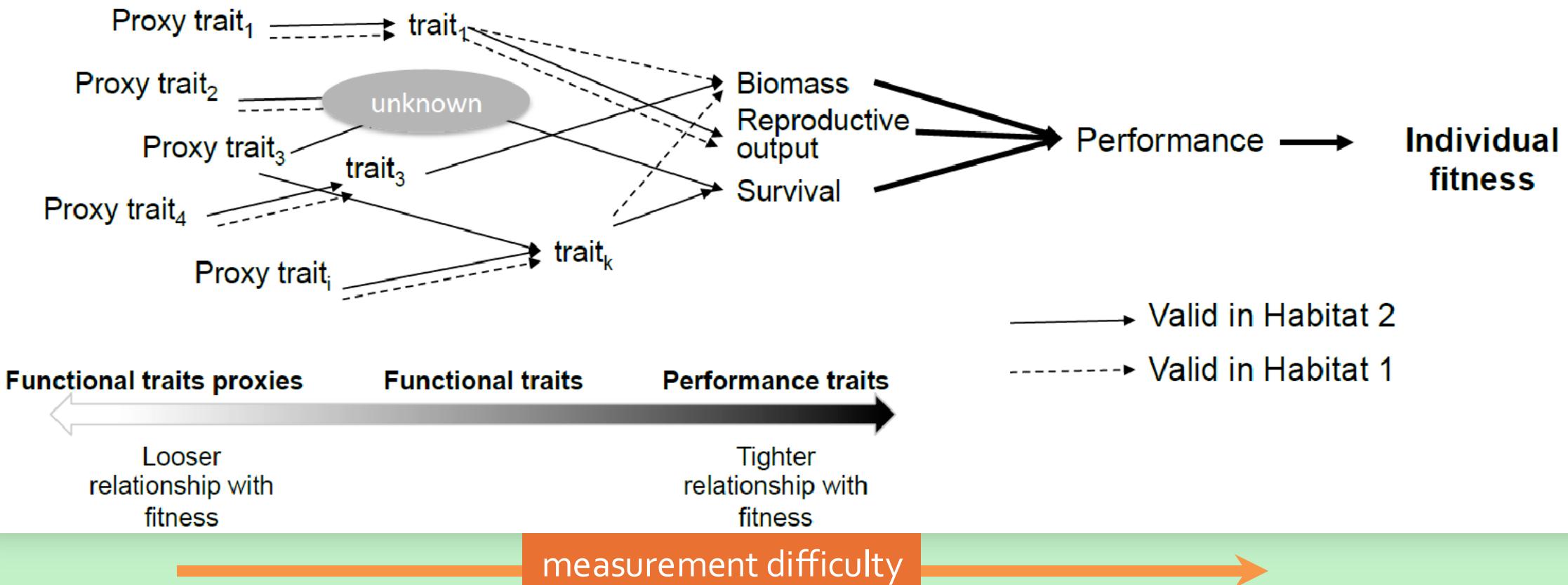
Trends in Ecology & Evolution

(Violle et al., 2007)

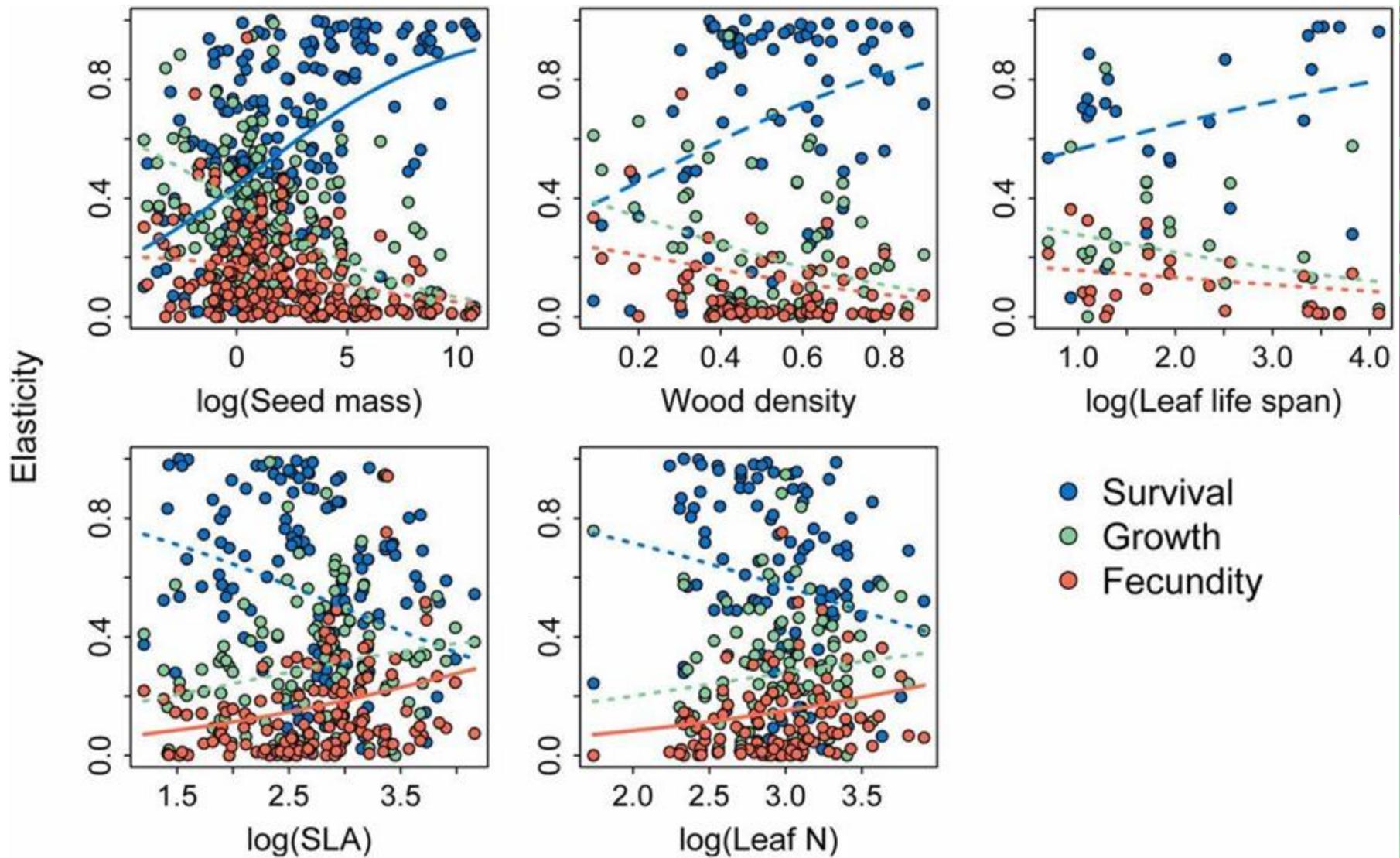


# What is a *functional* trait ?

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



# 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

## 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

# Many traits....

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

Those differences can be straightforward or more subtle



*Chrysophrys auratus*

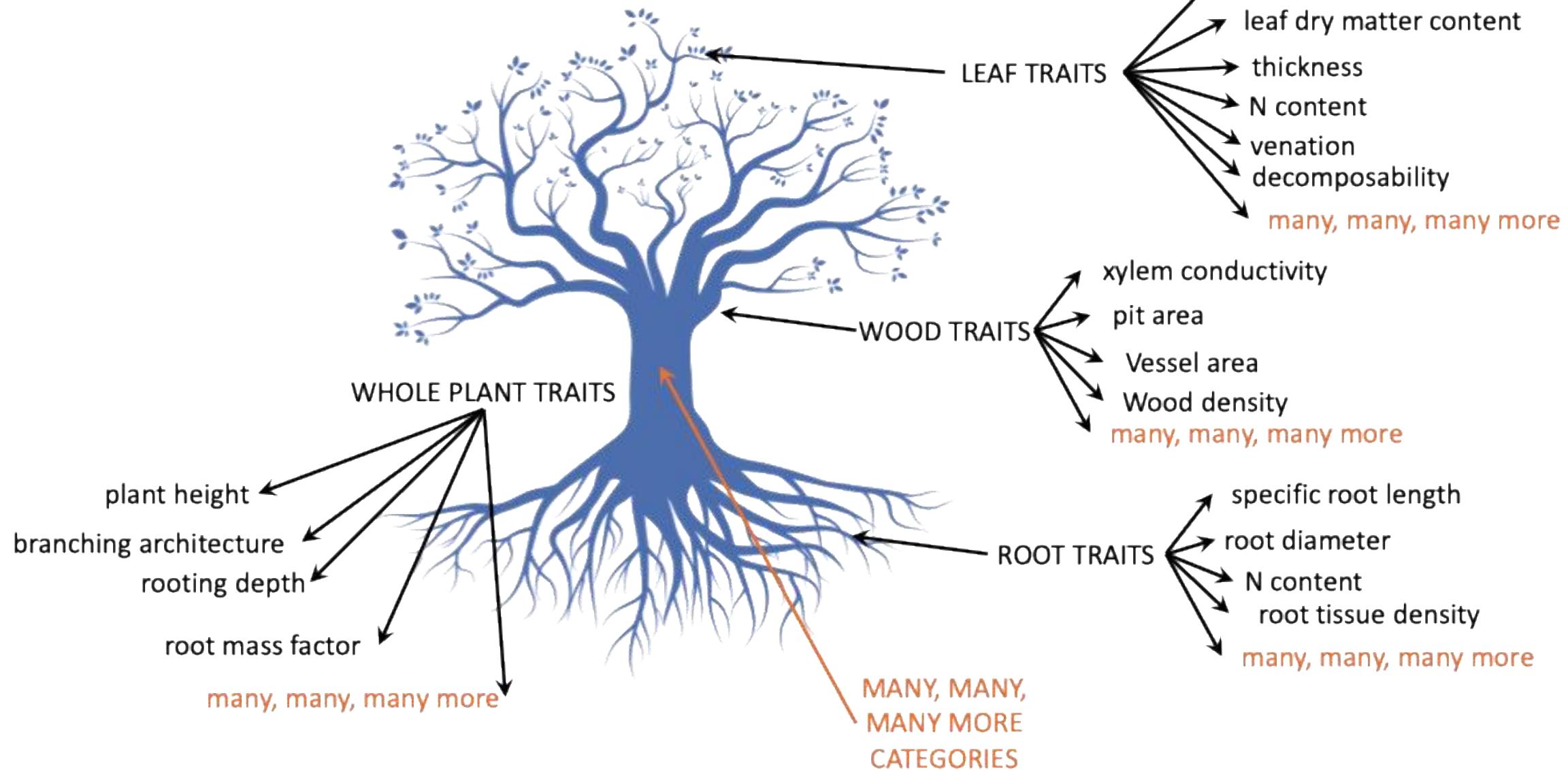


*Lethrinus mahsena*



*Lutjanus rivulatus*

# Many traits....



# Trait Syndromes and trade-offs

- **Trait Syndromes:**

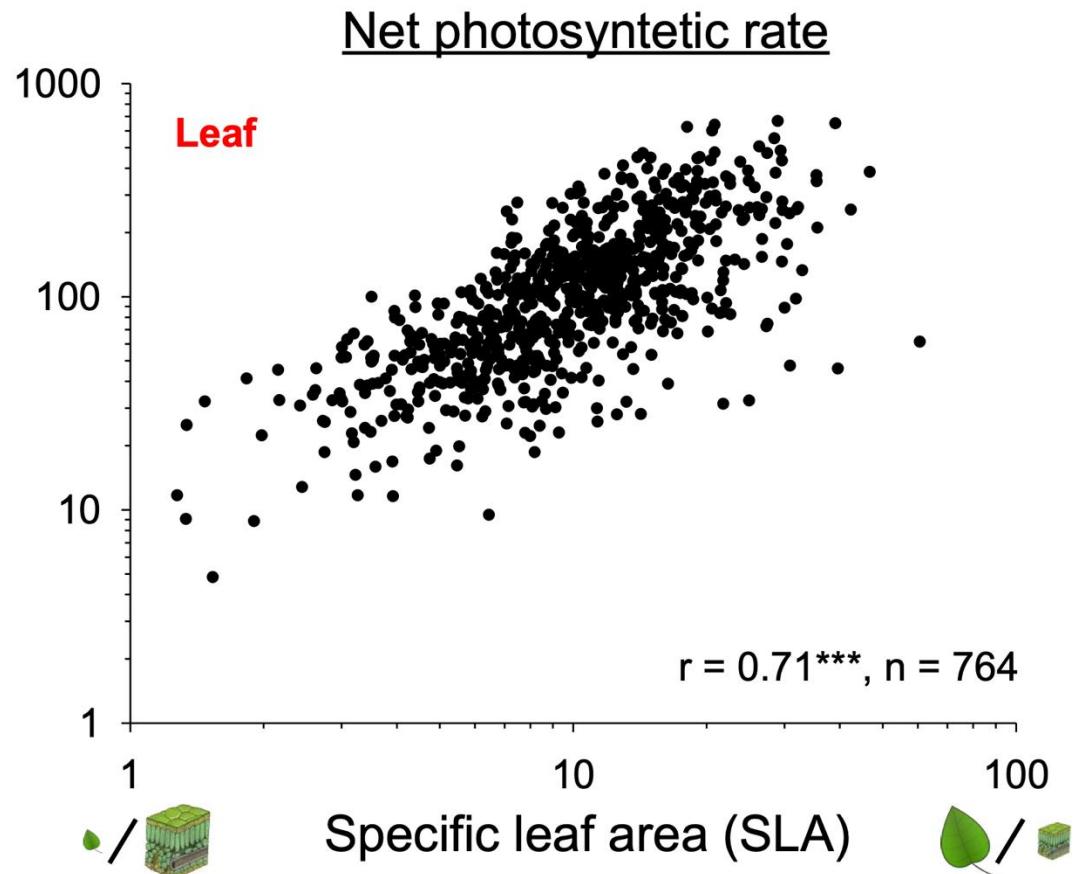
- Certain combinations of traits are often linked, forming syndromes (e.g., fast-growing species with short lifespans and high reproductive rates).

- **Trade-offs:**

- Trade-offs occur when species cannot optimize all traits due to resource allocation constraints (e.g., a plant can't both invest heavily in defense and rapid growth).

# Trait-based approach

- Example: link between photosynthetic rate and SLA



Trait trade-offs are key to understanding plant strategies and ecological dynamics.

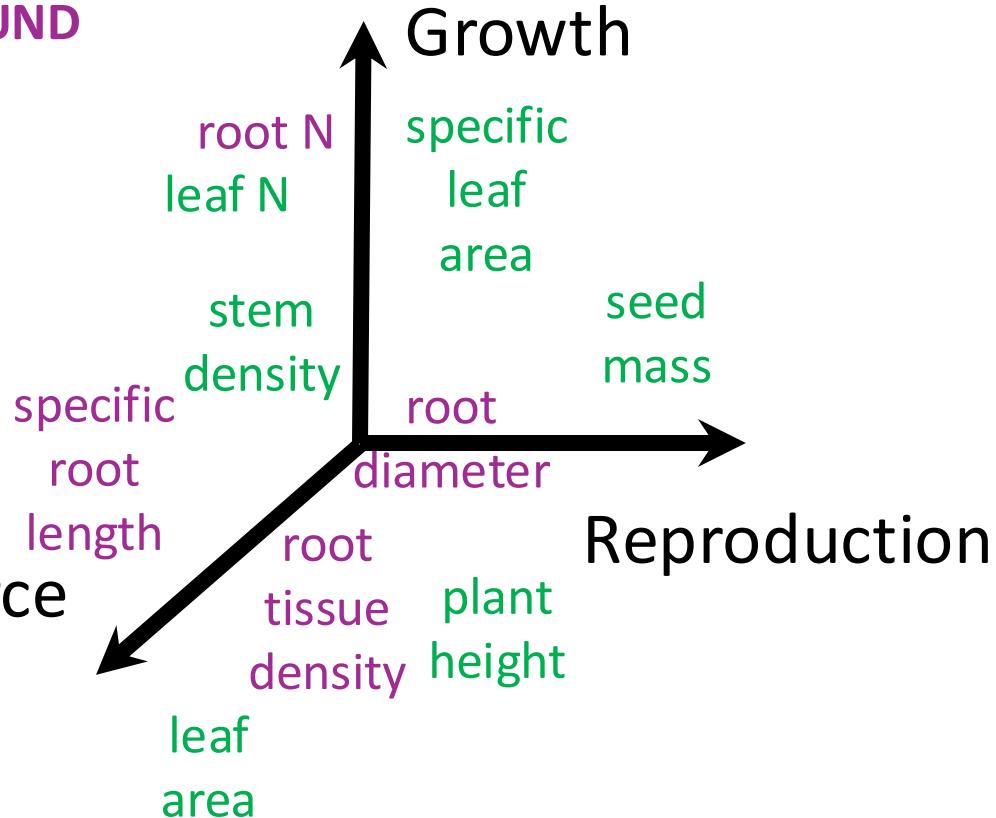
The trade-off between SLA and photosynthetic rate reflects the balance between fast growth and resource conservation in plants.

# Many traits....

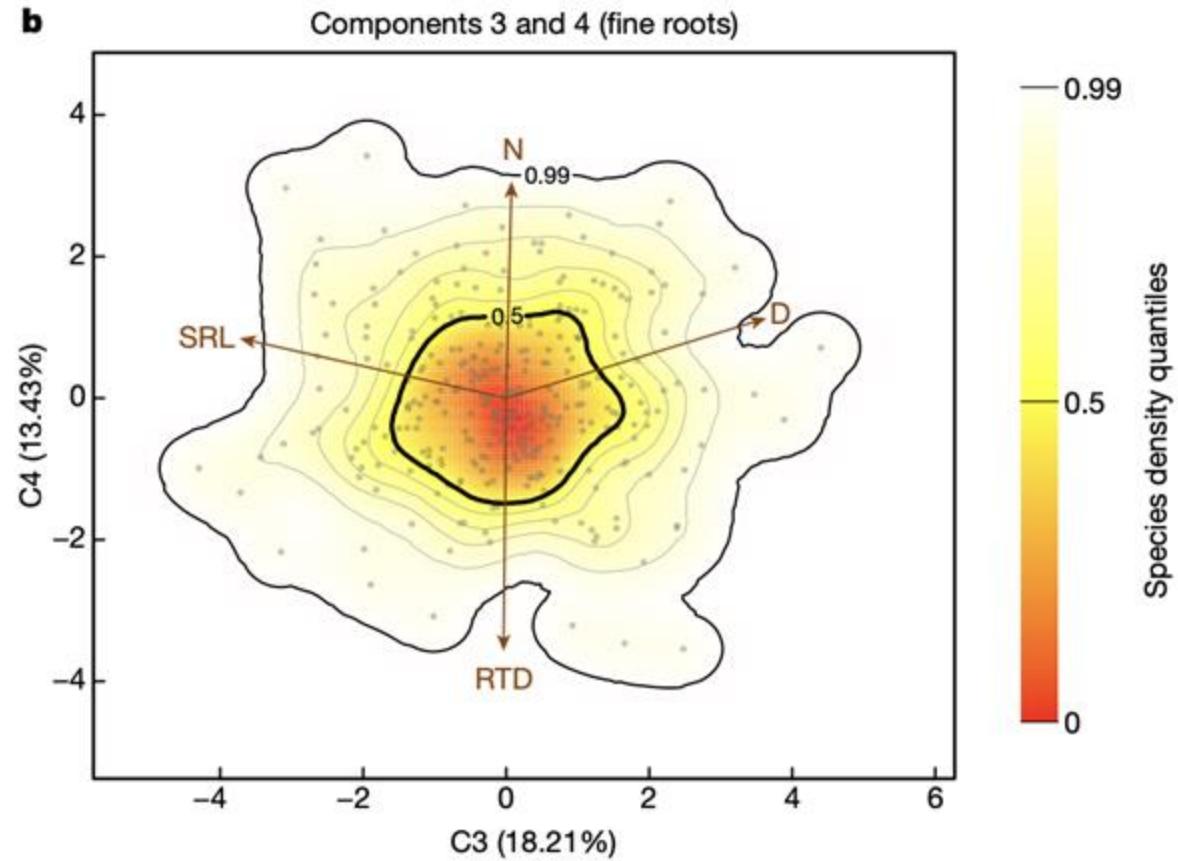
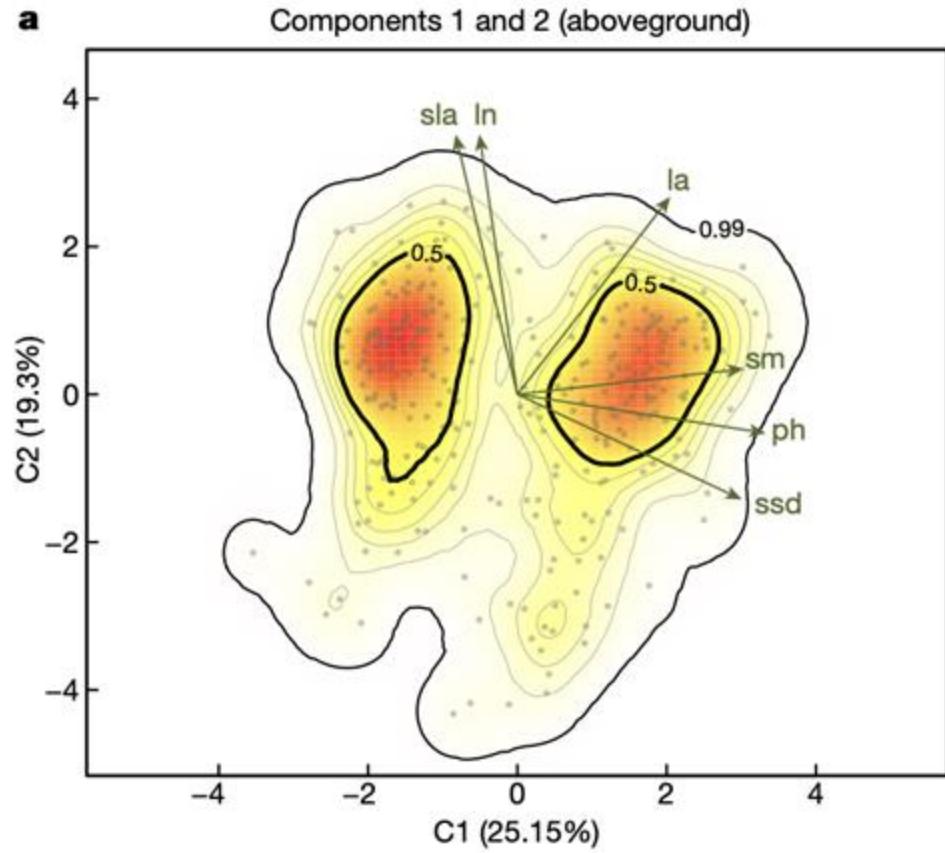


Survival/resource  
preemption

ABOVEGROUND  
BELOWGROUND



# Many traits....



# Linking traits to Ecosystem functioning

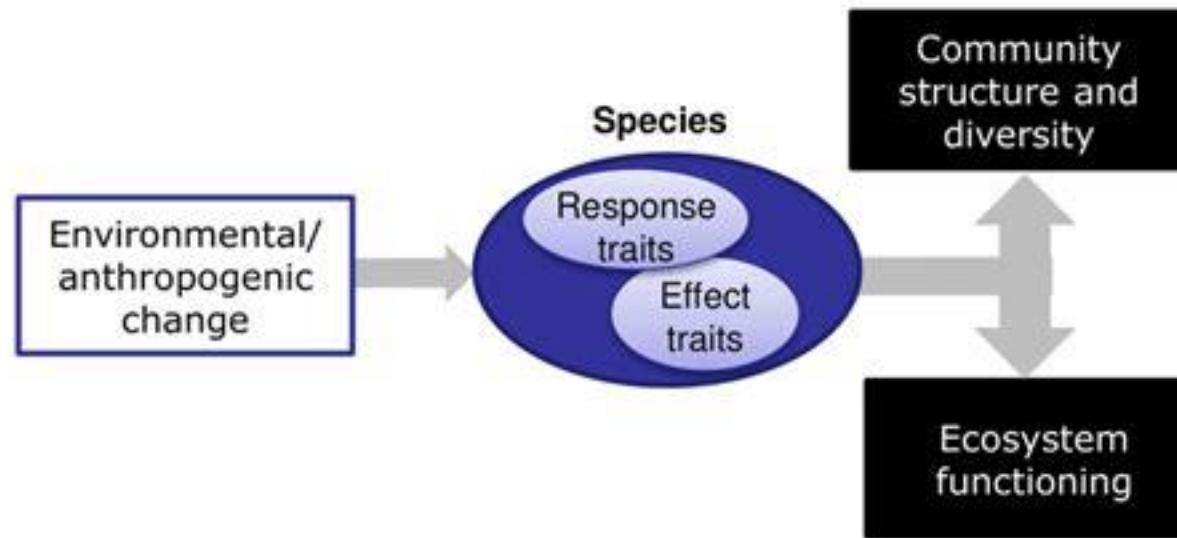
- **Functional Traits and Ecosystem Processes:**

- Functional traits directly influence key ecosystem functions like productivity, nutrient cycling, and stability.
- **Example:** Species with nitrogen-fixing abilities can increase soil nitrogen content, boosting productivity.

# Linking traits to Ecosystem functioning

- Response and Effect Framework

- Traits can be categorized as **response traits** (how species respond to environmental changes) and **effect traits** (how species influence ecosystem functioning).



# Linking traits to Ecosystem functioning

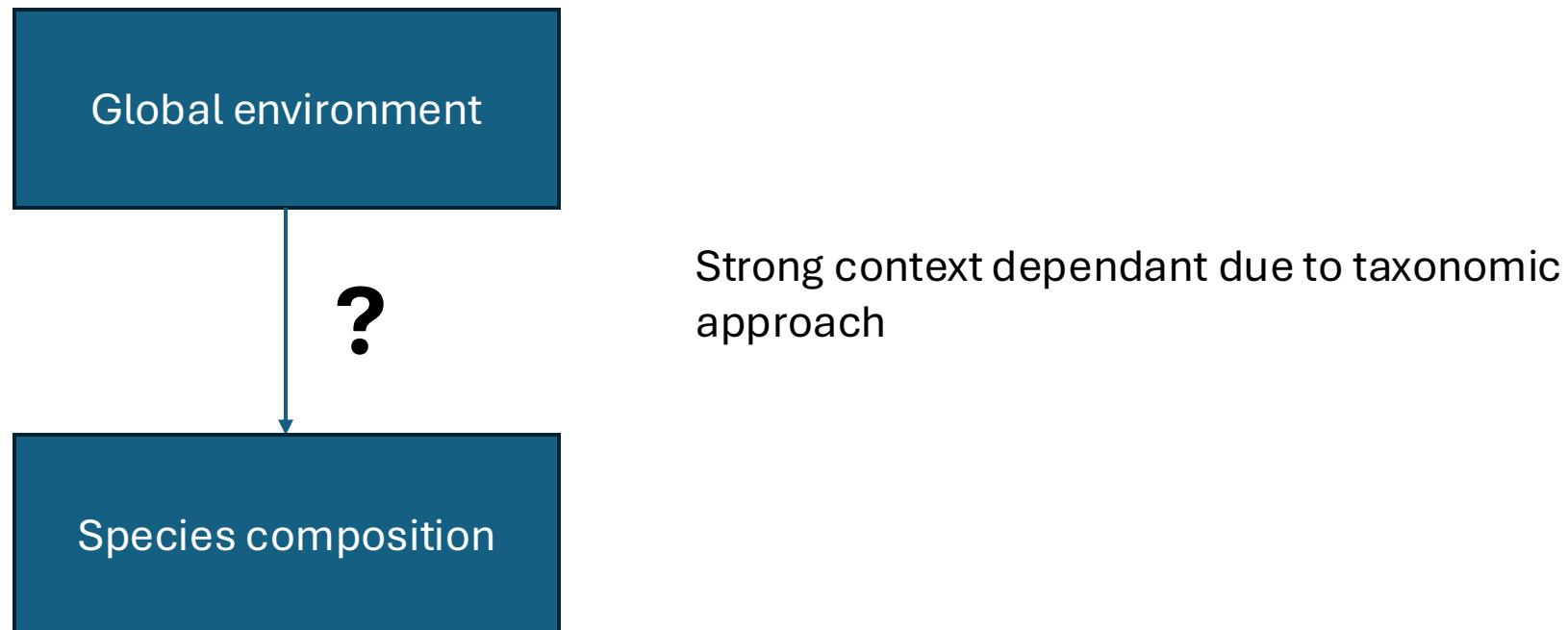
- **Response and Effect Framework**

- Traits can be categorized as **response traits** (how species respond to environmental changes) and **effect traits** (how species influence ecosystem functioning).
- **Example:** Leaf area as a response trait to drought conditions and an effect trait for regulating carbon cycling.

# **Community ecology and traits**

# General principles in community ecology

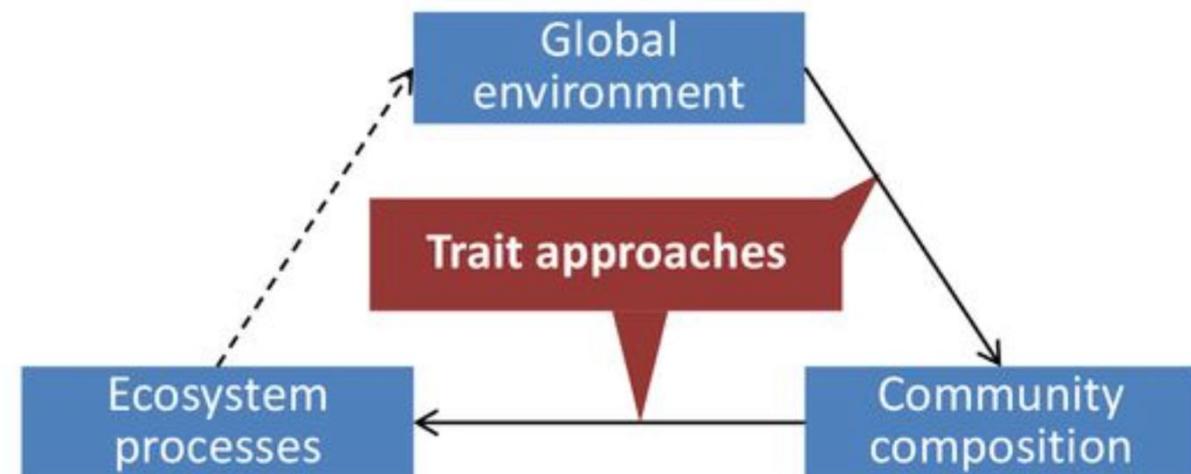
- Why do we observe a certain variety of species ?
- Why are some communities more species-rich than others?
- Why are some species present in a particular community but not in others ?



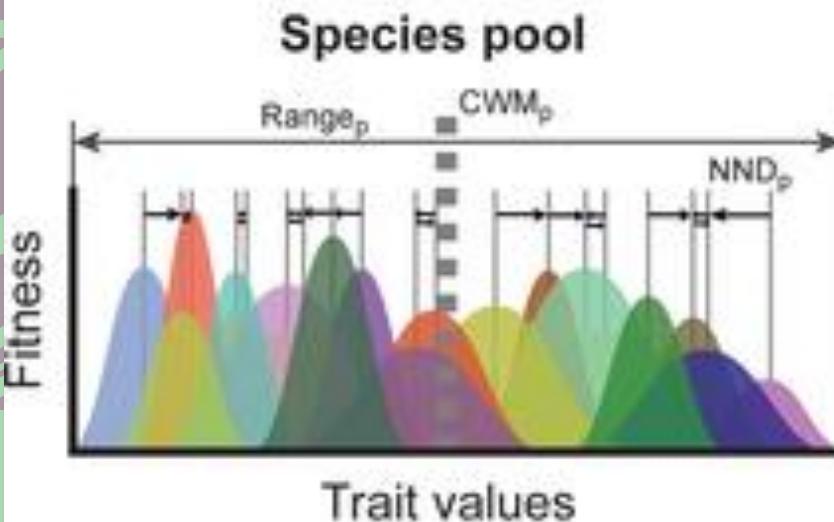
# Community ecology and traits

This understanding was traditionally mediated by species-based approaches.

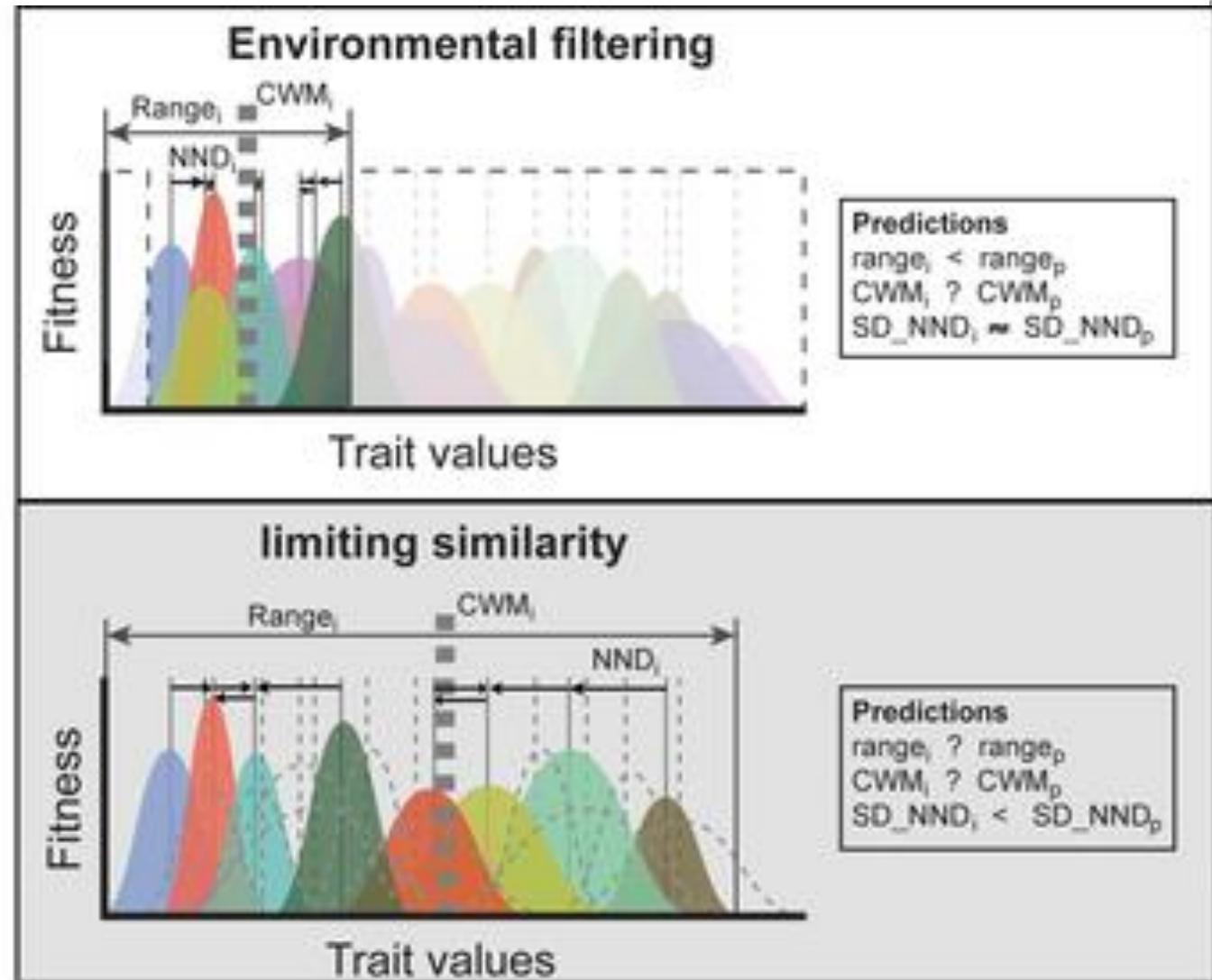
- More recently, such approaches were complemented by approaches based on traits.
- Trait-based approaches are popular, because they allow the direct connection of organism performance to its functions and to the functions of higher levels of organization such as populations, communities and ecosystems.



# 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



# Community Assembly Theories

- **Environmental Filtering:**

- Species with traits that match the local abiotic conditions (e.g., temperature, moisture) are more likely to establish and thrive.
- Example: In arid regions, plants with traits like deep root systems or water storage capacities dominate.



# Community Assembly Theories

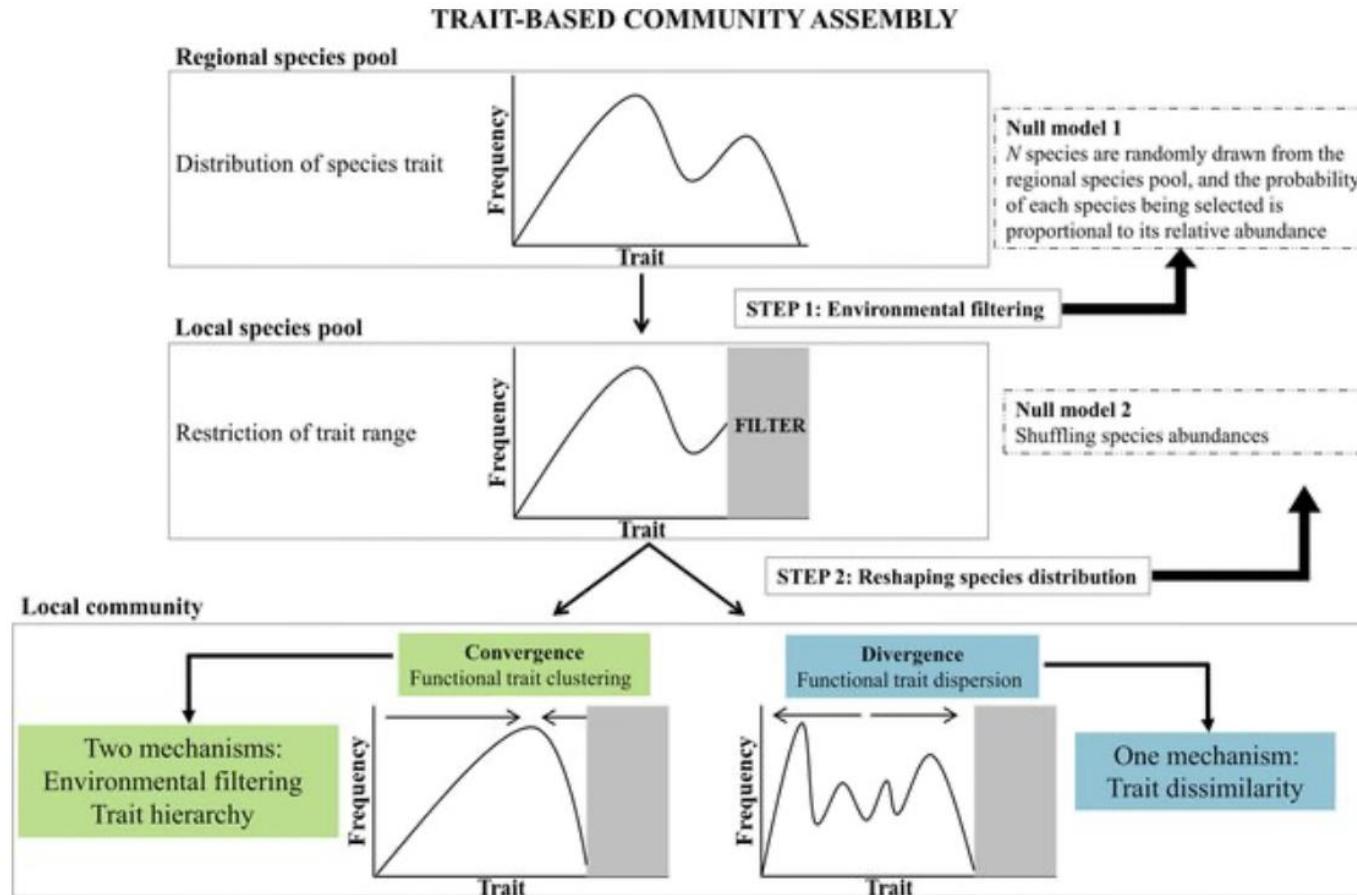
- **Environmental Filtering:**

- Species with traits that match the local abiotic conditions (e.g., temperature, moisture) are more likely to establish and thrive.
- Example: In arid regions, plants with traits like deep root systems or water storage capacities dominate.

- **Limiting similarity:**

- Coexistence is promoted by species occupying different niches (i.e., using different resources or traits that reduce competition).
- Example: Two plant species in a forest might have different leaf area sizes that allow them to specialize in different light conditions.

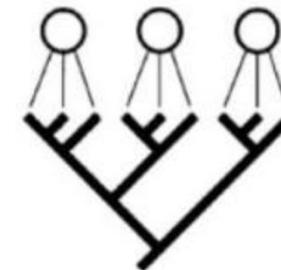
# Patterns of community structure



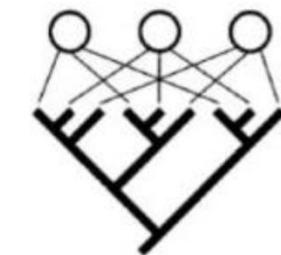
# Patterns of community structure

## Ecological interpretation

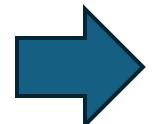
- Functional clustering
  - Co-occurring species are more closely related than expected by chance
- Functional dispersion
  - Co-occurring species are more distantly related than expected by chance
- Random patterns



Co-occurring species share a common ancestor



Co-occurring species have no shared common ancestor

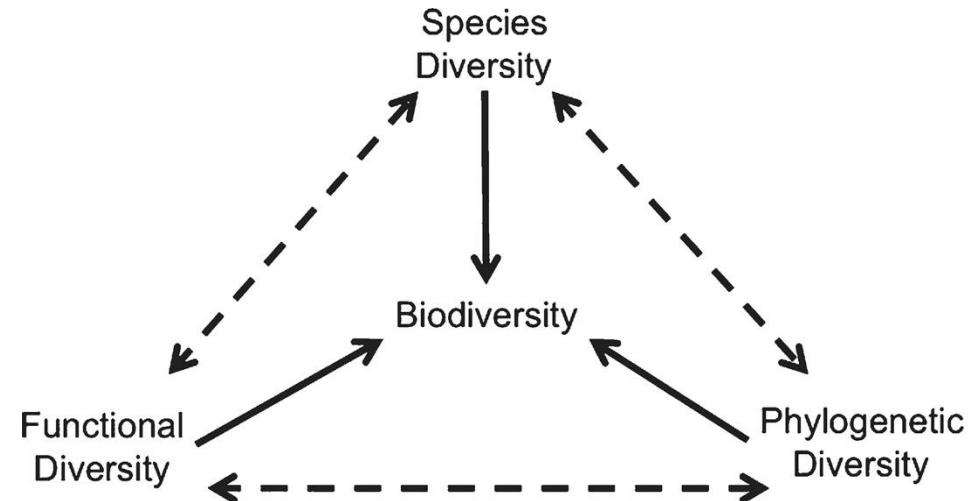


Can be tested by using **simulations** and **null models**

# Functional diversity indices

# Understanding indices

- **Definition of an Index:** A quantitative measure that summarizes complex ecological data into a single value to assess biodiversity.
- **Purpose of Indices:** Helps compare communities, understand ecological processes, and inform conservation strategies.
- **Types of Indices:** Indices can be based on taxonomic, functional, or phylogenetic diversity.

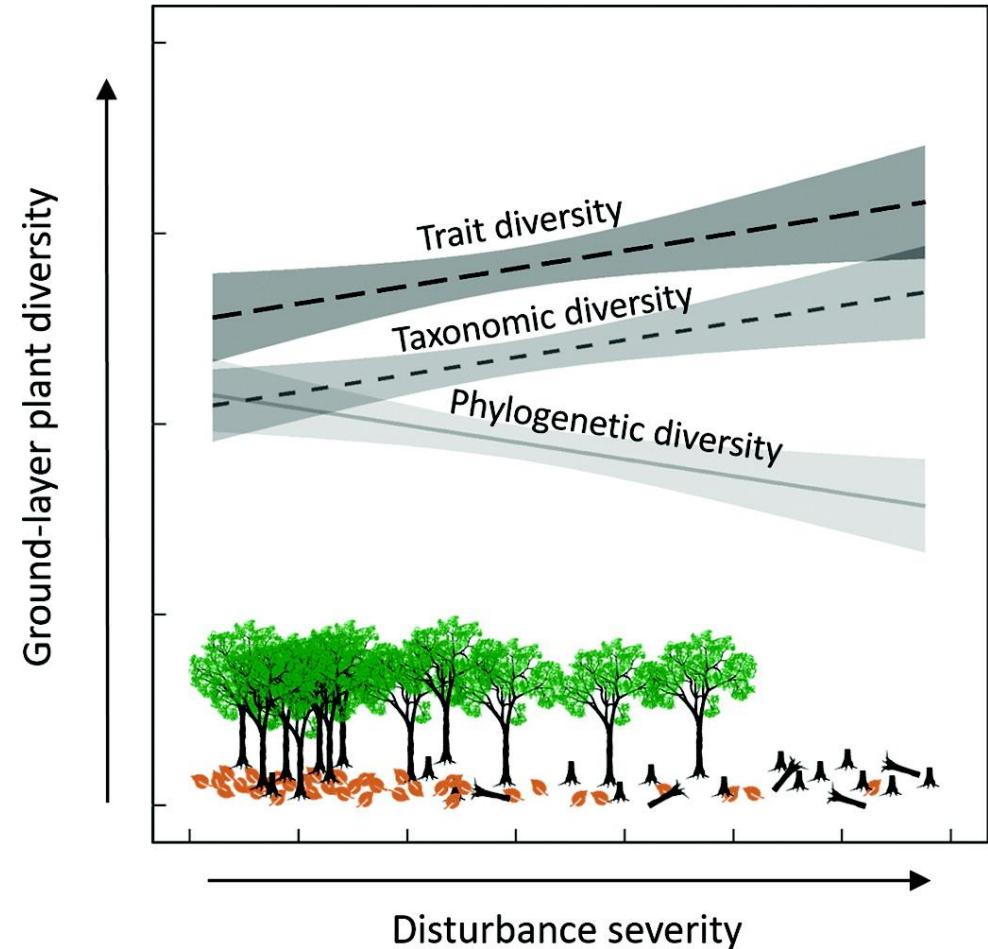


# Example of indices

- **Taxonomic Indices:** Measure biodiversity based on species identity and counts (e.g., species richness, Shannon diversity). Taxonomic indices do not consider functional traits or ecosystem roles.

- **Functional Indices:** Measure biodiversity based on the distribution and range of functional traits. Examples: Functional Richness (FRic), Functional Evenness (FEve), Functional Divergence (FDiv).

- **Comparison:** Taxonomic indices reflect species presence, while functional indices reflect species' roles and contributions to ecosystem functions.



# Functional trait diversity

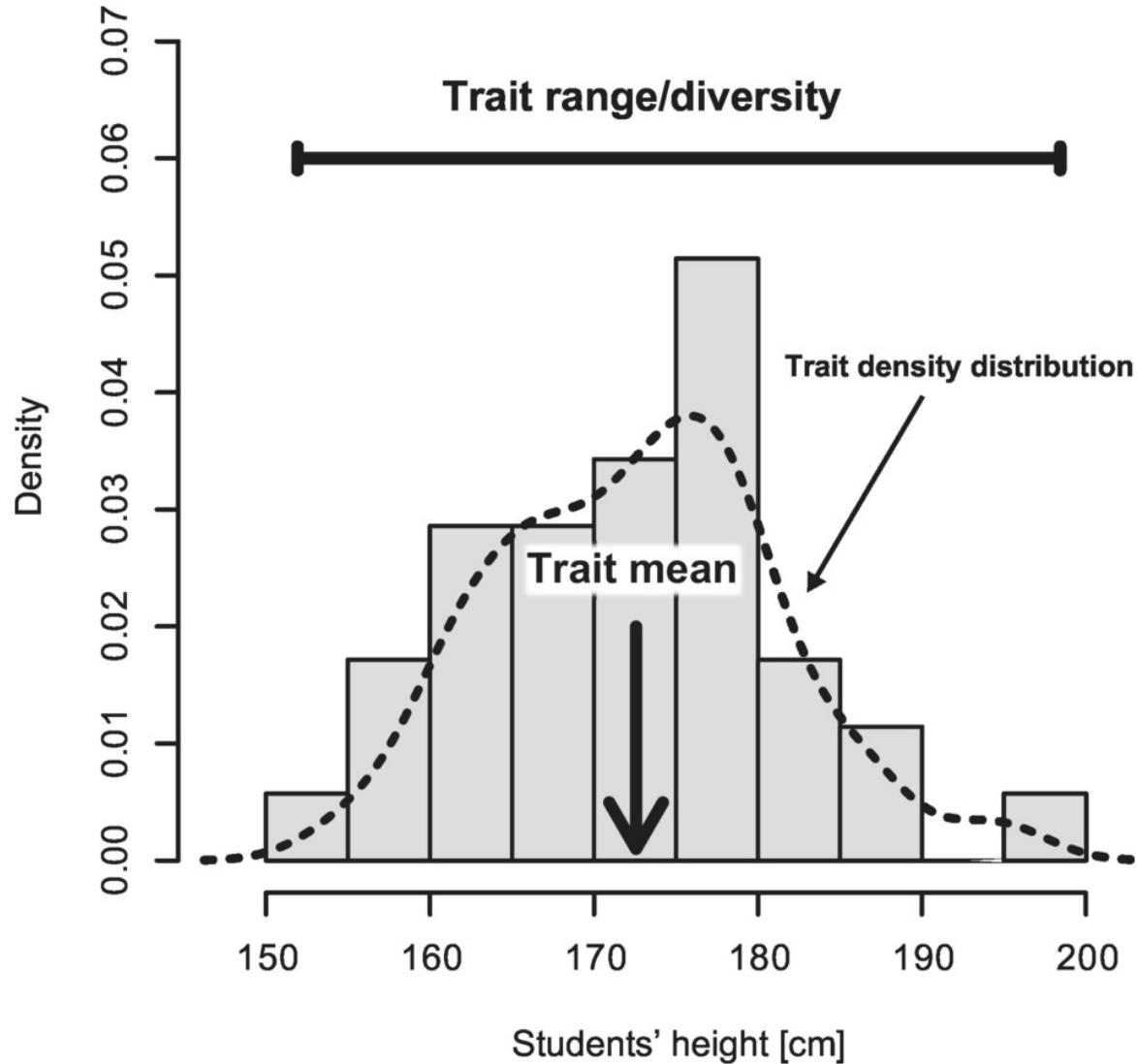
**Definition:** Measures the range and distribution of functional traits within community

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

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

# 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



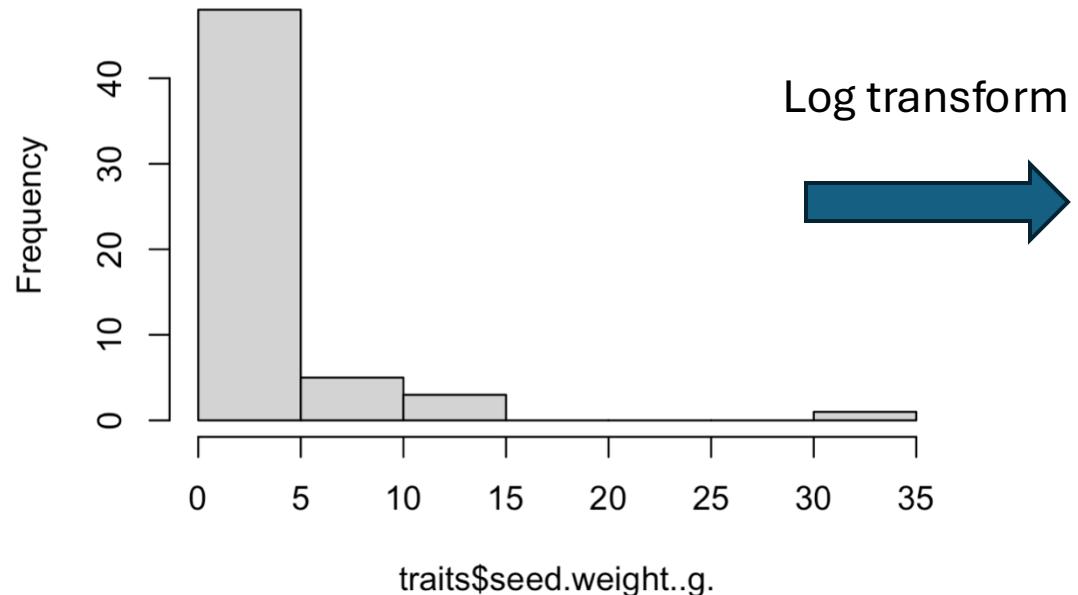
	seed.weight..g.	clonal	leaf
1	6.40	1	NA
2	2.36	1	5
3	4.00	2	4
4	3.16	2	NA
5	NA	1	NA
6	2.56	3	4
.	.	.	.

79 species

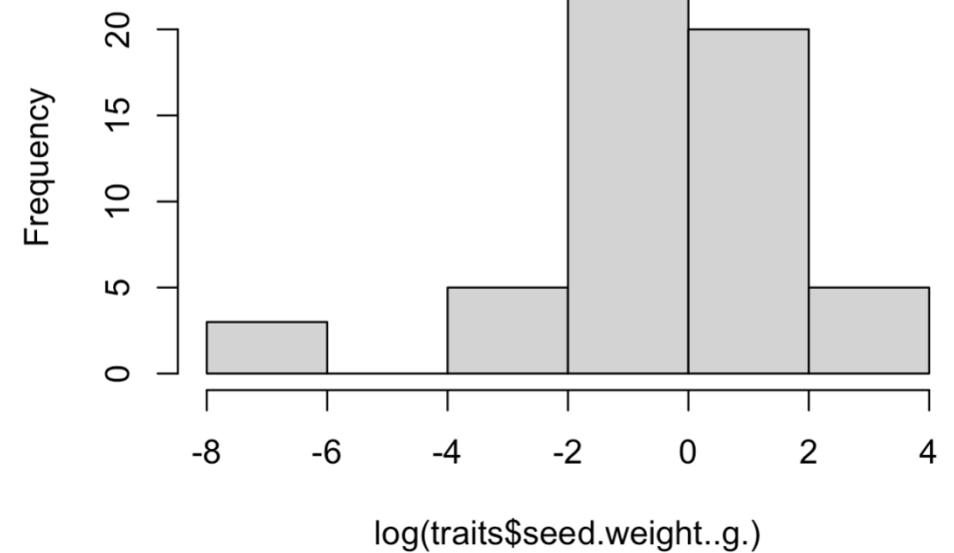
# Community functional trait structure

Sometimes, some adjustment are needed

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

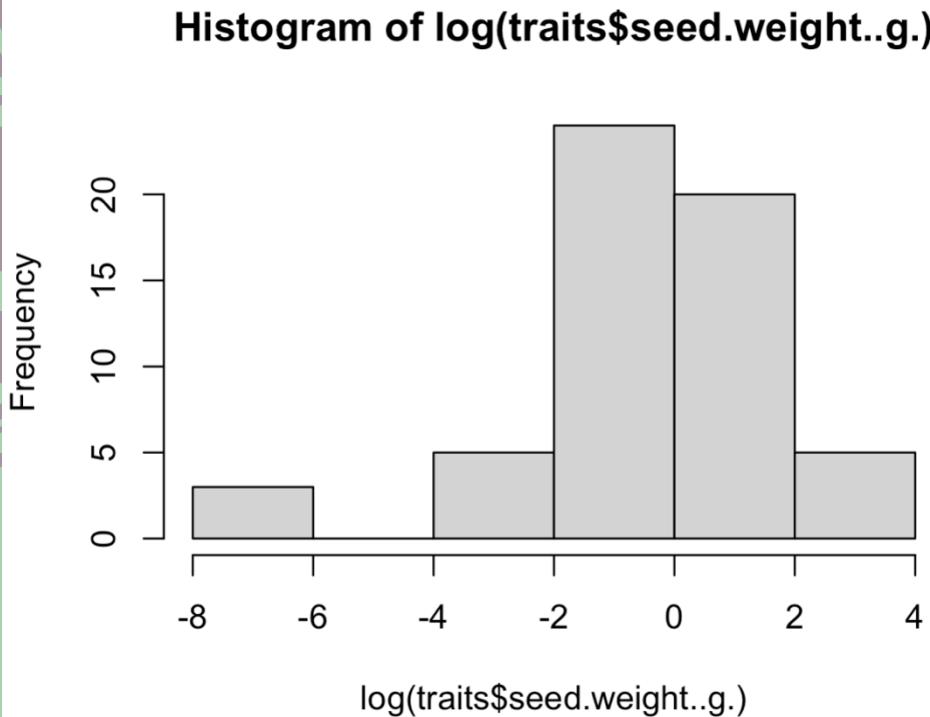


Histogram of log(traits\$seed.weight..g.)



```
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

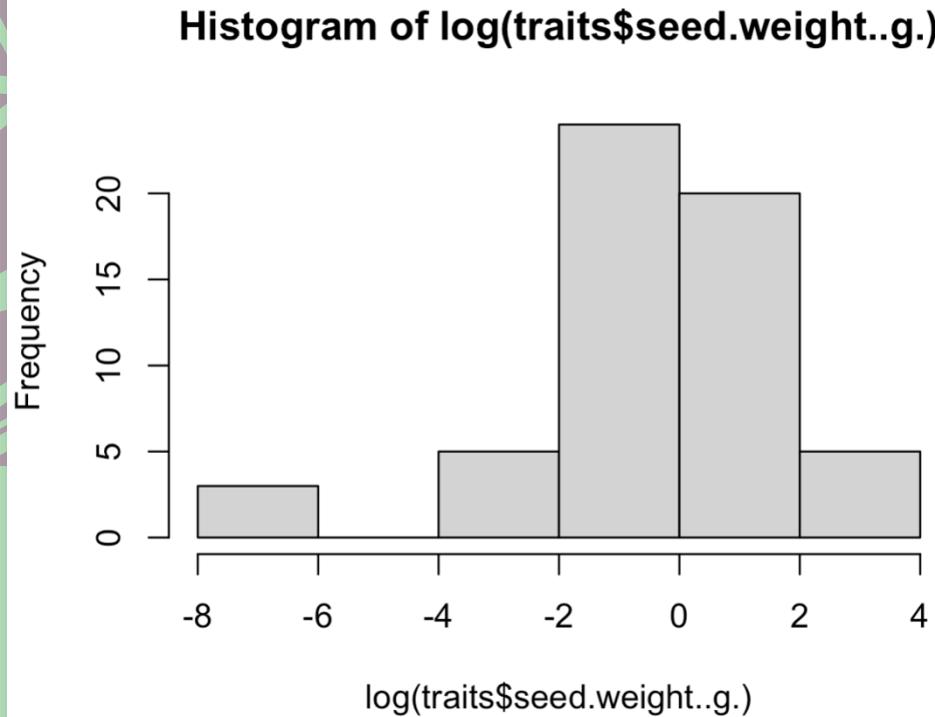
	seed.weight..g.	clonal	leaf
1	6.40	1	NA
2	2.36	1	5
3	4.00	2	4
4	3.16	2	NA
5	NA	1	NA
6	2.56	3	4

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.)`



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

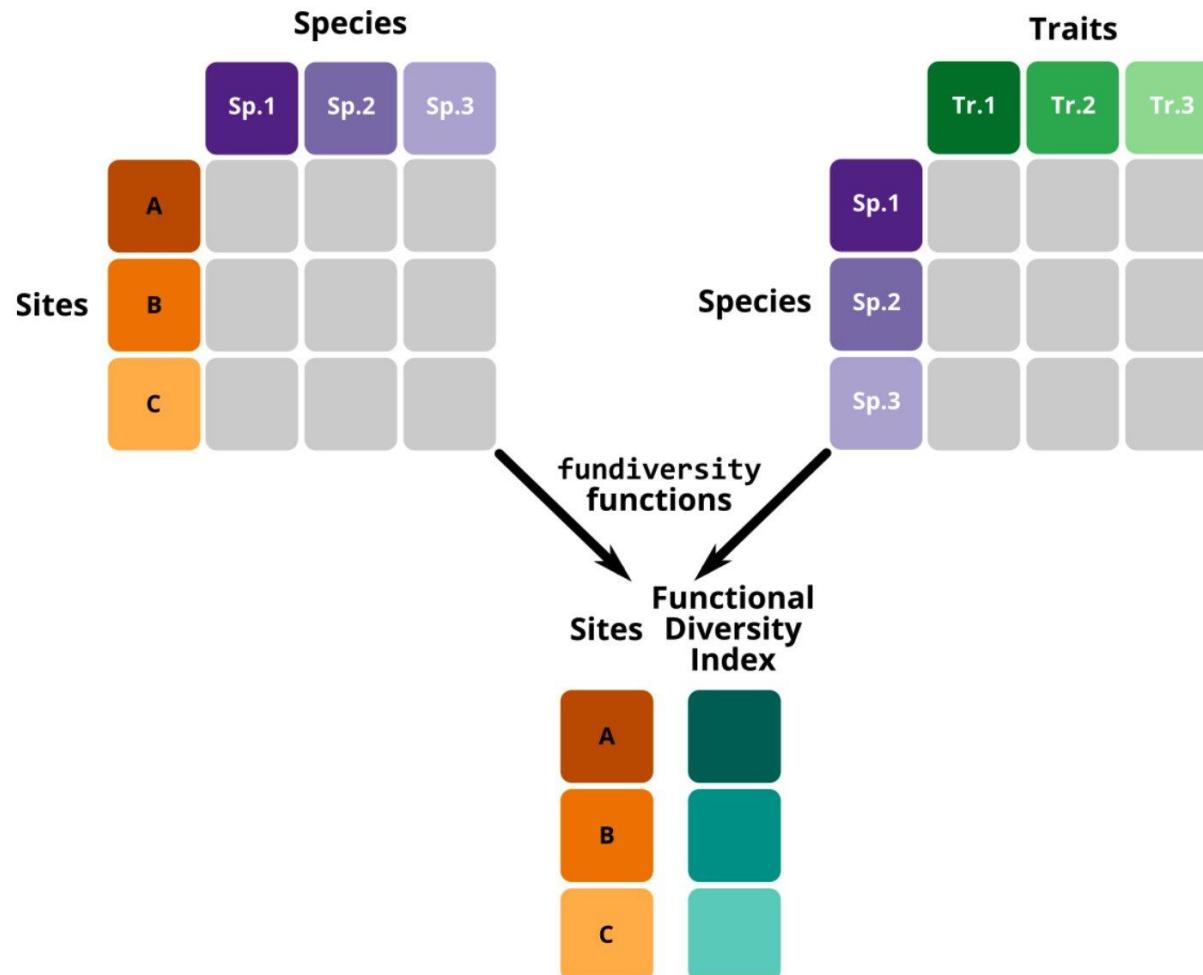
```
# CWM
mean.seed <- numeric() # empty numeric object
for (i in 1:nrow(vas.plants)) {
  mean.seed[i] <- weighted.mean(traits$seed.weight..g.,
                                w = vas.plants[i, ],
                                na.rm = T)
}
```

# Community functional trait structure

$CWM = \sum_{i=1}^N p_i x_i$	Sp1	Sp2	Sp3	MEAN
<b>Size of different individuals (cm)</b>	20 25 30 35 40	35 40 45	80	38.9
<b>Mean per species (<math>x_i</math>)</b>	30	40	80	50
<hr/>				SUM
<b>Species relative abundance (<math>p_i</math>)</b>	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, CMW.type = "all")
```

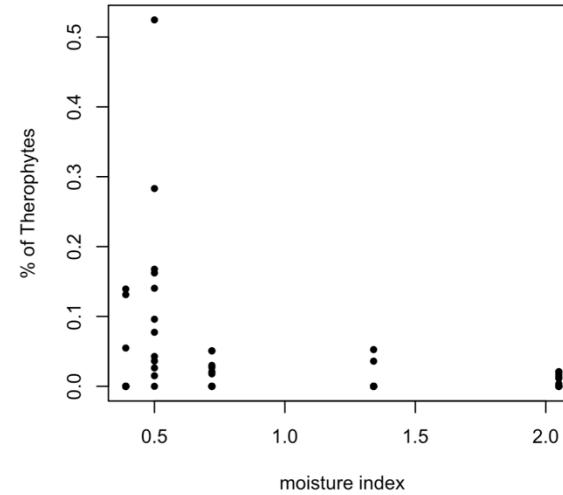
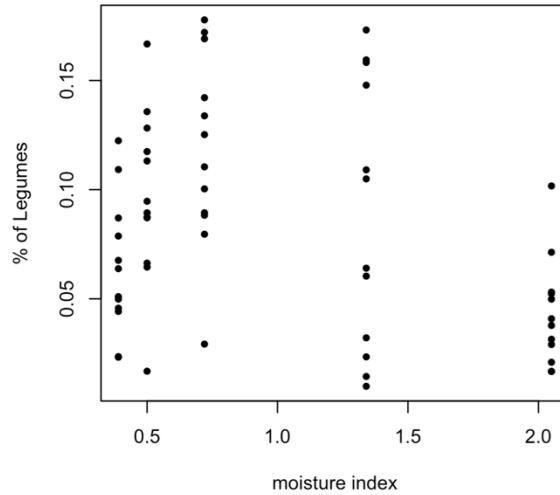
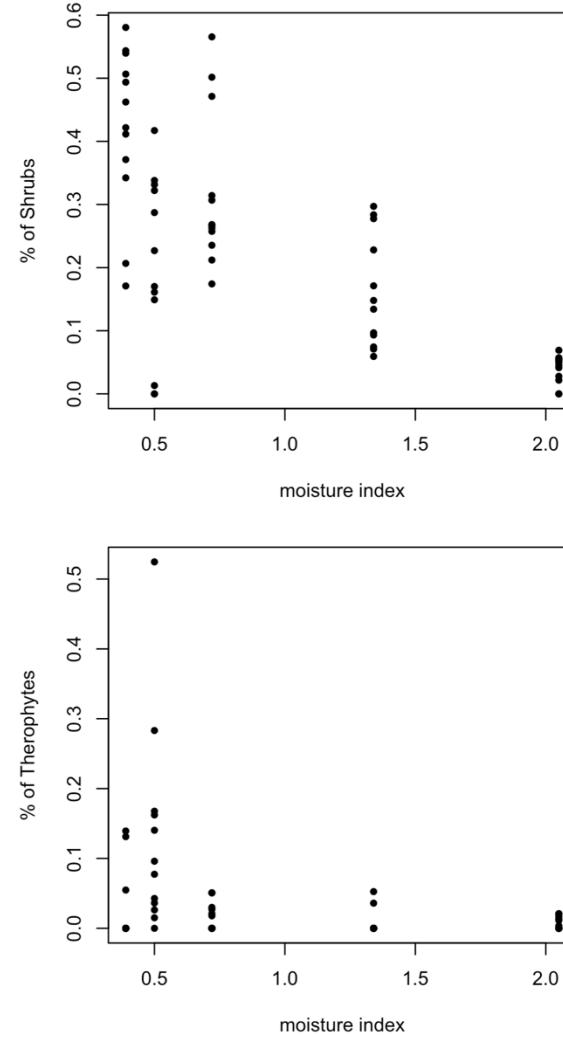
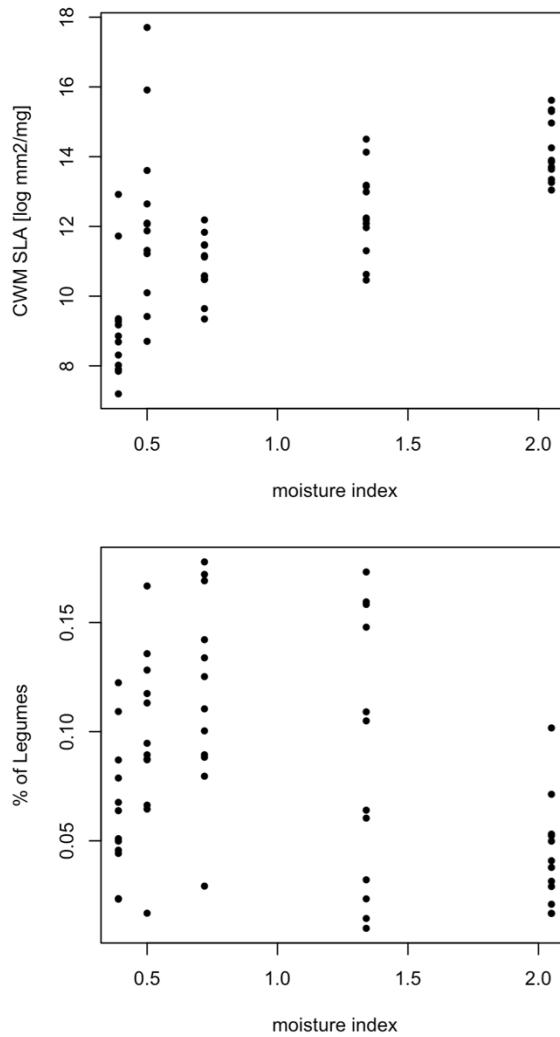
	GrowthForm_forb	GrowthForm_grass	GrowthForm_shrub	GrowthForm_subshrub	LEG_0	LEG_1	SLA	LF_Th	LF_G	LF_H
X1nograz.1	0.17441466	0.07487008	0.58044233	0.17027294	0.9557956	0.044204387	8.857775	0.00000000	0.00000000	0.17202123
X1nograz.2	0.22658585	0.08545117	0.50653372	0.18142925	0.9501596	0.049840427	9.173906	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

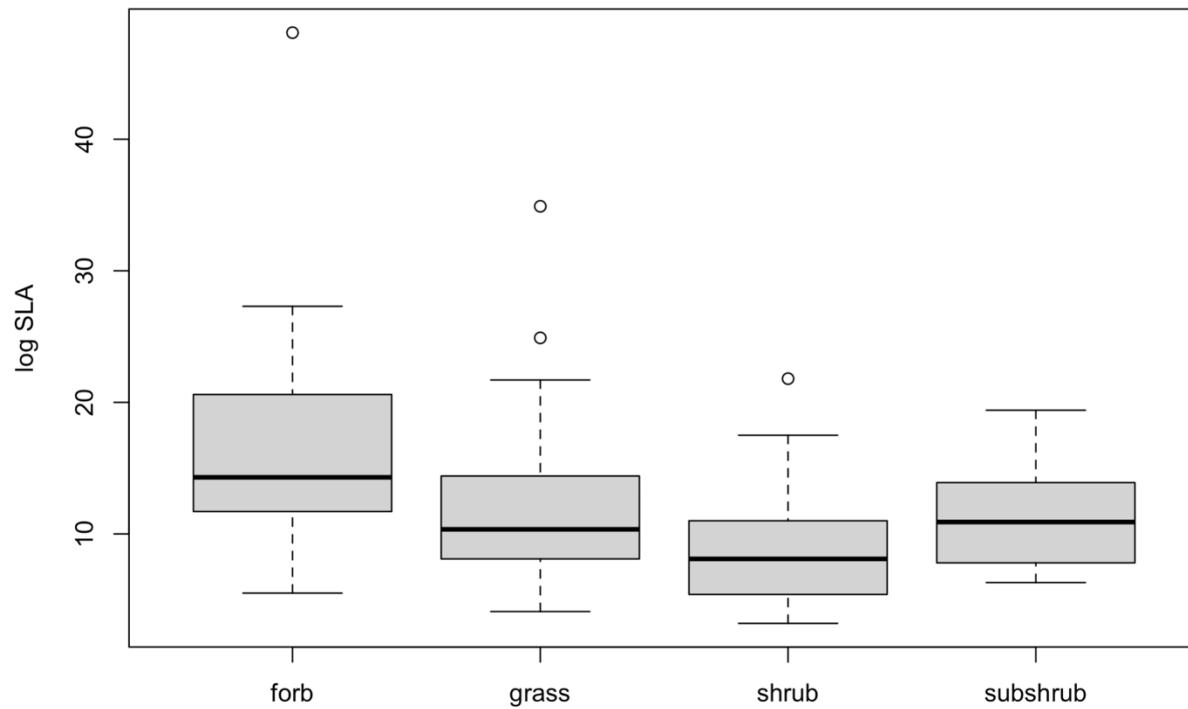
	vegbelt	grazing	moisture.index
1nograz.1	1	0	0.39
1nograz.2	1	0	0.39
1nograz.3	1	0	0.39
1nograz.4	1	0	0.39
1highgraz.1	1	2	0.39
1highgraz.2	1	2	0.39
1highgraz.3	1	2	0.39
1highgraz.4	1	2	0.39
1littlegraz.1	1	1	0.39

# 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

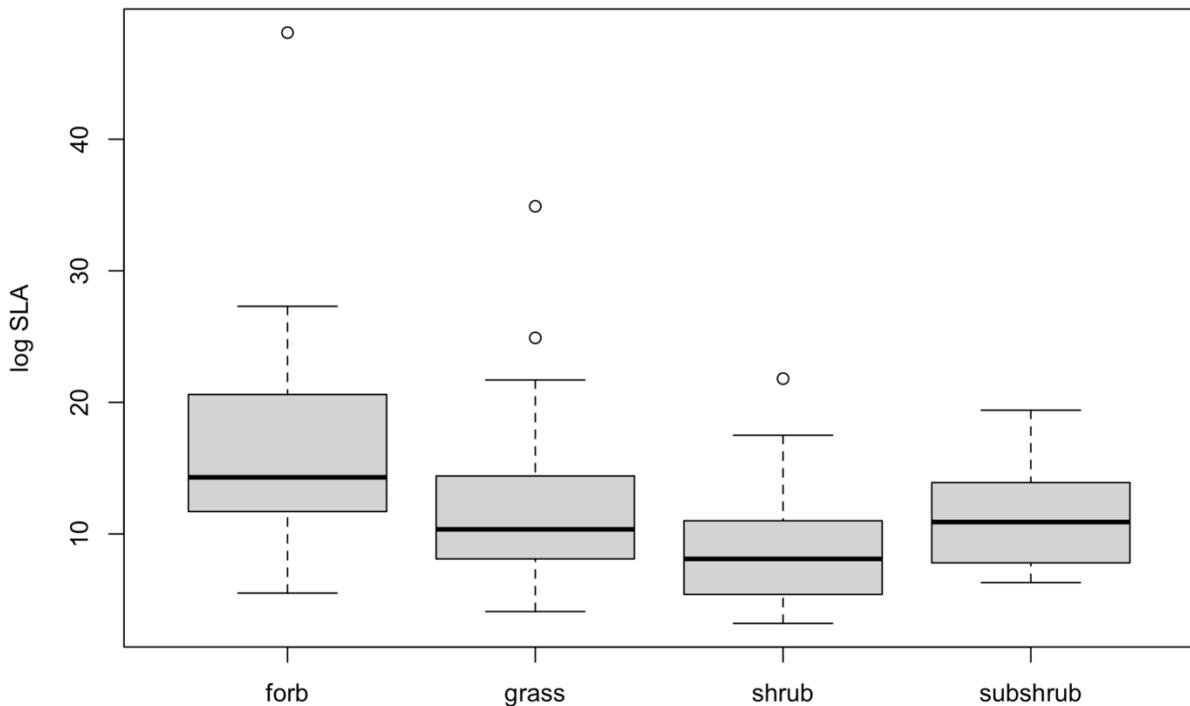


- The CWM SLA is increasing with moisture index, likely because of decrease in shrub species with moisture.
- In fact, the different growth forms tend to have different SLA.
- We can test it !

```
> 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 **

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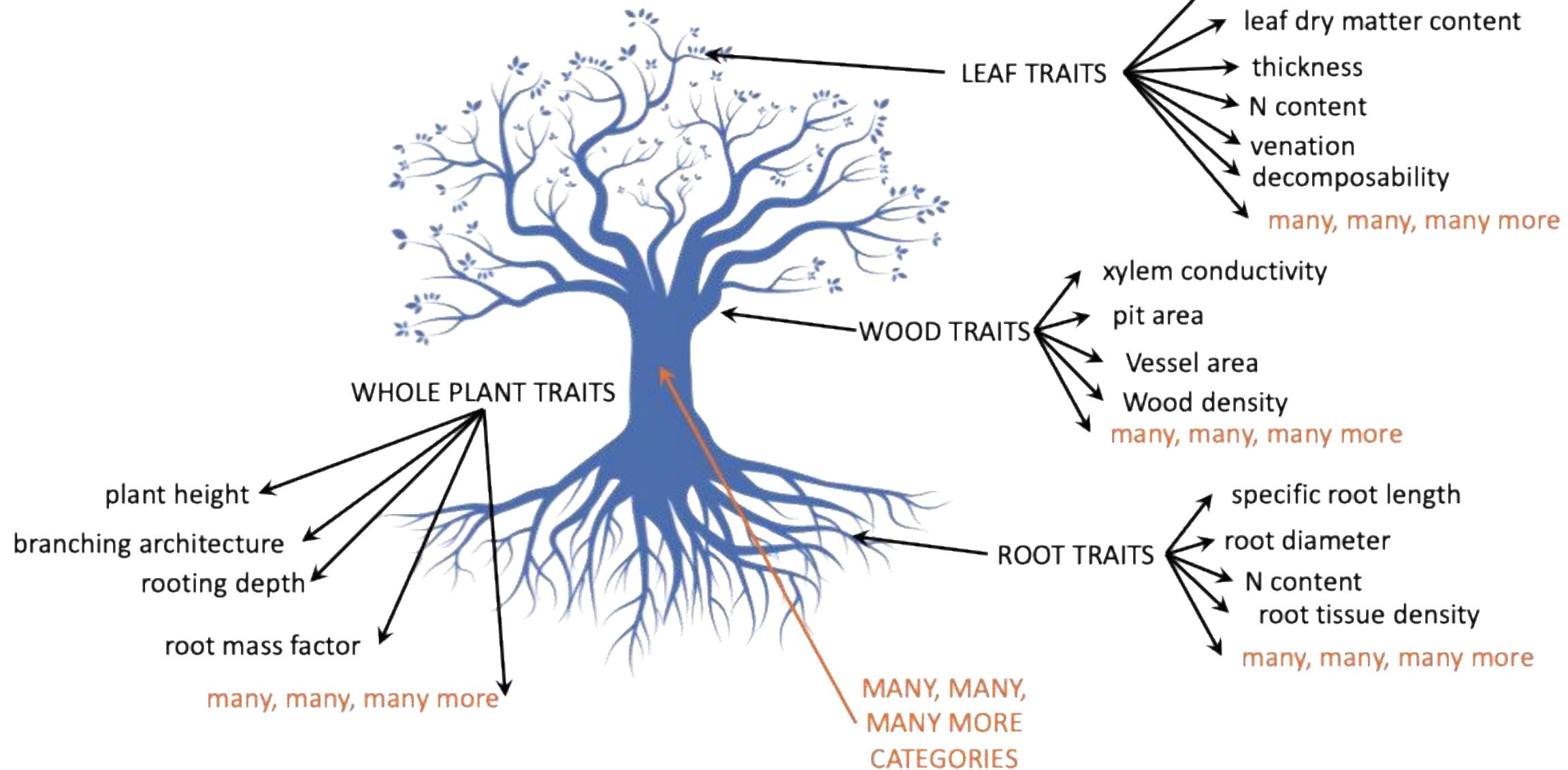
Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

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

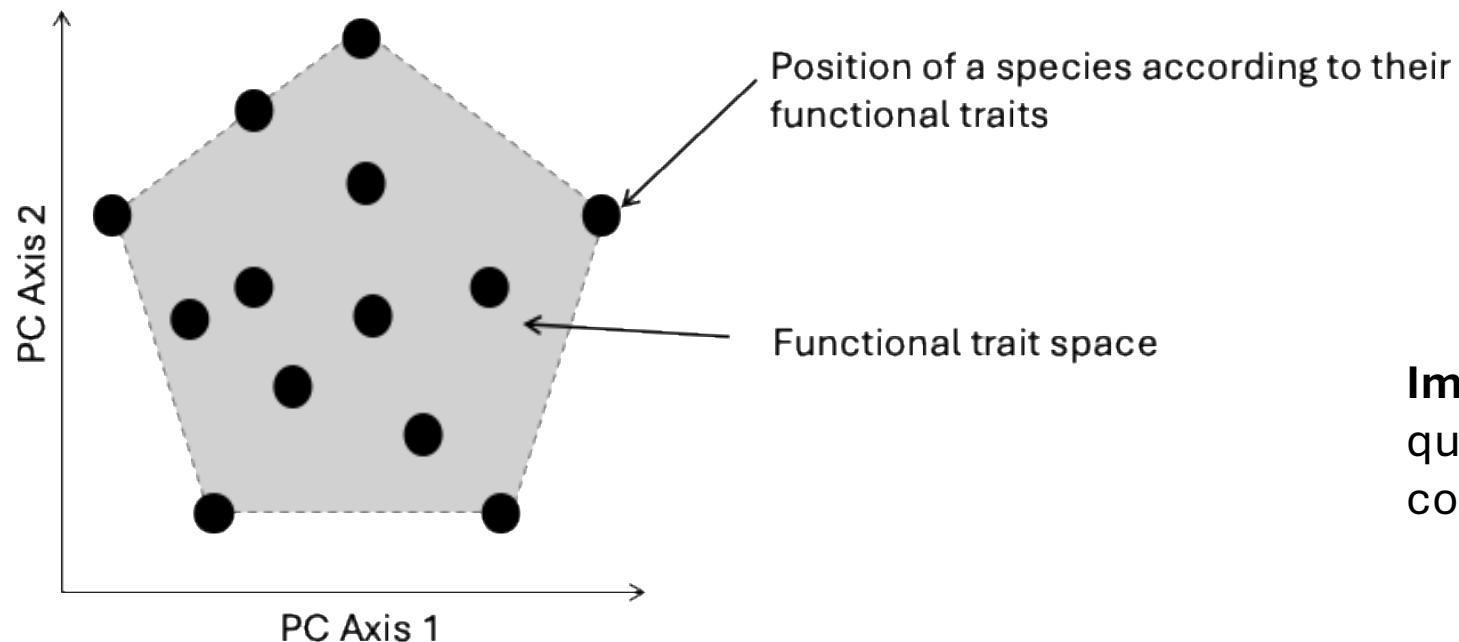
# Many traits....



# Functional trait space

**Functional Trait Space:** A multi-dimensional space where species are positioned based on their traits.

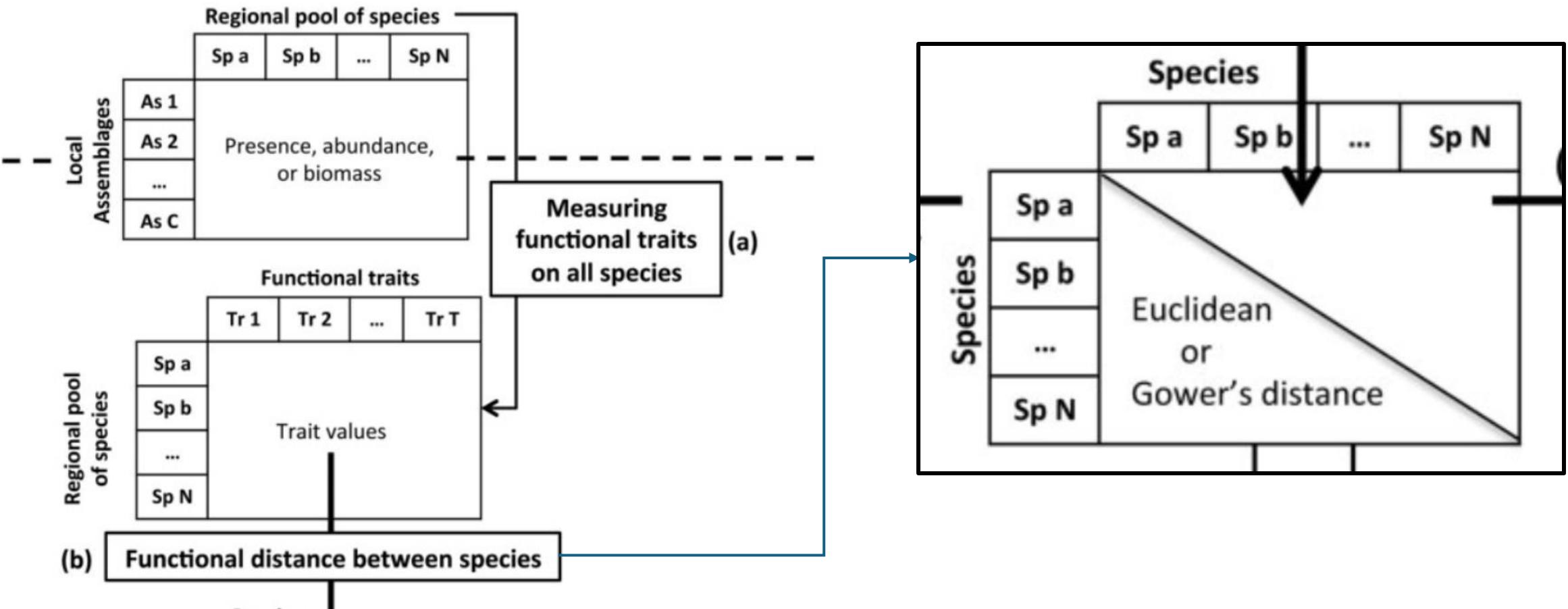
**Axes:** Each dimension (axis) represents a functional trait (e.g., leaf area, body size, root depth).



**Importance:** Helps visualize and quantify functional diversity, and assess community assembly mechanisms.

# How to build a functional trait space ?

Step 1. Compute functional distance between species



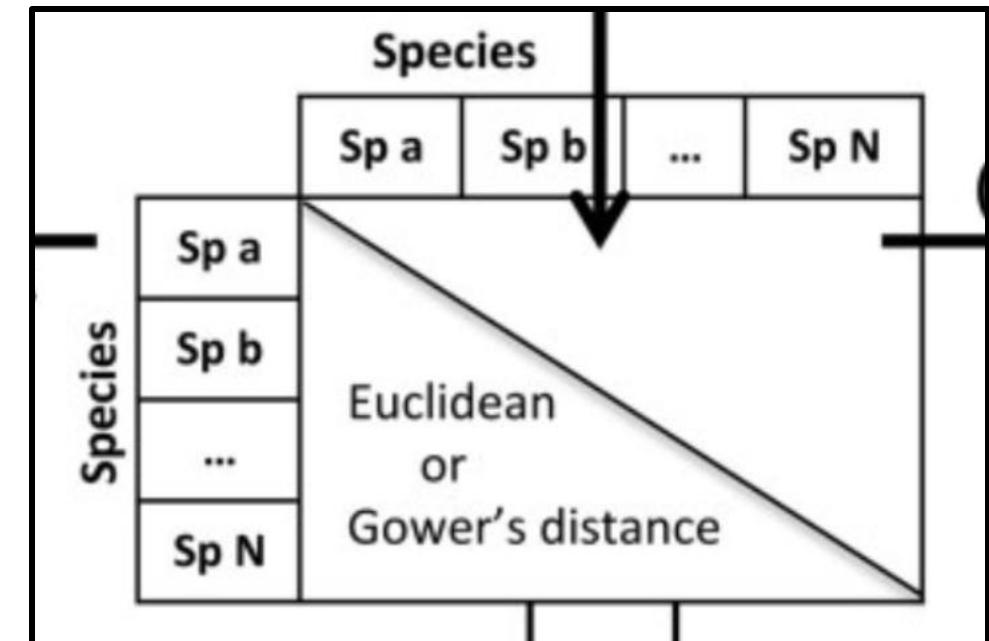
# How to build a functional trait space ?

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 build a functional trait space ?

## 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)
```

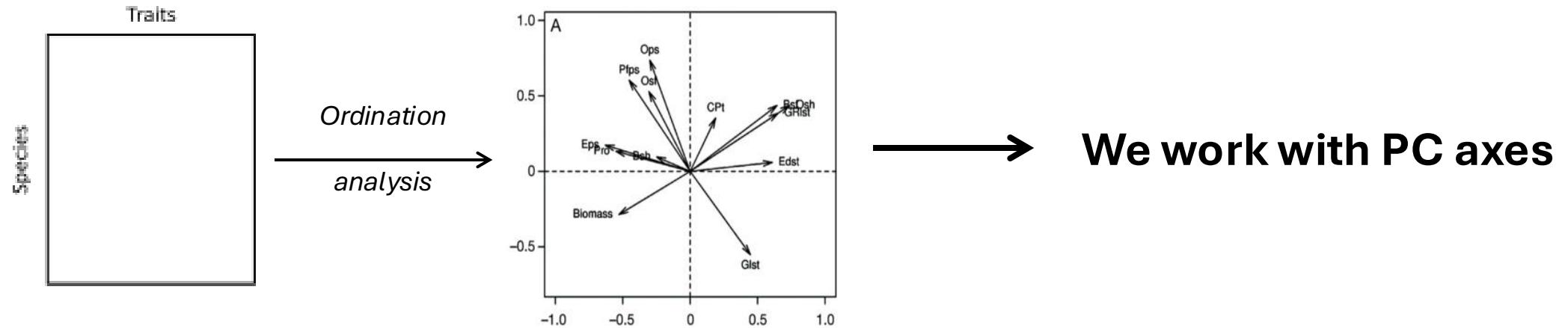
PCA is the most common method, but other methods exist.



PCA works only with continuous data

# How to build a functional trait space ?

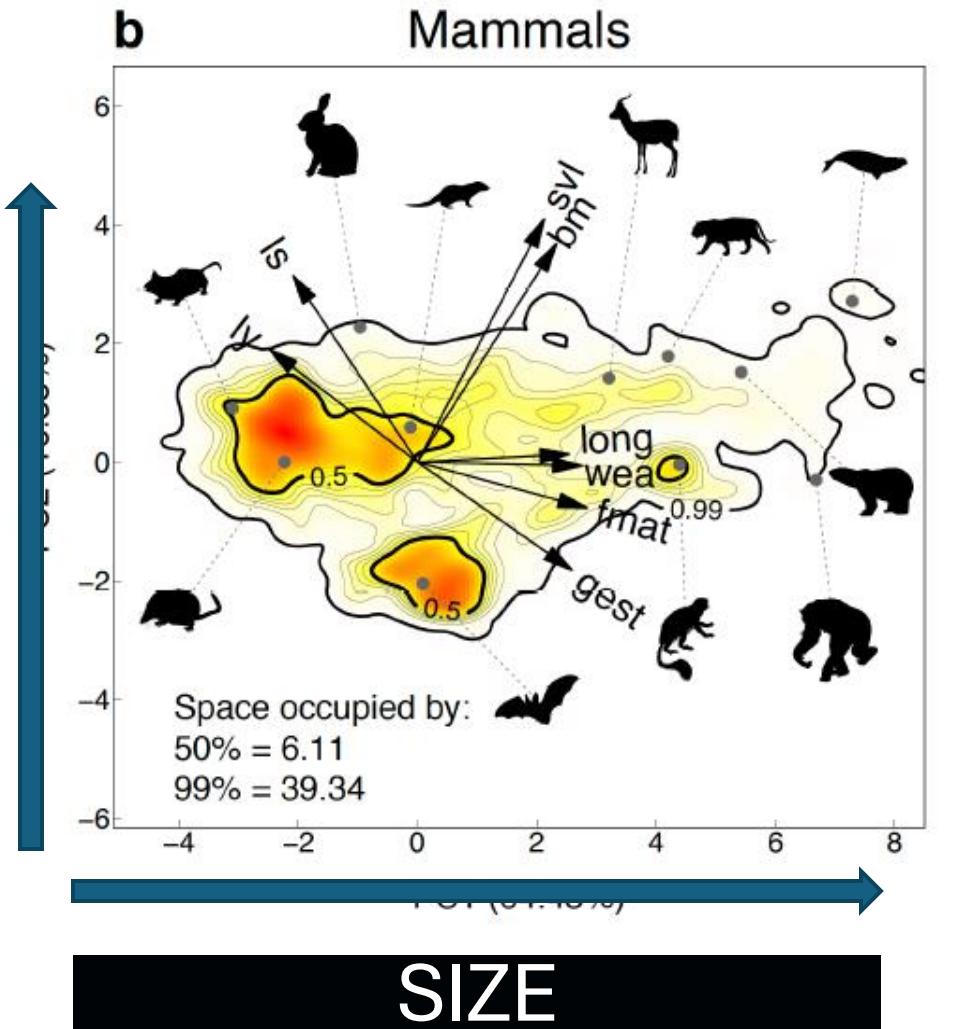
## Principal Component Analysis (PCA)



We work with PC axes

# Example on mammals

REPRODUCTION



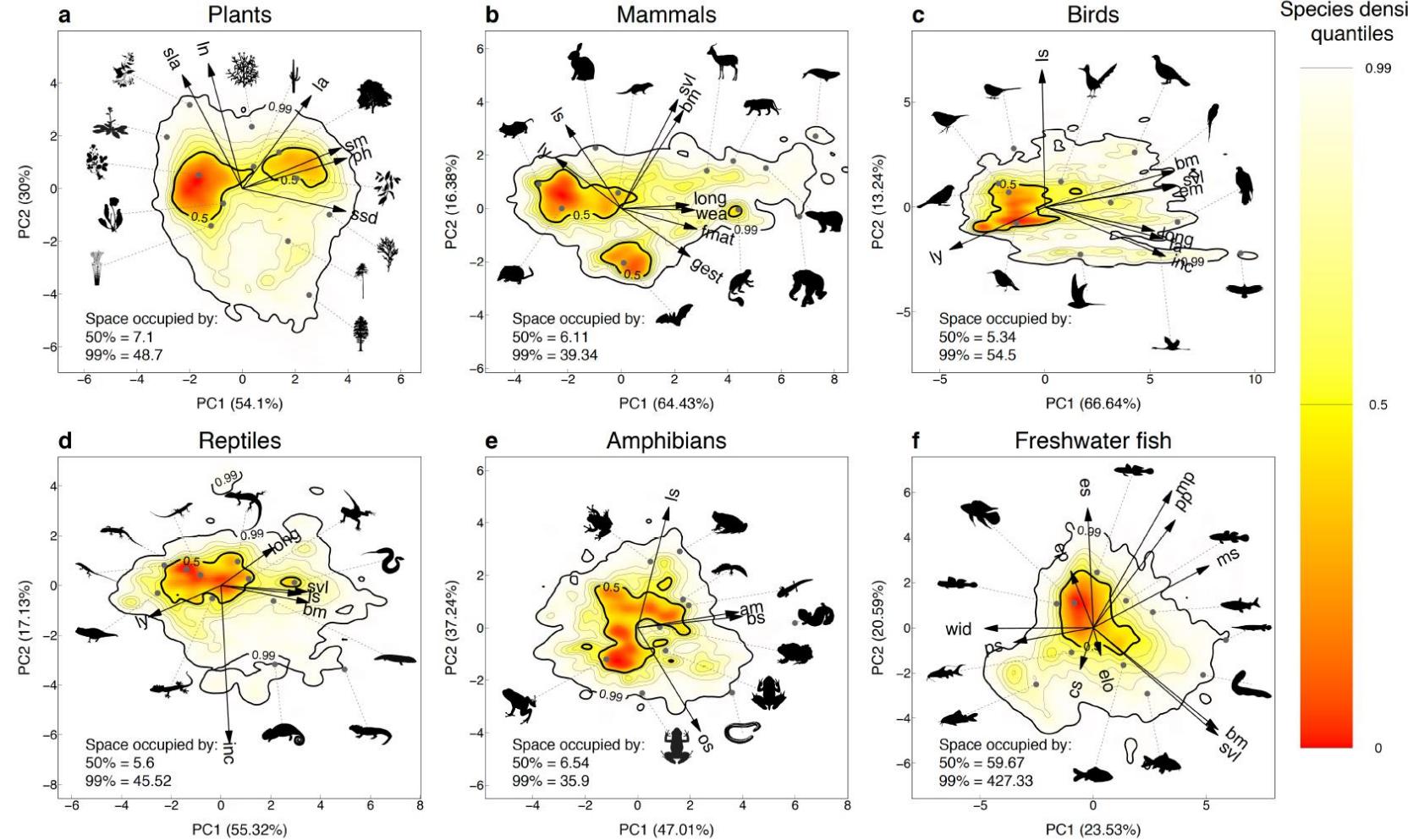
**Step 1: Collect Trait Data:** Gather functional trait data for the species in the community.

**Step 2: Standardize Trait Data:** Scale and center the data to ensure traits are comparable.

**Step 3: Use Dimensionality Reduction Techniques:** Apply Principal Component Analysis (PCA), Multidimensional Scaling (MDS), or PcoA to reduce the number of dimensions.

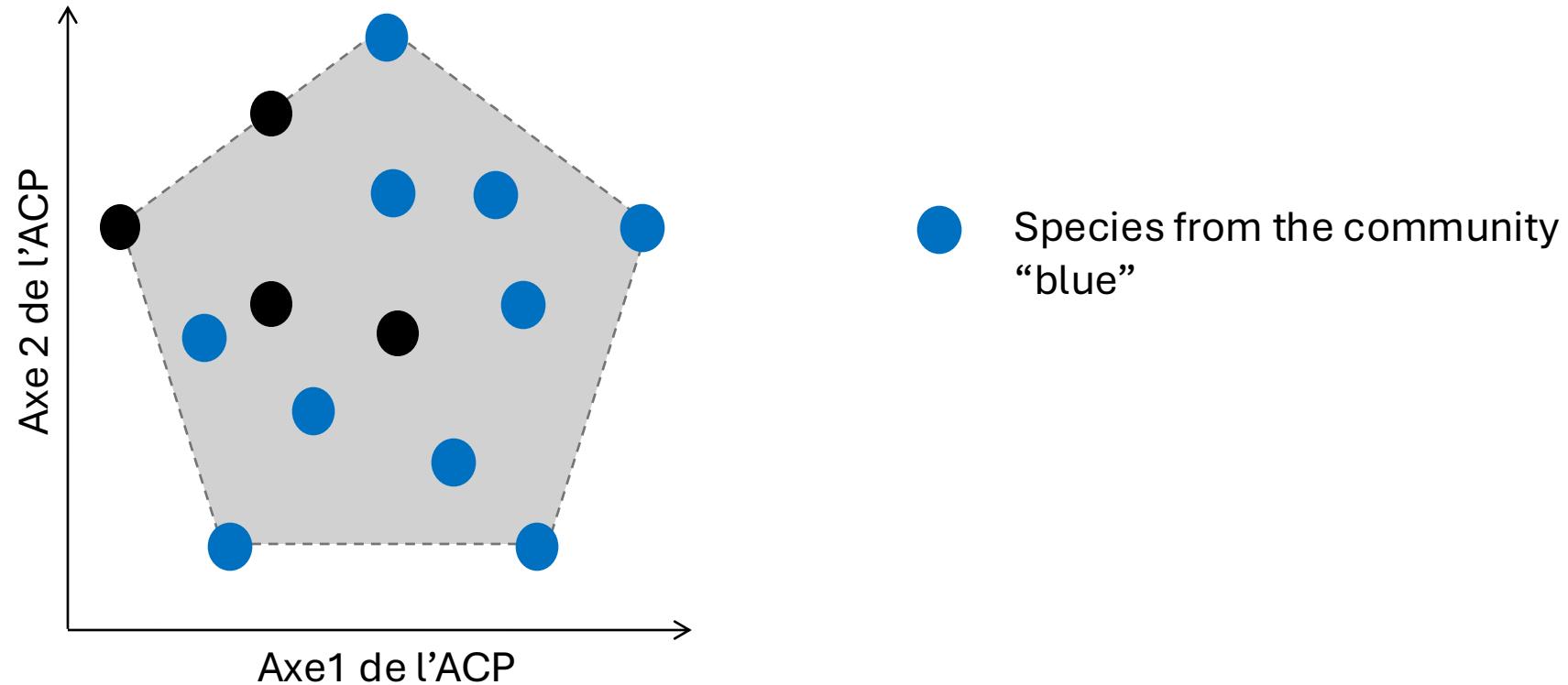
**Step 4: Plot Species in the Reduced Trait Space:** Each species is represented as a point in the multi-dimensional space.

# The functional space of vertebrates and plants

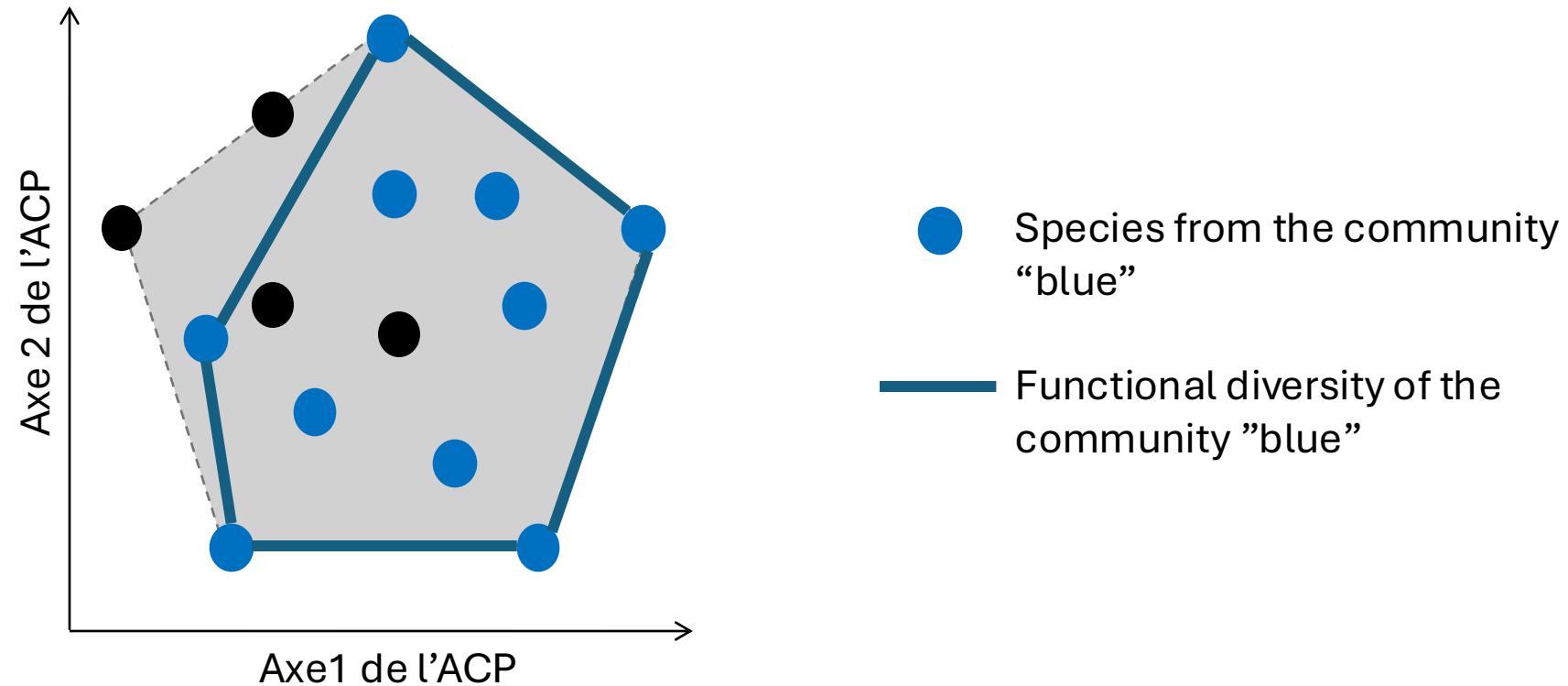


- Few dimensions
- High lumpiness (hotspot)
- Hotspots are close to the extremes (skewed occupation)

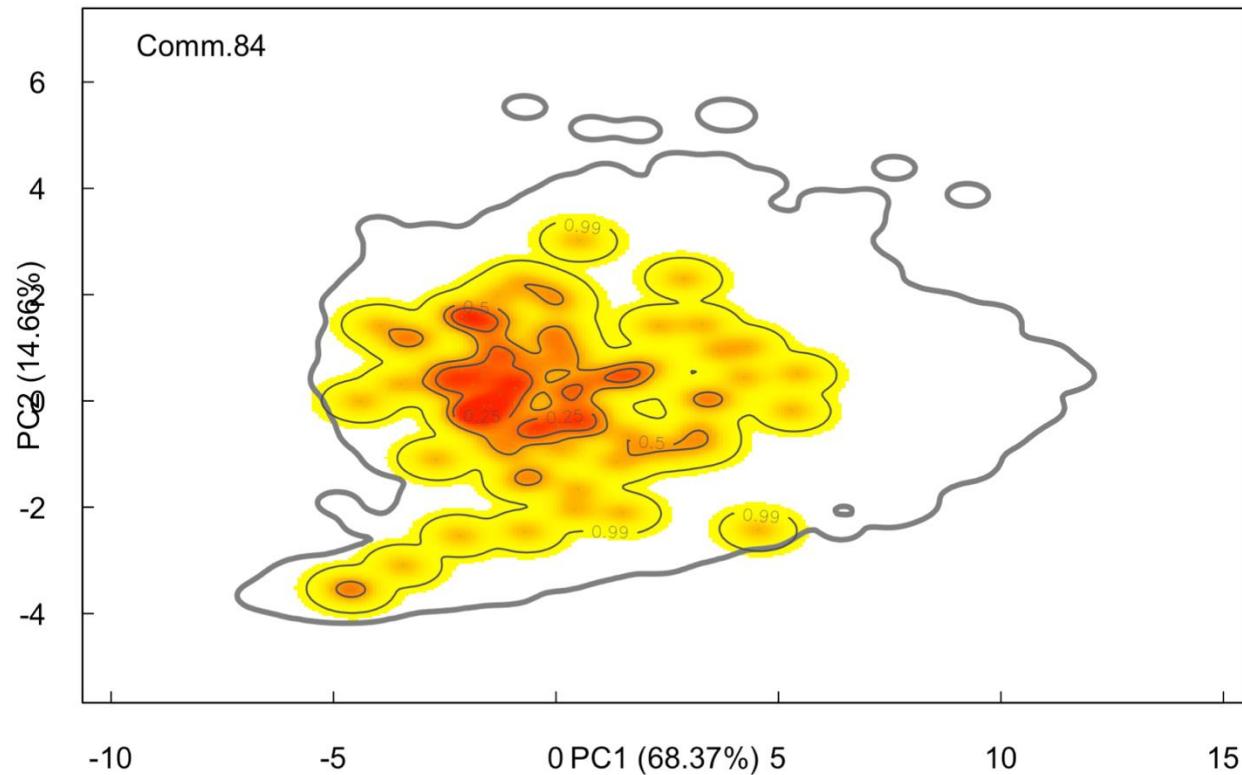
# Functional trait space and community



# Functional trait space and community



# Functional trait space and community



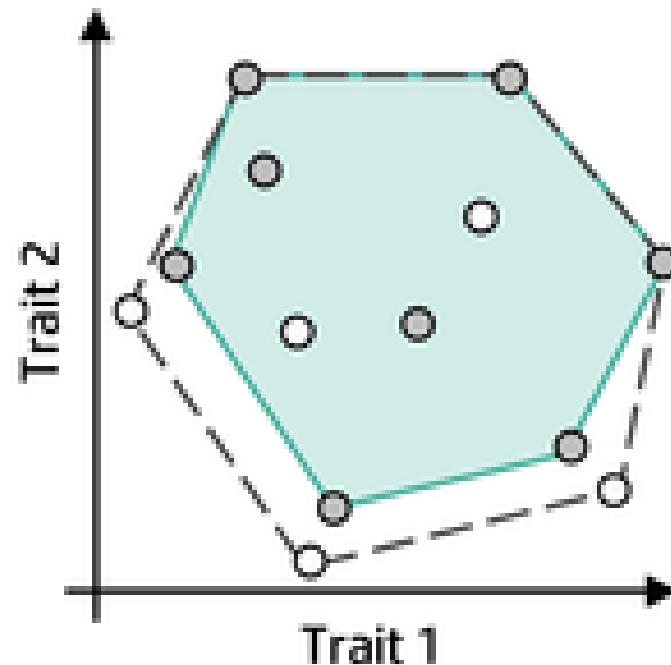
Species relative abundances ( $p_i$ )

	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
<b>Sum</b>	<b>1</b>	<b>1</b>	<b>1</b>	<b>1</b>

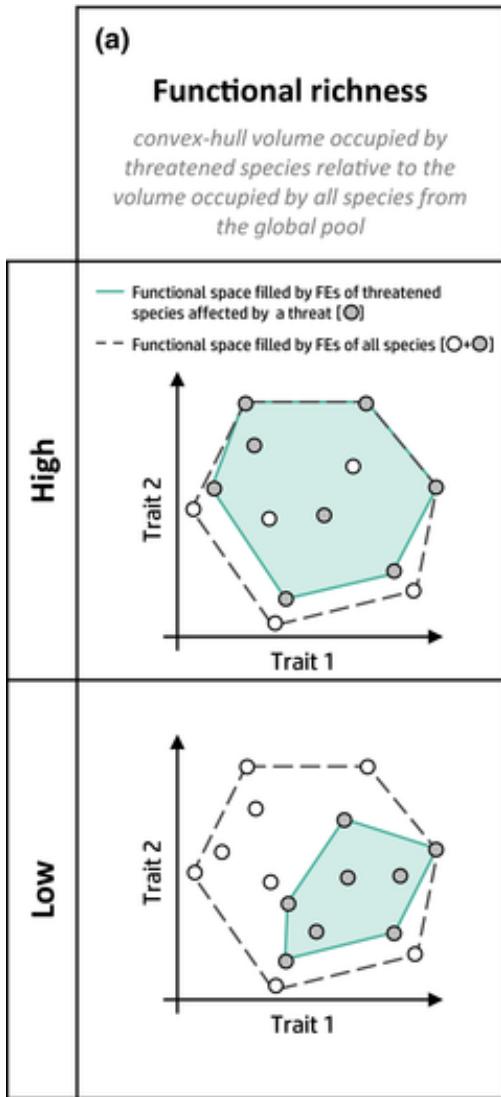
# How to calculate functional diversity ?

**Definition:** Functional diversity (FD) measures the range of functional traits within a community and reflects how species traits are distributed across ecological space.

**Importance:** FD provides insight into ecosystem functioning, resilience, and stability.



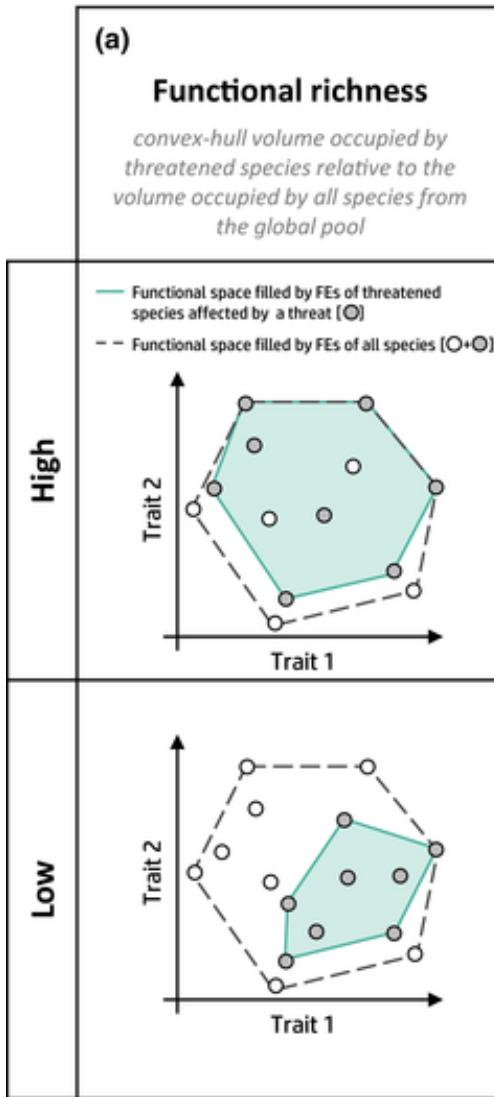
# How to calculate functional diversity ?



## Functional richness (FRic)

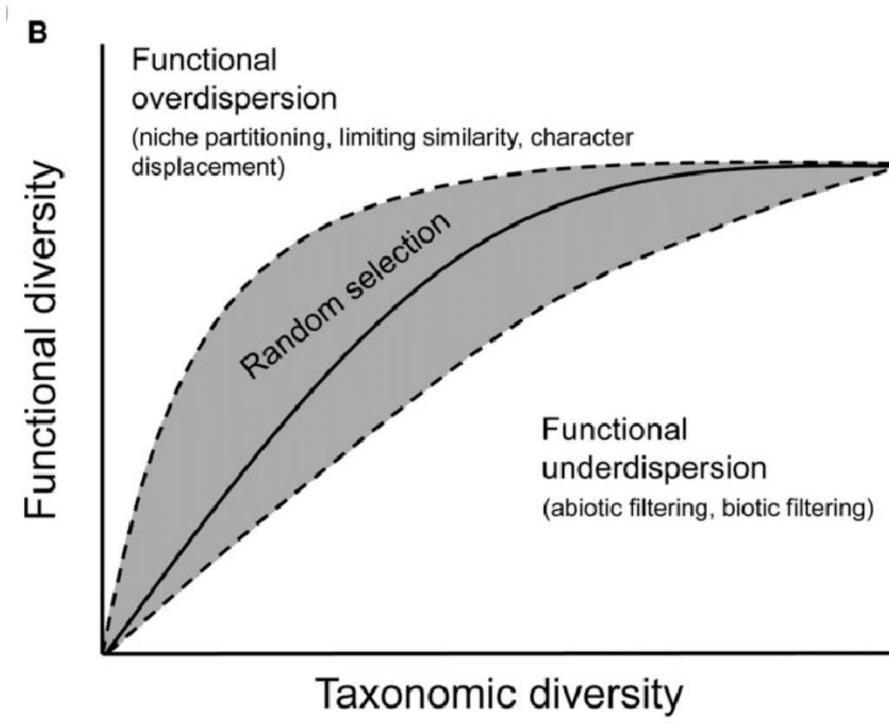
- measures the amount of trait space filled by a community. It is calculated by creating a convex hull that encompasses the trait values of all species in the community.
- FRic is used to assess how much of the total possible trait space is utilized by species within an ecosystem.
- High FRic indicates that species occupy a wide range of functional roles, contributing to ecosystem processes like productivity or nutrient cycling.
- Low FRic may suggest that functional roles are limited, which can reduce ecosystem resilience and function.

# Null model



## Functional richness (FRic)

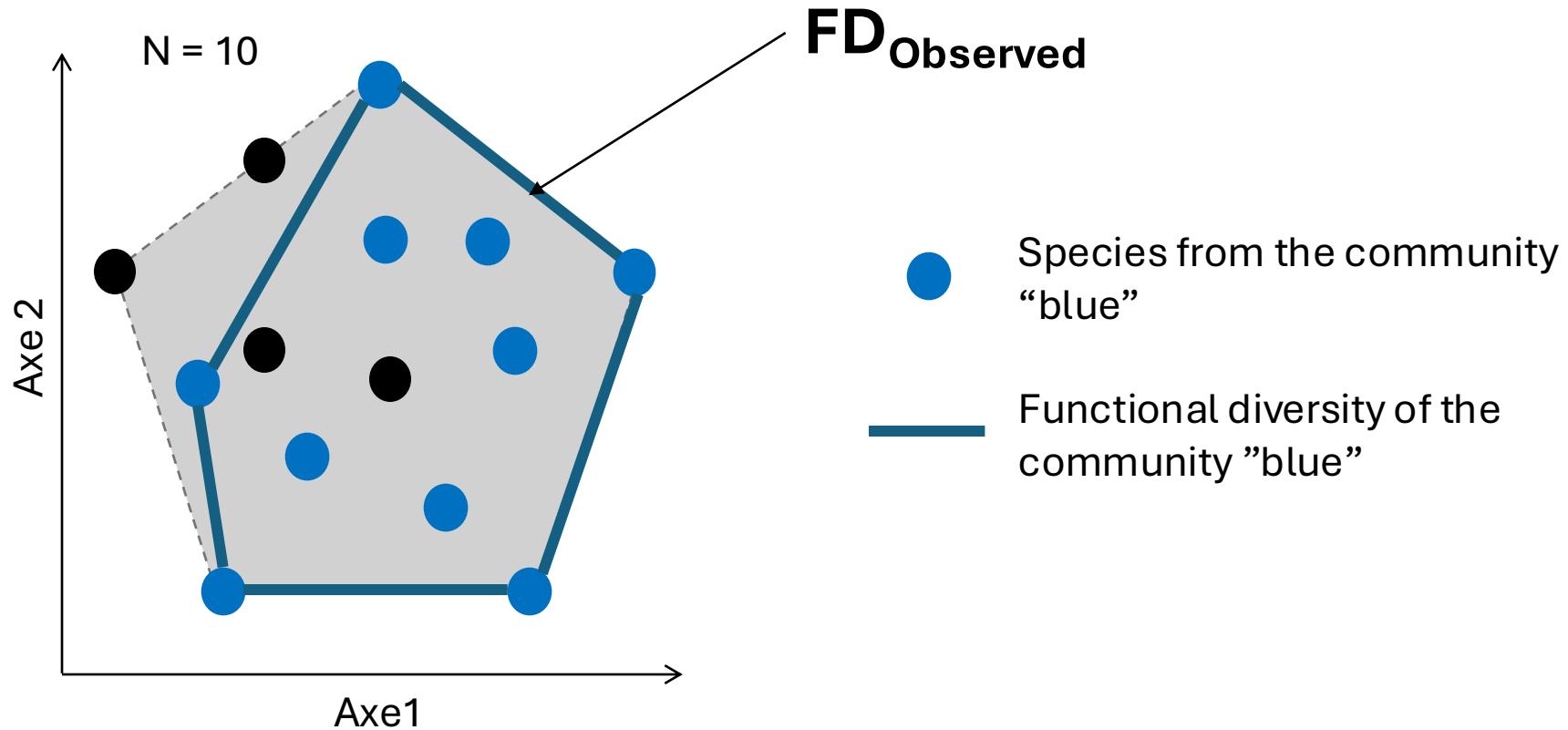
- Expected correlation with species richness



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

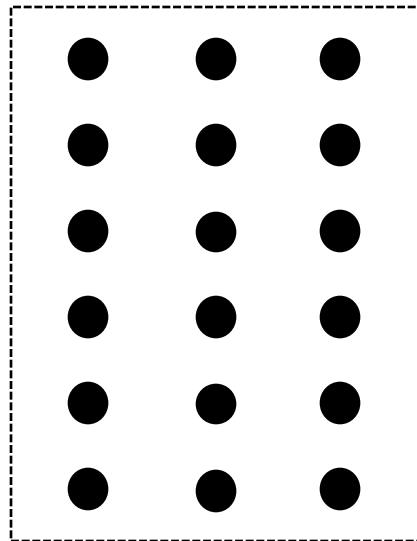
① Observed functional diversity ( $FD_{\text{Observed}}$ )



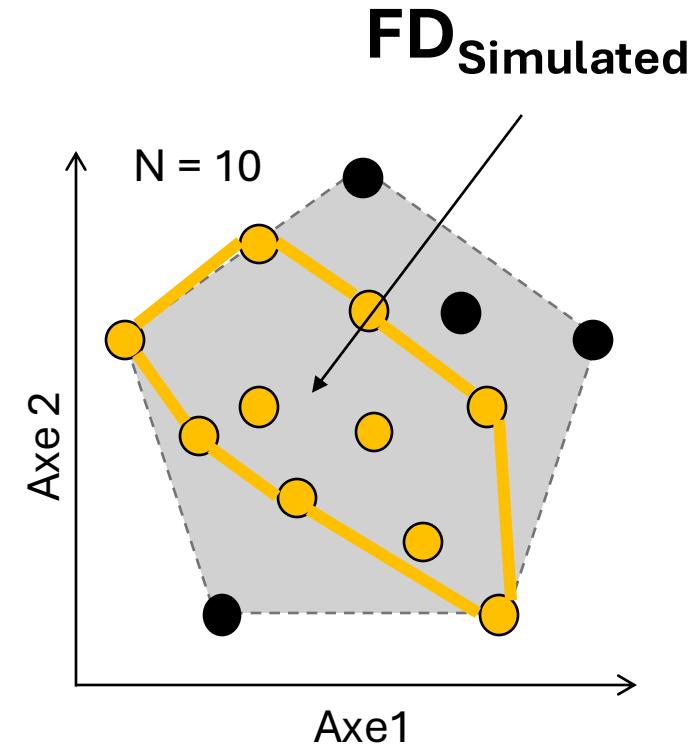
# Null model

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

**Species pool**

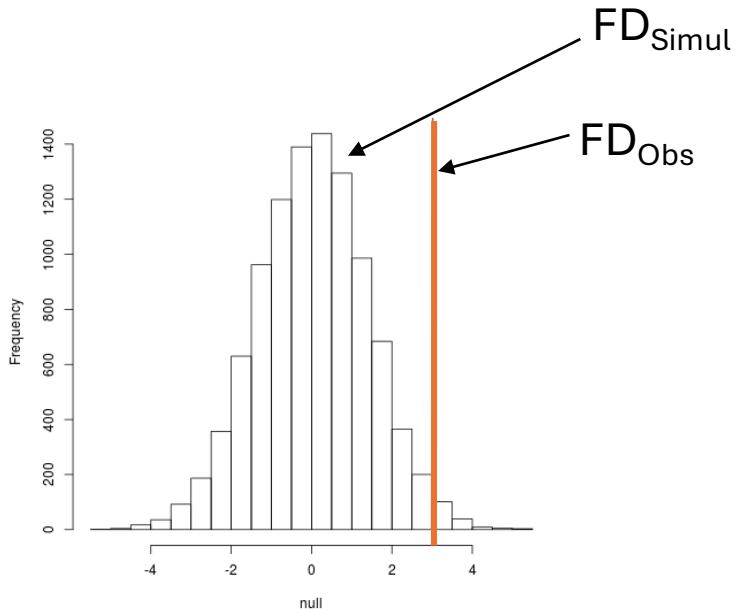


Random sp.



# Null model

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



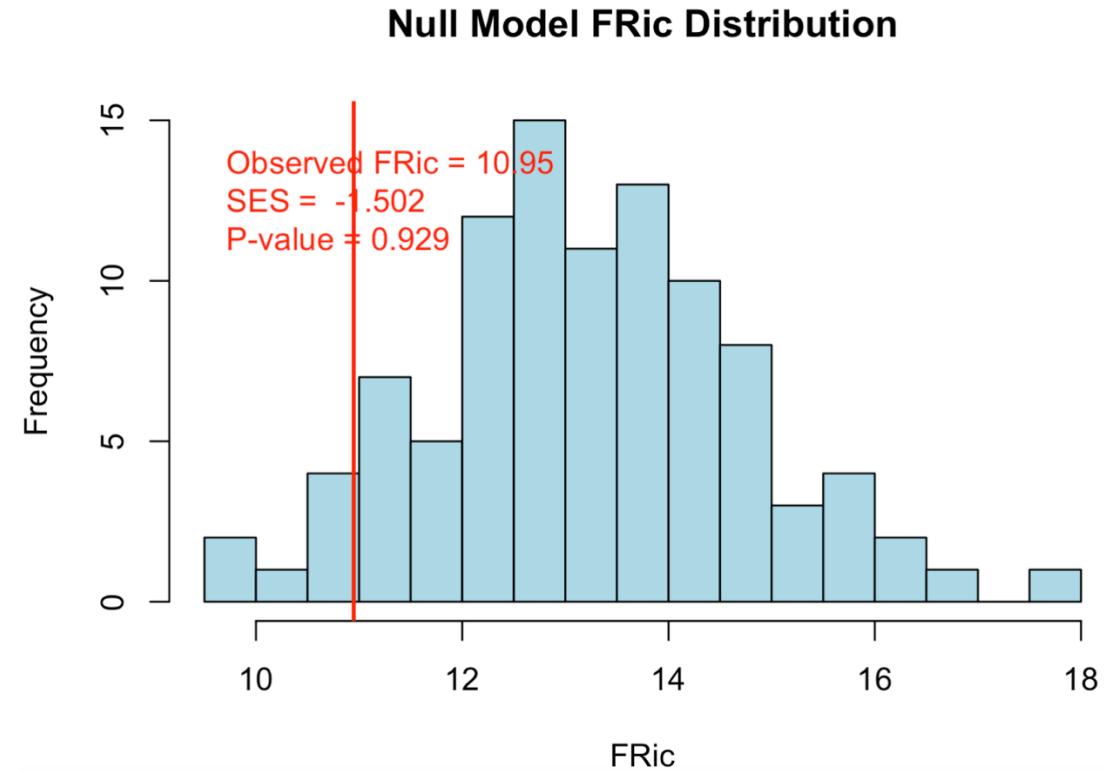
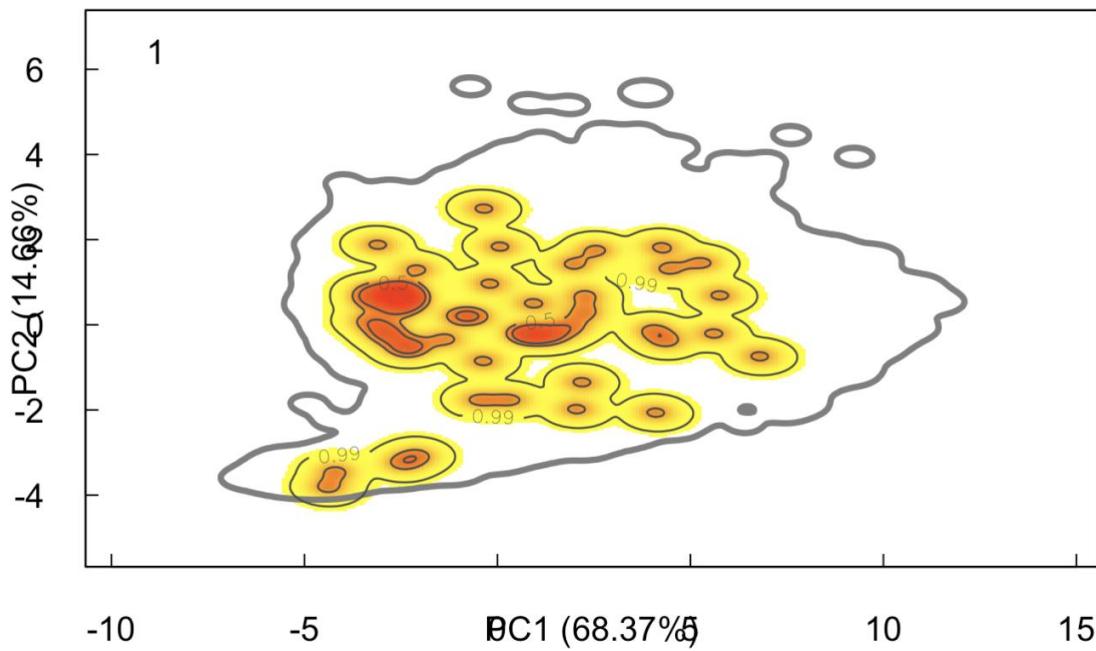
# Null model

- 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

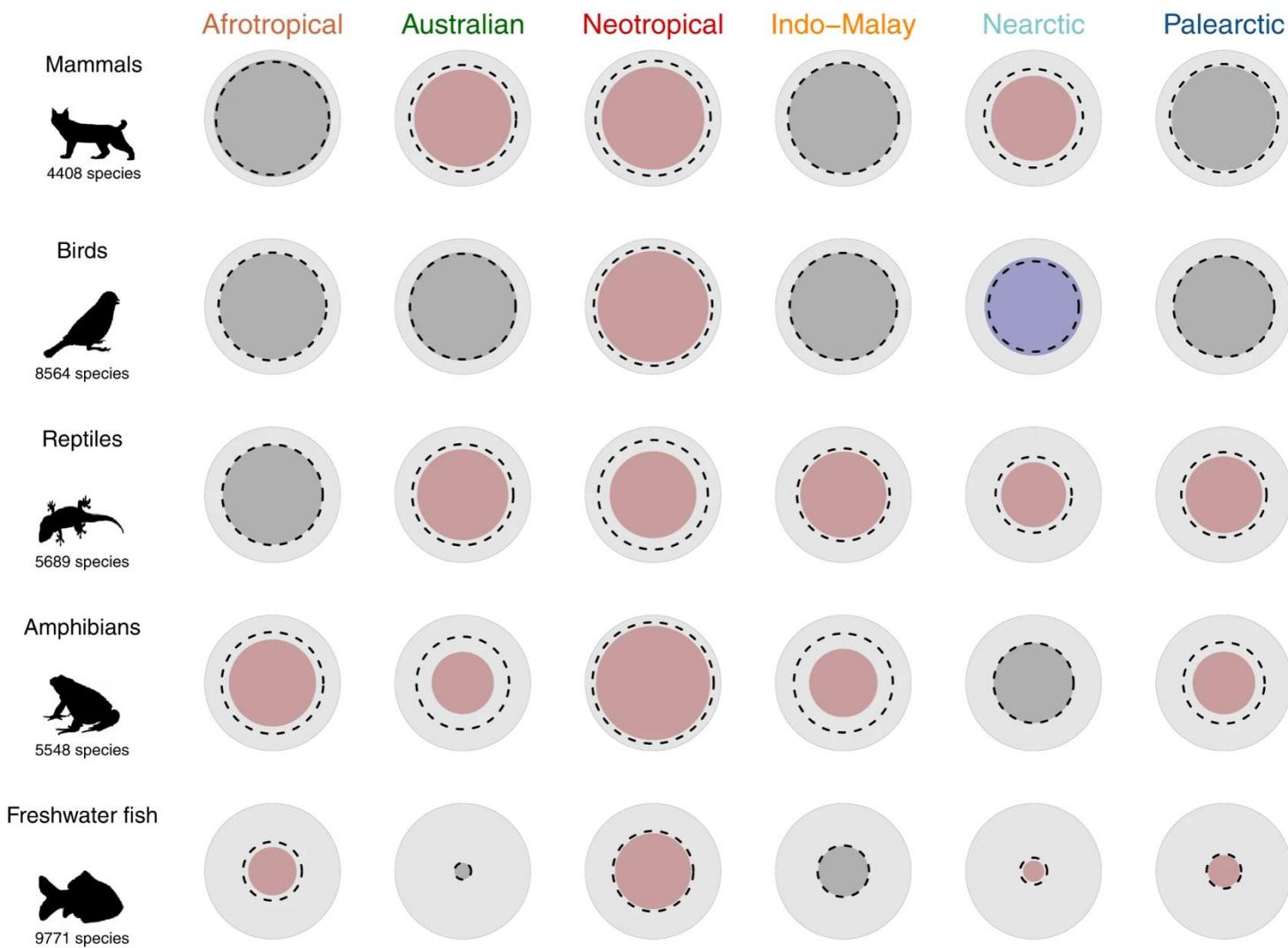
$$SES = (FD_{Obs} - \text{Mean}(FD_{Simul})) / \text{SD}(FD_{Simul})$$

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

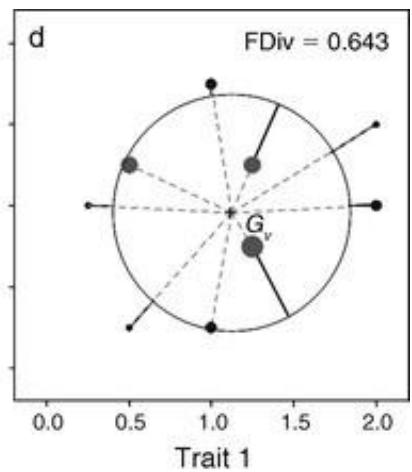
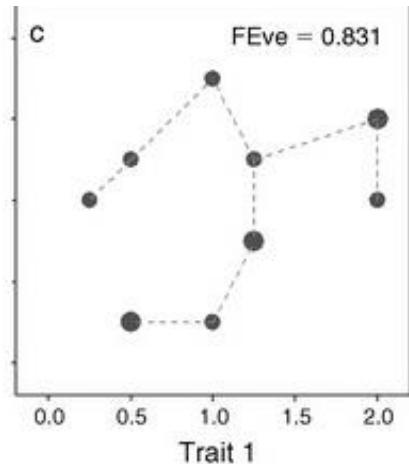
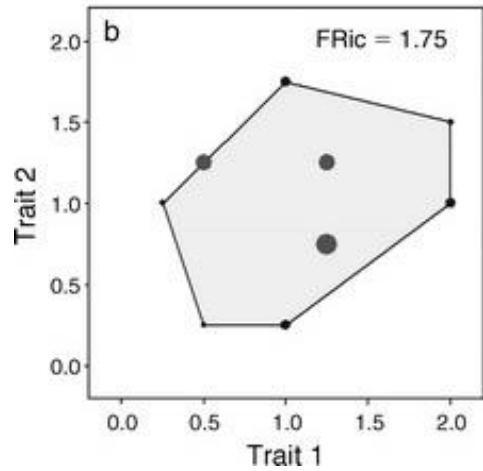
# Functional trait space and community



# Null model



# Different facets of functional diversity



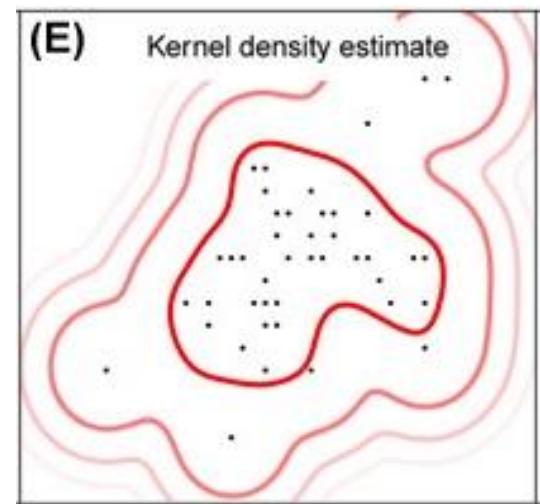
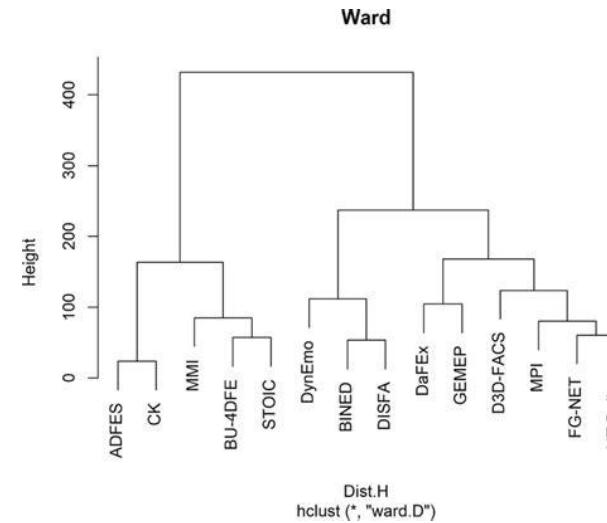
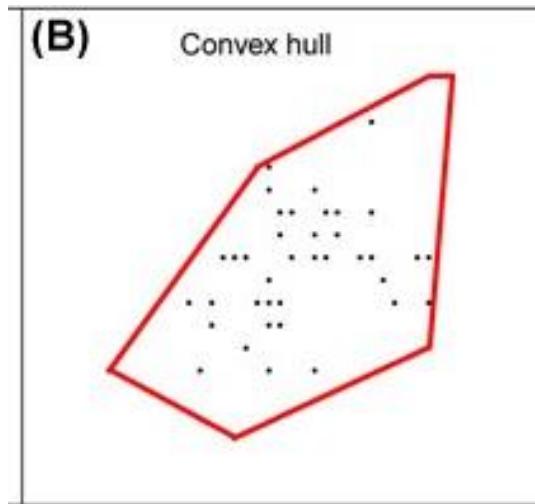
- **Functional Richness (FRic):** The range of trait values in a community, reflecting how much of the trait space is occupied.
- **Functional Evenness (FEve):** The regularity with which species traits are distributed across trait space.
- **Functional Divergence (FDiv):** The extent to which species traits differ from the average trait in a community, reflecting niche differentiation.

# Different approaches to calculate FD

**FD:** Describes the variety of functional traits in a community and how these traits affect ecosystem functioning.

**Common Metrics:** Convex hull (functional richness), functional evenness, functional divergence.

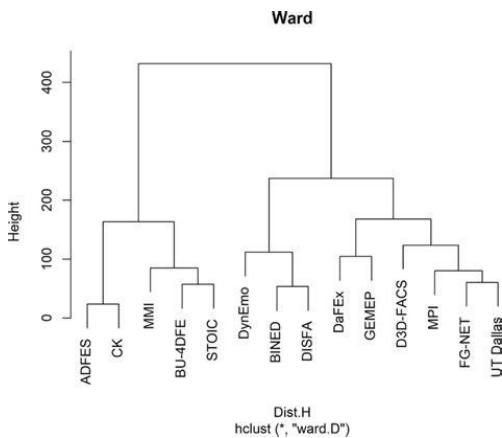
**Beyond Convex Hull:** Other methods like **Dendograms**, **Trait Probability Density (TPD)**, and **Hypervolumes** provide alternative ways to quantify FD.



# Different approaches to calculate FD

## Dendrogram-Based Quantification of FD

- **Definition:** A dendrogram represents species' trait similarities as hierarchical clusters, where branch lengths reflect trait differences.
- **FD as Branch Lengths:** The sum of branch lengths in the dendrogram represents functional diversity.
- **Advantages:** Good for hierarchical or clustered trait data, and allows visualization of trait relationships.



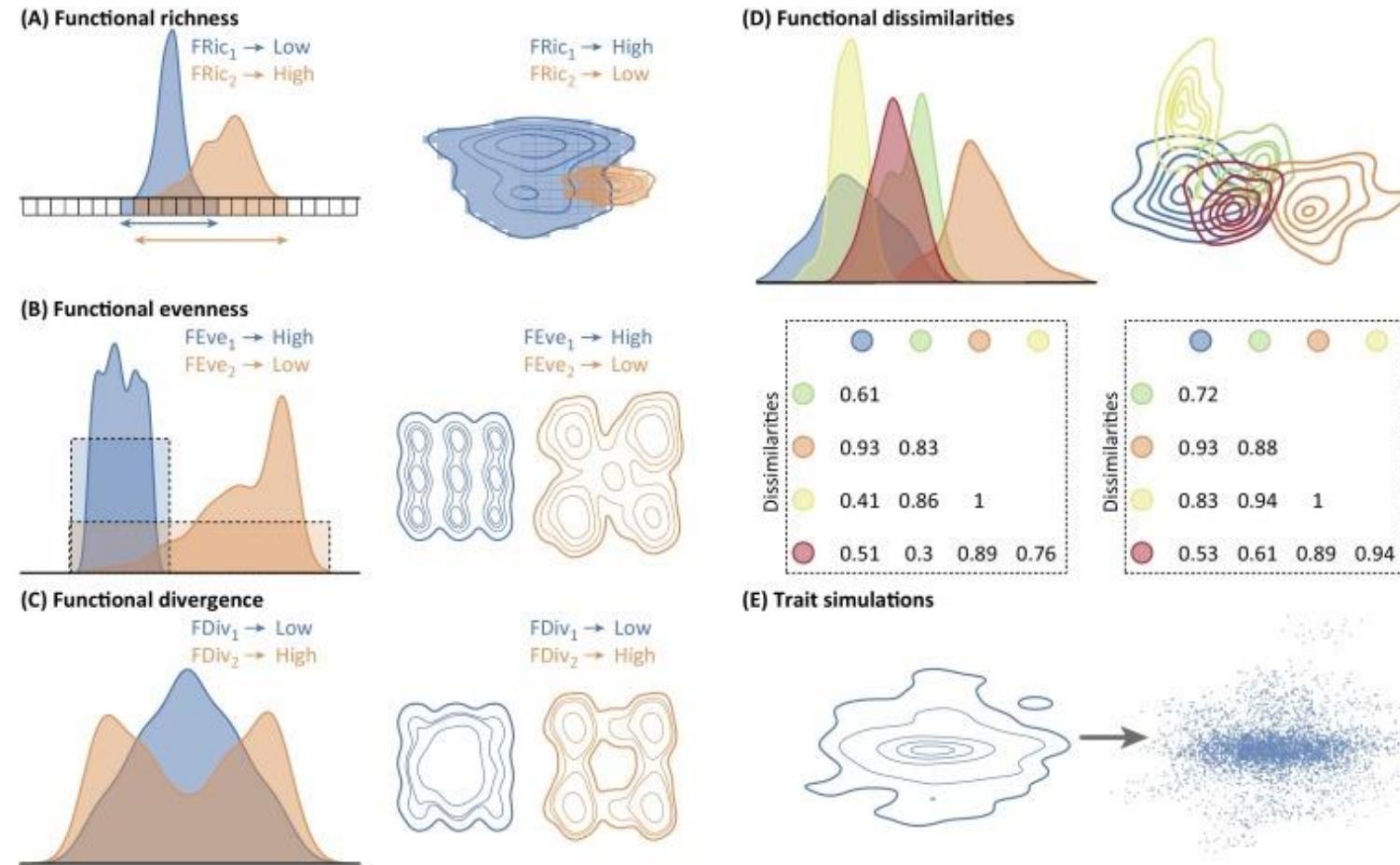
# Different approaches to calculate FD

## Dendrogram-Based Quantification of FD

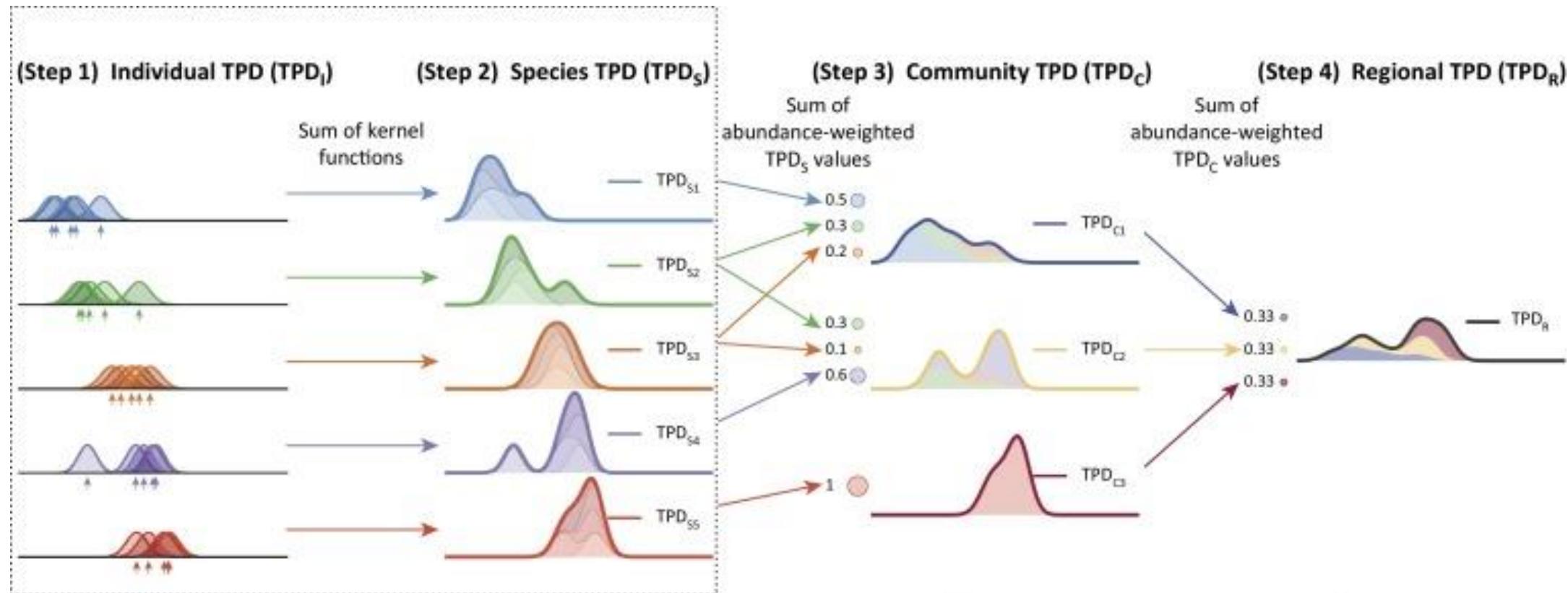
## Trait Probability Density (TPD) Approach

- **Definition:** TPD quantifies FD by estimating the probability distribution of trait values in a community.
- **Probability Distribution:** Each species contributes to the overall trait distribution based on its abundance and trait variation.
- **Advantages:** Captures intra-specific trait variation and the probability of encountering different traits in the community.

# Different approaches to calculate FD



# Different approaches to calculate FD



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

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

# Different approaches to calculate FD

- **Convex Hull:** Simple, but does not account for species abundance or trait distributions.
- **Dendrogram:** Hierarchical, useful for visualizing trait relationships, but may oversimplify trait complexity.
- **Trait Probability Density:** Accounts for abundance and intra-specific trait variation, but requires more complex estimation.

# **Application**

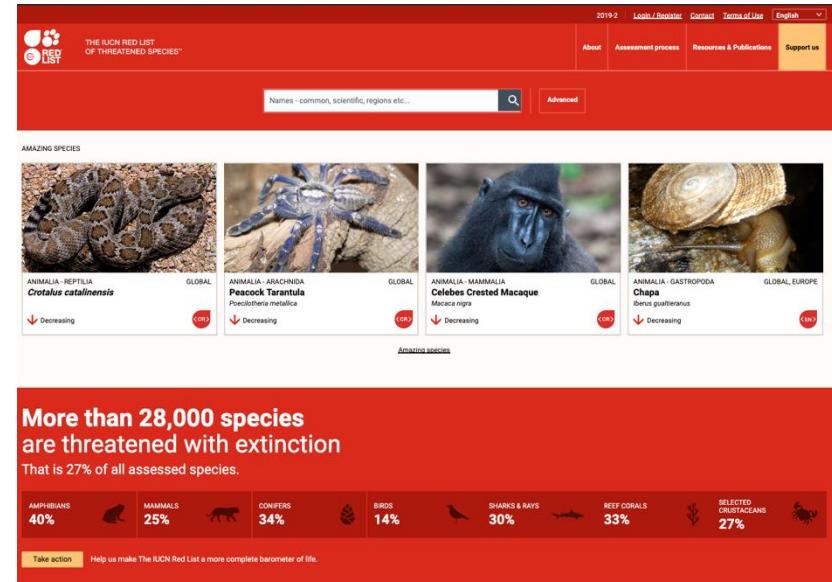
# Causes of extinction

## Low abundance

- Isolation
- Allee effect

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

## Species conservation strategies



# Causes of extinction

## Low abundance

- Isolation
- Allee effect

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

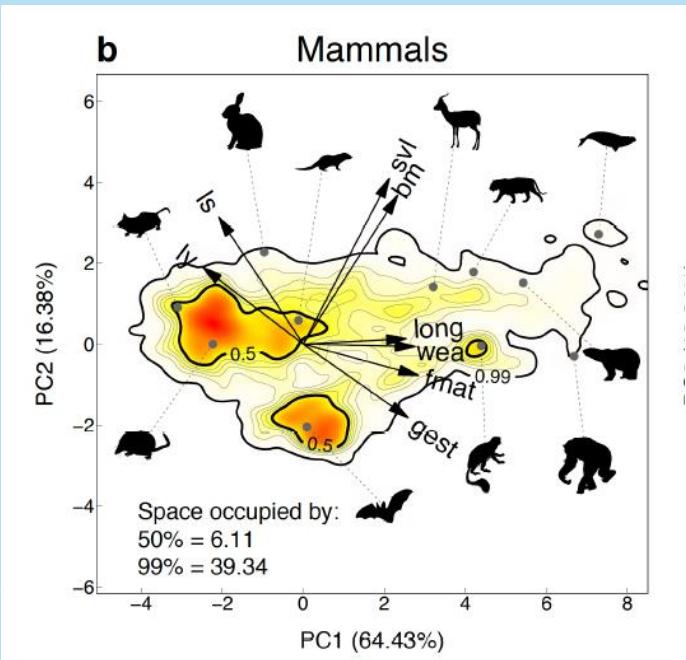
## Species-specific risk

- Traits
- Phylogenetic

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

# Causes of extinction

## Traits

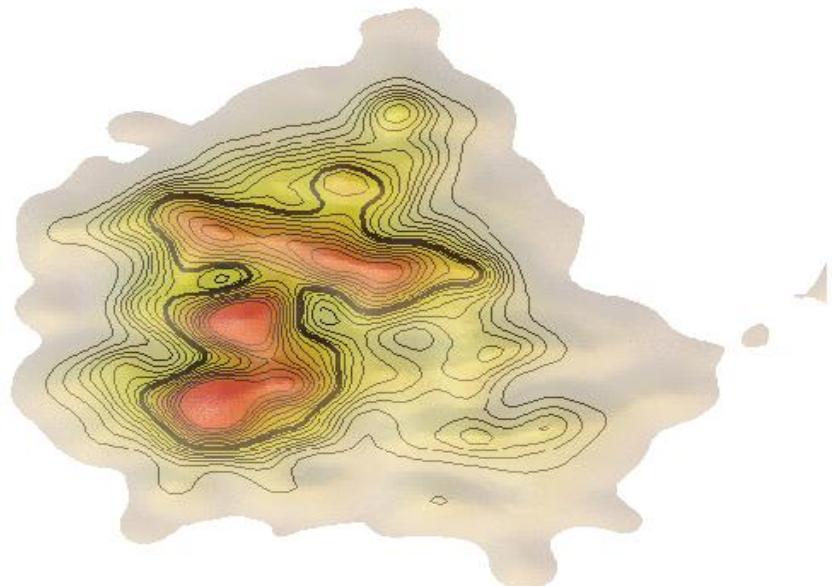


## IUCN Red List



# Causes of extinction

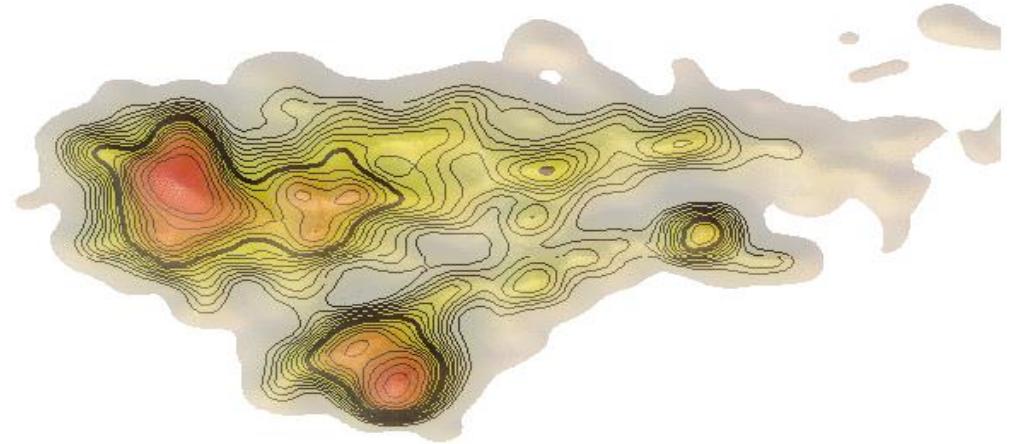
Amphibians



Spectrum before extinctions

Spectrum after extinctions

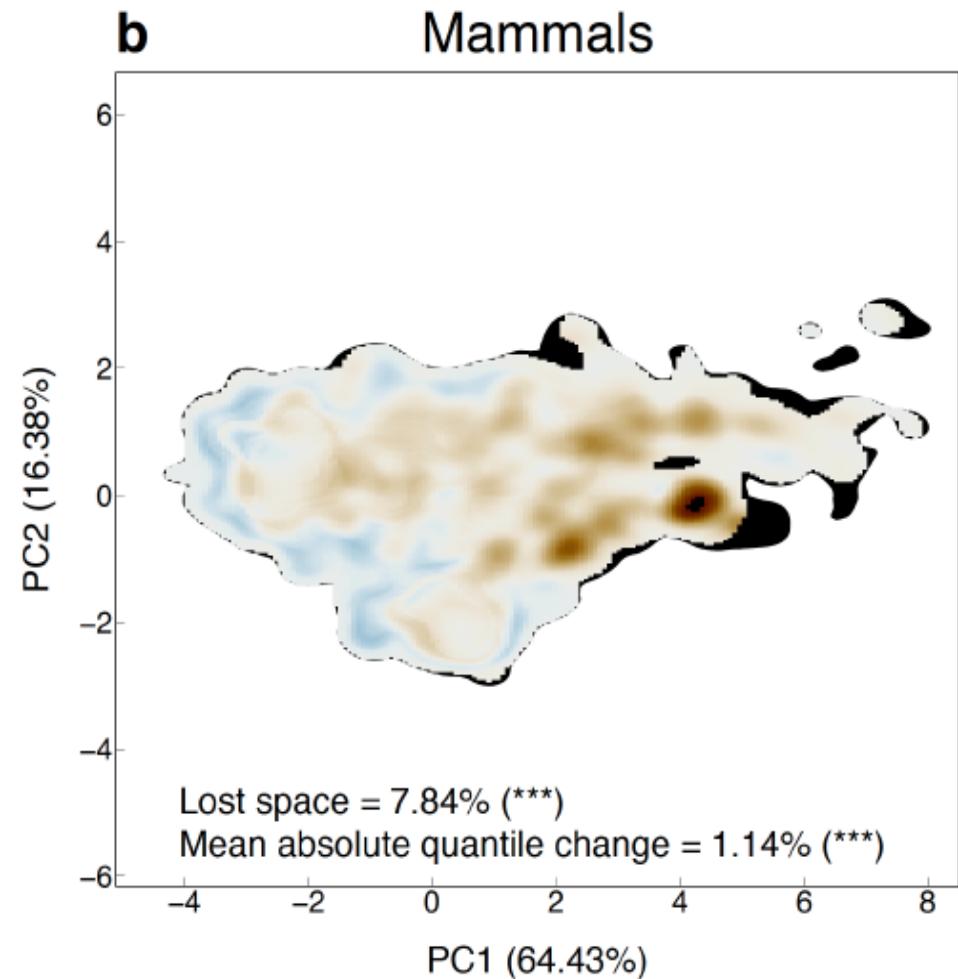
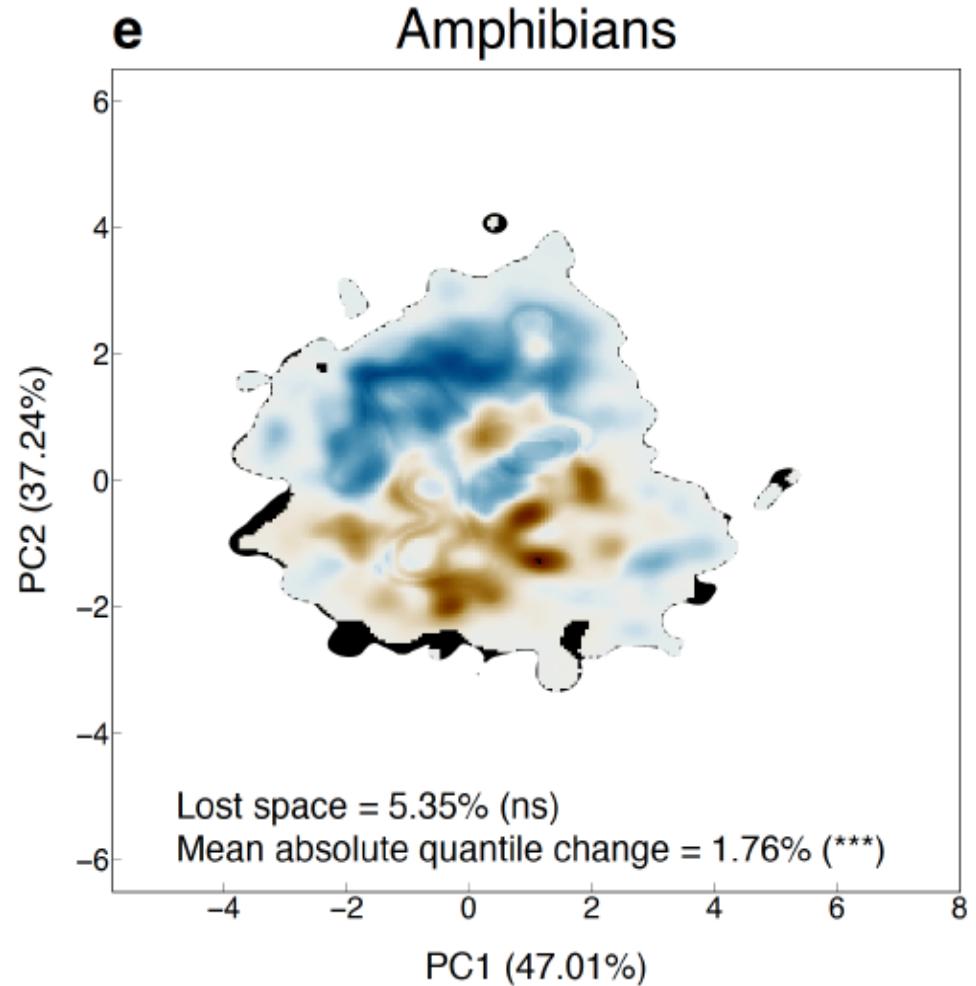
Mammals



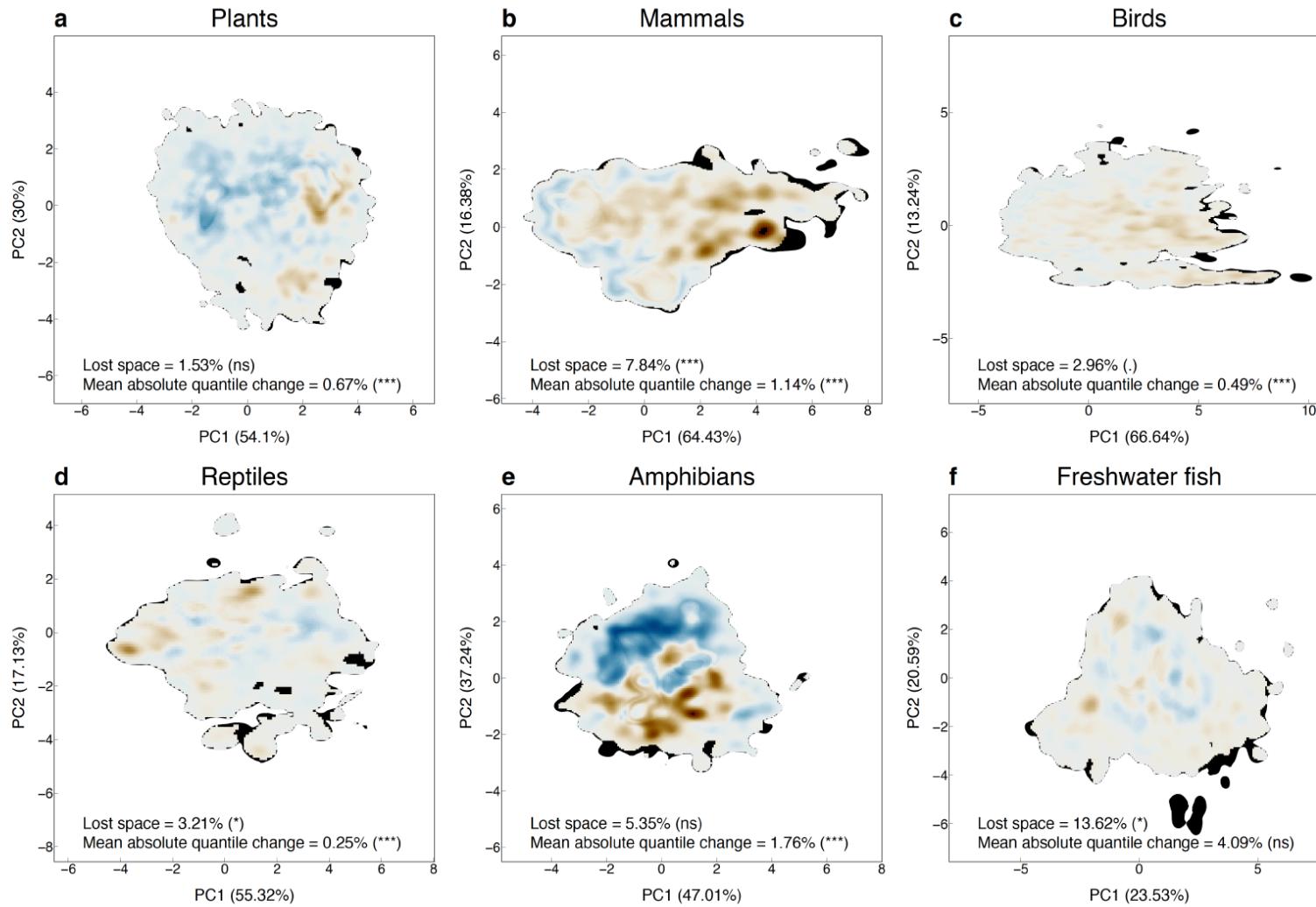
Spectrum before extinctions

Spectrum after extinctions

# Causes of extinction



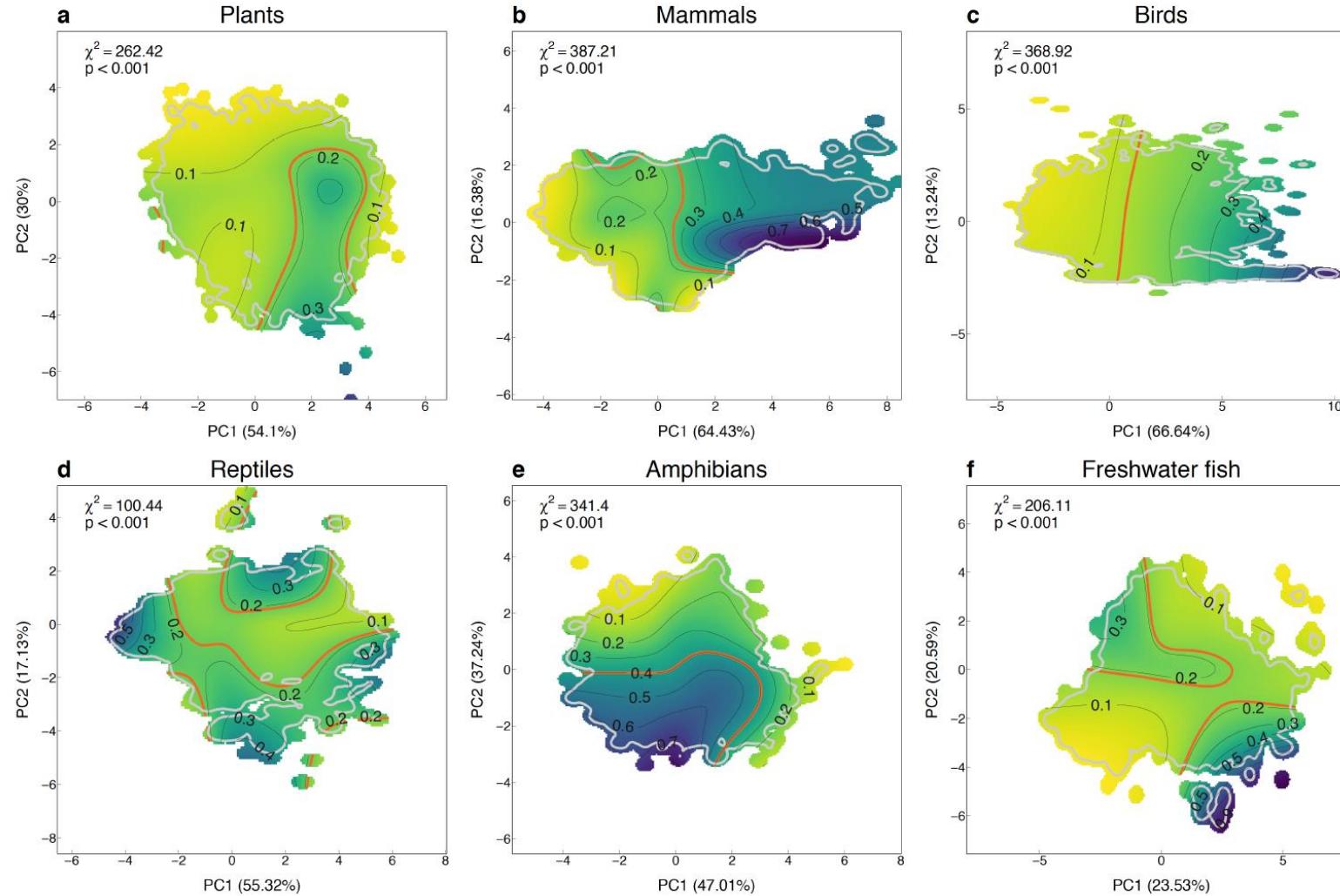
# *Global spectra of 6 terrestrial groups*



## Changes in functional spectra

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

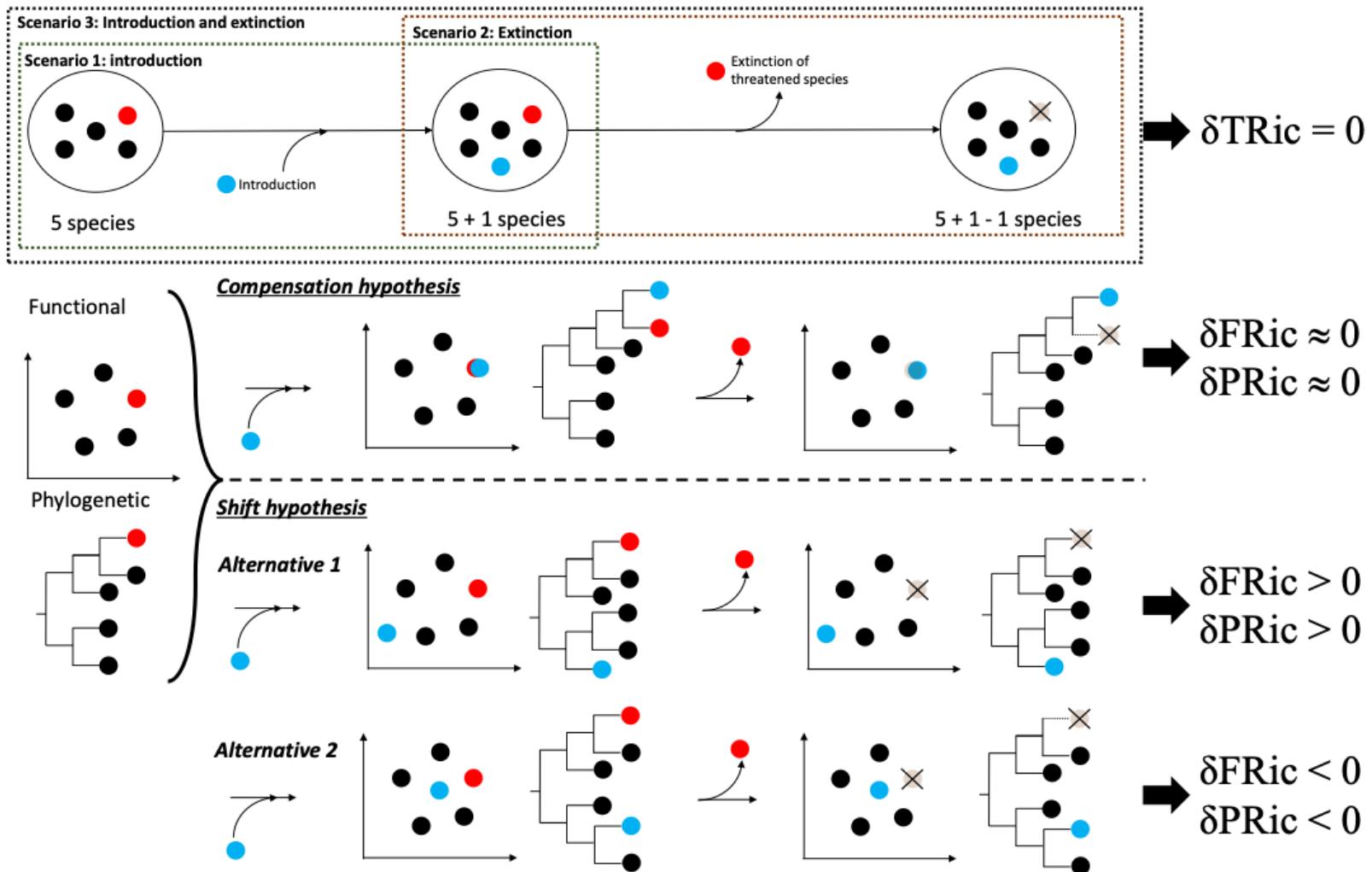
# *Global spectra of 6 terrestrial groups*



## Threatened species

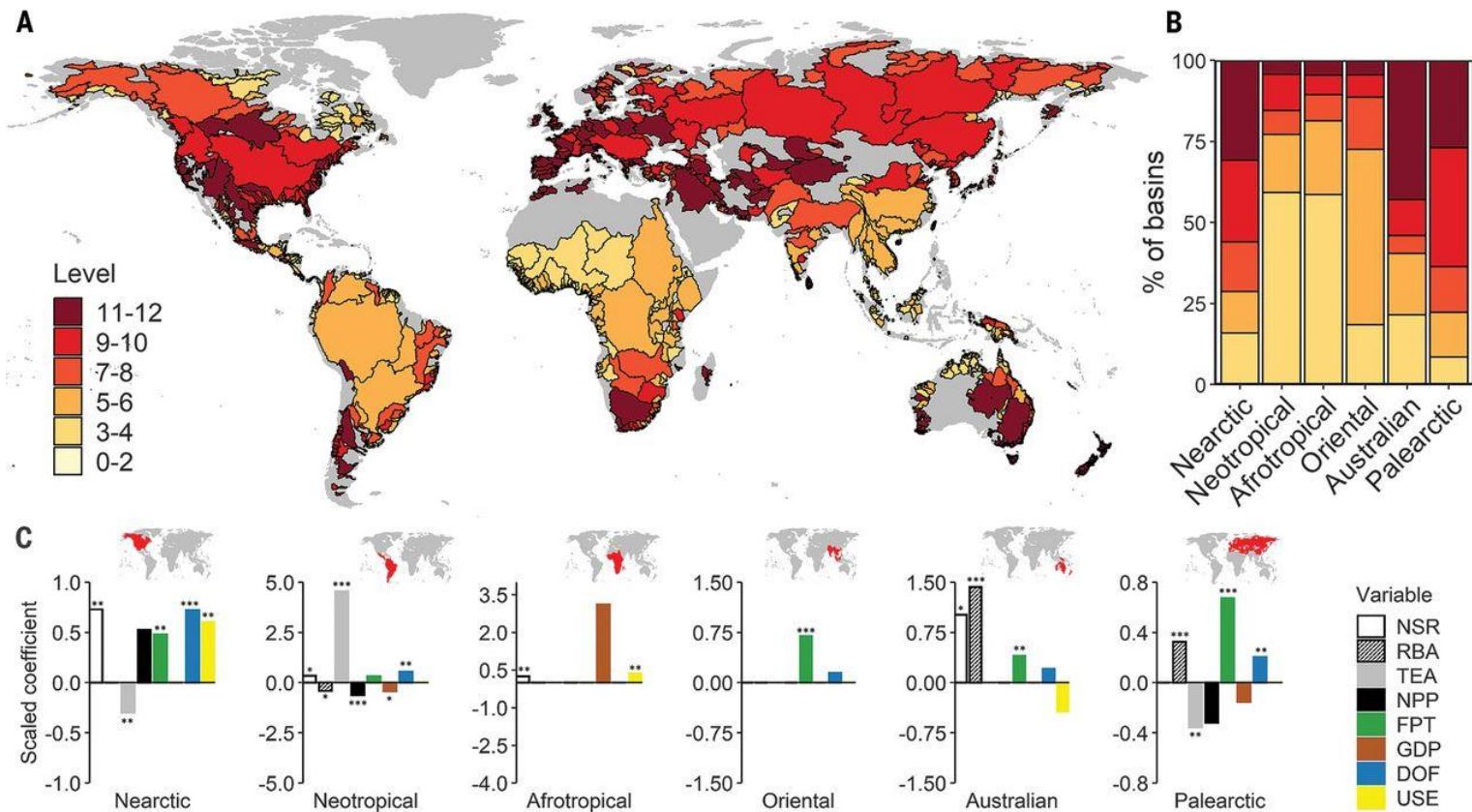
- Large
- “Slow” pace of life
- Low fecundity
- Up to 8x difference in threat risk
- High variability

# Introduction/extinction

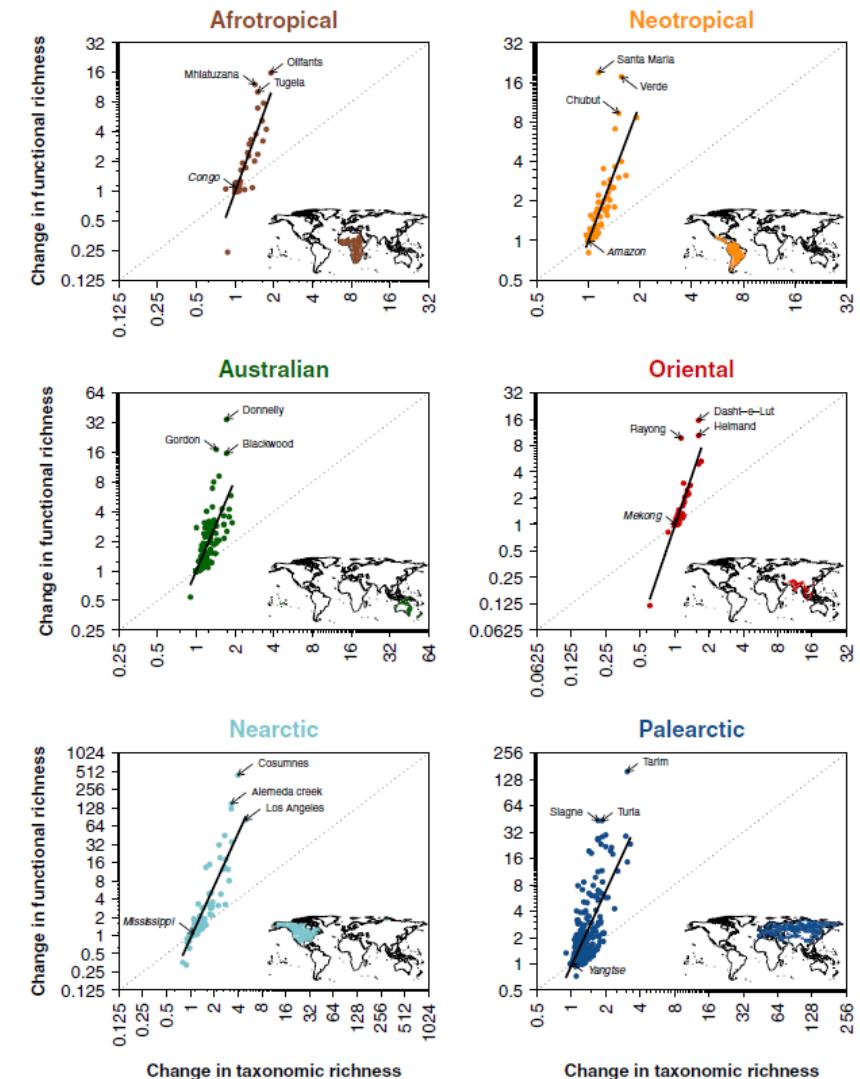


# Introduction/extinction

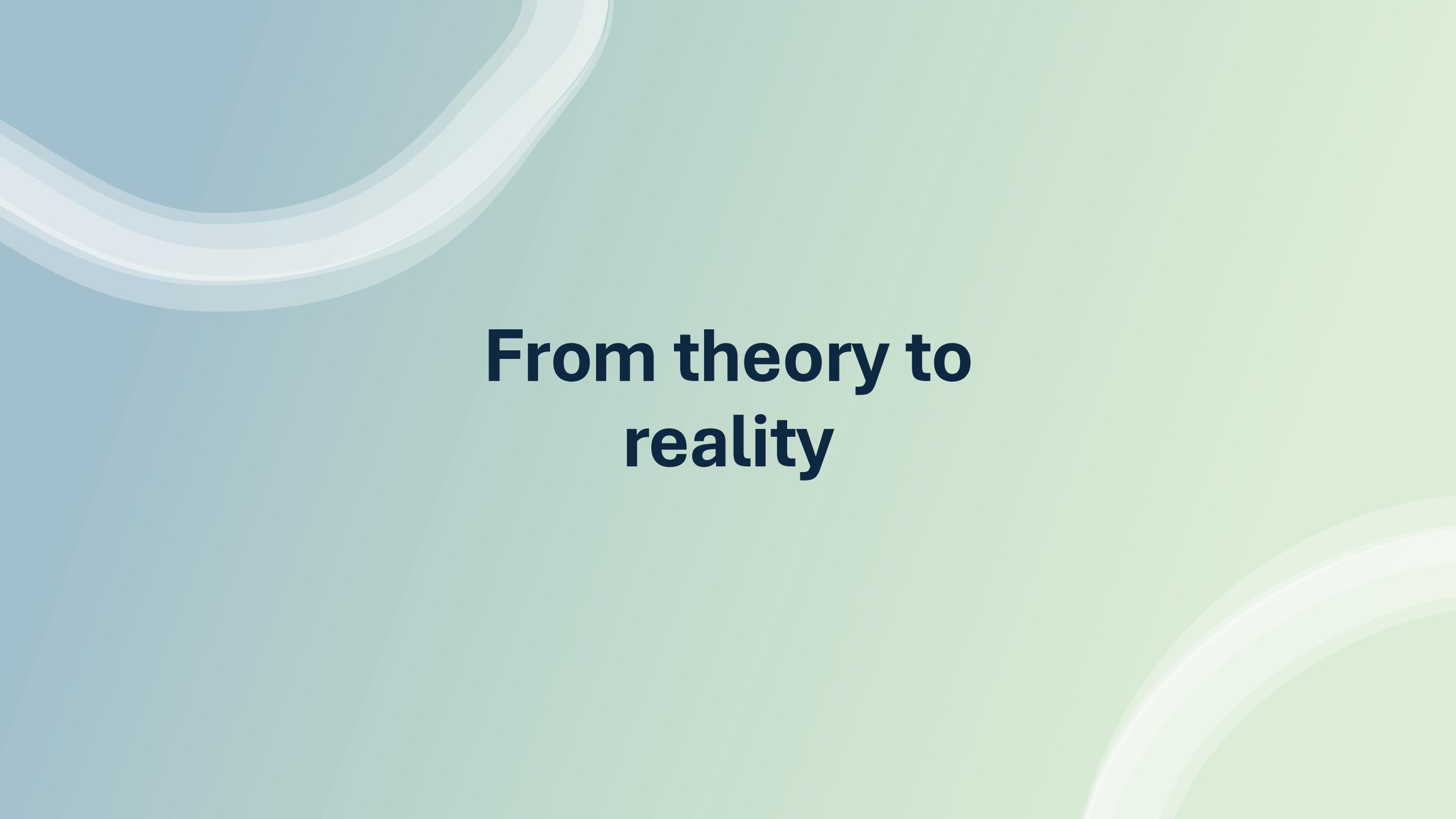
Non-native species are functional distinct than native species



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

# 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

# Mammals: Imputation values



- Six life-history traits
- IUCN Threatened species

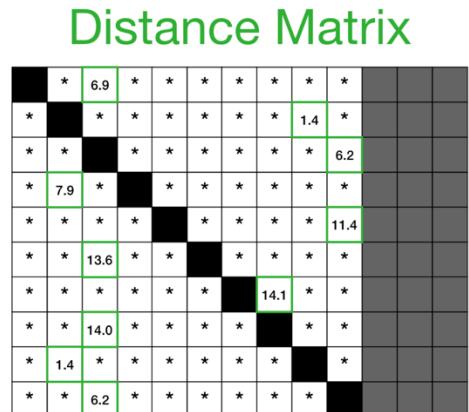
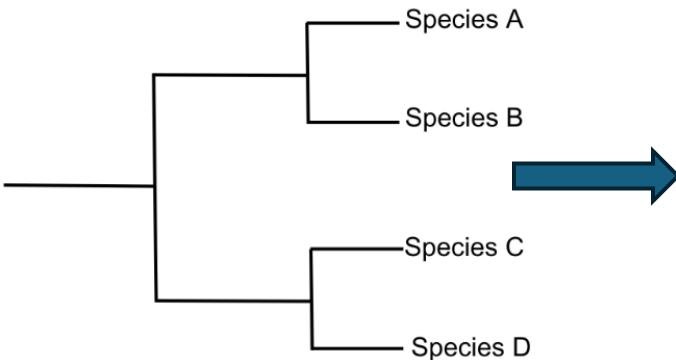
- NA: values not measured
- Remove sp.
  - Impute values

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

# Mammals: Imputation values



- Using phylogenetic data
  - Hypotheses: Closely related species shared similar functional traits.



PCA

	Eigen.3	Eigen.4	Eigen.5	Eigen.6
1	-1.251688	-0.1279389	-0.2622112	-0.2561482
2	-1.251641	-0.1279329	-0.2621959	-0.2561324
3	-1.251610	-0.1279288	-0.2621855	-0.2561217
4	-1.251635	-0.1279320	-0.2621937	-0.2561301
5	-1.251652	-0.1279342	-0.2621993	-0.2561359
6	-1.249919	-0.1277099	-0.2616278	-0.2555446
7	-1.251567	-0.1279232	-0.2621714	-0.2561070
8	-1.250120	-0.1277360	-0.2616944	-0.2556135
9	-1.250804	-0.1278245	-0.2619200	-0.2558469
10	-1.250205	-0.1277470	-0.2617224	-0.2556425
11	-1.250488	-0.1277836	-0.2618157	-0.2557390
12	-1.250289	-0.1277578	-0.2617501	-0.2556711
13	-1.249404	-0.1276433	-0.2614583	-0.2553692
14	-1.249873	-0.1277040	-0.2616128	-0.2555291

10 first eigenvalues

This analysis is time consuming; Already done in the dataset

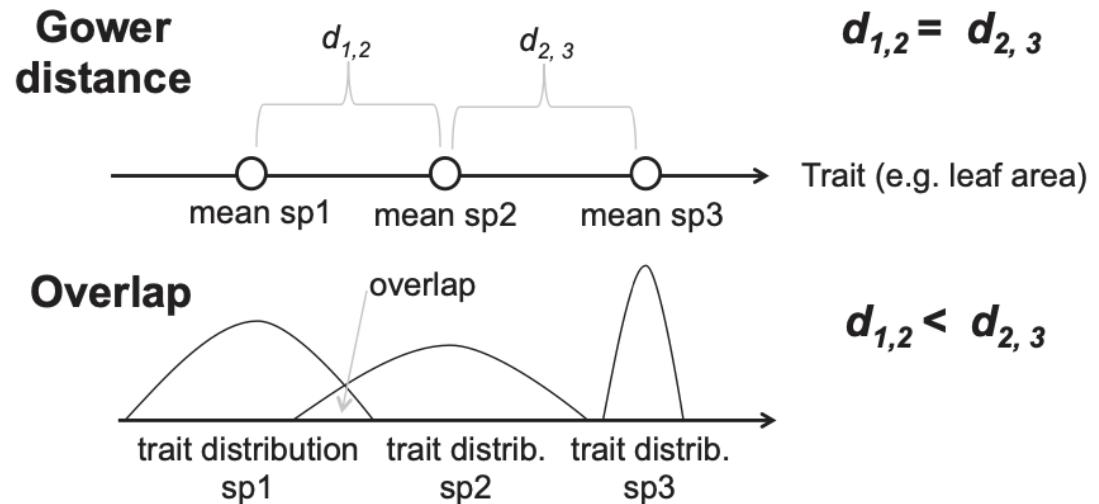
# Fish: Intra specific variability



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

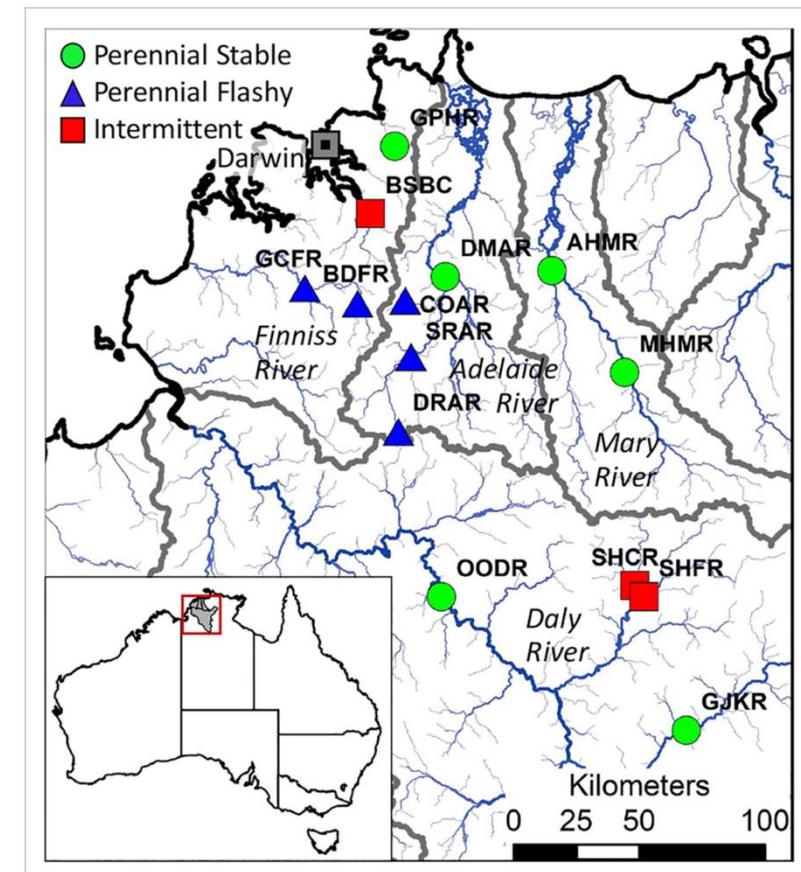


# Fish: Intra specific variability



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



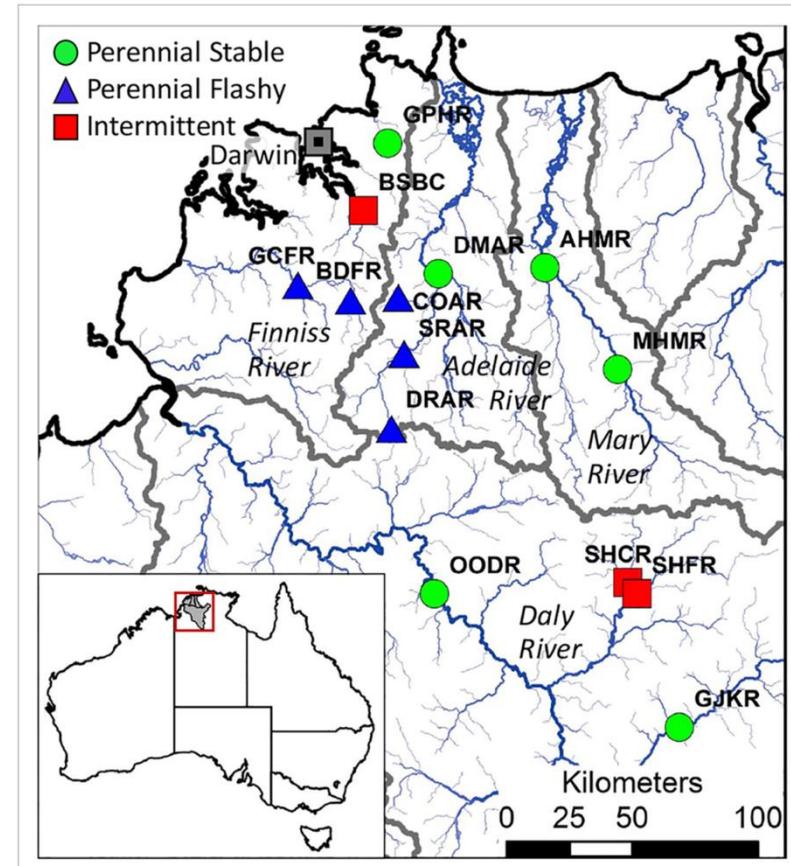
Code	Name	Protocol for measurement
Bl	Body length	Standard length (snout-to-caudal fin basis)
Bd	Body depth	Maximum body depth
Hd	Head depth	Head depth at the vertical of eye
CPd	Caudal peduncle depth	Minimum depth of the caudal peduncle
CFd	Caudal fin depth	Maximum depth of the caudal fin
Ed	Eye diameter	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 <sup>2</sup> )	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



**Let's go !**

# 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