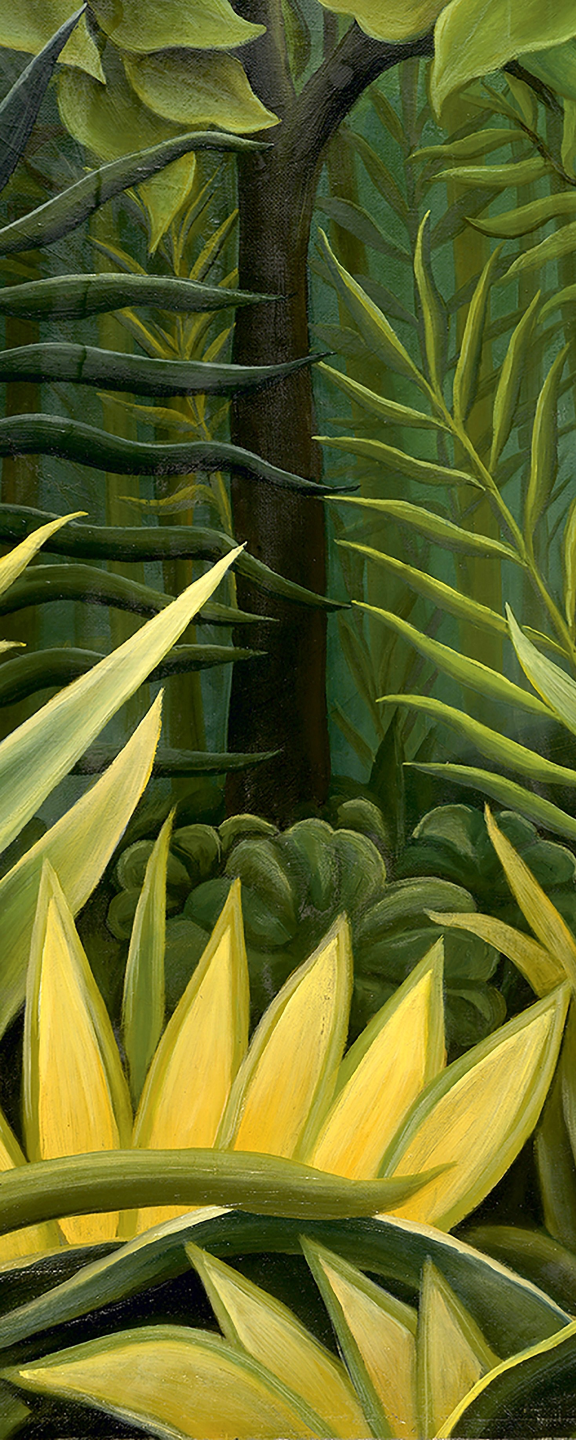

Quantifying functional diversity in community ecology

François Rigal
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Data accessibility

https://github.com/frigal001

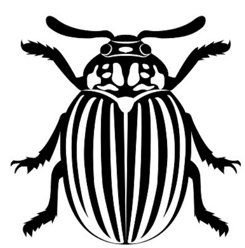
Plan

1. Basic definitions & statistical units
2. Functional diversity metrics
3. Overview of the current FD frameworks
4. Type of traits & distances
5. Study cases and R packages
6. Trait-based community assembly & null models

1. Basic definitions & statistical units

« Functional traits are morphological and phenological characteristics of an organism or species that express aspects of its ecological strategy, scale up from individuals to properties of populations, communities and ecosystems, and can be used to quantify dimensions of ecological variation across organisms, populations, species, communities and ecosystems ».

In Schrader et al., 2021. A roadmap to plant functional island biogeography. Biological Reviews.



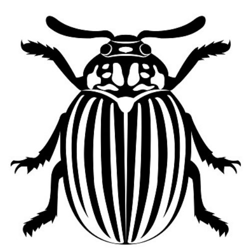
1. Basic definitions & statistical units

Functional diversity is the extent of functional differences among the species in a community.

Functional diversity of a community is the multidimensional space defined by the functional traits of the constituent species.

Functional diversity is the diversity component measuring the diversity of organism characteristics that relates to their interactions with their abiotic and biotic environment.

From Tilman, D. (2001). Functional diversity. Encyclopedia of biodiversity; Petchey, O. L., & Gaston, K. J. (2006). Functional diversity: back to basics and looking forward. Ecology letters; Pollock, L. J., O'connor, L. M., Mokany, K., Rosauer, D. F., Talluto, M. V., & Thuiller, W. (2020). Protecting biodiversity (in all its complexity): new models and methods. Trends in Ecology & Evolution.



1. Basic definitions & statistical units

Island functional diversity is an emerging discipline with a great potential to close the gap between the study of **species characteristics** and **island biogeography**.

Functional biogeography of oceanic islands and the scaling of functional diversity in the Azores

Robert J. Whittaker[a,b,1], François Rigal[c], Paulo A.V. Borges[c], Pedro Cardoso[c,d,e], Sofia Terzopoulou[c,f], Fernando Casanoves[g], Laura Pla[h], François Guilhaumon[c,i], Richard J. Ladle[a,j], and Kostas A. Triantis[a,c,f]

Drouetus borgesi (Azores)

SCIENCE ADVANCES | RESEARCH ARTICLE

ECOLOGY

Loss of functional diversity through anthropogenic extinctions of island birds is not offset by biotic invasions

Ferran Sayol[1,2,3]*, Robert S. C. Cooke[2,3,4], Alex L. Pigot[1], Tim M. Blackburn[1,5], Joseph A. Tobias[6], Manuel J. Steinbauer[7], Alexandre Antonelli[2,3,8,9], Søren Faurby[2,3]

Hawaiian finches

RESEARCH ARTICLE

Global Ecology and Biogeography A Journal of Macroecology WILEY

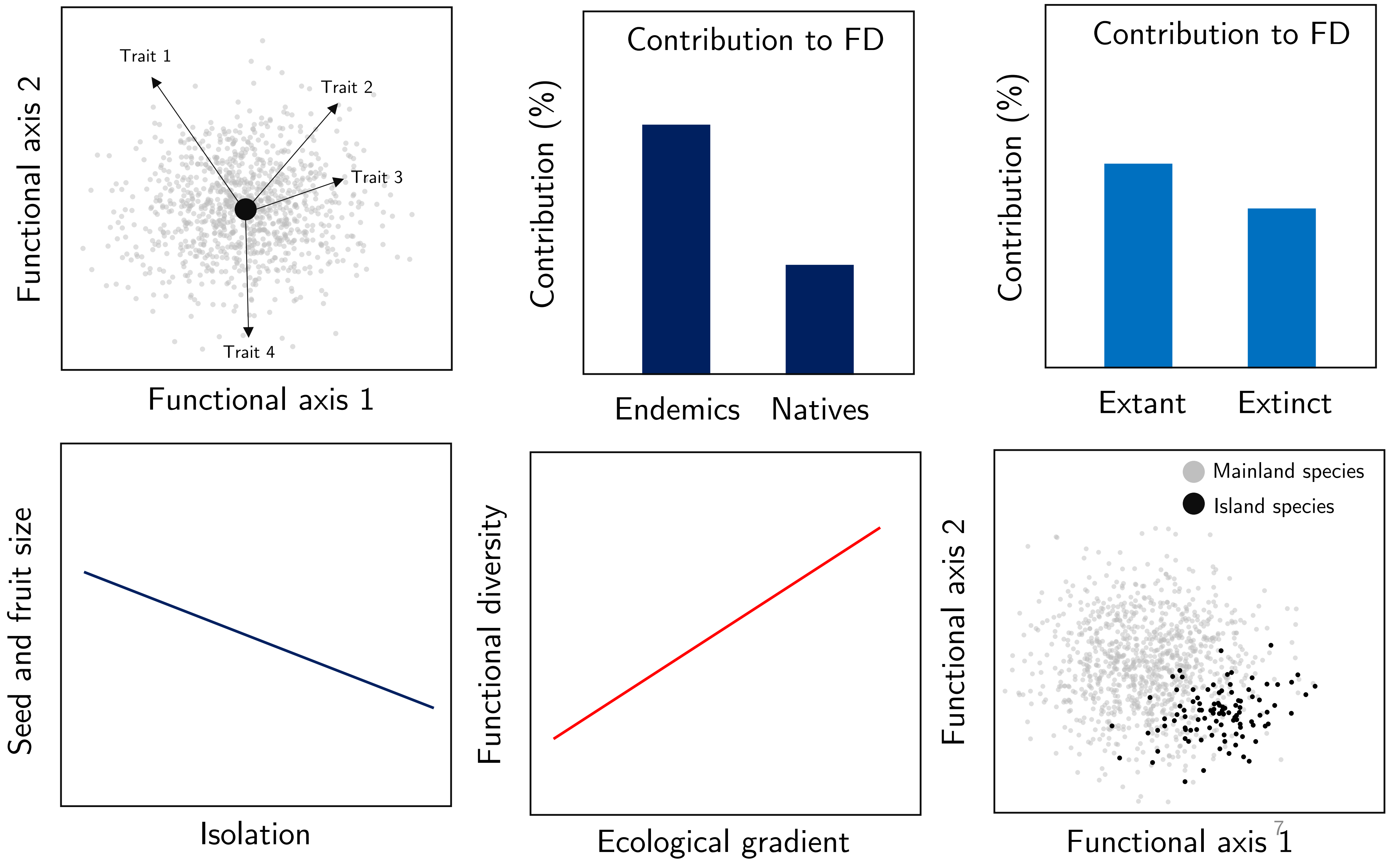
Climatic and biogeographical drivers of functional diversity in the flora of the Canary Islands

Dagmar M. Hanz[1] | Vanessa Cutts[2] | Martha Paola Barajas-Barbosa[3,4,5] | Adam C. Algar[6] | Carl Beierkuhnlein[7,8,9] | José-María Fernández-Palacios[10] | Richard Field[2] | Holger Kreft[3] | Manuel J. Steinbauer[8,11,12] | Patrick Weigelt[3] | Severin D. H. Irl[1,8]

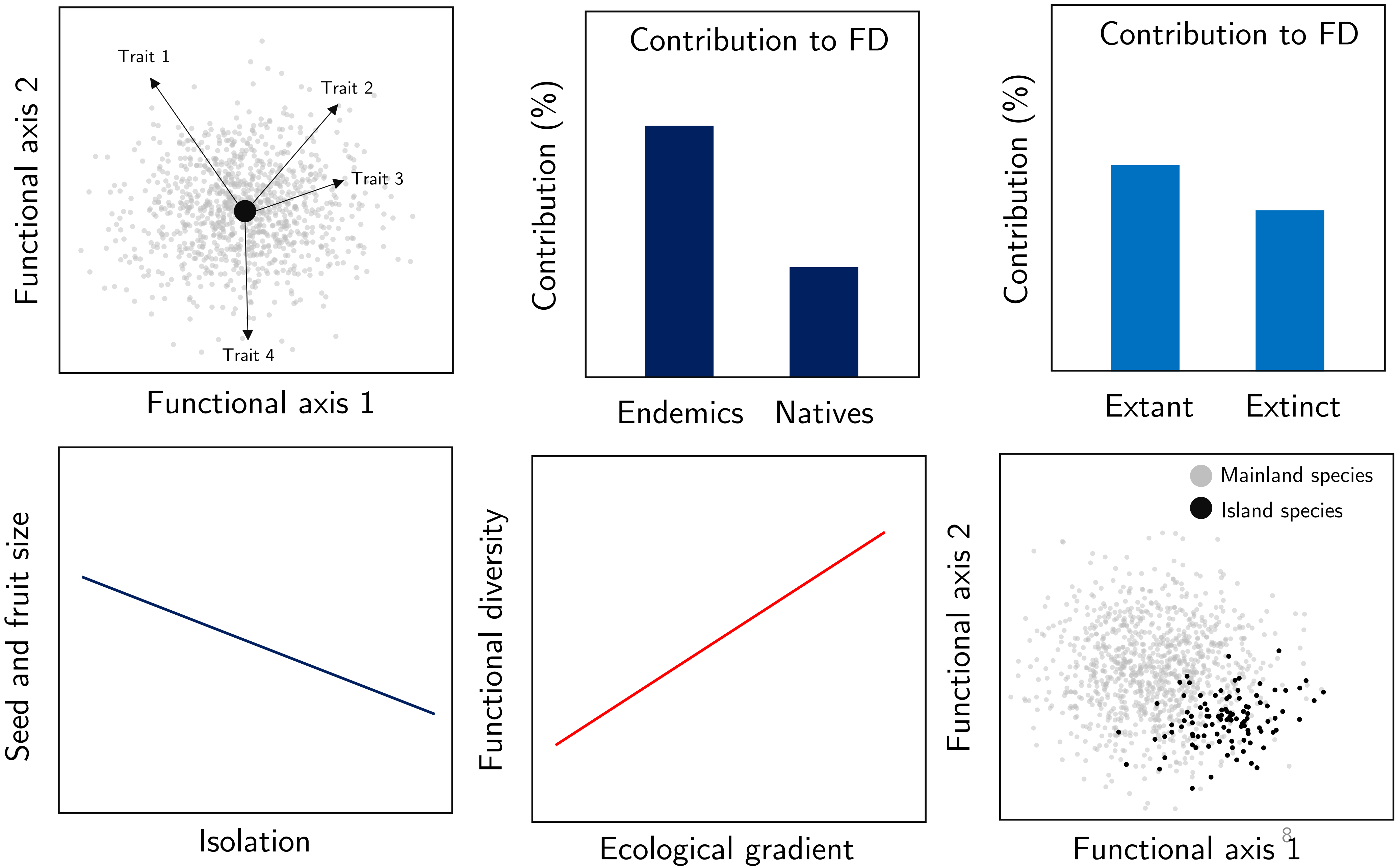
Echium (Canary Islands)

Schrader, J., Wright, I. J., Kreft, H., & Westoby, M. (2021). A roadmap to plant functional island biogeography. Biological Reviews, 96(6), 2851-2870.

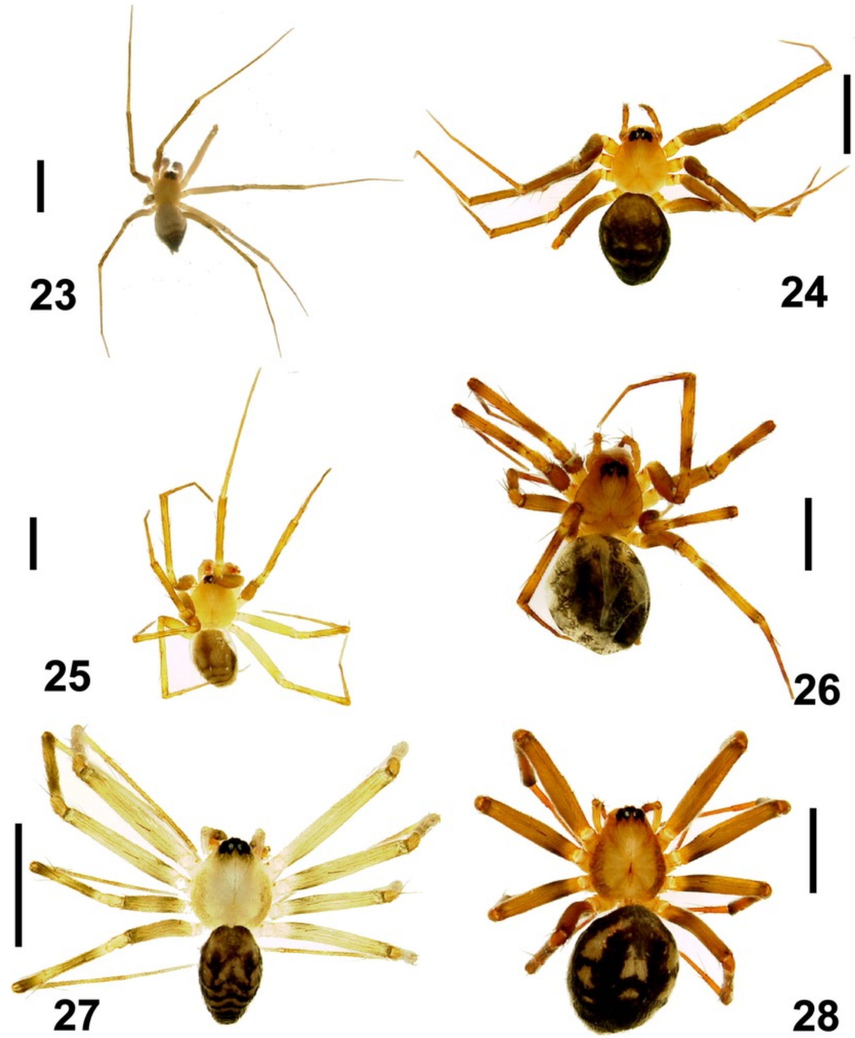
1. Basic definitions & statistical units



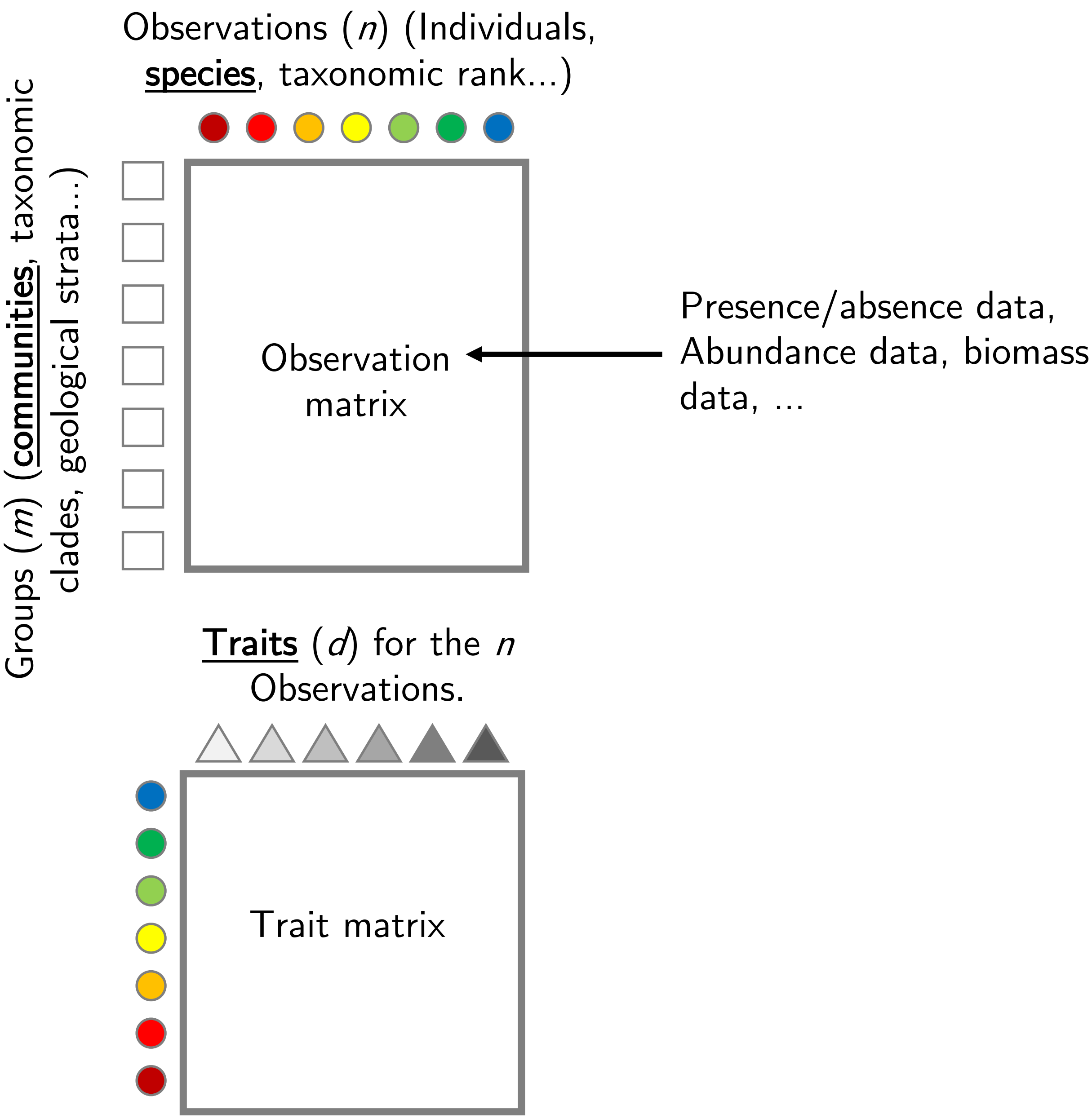
1. Basic definitions & statistical units



1. Basic definitions & statistical units

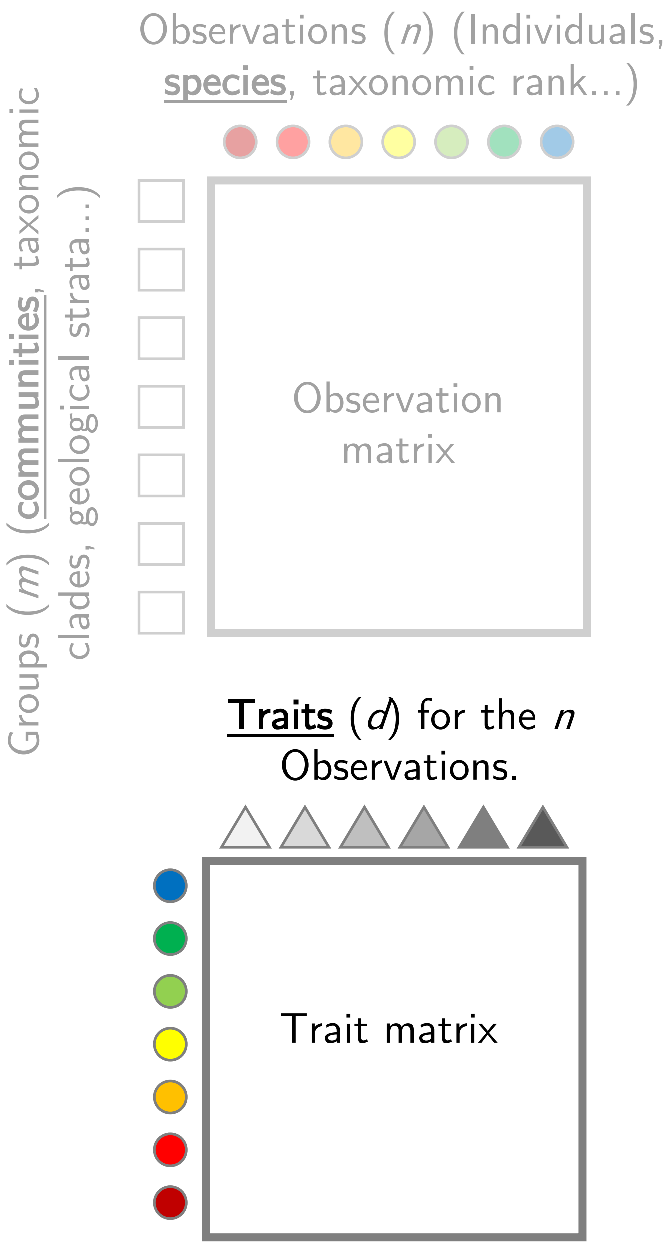


1. Basic definitions & statistical units

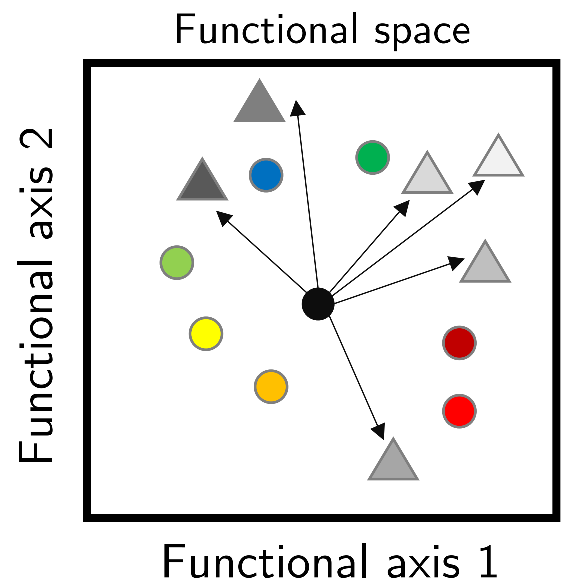


Mammola, S., Carmona, C. P., Guillerme, T., & Cardoso, P. (2021). Concepts and applications in functional diversity. *Functional Ecology*, *35*(9), 1869-1885.

1. Basic definitions & statistical units

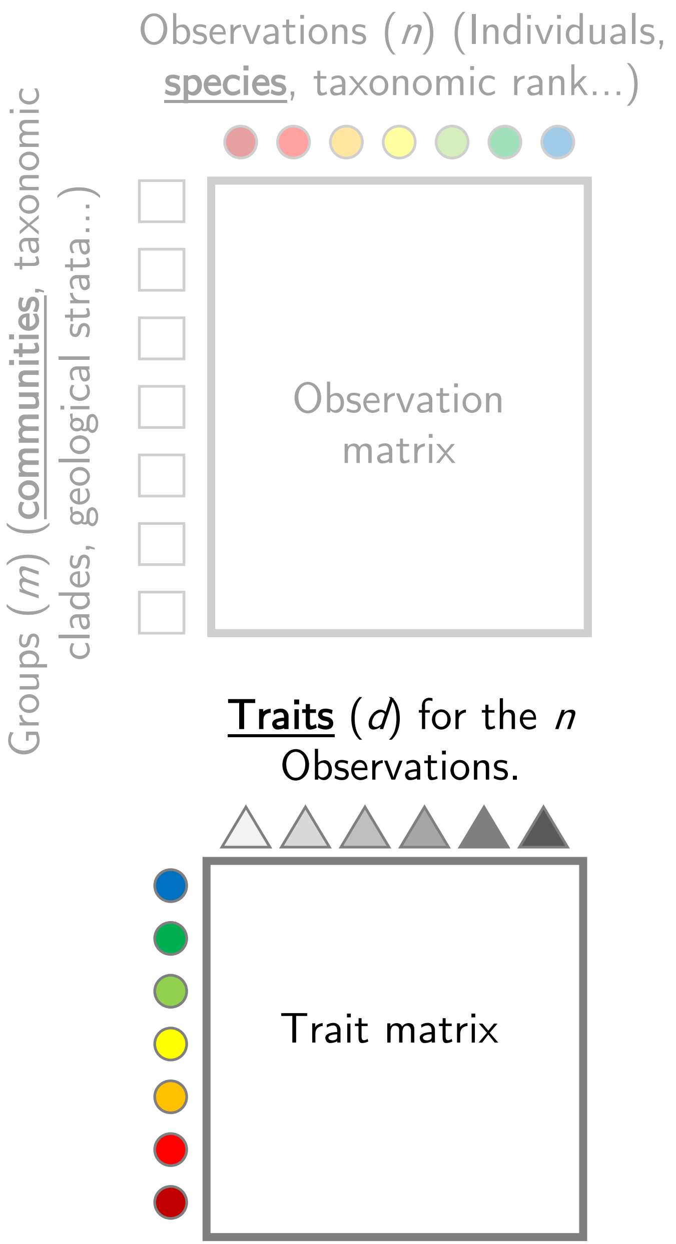


Functional space: Graphical visualisation of the trait matrix.



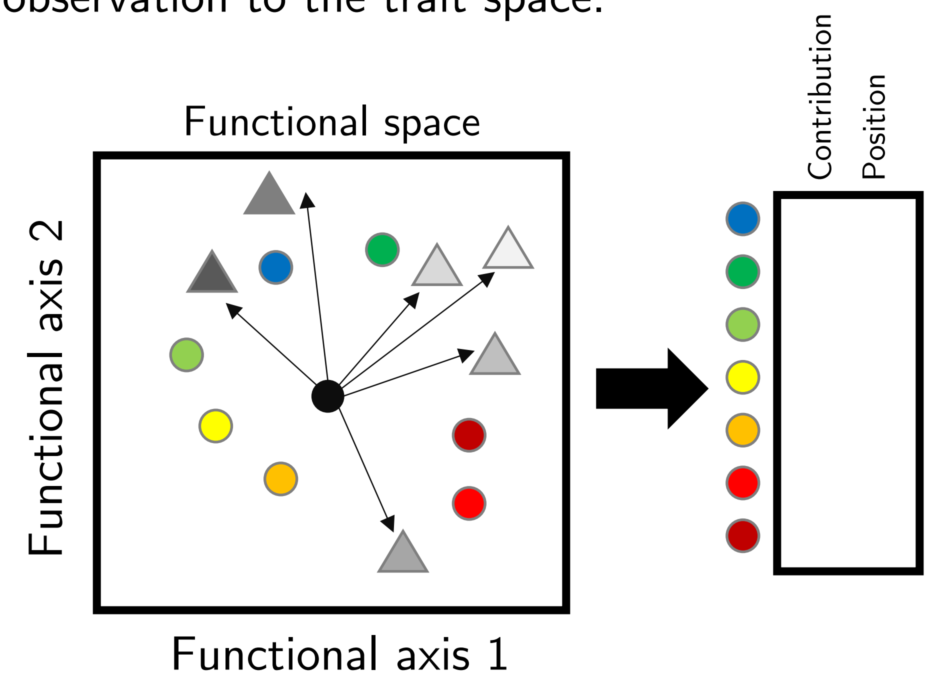
Mammola, S., Carmona, C. P., Guillerme, T., & Cardoso, P. (2021). Concepts and applications in functional diversity. *Functional Ecology*, *35*(9), 1869-1885.

1. Basic definitions & statistical units



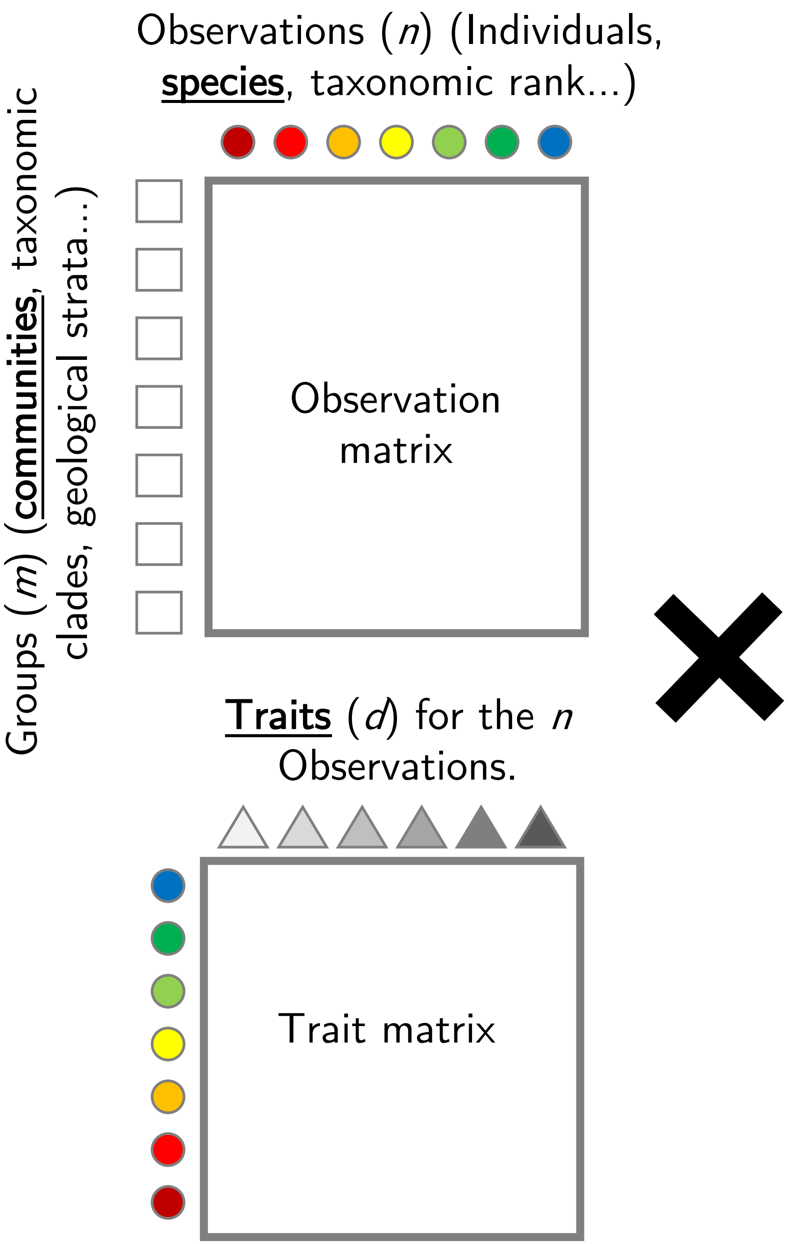
Functional metric: Index that attempts to summarise intrinsic features of the variation in the trait space.

A. Observation-based (**species-based**) metric: Index measuring the position and contribution of each observation to the trait space.



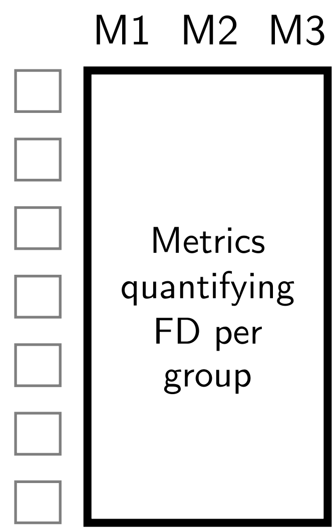
Mammola, S., Carmona, C. P., Guillerme, T., & Cardoso, P. (2021). Concepts and applications in functional diversity. *Functional Ecology*, *35*(9), 1869-1885.

1. Basic definitions & statistical units



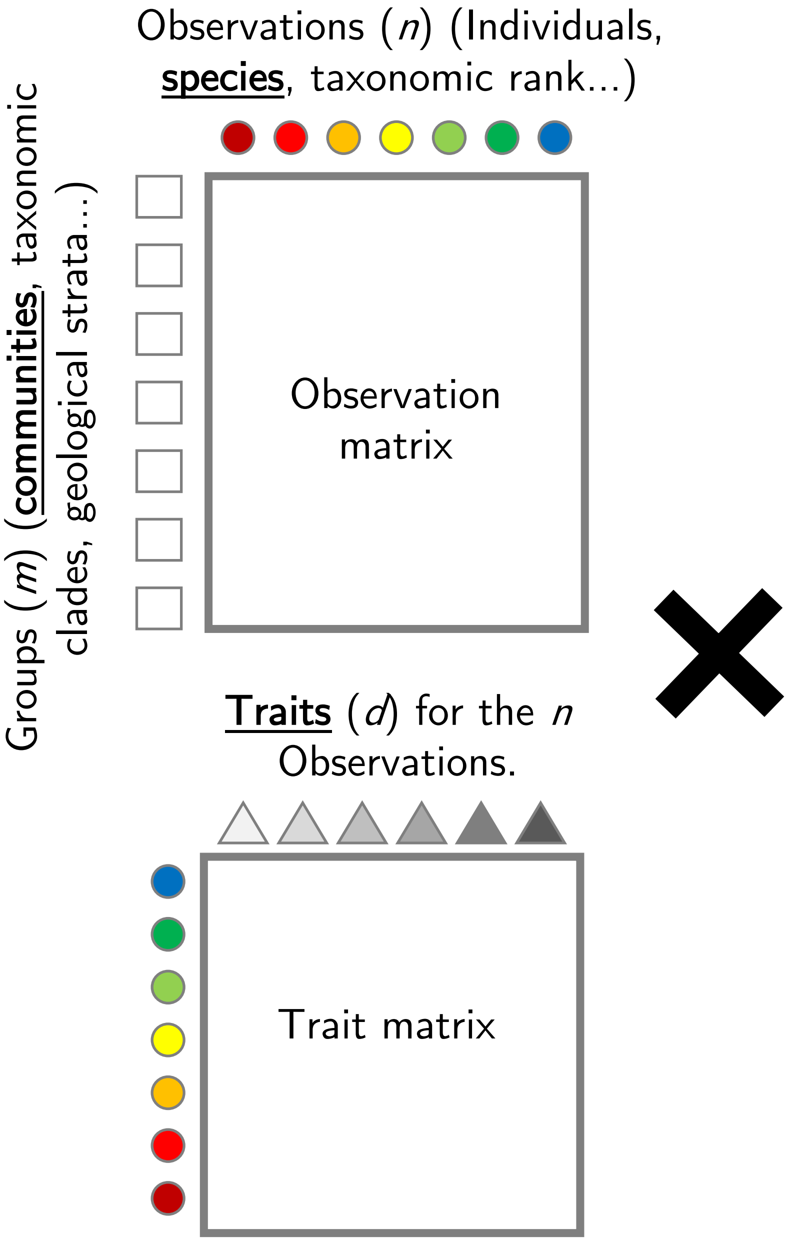
Functional metric: Index that attempts to summarise intrinsic features of the variation in the trait space.

B. Group-based (**community-based**) metric: Index measuring the variation in the trait space of each group.



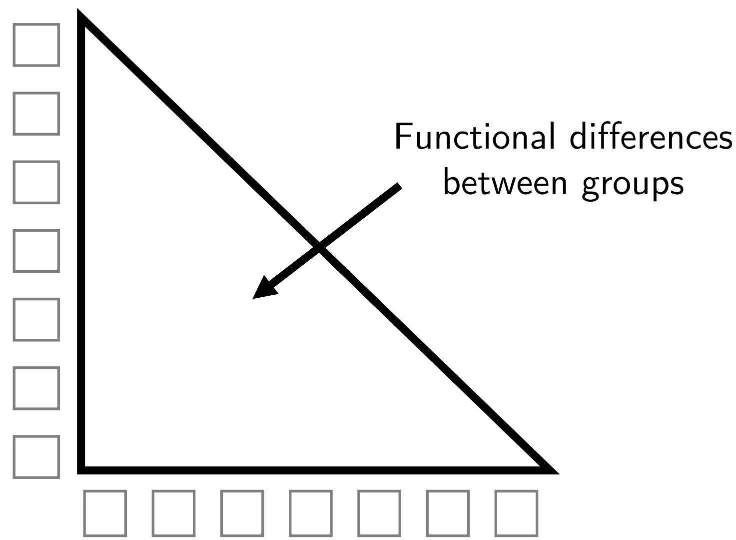
Mammola, S., Carmona, C. P., Guillerme, T., & Cardoso, P. (2021). Concepts and applications in functional diversity. *Functional Ecology*, *35*(9), 1869-1885.

1. Basic definitions & statistical units



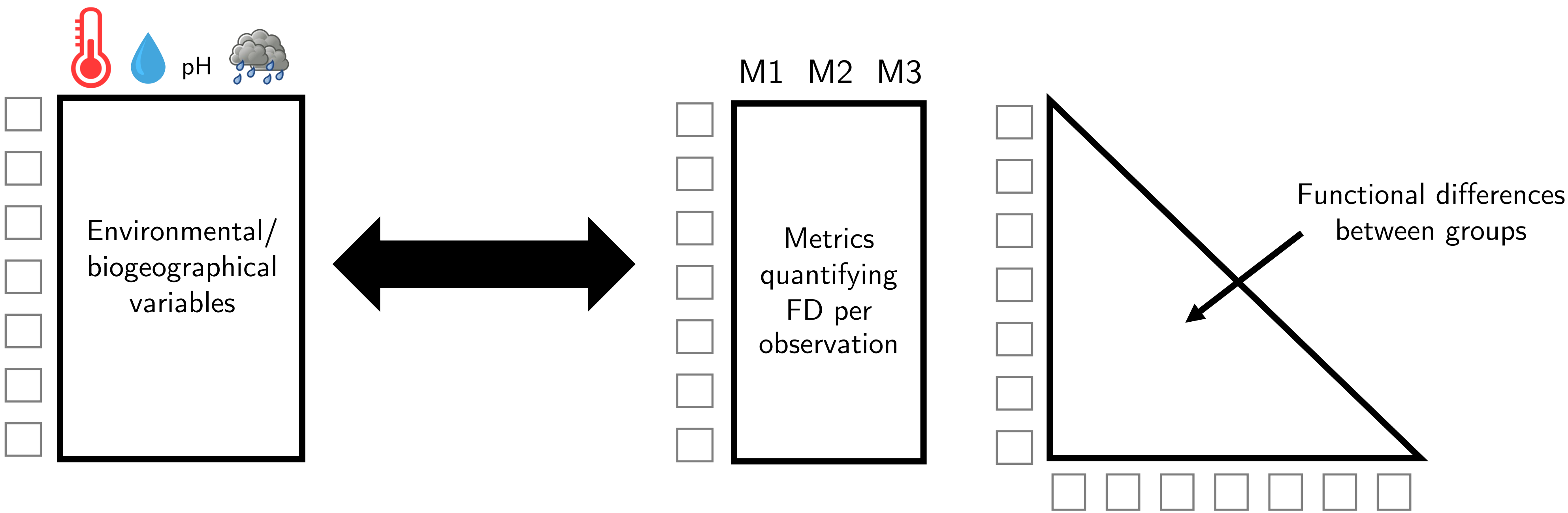
Functional metric: Index that attempts to summarise intrinsic features of the variation in the trait space.

A. Between groups based (**between community-based**) metrics: Index measuring differences in the trait space occupation between groups.



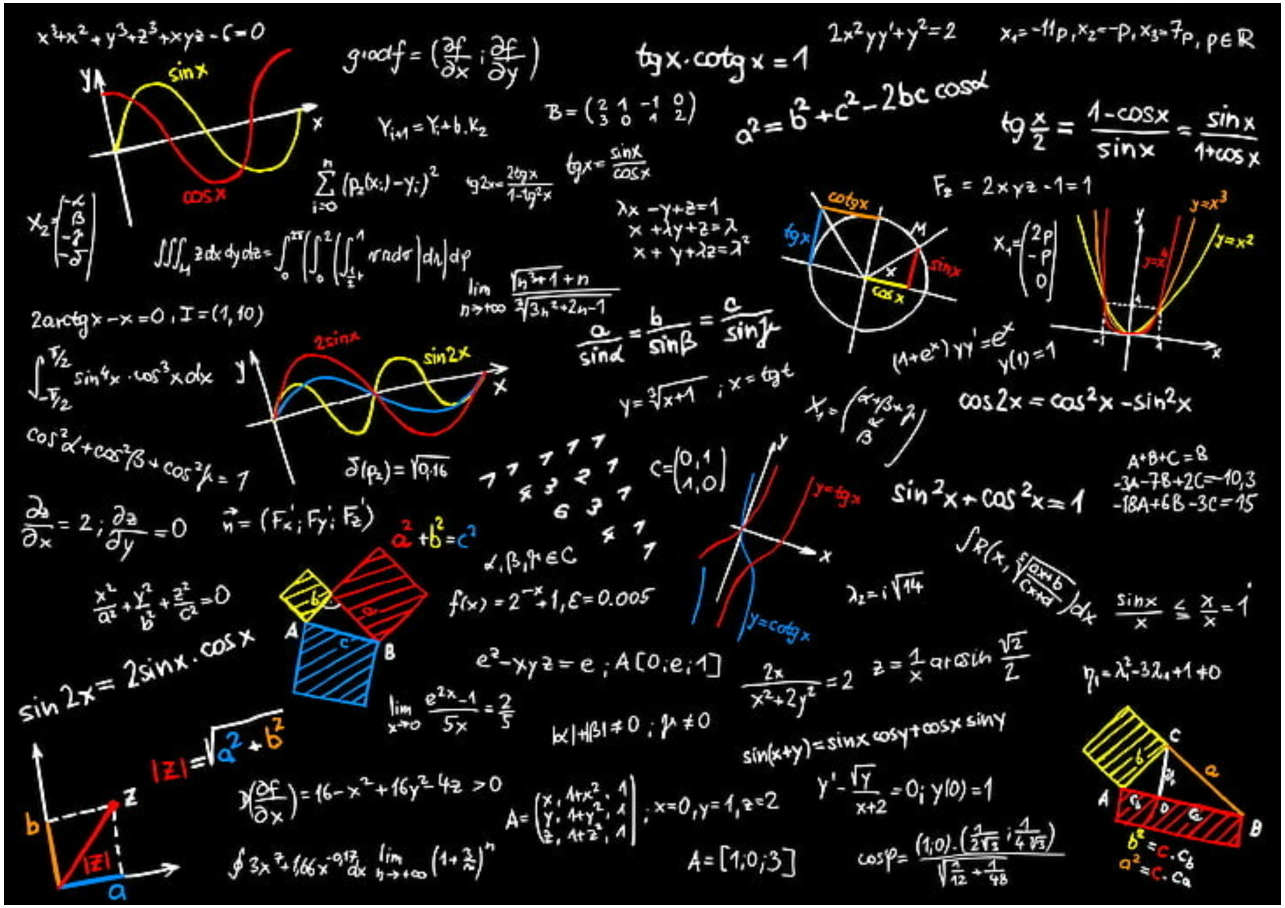
Mammola, S., Carmona, C. P., Guillerme, T., & Cardoso, P. (2021). Concepts and applications in functional diversity. *Functional Ecology*, *35*(9), 1869-1885.

1. Basic definitions & statistical units



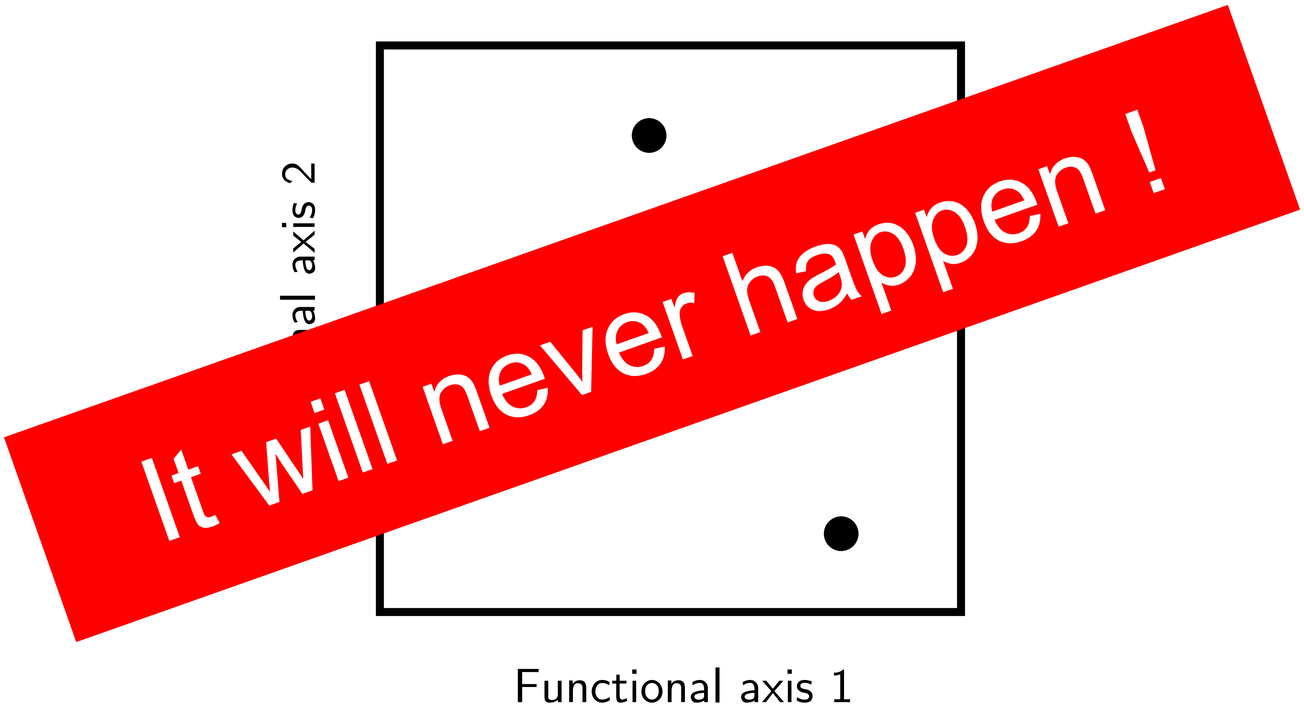
Mammola, S., Carmona, C. P., Guillerme, T., & Cardoso, P. (2021). Concepts and applications in functional diversity. *Functional Ecology*, *35*(9), 1869-1885.

2. Functional diversity metrics



2. Functional diversity metrics

Two traits – Not correlated (orthogonal) – quantitative continuous



2. Functional diversity metrics

A. Observation-based metrics

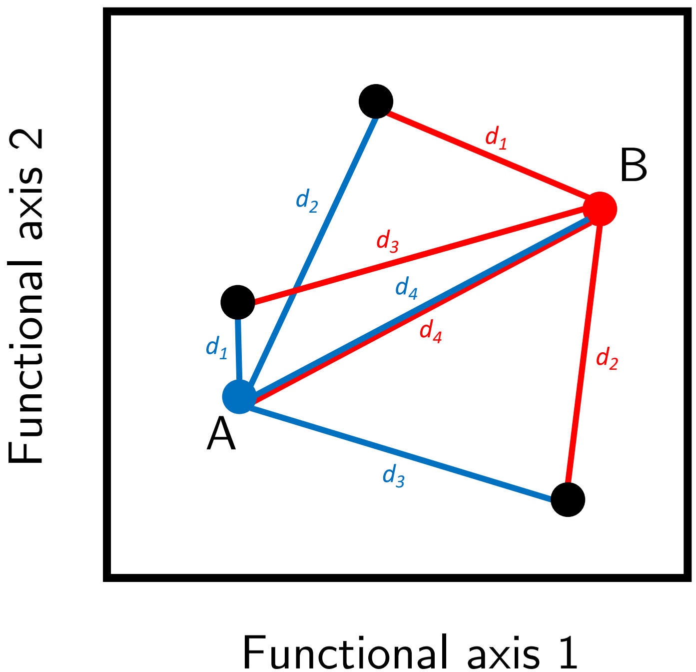
- Originality
- Uniqueness
- Contribution

Pavoine, S. et al. A. B. (2005). Is the originality of a species measurable?. *Ecology Letters*, *8*(6), 579-586.
Mouillot, D. et al. (2013). A functional approach reveals community responses to disturbances. *Trends in ecology & evolution*, *28*(3), 167-177.
Mammola, S. et al. (2021). Concepts and applications in functional diversity. *Functional Ecology*, *35*(9), 1869-1885.

2. Functional diversity metrics

A. Observation-based metrics

Originality A < B

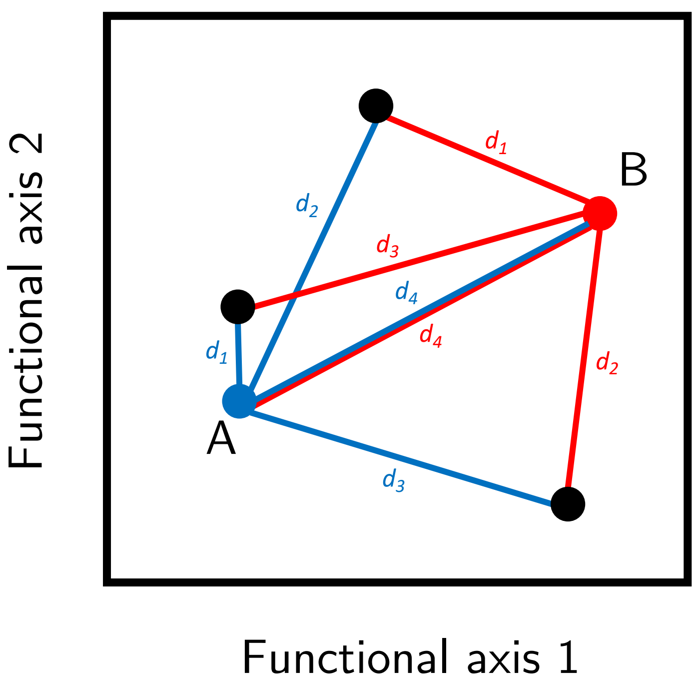


Average dissimilarity between an observation (species) and all others in a community.

2. Functional diversity metrics

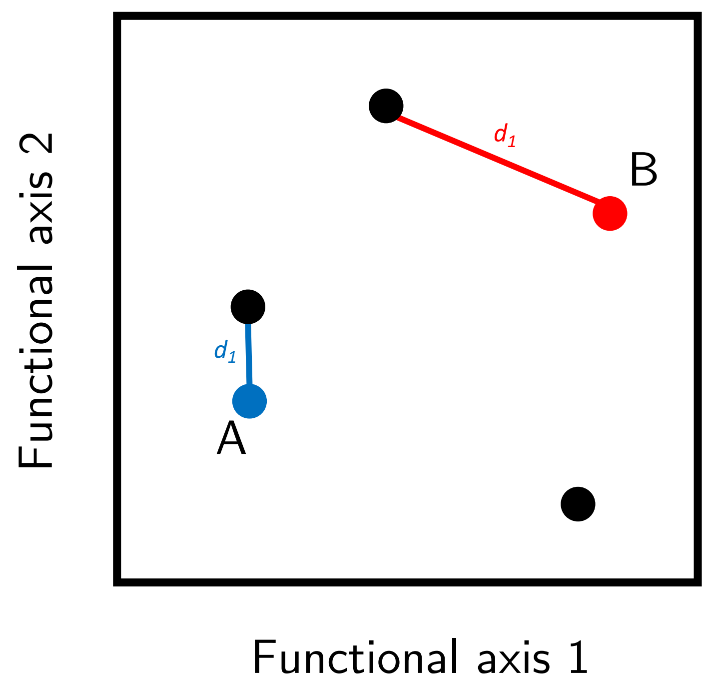
A. Observation-based metrics

Originality A < B



Average dissimilarity between an observation (species) and all others in a community.

Uniqueness A < B

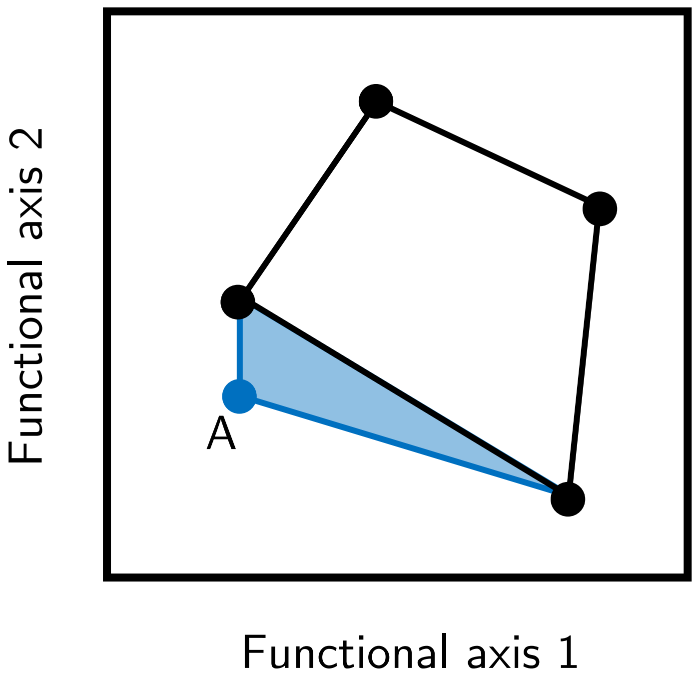


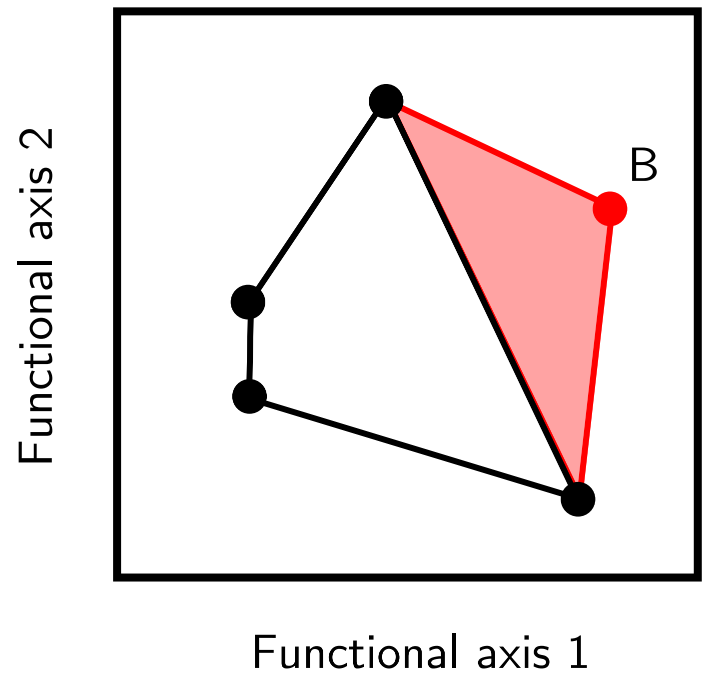
Dissimilarity between each observation (species) and the single closest in a community.

2. Functional diversity metrics

A. Observation-based metrics

Contribution A < B





Contribution of each observation (species) to the total FD.

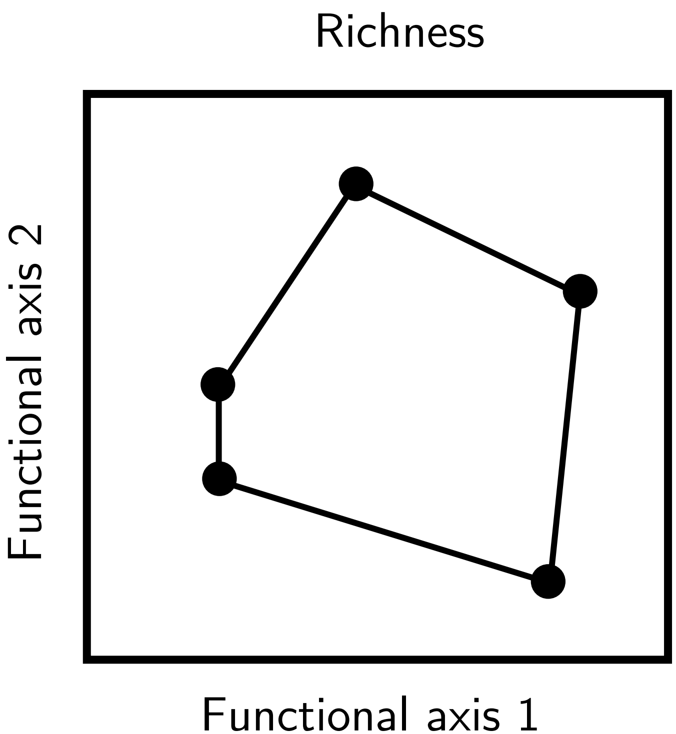
2. Functional diversity metrics

B. Group-based metrics

- Richness
- Divergence
- Regularity

2. Functional diversity metrics

B. Group-based metrics



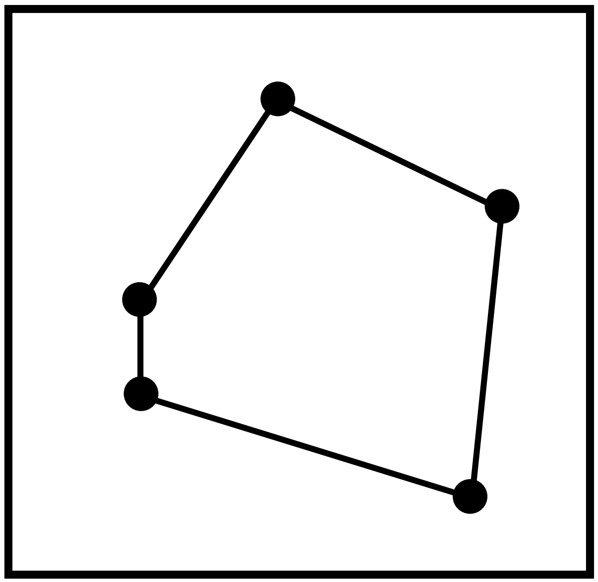
What is the size of the trait space ?

2. Functional diversity metrics

B. Group-based metrics

Functional axis 2

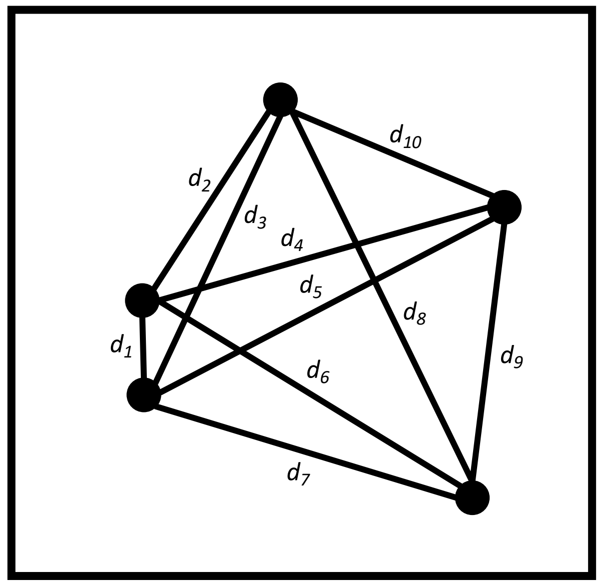
Richness



Functional axis 1

What is the size of the trait space ?

Divergence (dispersion)



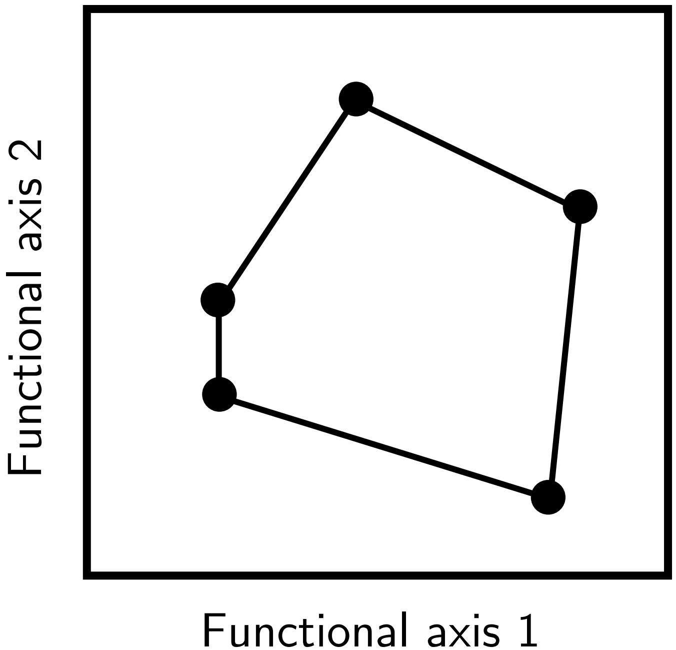
Functional axis 1

How dispersed is the trait space ?

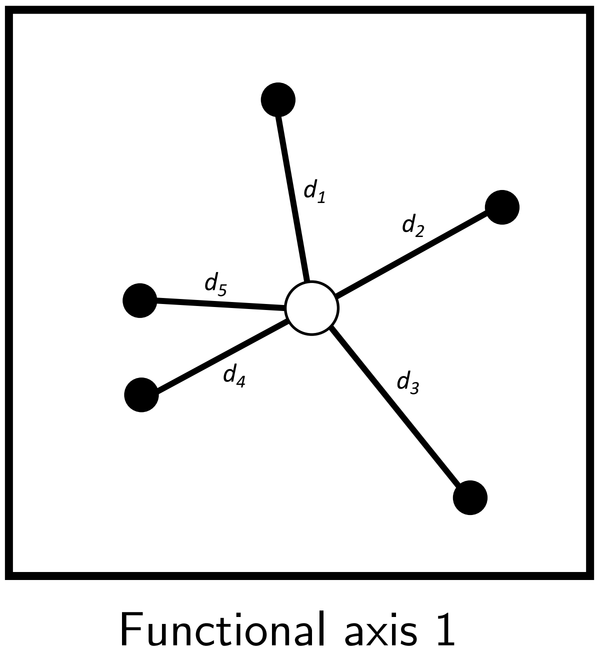
2. Functional diversity metrics

B. Group-based metrics

Richness



Divergence (dispersion)

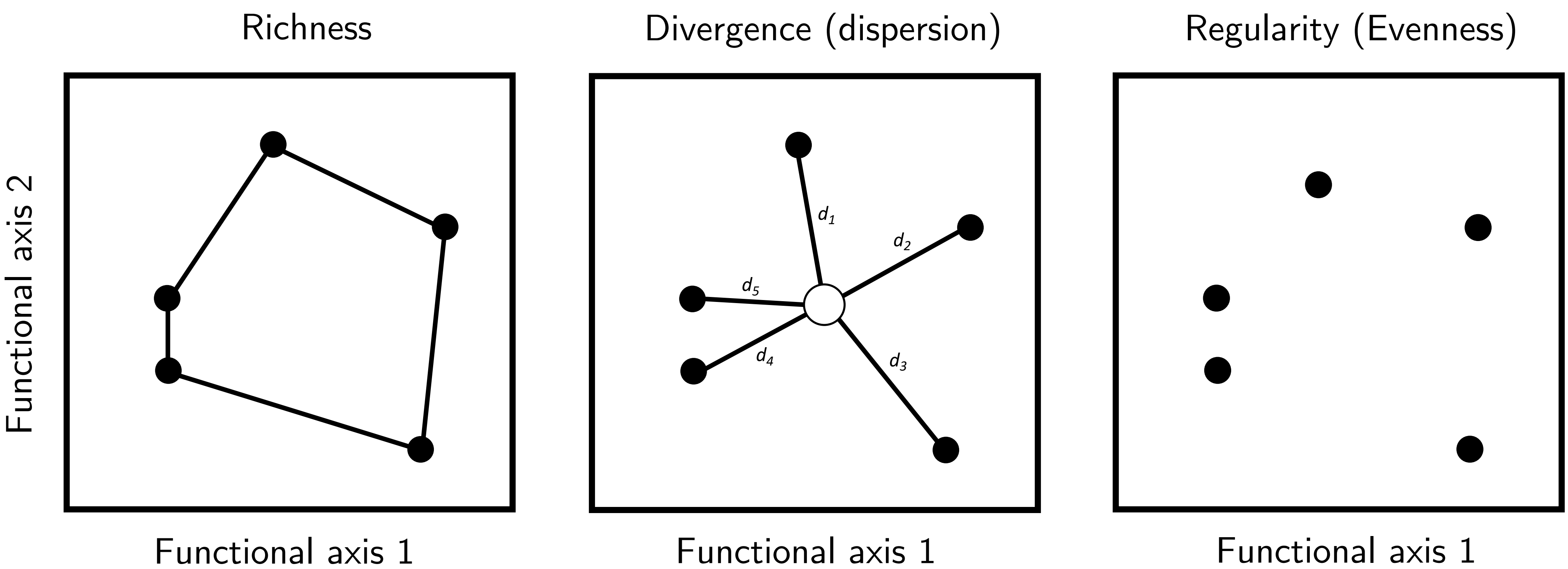


What is the size of the trait space ?

How dispersed is the trait space ?

2. Functional diversity metrics

B. Group-based metrics



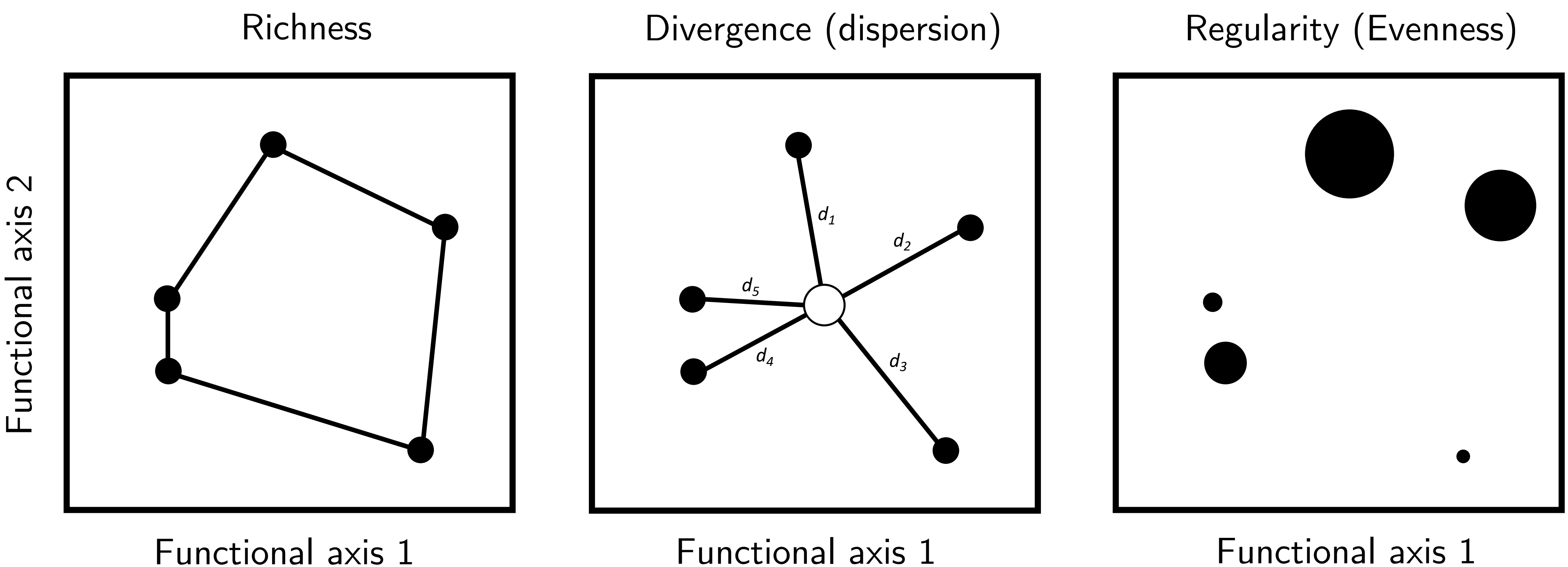
What is the size of the trait space ?

How dispersed is the trait space ?

How regular is the trait space ?

2. Functional diversity metrics

B. Group-based metrics

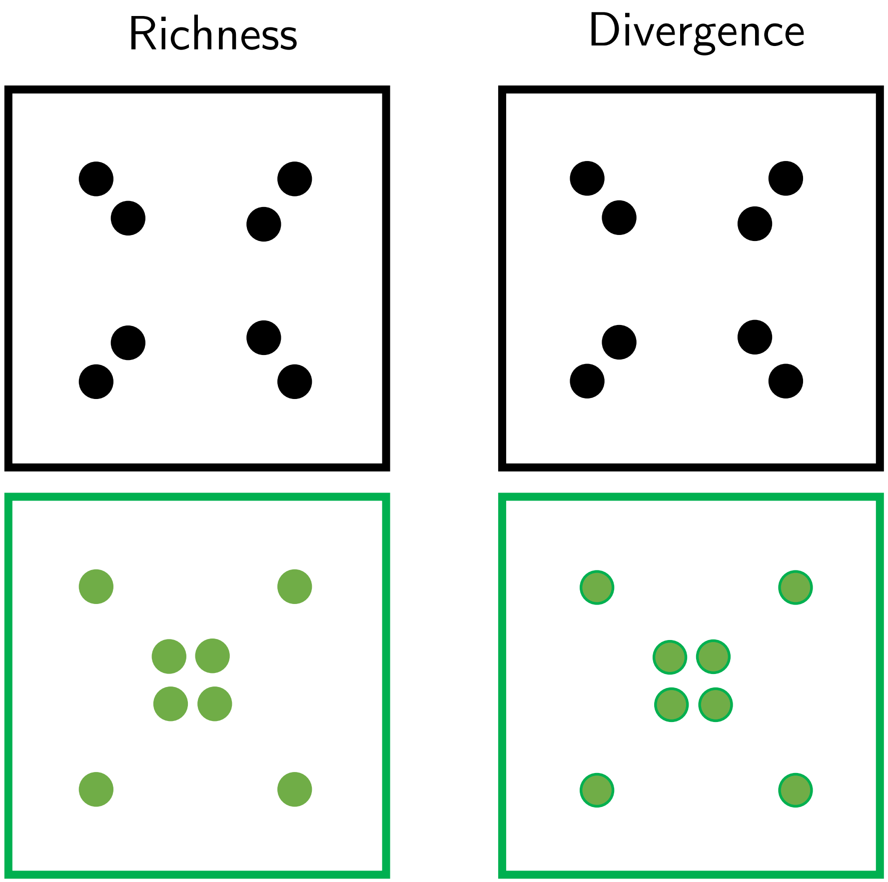


What is the size of the trait space ?

How dispersed is the trait space ?

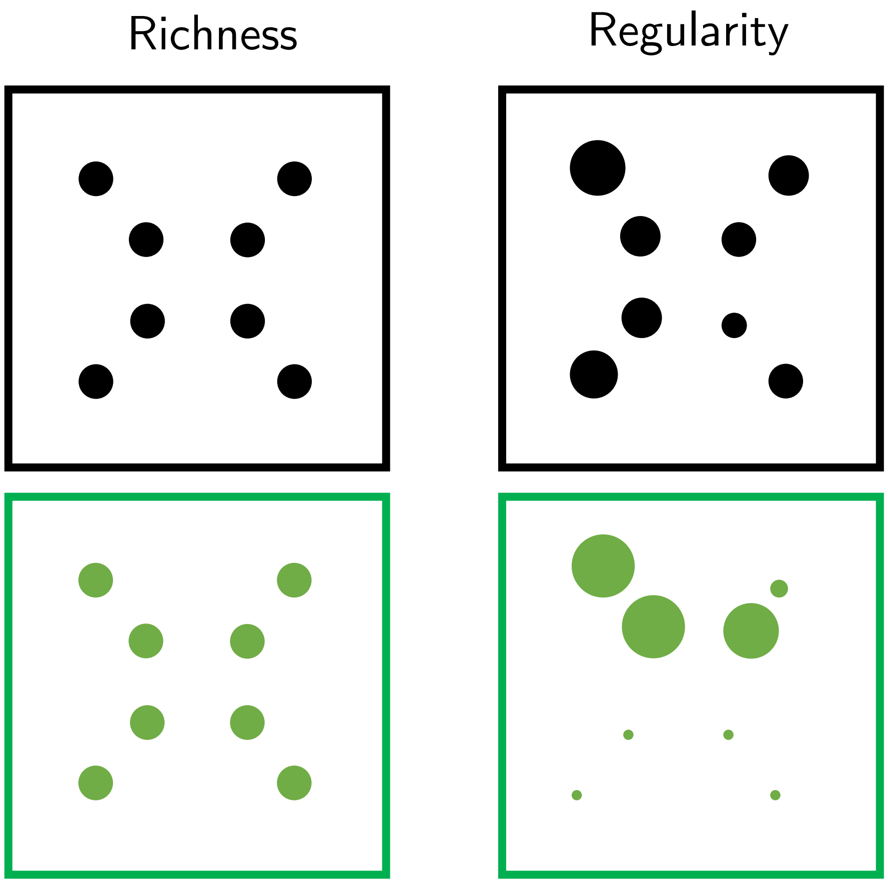
How regular is the trait space ?

B. Group-based metrics



2. Functional diversity metrics

B. Group-based metrics



2. Functional diversity metrics

C. Between Groups metrics

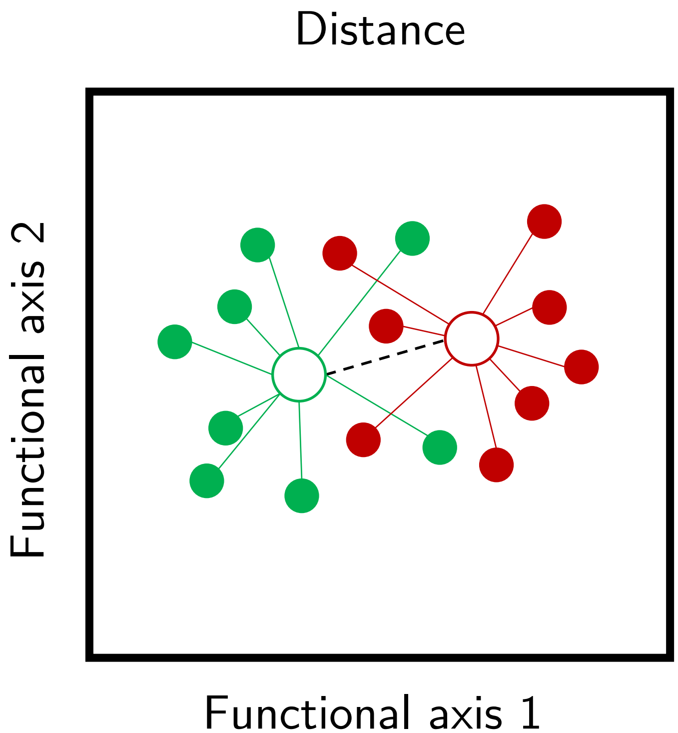
- Distance
- Beta diversity (Jaccard)

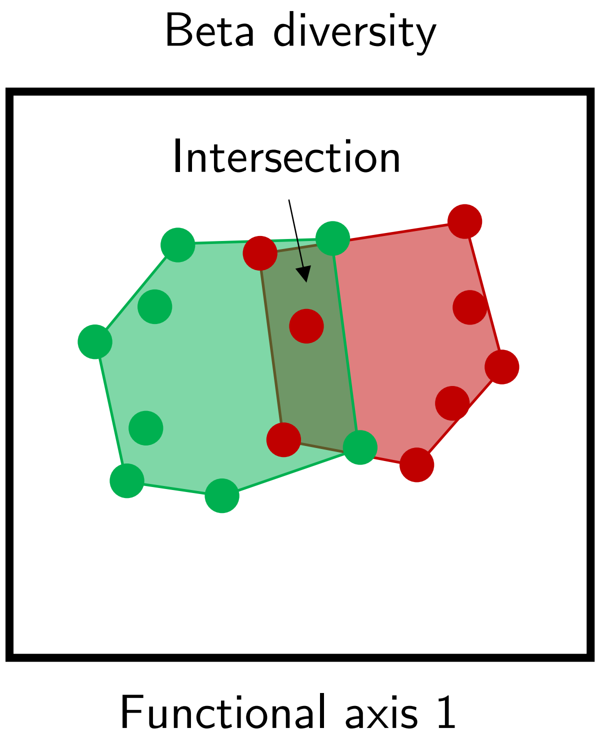
PEDRO CARDOSO (Wednesday, 27th and Friday 28th)

- Partitioning phylogenetic and functional beta diversity
- Phylogenetic (richness, dispersion, evenness)

2. Functional diversity metrics

C. Between Groups metrics





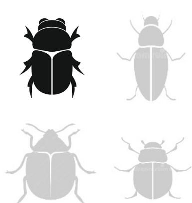
How distant are the trait spaces ?

What proportion of the functional space is (not) shared by the trait spaces?

2. Functional diversity metrics

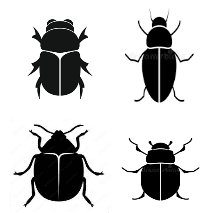
To sum up…

Observation-based metrics



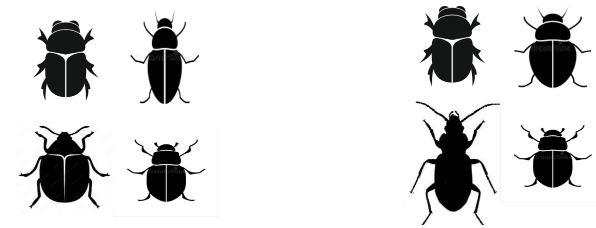
- Originality
- Uniqueness
- Contribution

Group-based metrics



- Richness
- Divergence
- Regularity

Between groups metrics



- Distance
- Beta

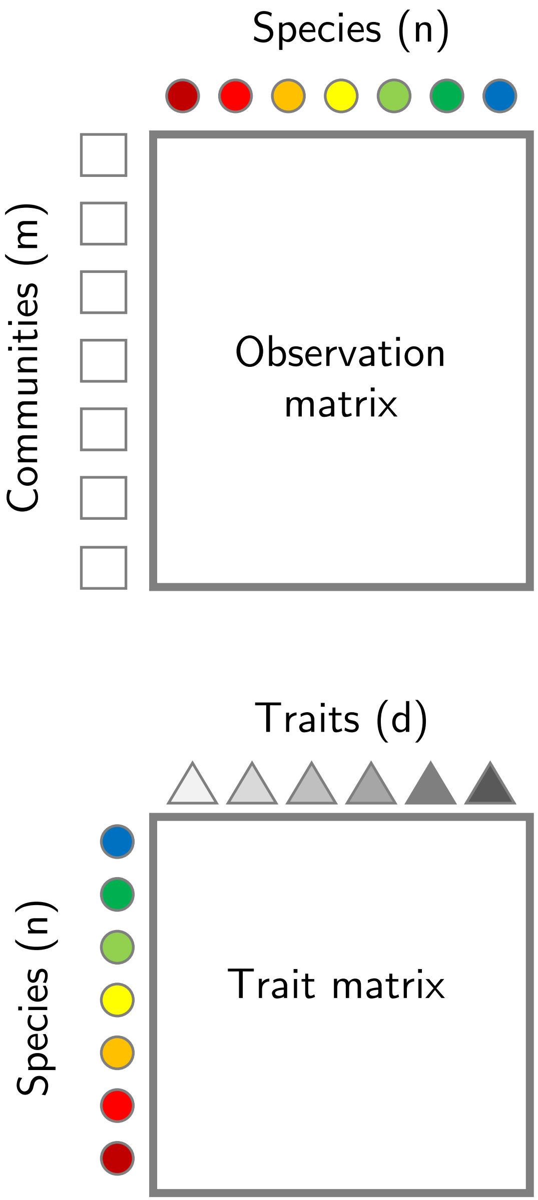
3. Overview of the current FD frameworks

3. Overview of the current FD frameworks

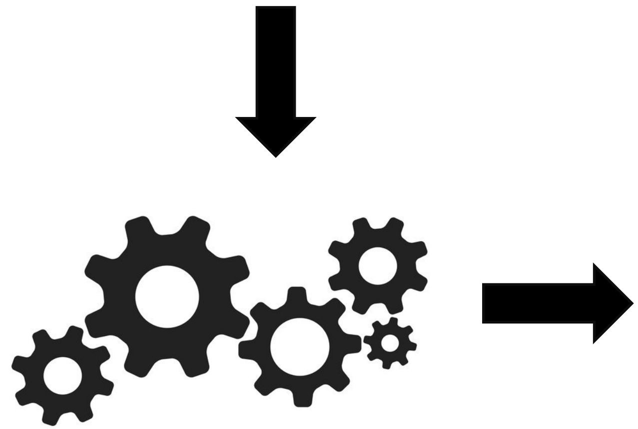
- Dissimilarity-based framework
- Multidimensional space framework

Pavoine, S., & Bonsall, M. B. (2011). Measuring biodiversity to explain community assembly: a unified approach. Biological Reviews, 86(4), 792-812.
Mammola, S., Carmona, C. P., Guillerme, T., & Cardoso, P. (2021). Concepts and applications in functional diversity. Functional Ecology, 35(9), 1869-1885.

3. Overview of the current FD frameworks



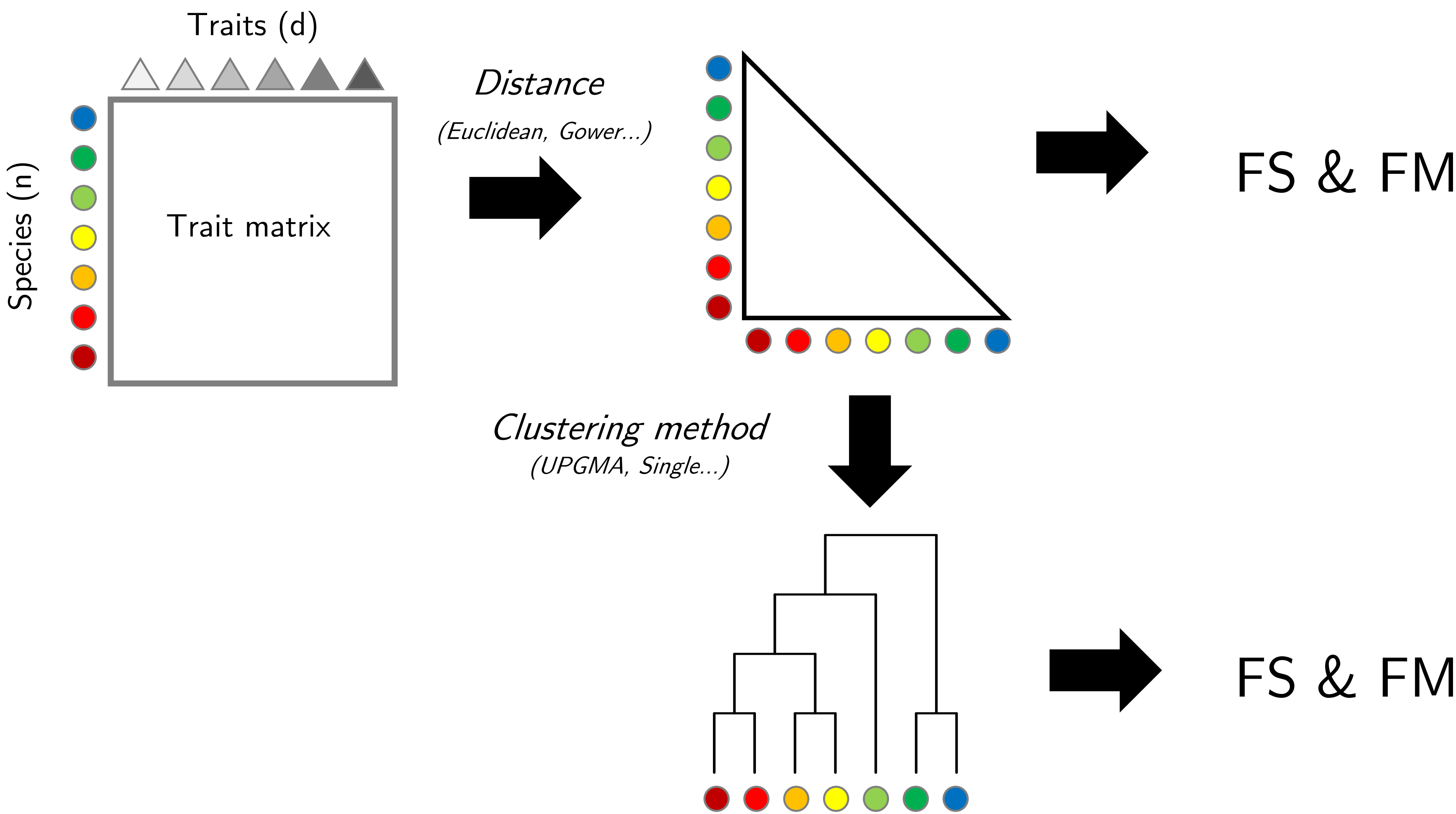
Framework: general mathematical approach for estimating the trait space and its properties.



Building functional space & computing functional metrics

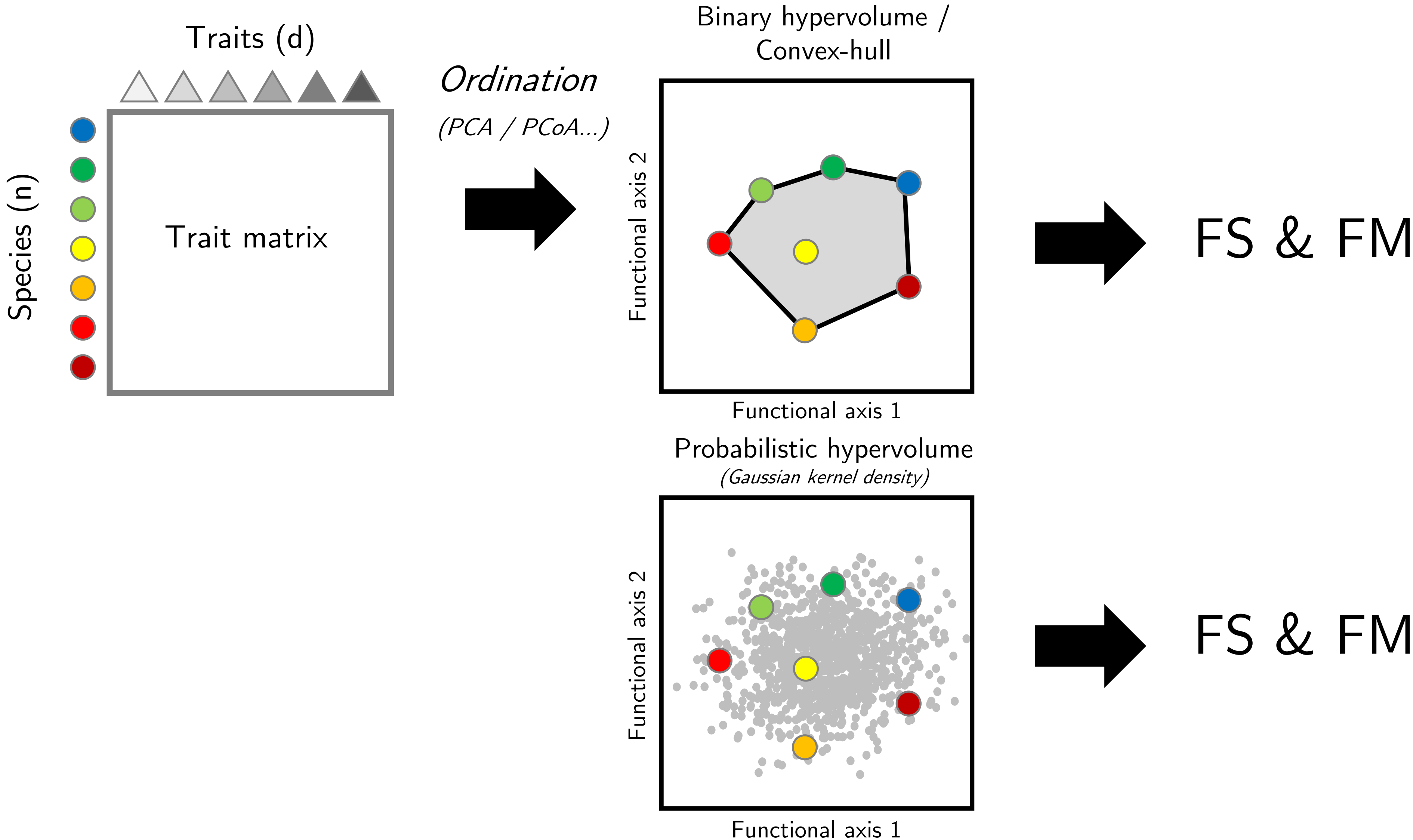
3. Overview of the current FD frameworks

A. Dissimilarity-based framework *(non-dimensional approach)*

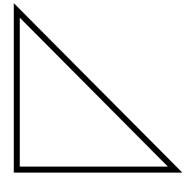
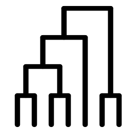
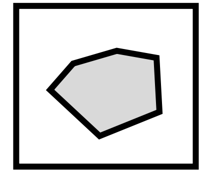
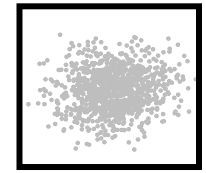


3. Overview of the current FD frameworks

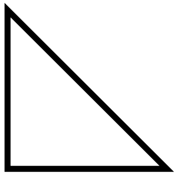
B. Multidimensional space framework *(hypervolumes)*



3. Overview of the current FD frameworks

				
Observation-based metrics				
○ Originality	✕	✕		✕
○ Uniqueness	✕	✕		
○ Contribution		✕	✕	✕
Group-based metrics				
○ Richness		✕	✕	✕
○ Divergence	✕	✕		✕
○ Regularity	✕	✕		✕
Between groups metrics				
○ Distance	✕	✕		✕
○ Overlap		✕	✕	✕

3. Overview of the current FD frameworks



A. Observation-based metrics

For observation 1

	obs1	obs2	obs3	obs4	obs5	obs6	obs7
obs2	1						
obs3	2	1.5					
obs4	3	2.5	4				
obs5	0.5	2	5	6			
obs6	1	5	0.5	2	1		
obs7	2	2	6	1	1.5	2	
obs8	3	1	2	2	1	3.5	1

$$Originality_1 = \frac{(1+2+3+0.5+1+2+3)}{7} = 1.78$$

$$Uniqueness_1 = 0.5$$

$$Contribution_1 = NA$$

For originality, possibility to weight each distance with the relative abondance of the other species of the pair. No need to weight for uniqueness.

Grenié, M. et al. (2017). funrar: An R package to characterize functional rarity. *Diversity and Distributions*, *23*(12), 1365-1371.

3. Overview of the current FD frameworks

B. Group-based metrics

	obs1	obs2	obs3	obs4	obs5	obs6	obs7
obs2	1						
obs3	2	1.5					
obs4	3	2.5	4				
obs5	0.5	2	5	6			
obs6	1	5	0.5	2	1		
obs7	2	2	6	1	1.5	2	
obs8	3	1	2	2	1	3.5	1

$$Richness = NA$$

Mean Pairwise distance (MPD)

$$Divergence = \frac{(1 + 2 + 1.5 + 3 + 2.5 + 4)}{6} = 2.33$$

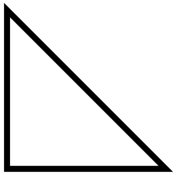
$$Regularity = FEve$$ See details in Villeger et al. 2018

Possibility to weight each distance with the product of the relative abondance of the two species.

Indices RaoQ and FDis are also available for divergence but all are highly correlated between each others. See also Hill numbers for similar indices with different weights for abundance.

Villéger, S. et al. (2008). New multidimensional functional diversity indices for a multifaceted framework in functional ecology. Ecology, 89(8), 2290-2301.

3. Overview of the current FD frameworks



C. Between groups metrics

The distance between the red and green is the mean of the pairwise distance calculated between the species of the two communities.

	obs1	obs2	obs3	obs4	obs5	obs6	obs7
obs2	1						
obs3	2	1.5					
obs4	3	2.5	4				
obs5	0.5	2	5	6			
obs6	1	5	0.5	2	1		
obs7	2	2	6	1	1.5	2	
obs8	3	1	2	2	1	3.5	1

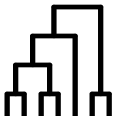
$$Distance_{G,R} = \frac{(0.5 + 2 + 5 + 6 + 1 + \ \dots)}{16} = 2.56$$

$$Beta\ Jaccard_{G,R} = NA$$

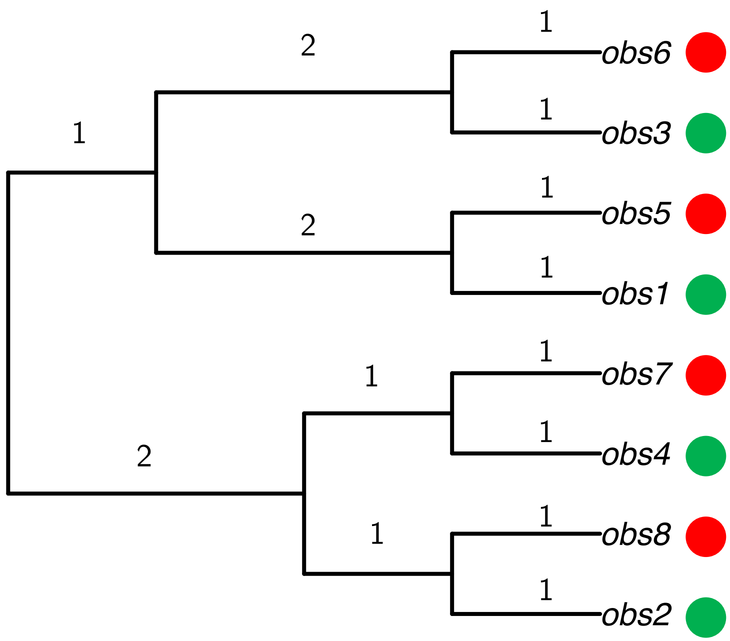
Possibility to weight each distance with the product of the relative abondance of the two species.

Index RaoQ for Beta diversity is also available for distance but it is highly correlated with the one above.

3. Overview of the current FD frameworks



! Distances in a tree are called cophenetic distances



A. Observation-based metrics

For observation 1

Cophenetic distance in the tree between obs1 and obs2 is 1+2+1+2+1+1=8

$$Originality_1 = \frac{(8+6+8+2+6+8+8)}{7} = 6.57$$

$$Uniqueness_1 = 2$$

$$Contribution_1 = 1 + \frac{2}{2} + \frac{1}{4} = 2.25$$

Branch length divided by the number of species sharing the branch

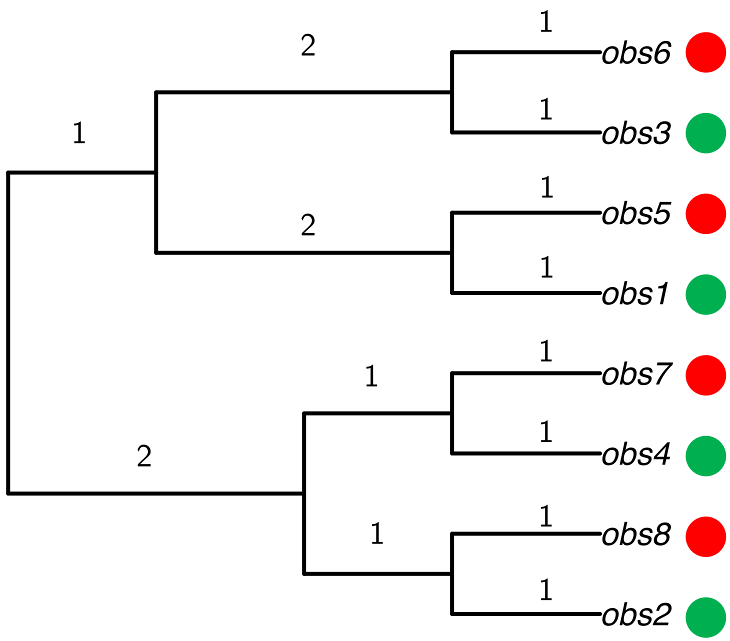
Possibility to weight each distance with the product of the relative abondance of the two species.

Sum of the contribution is equal to the sum of all the branch lengths in the tree. Possibility to weight each contribution with the relative abondance of the species.

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C., & Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PloS one*, *2*(3), e296.

3. Overview of the current FD frameworks

B. Group-based metrics



Sum of the branch lengths (Petchey & Gaston 2002)

$$\color{green}{Richness} = 1 + 1 + 2 + 2 + 1 + 2 + 1 + 1 + 1 + 1 = 13$$

Mean pairwise cophenetic distance

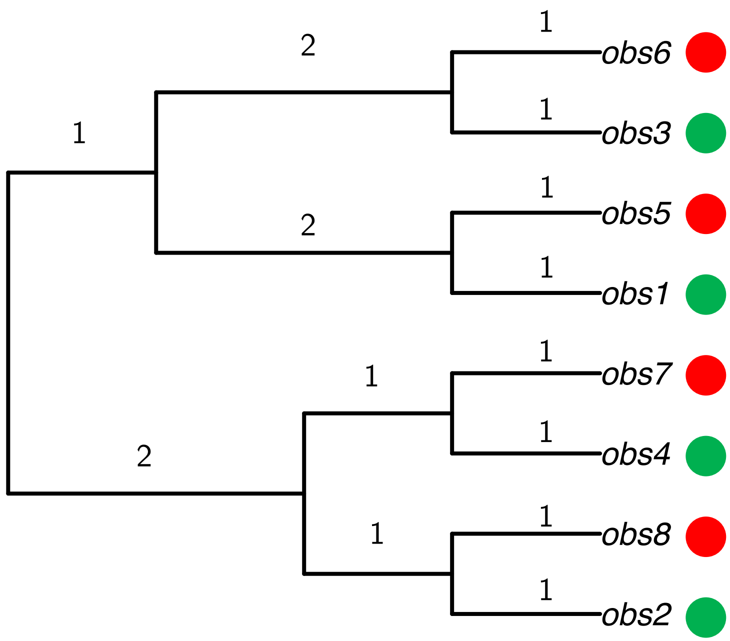
$$\color{green}{Divergence} = \frac{(8 + 6 + 8 + 8 + 4 + 8)}{6} = 7$$

Possibility to weight each distance with the product of the relative abondance of the two species.

Indices RaoQ with trees is also available for divergence but all are highly correlated between each others. See also Hill numbers for similar indices with different weights for abundance.

Petchey, O. L., & Gaston, K. J. (2002). Functional diversity (FD), species richness and community composition. *Ecology letters*, *5*(3), 402-411.

3. Overview of the current FD frameworks



B. Group-based metrics

For *evenness*, we need the contribution of the four species in the green community: obs1=3.5; obs2=3; obs3=3.5; obs4=3

Camargo's formula

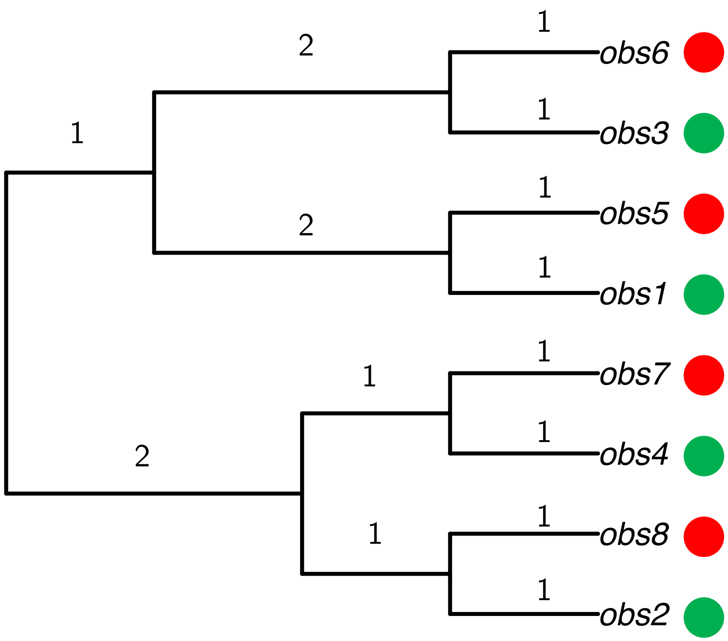
$$Evenness = 1 - \frac{|3.5-3| + |3.5-3.5| + |3.5-3| + |3-3.5| + |3.5-3.5| + |3.5-3|}{6} = 0.66$$

1-the sum of the absolute difference between pairs of contributions divided by the number of pairs.

Possibility to weight each contribution with the relative abondance of the species.

Camargo, J.A. (1993) Must dominance increase with the number of subordinate species in competitive interactions? *Journal of Theoretical Biology*, **161**, 537–542.

3. Overview of the current FD frameworks



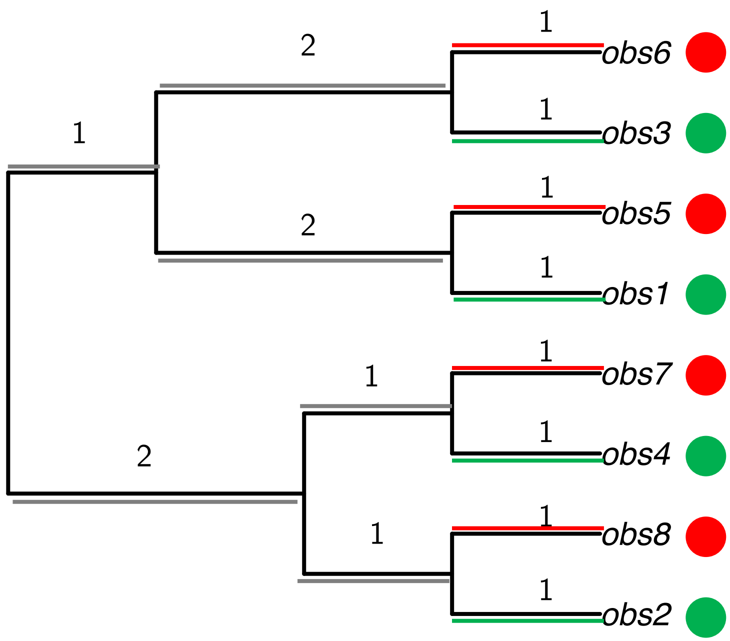
C. Between groups metrics

As for the dissimilarity matrix, the distance between the red and green is the mean of the pairwise distance calculated between the species of the two communities.

$$Distance_{G,R} = \frac{(2+6+8+8+8+\ \ldots)}{16} = 5.75$$

Possibility to weight each distance with the product of the relative abondance of the two species.

C. Between groups metrics



$$Beta\ Jaccard_{G,R} = \frac{b+c}{a+b+c}$$

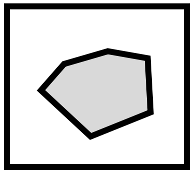
a = Shared branch lengths between green and red
b = Branch lengths found only in green
c = Branch lengths found only in red

$$Beta\ Jaccard_{G,R} = \frac{(4+4)}{4+4+9} = 0.47$$

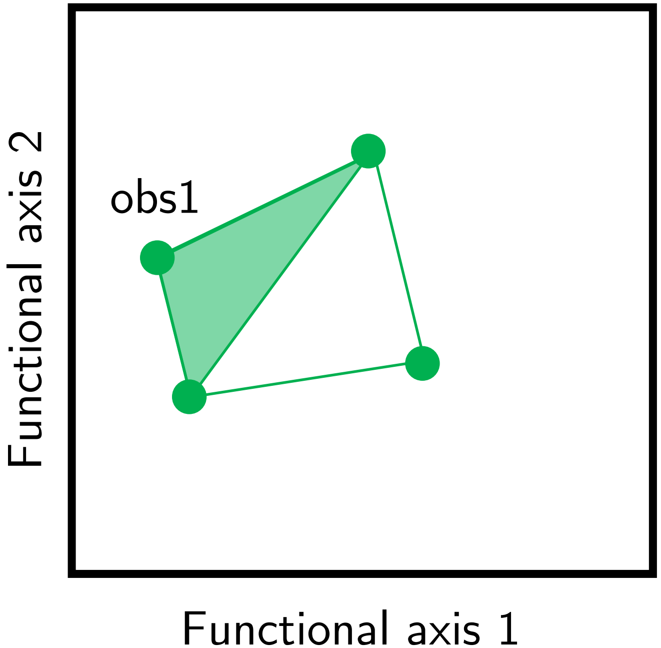
Possibility to weight each branch length with the relative abondance of the species.

Cardoso, P., Rigal, F., Carvalho, J. C., Fortelius, M., Borges, P. A., Podani, J., & Schmera, D. (2014). Partitioning taxon, phylogenetic and functional beta diversity into replacement and richness difference components. *Journal of Biogeography*, *41*(4), 749-761.

3. Overview of the current FD frameworks



A. Observation-based metrics

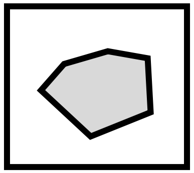


$$Originality \quad = NA$$

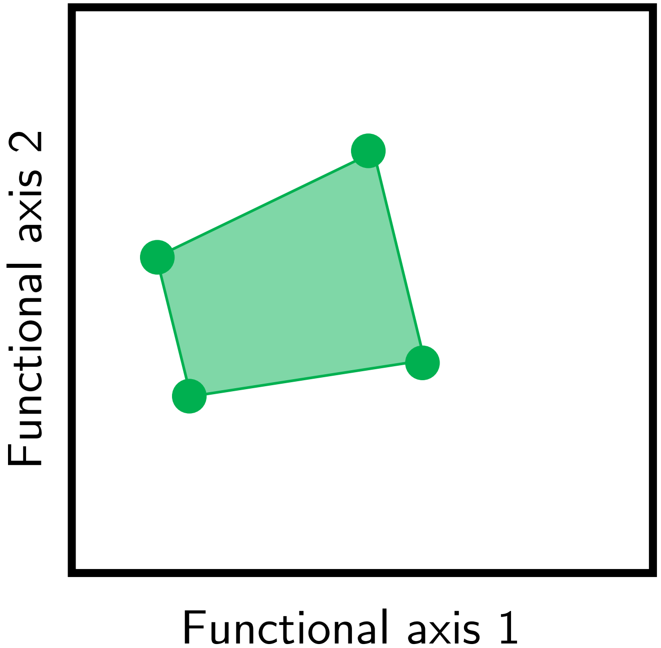
$$Uniqueness \quad = NA$$

Contribution of each observation to the total surface/volume of a convex hull is calculated as the difference in surface/volume between the total convex hull and a second surface/volume lacking this specific observation.

3. Overview of the current FD frameworks



B. Group-based metrics



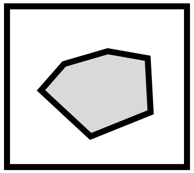
Richness is the minimum convex hull which includes all the species of the group; Richness is then the surface / volume inside this hull.

$Divergence = NA$

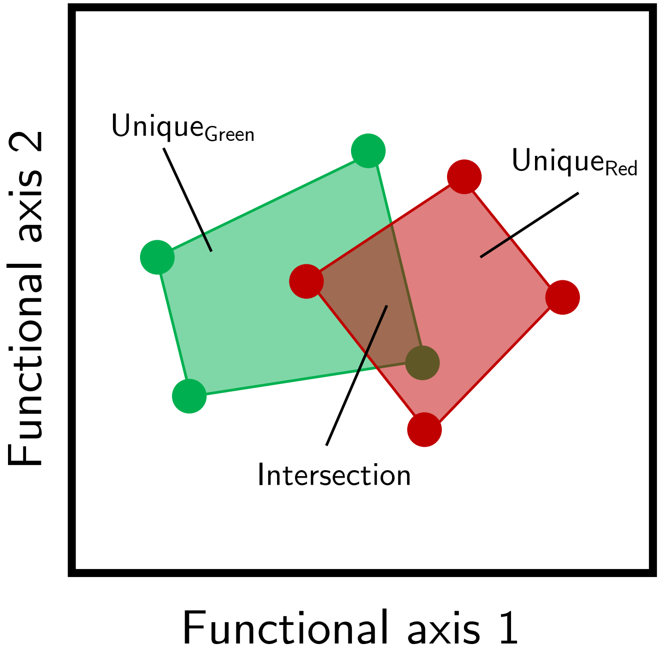
$Evenness = NA$

Cornwell, W. K., Schwilk, D. W., & Ackerly, D. D. (2006). A trait-based test for habitat filtering: convex hull volume. *Ecology*, *87*(6), 1465-1471.

3. Overview of the current FD frameworks



C. Between groups metrics

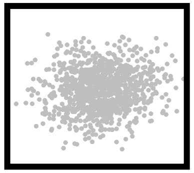


$$Distance_{G,R} = NA$$

$$Beta\ Jaccard_{G,R} = \frac{Unique_{Green} + Unique_{Red}}{Unique_{Green} + Unique_{Red} + Intersection}$$

Cornwell, W. K., Schwilk, D. W., & Ackerly, D. D. (2006). A trait-based test for habitat filtering: convex hull volume. *Ecology*, *87*(6), 1465-1471.

3. Overview of the current FD frameworks



Global Ecology and Biogeography, (Global Ecol. Biogeogr.) (2014) **23**, 595–609

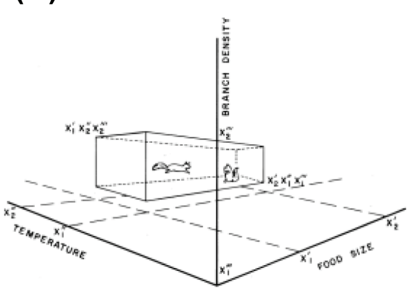
The *n*-dimensional hypervolume

Benjamin Blonder[1,2,3*], Christine Lamanna[2,4], Cyrille Violle[5] and Brian J. Enquist[1,2,6]

Benjamin Blonder
University of Arizona

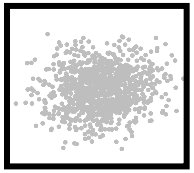
Rooted in the concept of the Hutchinsonian hypervolume of species niche.

(A)

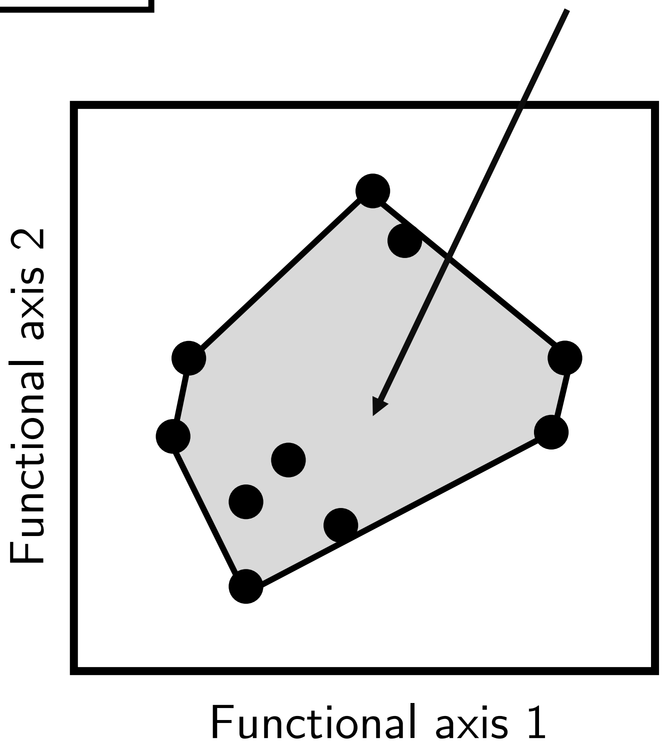


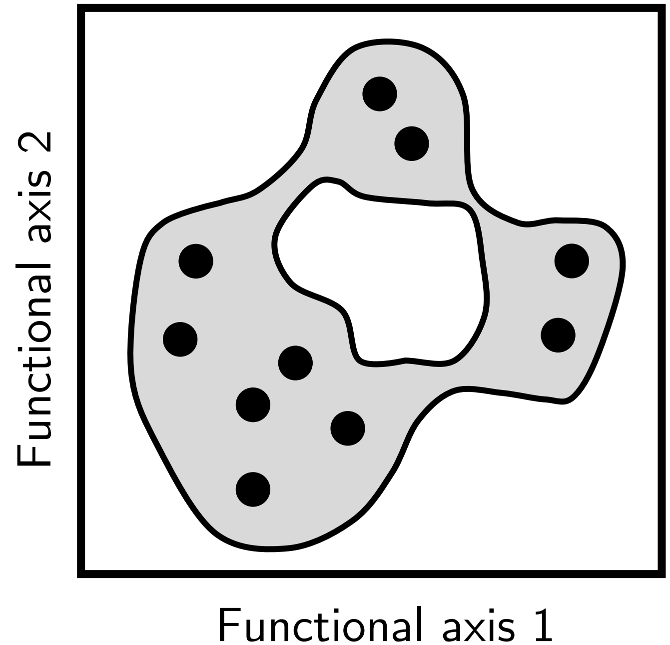
George Evelyn Hutchinson

3. Overview of the current FD frameworks



Empty space=overestimation of the trait space





E-Article

Do Hypervolumes Have Holes?

Benjamin Blonder*

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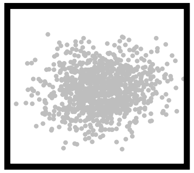
Submitted May 13, 2015; Accepted October 23, 2015; Electronically published February 15, 2016

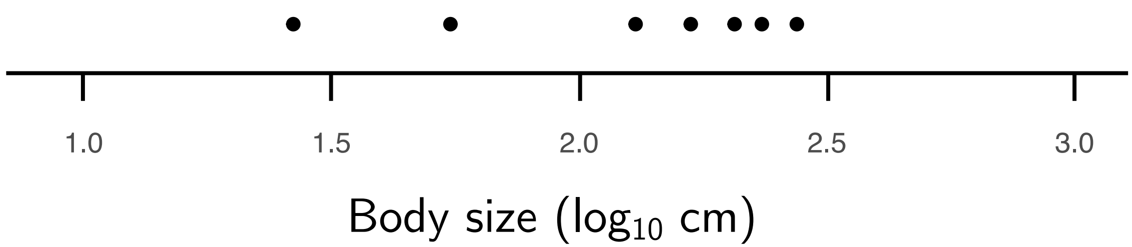
Online enhancements: video.

3. Overview of the current FD frameworks



Let's start with a single-trait approach

Ptilinopus huttoni (Austral Islands)



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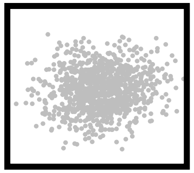

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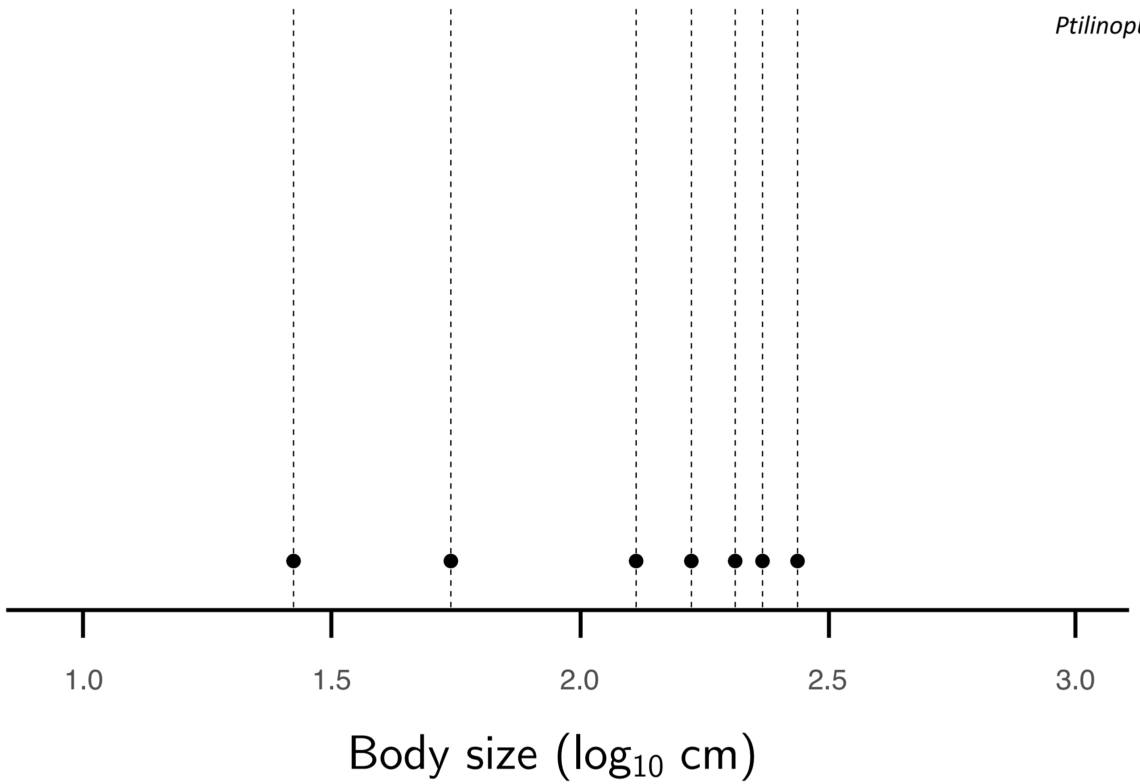

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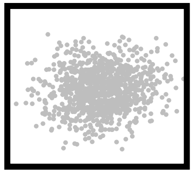
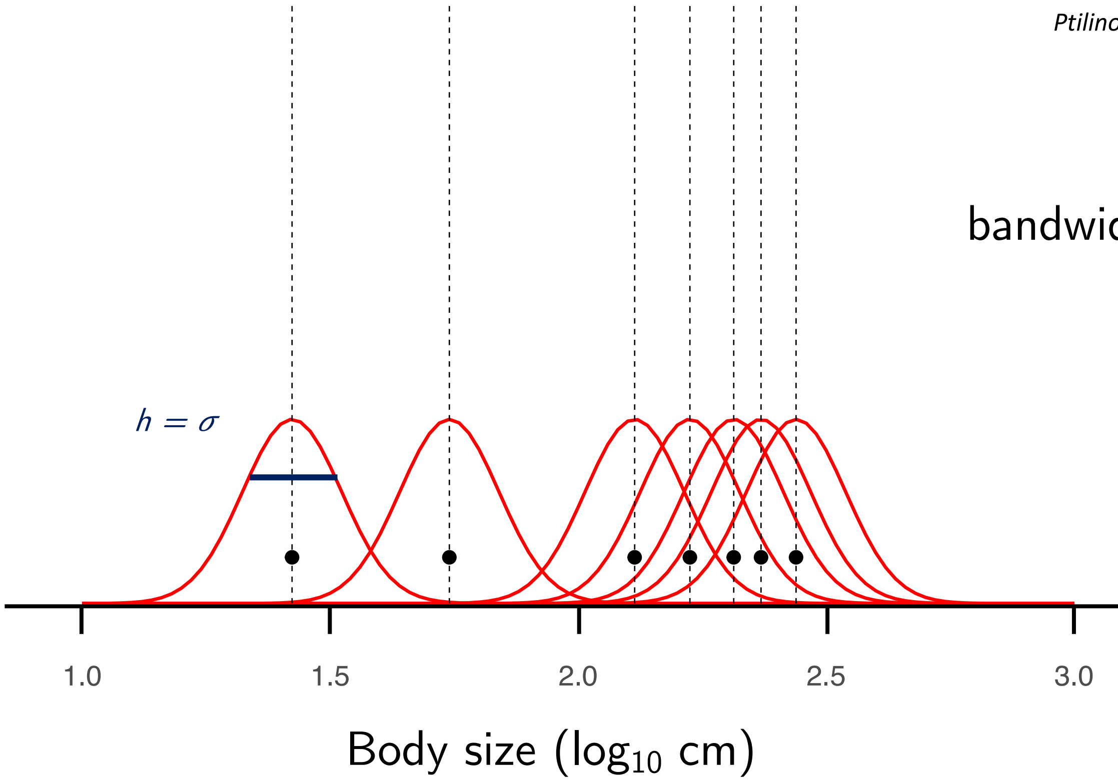


Let's start with a single-trait approach

Ptilinopus huttoni (Austral Islands)

bandwidth $(h) = 0.1$



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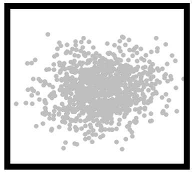
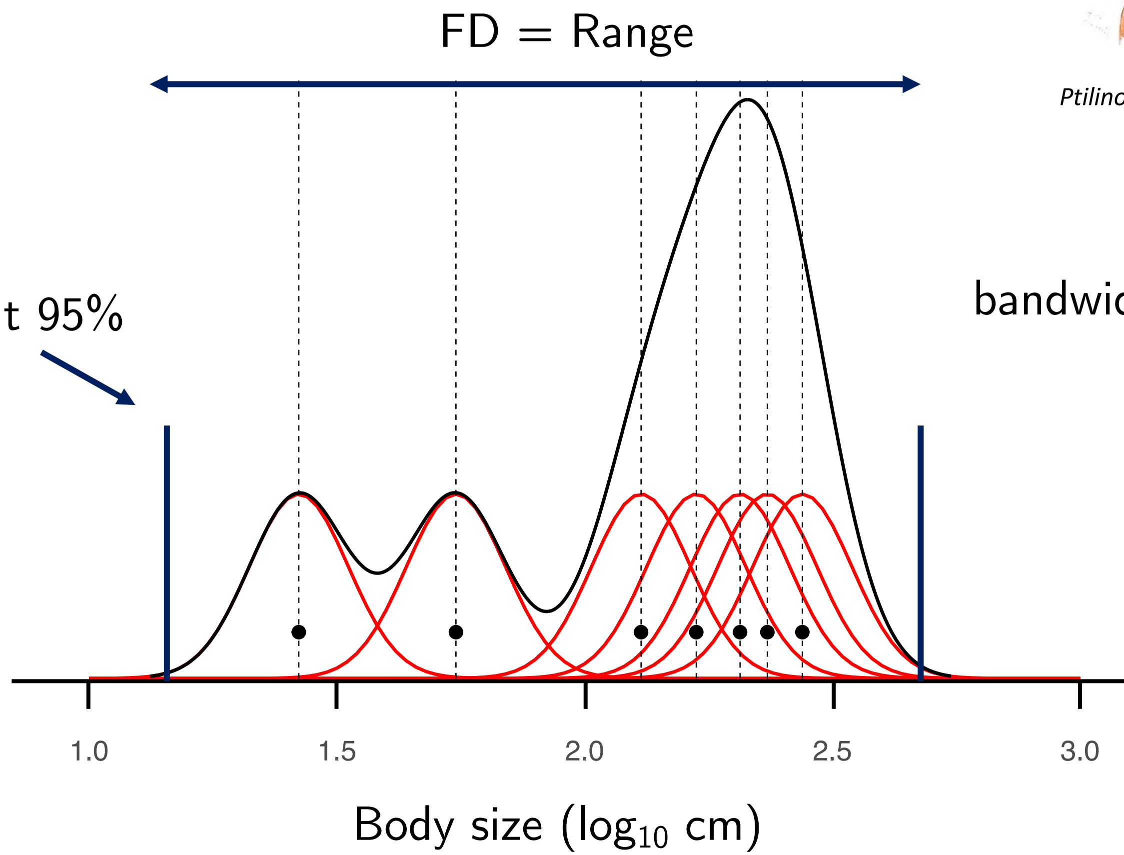


Let's start with a single-trait approach

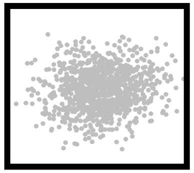
Ptilinopus huttoni (Austral Islands)

Threshold: quantile at 95%



bandwidth $(h) = 0.1$

3. Overview of the current FD frameworks

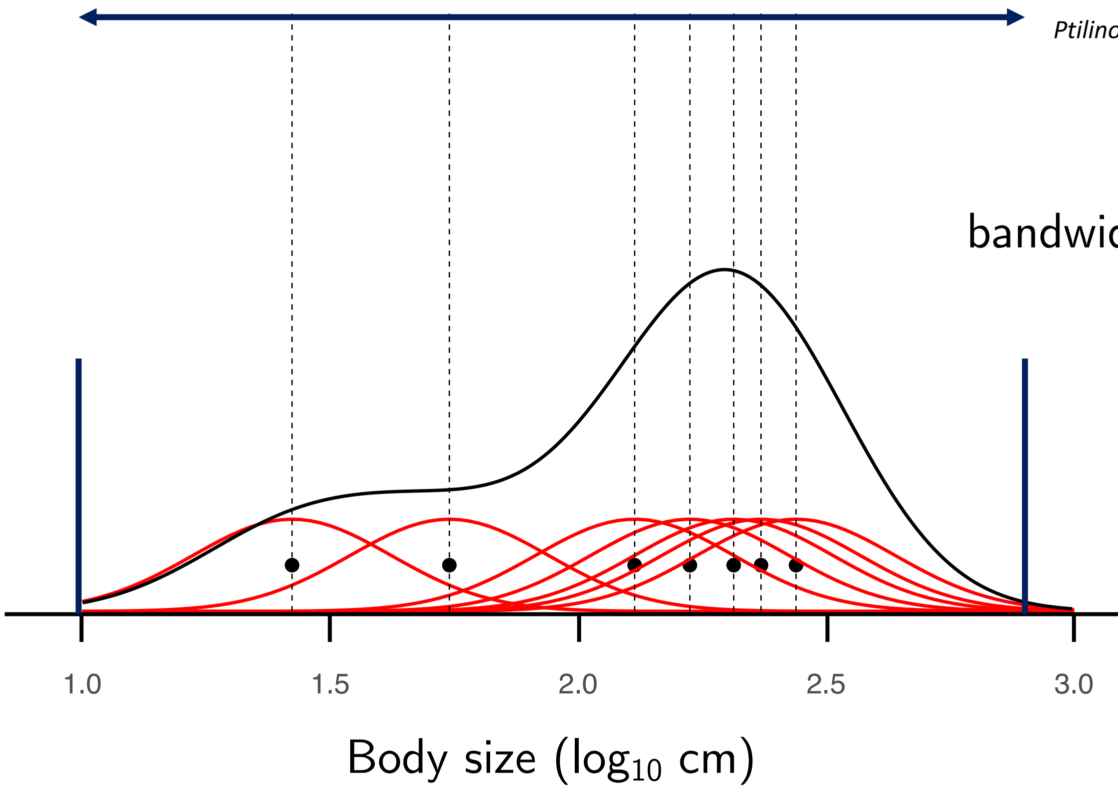


Let's start with a single-trait approach

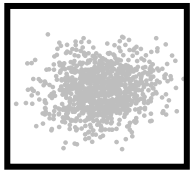
Ptilinopus huttoni (Austral Islands)

FD = Range

bandwidth *(h)* = 0.2

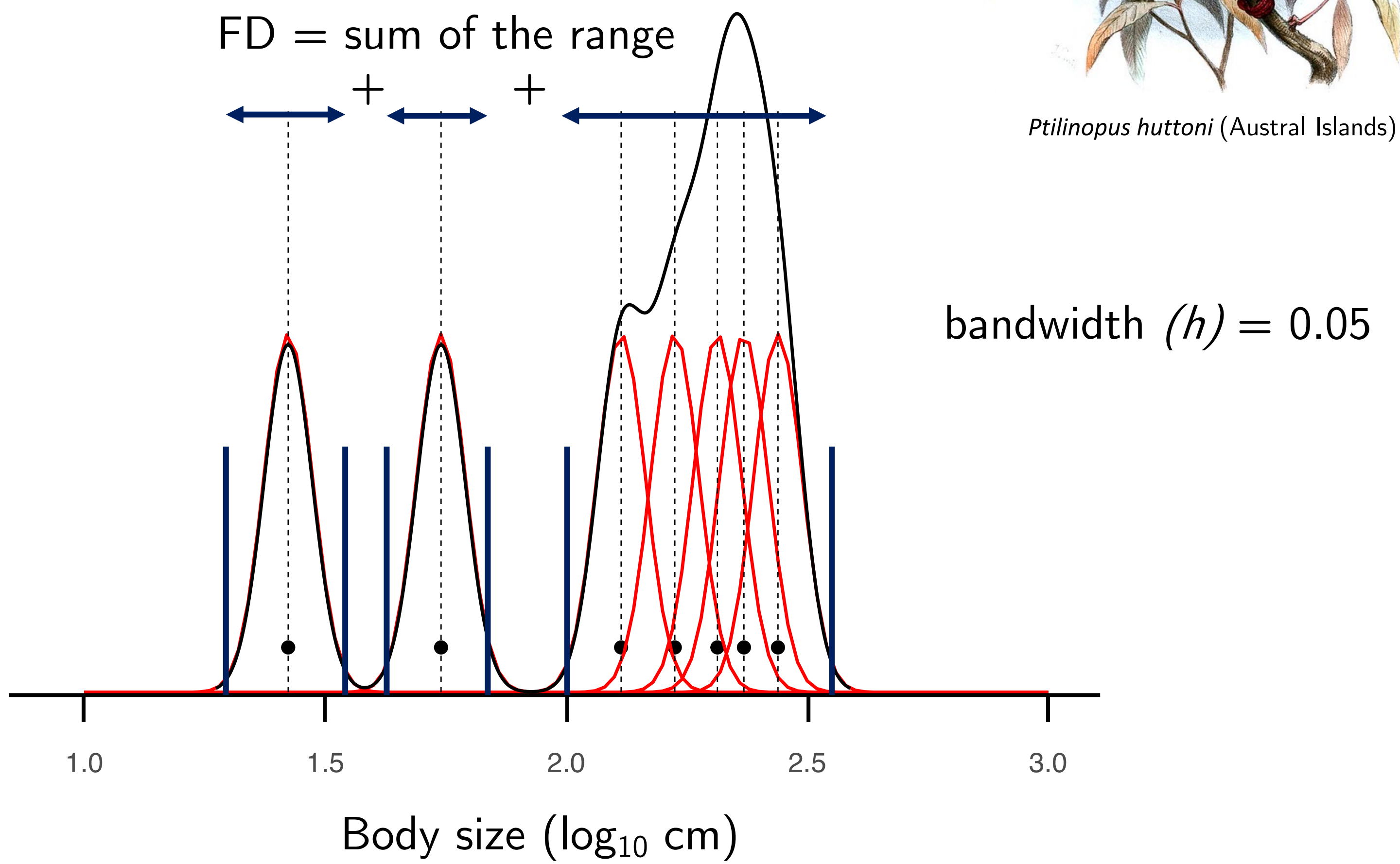


3. Overview of the current FD frameworks



Let's start with a single-trait approach

Ptilinopus huttoni (Austral Islands)



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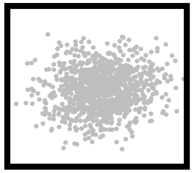
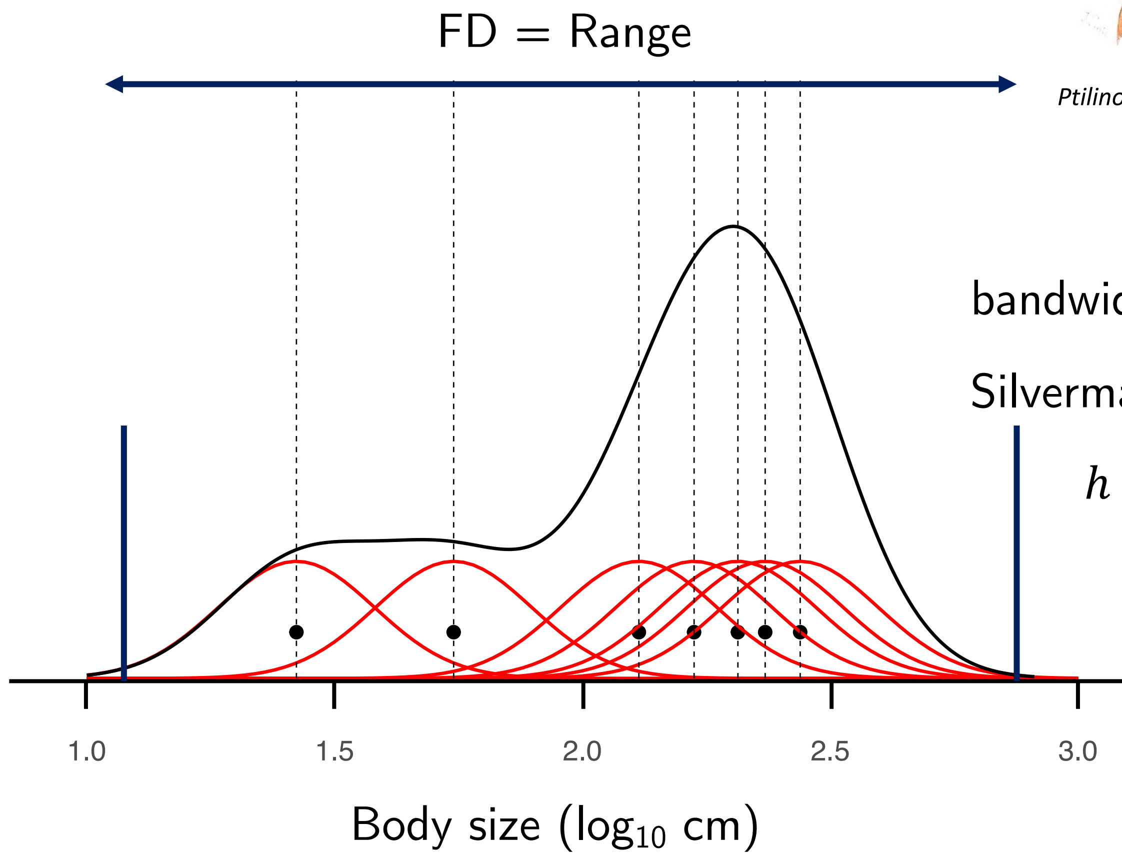


Let's start with a single-trait approach

Ptilinopus huttoni (Austral Islands)



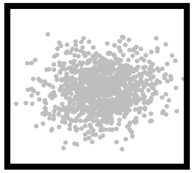
bandwidth *(h)* = 0.1575

Silverman's rule of thumb:

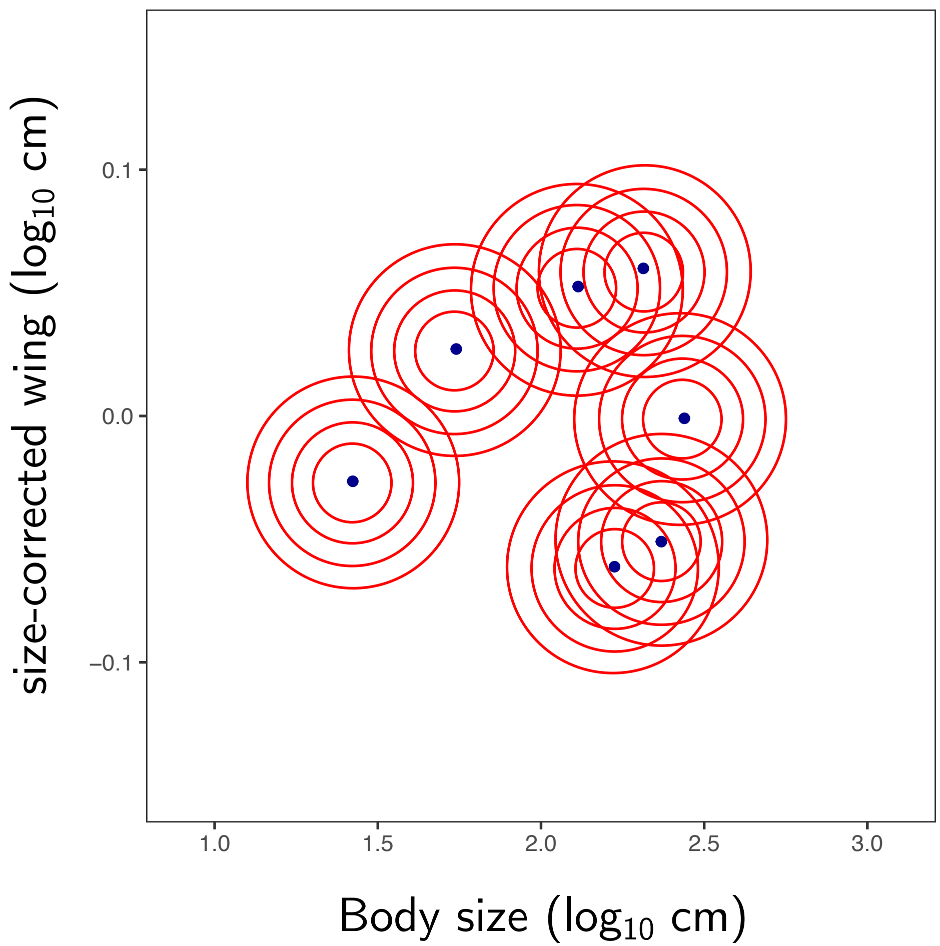
$$h = 1.06\,\hat{\sigma}\,n^{-\frac{1}{5}}$$

Silverman, B.W. Density Estimation for Statistics and Data Analysis (1986) London: Chapman and Hall

3. Overview of the current FD frameworks



...and with two traits...



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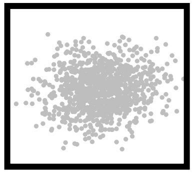
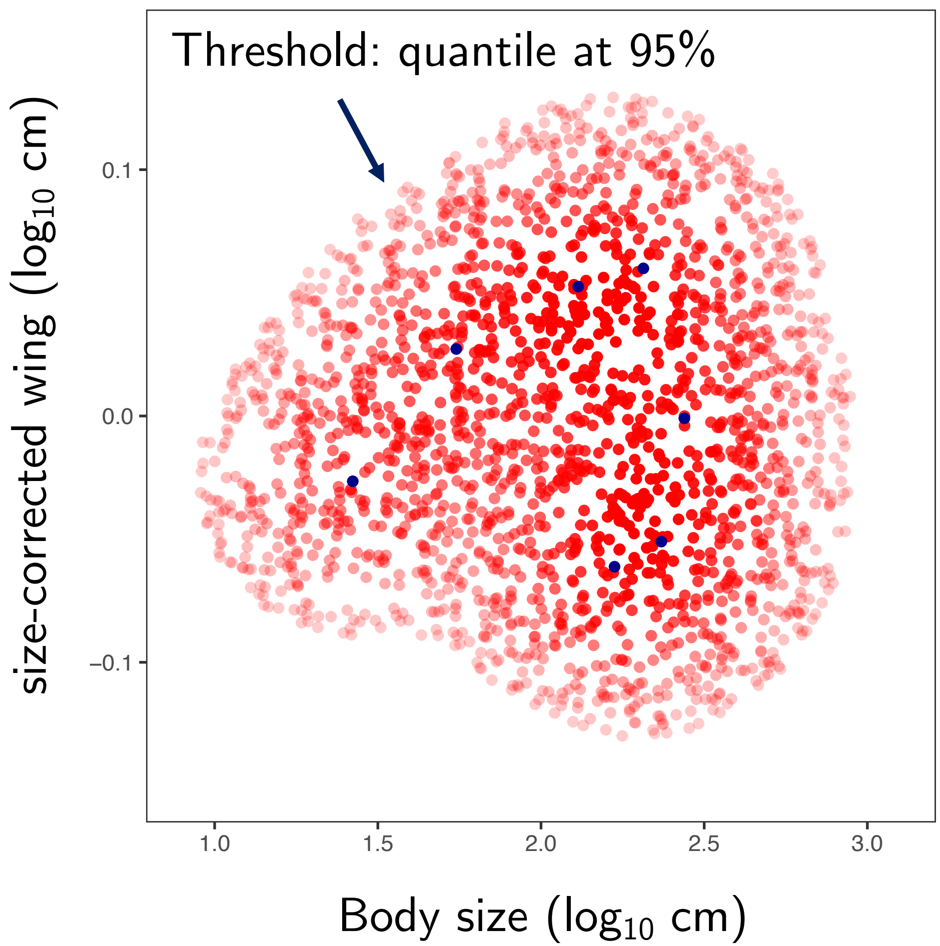


and with two traits...



Ptilinopus huttoni (Austral Islands)

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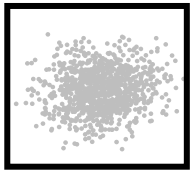
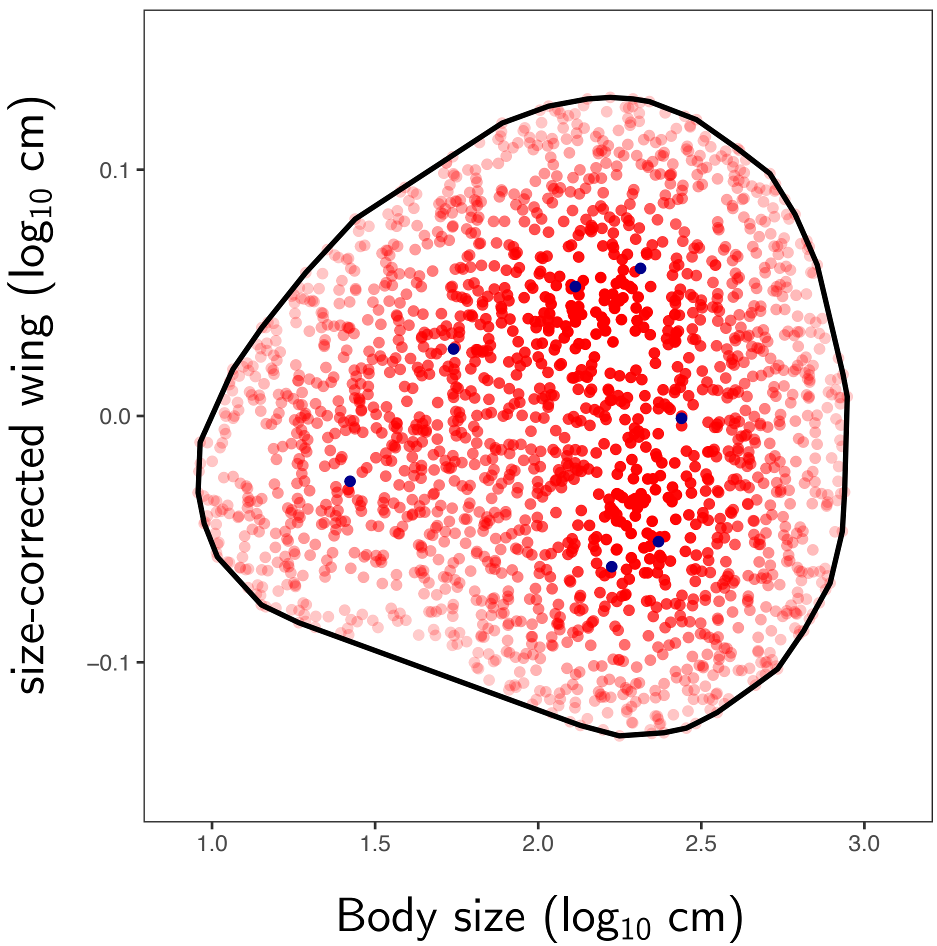


and with two traits...



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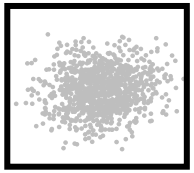

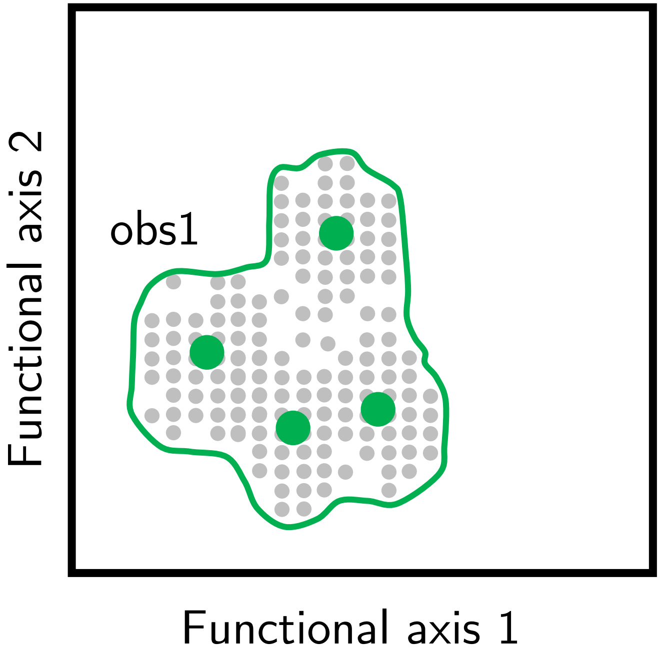

<u>**Incorporating abundance data:**</u>

Each observation can be weighted by replicating it based on its abundance in the estimation of the hypervolume. If Obs1 is replicated 10 times (e.g. 10 individuals for a species), it will appears 10 times during the construction of hypervolume.

All following metrics can be calculated with or without abundance data.

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C., & Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PloS one*, *2*(3), e296.

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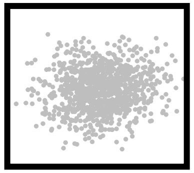
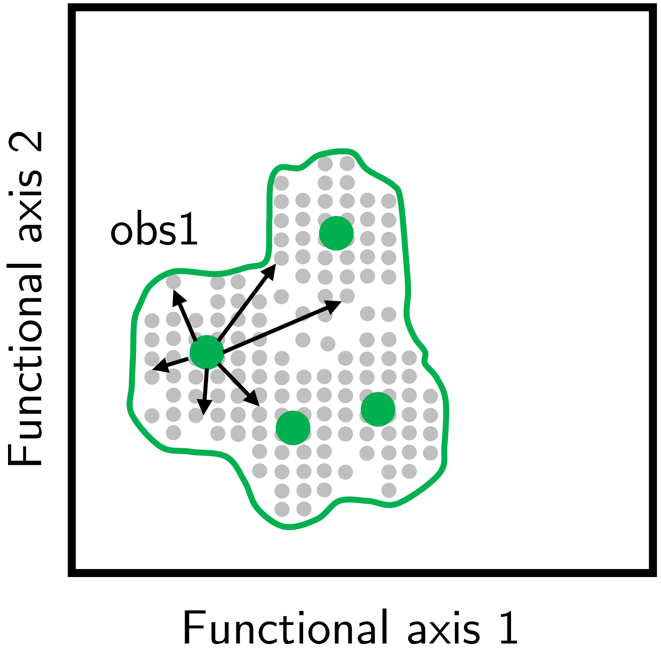


A. Observation-based metrics

For observation 1

Originality$_1$ is average distance between each observation to a sample of stochastic points within the boundaries of the hypervolume

Uniqueness$_1$ $= NA$



Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C., & Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PloS one*, *2*(3), e296.

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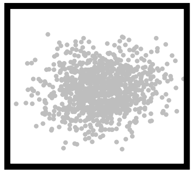
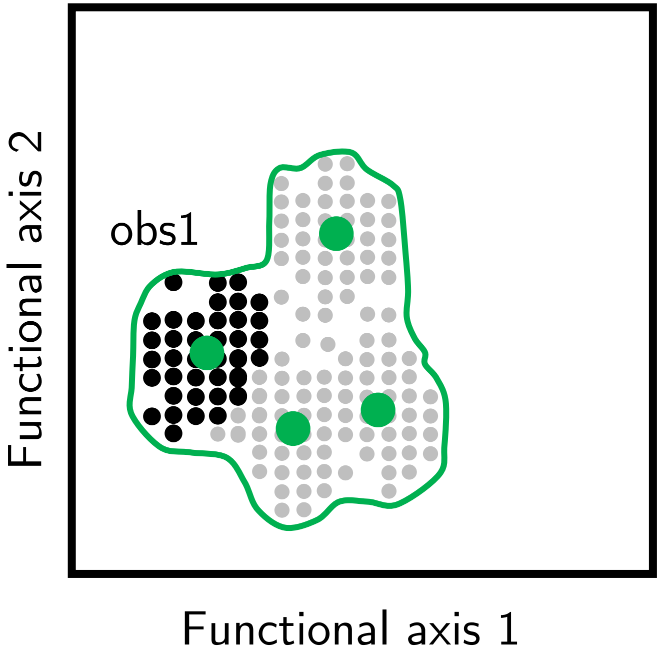


A. Observation-based metrics

For observation 1



Originality$_1$ is average distance between each observation to a sample of stochastic points within the boundaries of the hypervolume

Uniqueness$_1$ = NA

Contribution$_1$ is measured as the proportion of random points that is closer to obs1 multiplied by the total hypervolume of the group.

Contribution can also be measured using the « leave one out » apporach as for convex-hull.

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C., & Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PloS one*, *2*(3), e296.

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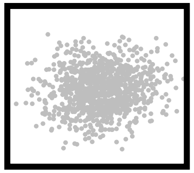
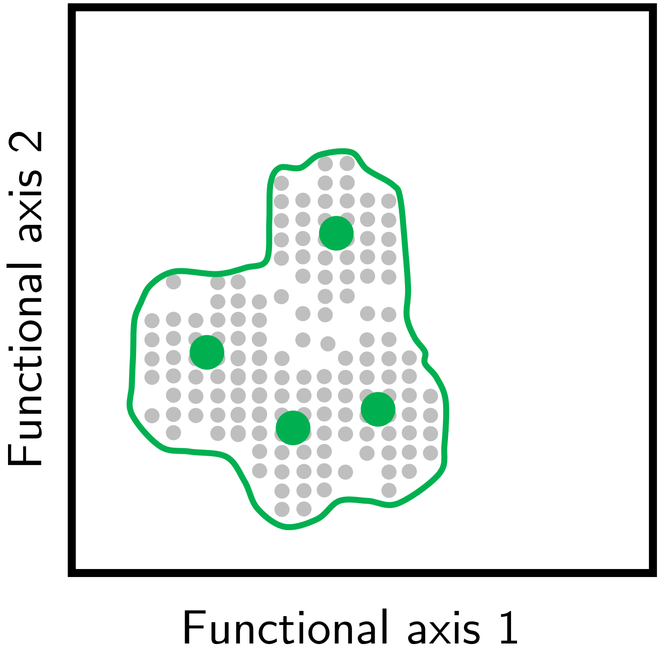


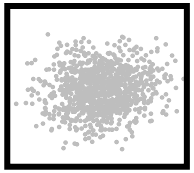
B. Group-based metrics



Richness is the total surface/volume of the functional hyperspace.

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C., & Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PloS one*, *2*(3), e296.

3. Overview of the current FD frameworks



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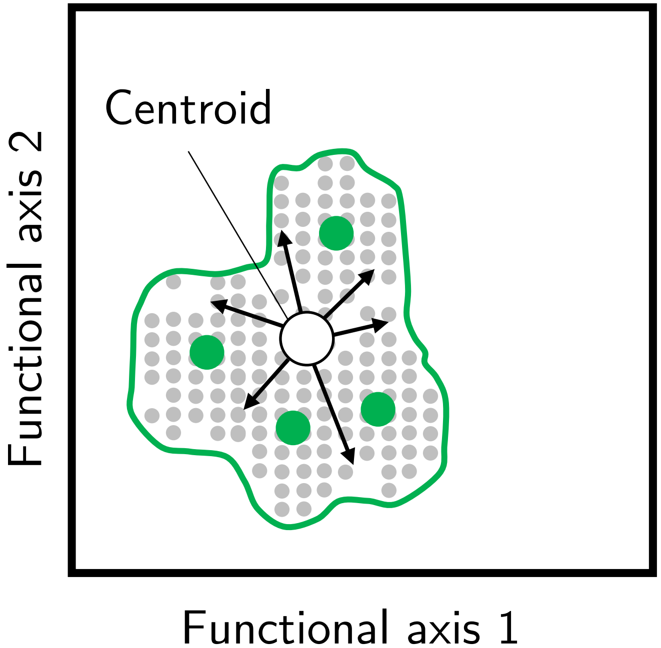
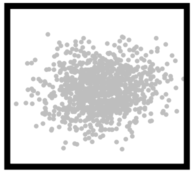


Richness is the total surface/volume of the functional hyperspace.

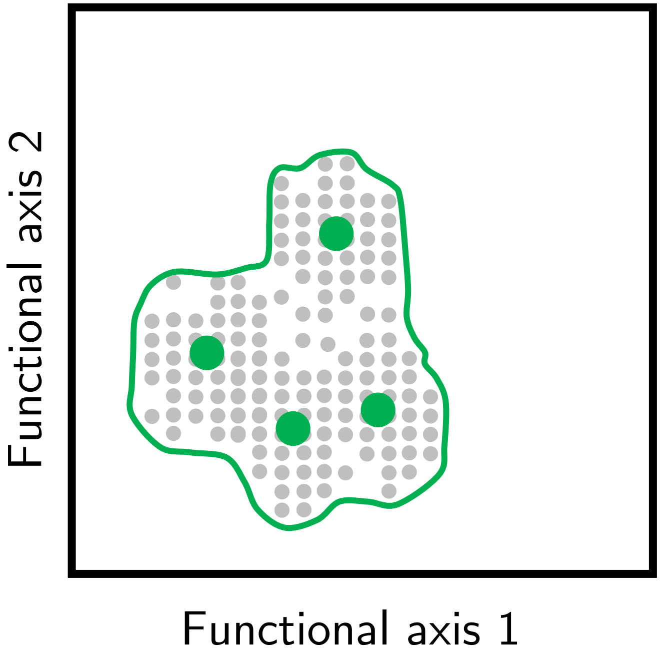
Divergence is calculated as the average distance between a sample of stochastic points and the hypervolume centroid.

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C., & Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PloS one*, *2*(3), e296.

3. Overview of the current FD frameworks



B. Group-based metrics



Richness is the total surface/volume of the functional hyperspace.

Divergence is calculated as the average distance between a sample of stochastic points and the hypervolume centroid.

Evenness is calculated as the overlap between the calculated hypervolume and a second, imaginary hypervolume where traits are evenly distributed within their possible range (and abundance evenly distributed between the observations!)

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C., & Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PloS one*, *2*(3), e296.

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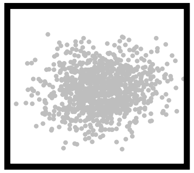

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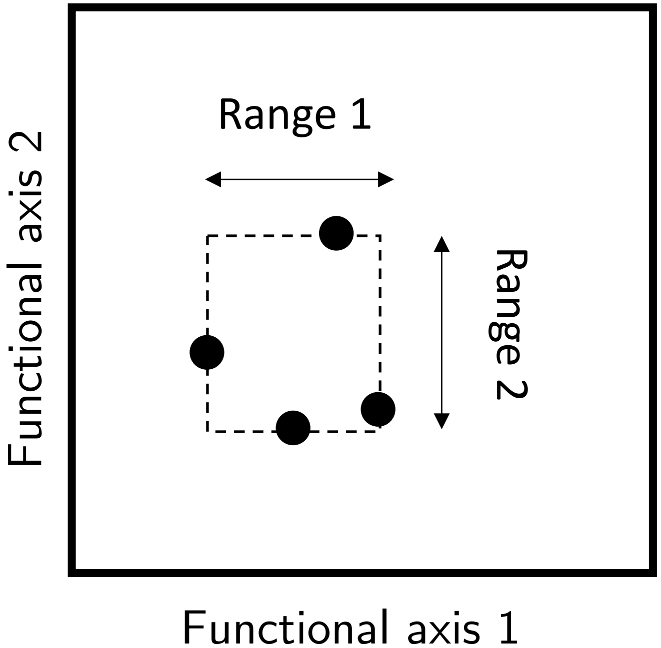

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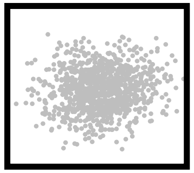

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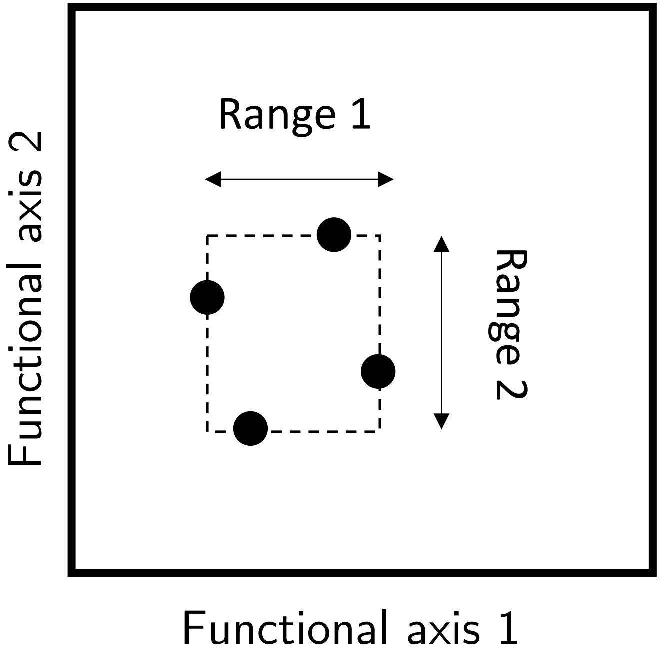

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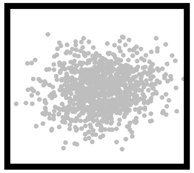

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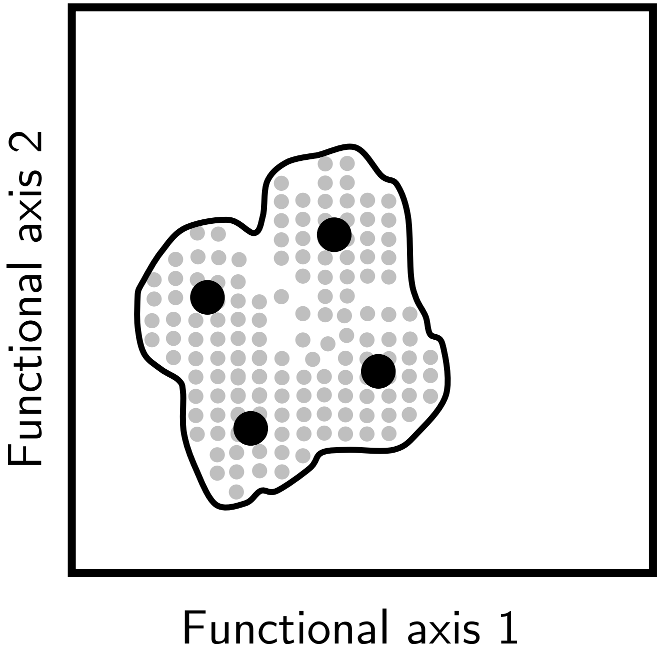

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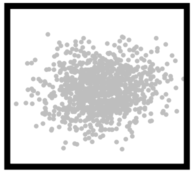

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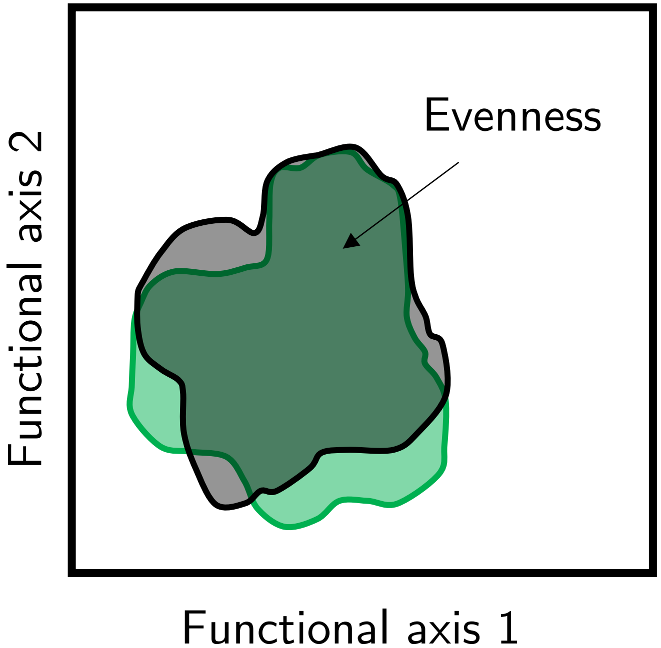

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Divergence is calculated as the average distance between a sample of stochastic points and the hypervolume centroid.

Evenness is calculated as the overlap between the calculated hypervolume and a second, imaginary hypervolume where traits are evenly distributed within their possible range.

If the 2 hypervolumes are the same = overlap is max and evenness is 1.

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C., & Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PloS one*, *2*(3), e296.

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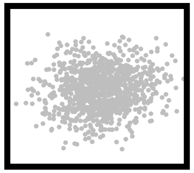
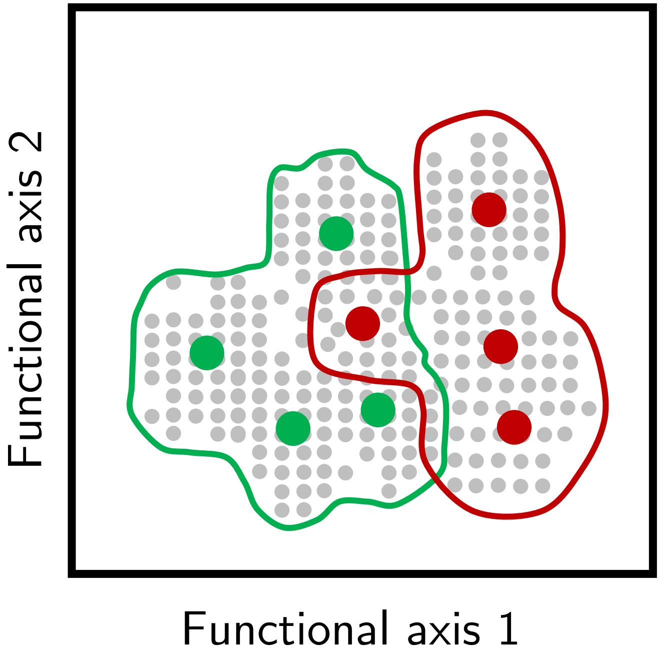


C. Between groups metrics



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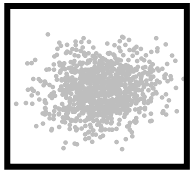

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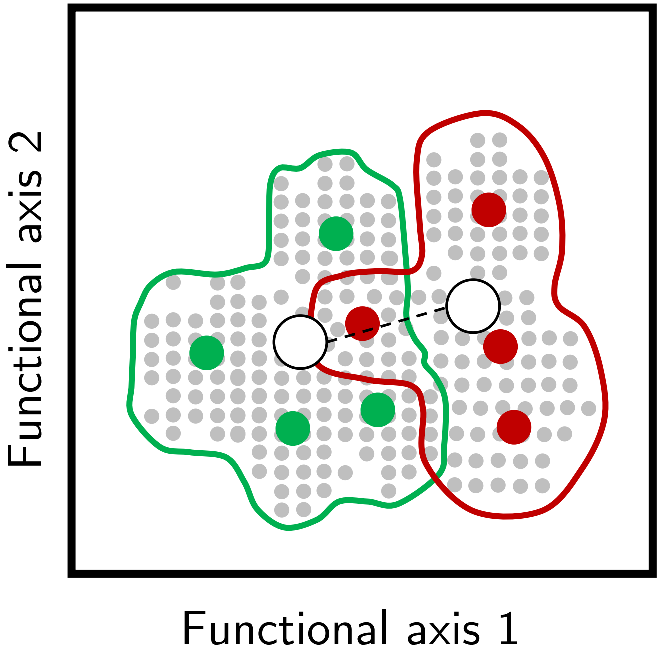

Distance = Still the possibility to calculate the distance between the hypervolume centroids as for the dissimilarity-based framework.

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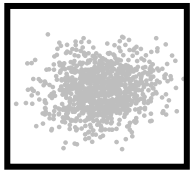

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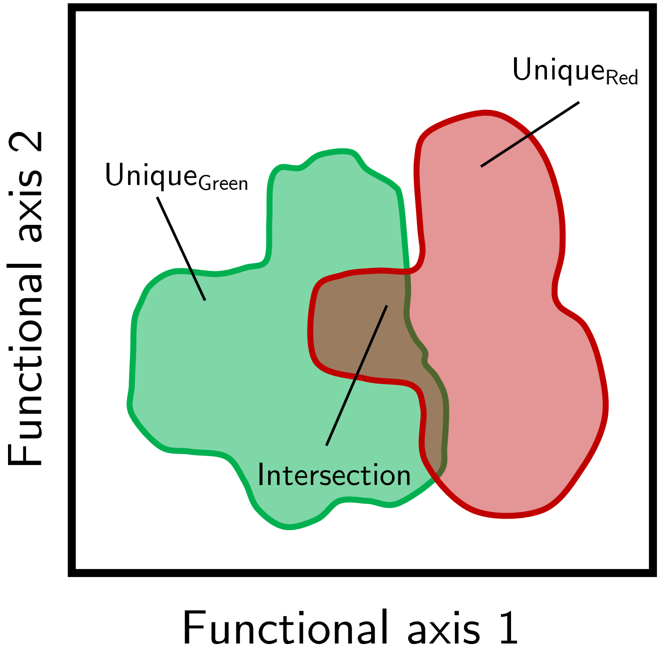


Distance = Still the possibility to calculate the distance between the hypervolume centroids as for the dissimilarity-based framework.

$$Beta\ Jaccard_{G,R} = \frac{Unique_{Green} + Unique_{Red}}{Unique_{Green} + Unique_{Red} + Intersection}$$

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C., & Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PloS one*, *2*(3), e296.

4. Type of traits & distances

4. Type of traits & distances

Traits must be measured or collected in the literature, and depending on the information itself, the instruments or experts involved, the variables will have different characteristics.

1) Continuous variables (quantitative variables): body size, plant height, leaf area, etc.

2) Ordinal variables: small/large; high vs low dispersal ability, etc.

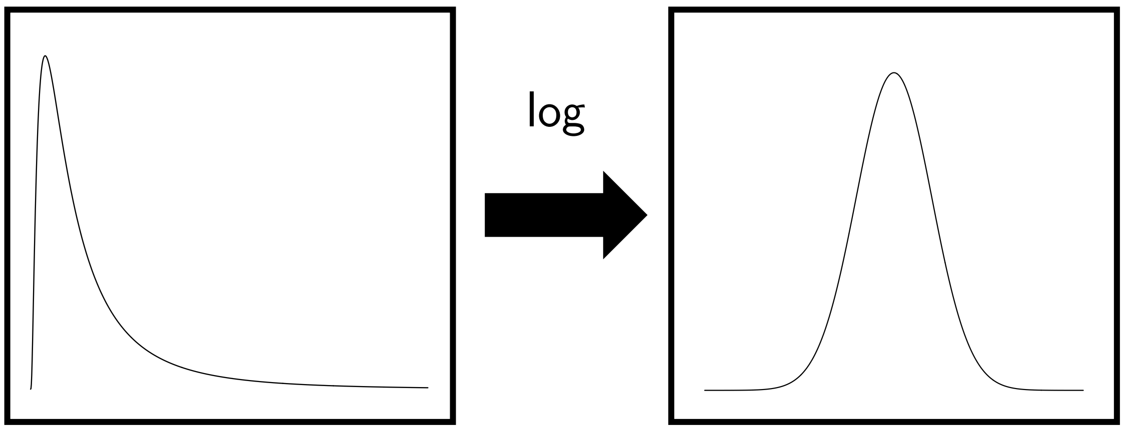
3) Categorical variables (Qualitative variables): colour of the petals feeding behavior (herbivorous, predators), etc.

How to code your functional traits ?

4. Type of traits & distances

1) Continuous variables (quantitative variables):

Almost nothing to do...except transformations to approximate normality and avoid the influence of extreme values



4. Type of traits & distances

2) Ordinal variables:

Obs	Trait
Obs 1	small (1)
Obs 2	medium (2)
Obs 3	large (3)

Replace each category by its rank

4. Type of traits & distances

3) Categorical variables

Obs	Trait
Obs 1	blue
Obs 2	red
Obs 3	green

For the case of dichotomous variables (e.g. YES/NO), possibility to code the trait as a binary variable.

4. Type of traits & distances

3) Categorical variables

Obs	red	blue	green
Obs 1	0	1	1
Obs 2	1	0	0
Obs 3	0	1	0

Multichoice binary variables if some observations belong to multiple categories

4. Type of traits & distances

3) Categorical variables

Obs	red	blue	green
Obs 1	0	1	1
Obs 2	1	0	0
Obs 3	0	1	0

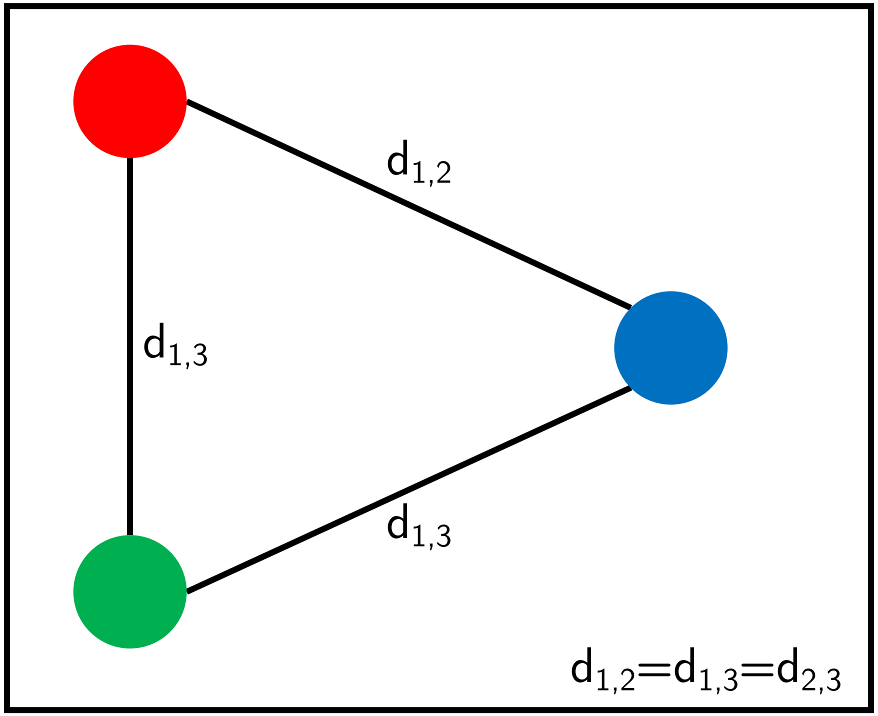
WHY NOT CREATE A NEW CATEGORY BLUE-GREEN?

Multichoice binary variables if some observations belong to multiple categories

4. Type of traits & distances

3) Categorical variables

Obs	Trait
Obs 1	blue
Obs 2	red
Obs 3	green

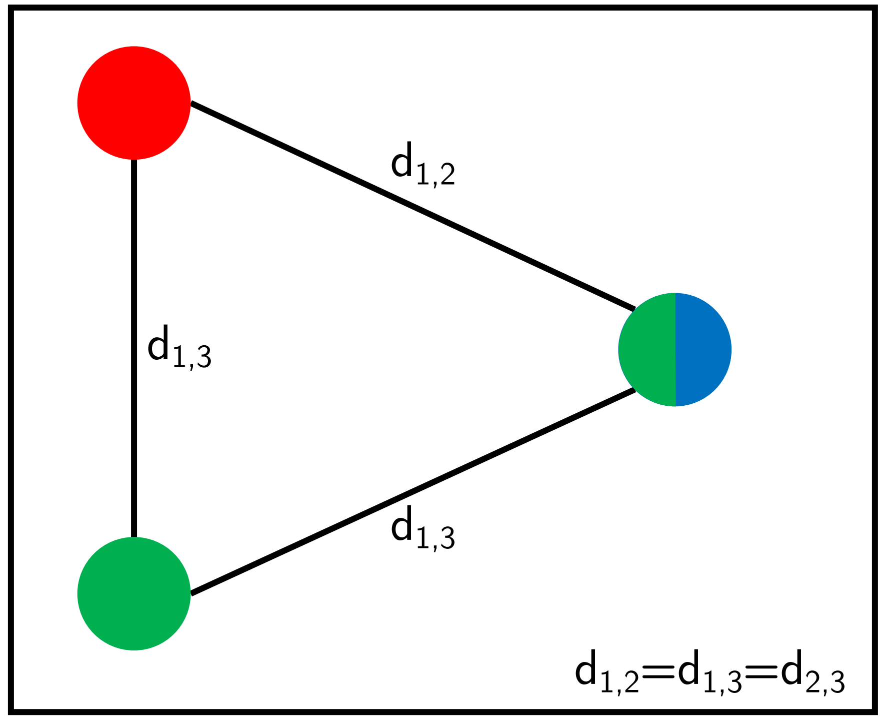


Multichoice binary variables if some observations belong to multiple categories

4. Type of traits & distances

3) Categorical variables

Obs	Trait
Obs 1	blue-green
Obs 2	red
Obs 3	green

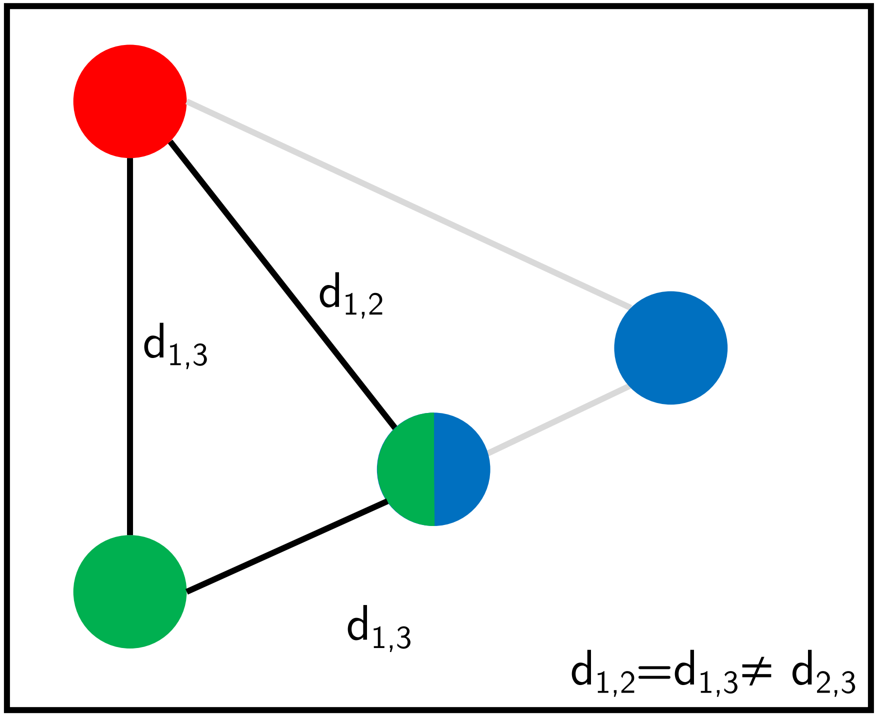


Multichoice binary variables if some observations belong to multiple categories

4. Type of traits & distances

3) Categorical variables

Obs	Trait
Obs 1	blue-green
Obs 2	red
Obs 3	green



Multichoice binary variables if some observations belong to multiple categories

4. Type of traits & distances

3) Categorical variables

Obs	red	blue	green
Obs 1	0	1	1
Obs 2	1	0	0
Obs 3	0	1	0

Multichoice binary variables if some observations belong to multiple categories

4. Type of traits & distances

3) Categorical variables

Obs	auto	insect	wind	
Obs 1	0.3	0.3	0.4	$\sum = 1$
Obs 2	0	0.5	0.5	$\sum = 1$
Obs 3	0.8	0	0.2	$\sum = 1$

Example: for plant, respective frequency of autopollination, pollination by insects and pollination by wind.

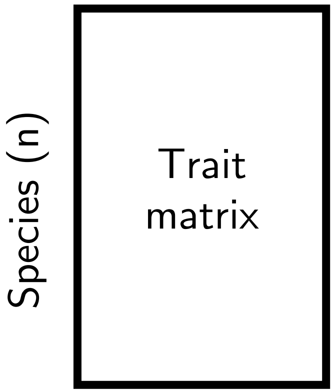
Fuzzy coding if observations belong to more than one category and each category can be expressed as a proportion.

Chevene, F., Doleadec, S., & Chessel, D. (1994). A fuzzy coding approach for the analysis of long-term ecological data. *Freshwater biology*, *31*(3), 295-309.

The question of the distance

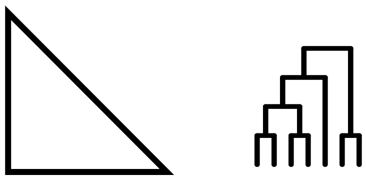
4. Type of traits & distances

The question of the distance

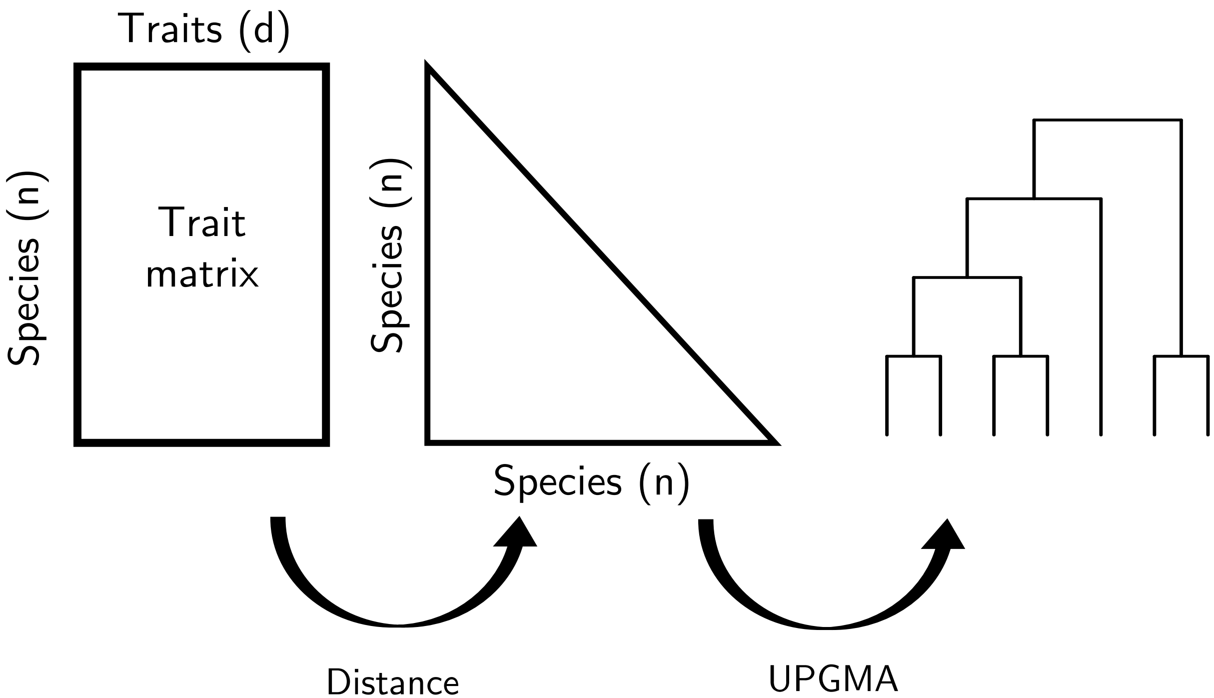


4. Type of traits & distances

The question of the distance



Dissimilarity-based framework *(non-dimensional approach)*



4. Type of traits & distances

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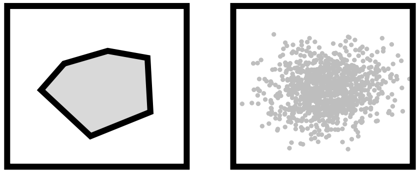
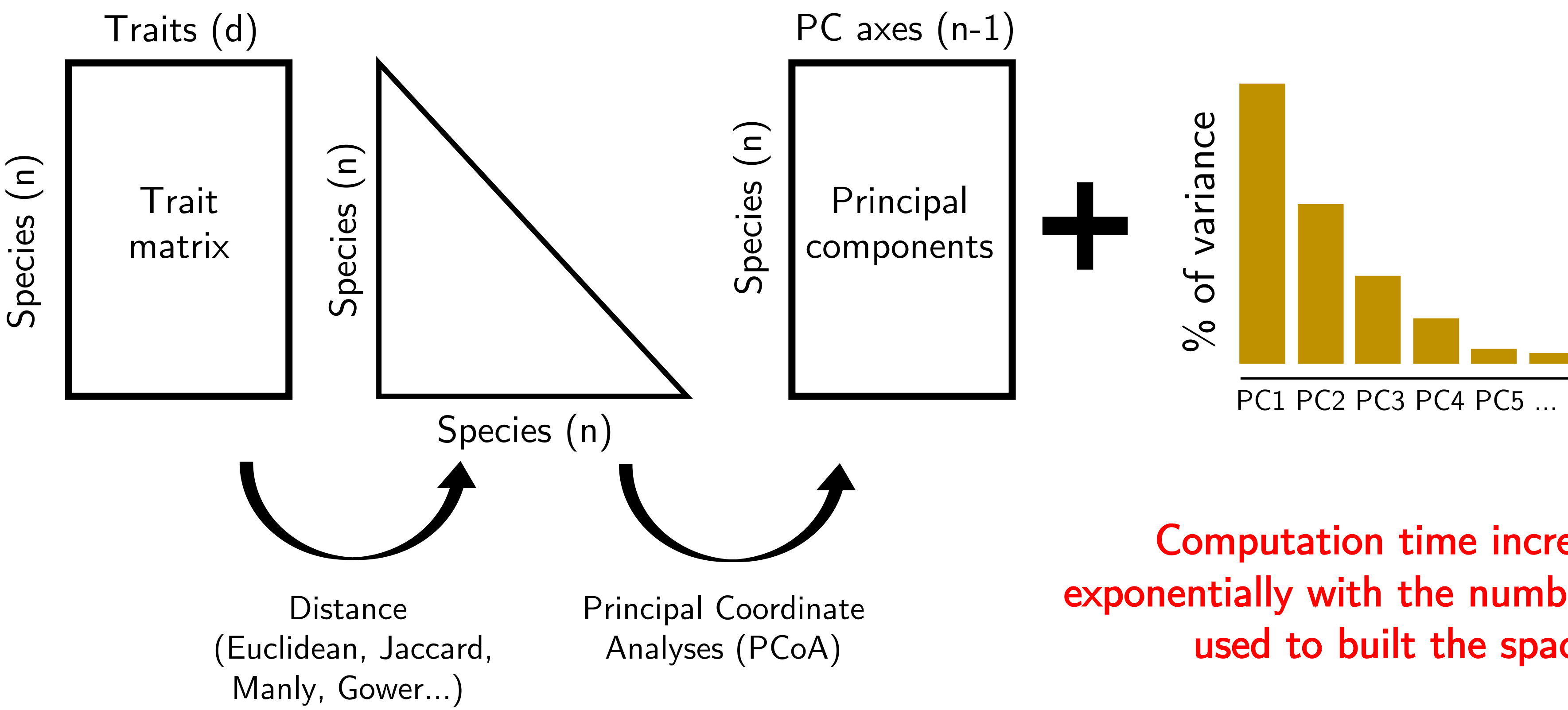


Multidimensional space framework *(hypervolumes)*

How can I get independent functional axes from the trait matrix to create my multidimensional space?



Computation time increases exponentially with the number of axes used to built the space.

The question of the distance

If all traits are continuous = **Euclidean distance**

$$d(p,q) = \sqrt{(p_1 - q_1)^2 + (p_2 - q_2)^2 + \ldots + (p_n - q_n)^2}$$

Obs	body length (mm)	antenna (mm)
Obs 1	10	1.5
Obs 2	20	1.3
Obs 3	30	1.4

	Obs 1	Obs 2
Obs 2	10.002	
Obs 3	20.00025	10.0005

The question of the distance

If all traits are continuous = **Euclidean distance**

Data need to be scaled for the measurements to have the same weight.

$$(x_i - \mu)/\sigma$$

Obs	body length (mm)	antenna (mm)
Obs 1	-1	1
Obs 2	0	-1
Obs 3	1	0

Body length for Obs 1 becomes (10-20)/10 = -1

Antenna for Obs 1 becomes (1.5-1.4)/0.1 = 1

	Obs 1	Obs 2
Obs 2	2.24	
Obs 3	2.24	1.41

The question of the distance

If all traits are multichoice variables = **Jaccard's distance**

$$D_{ij} = \frac{b+c}{a+b+c}$$

a= number of categories common to obs *i* and *j*
b= number of categories exclusive to the obs *i*
c= number of categories exclusive to the obs *j*

The question of the distance

If all traits are multichoice variables = **Jaccard's distance**

$$D_{ij} = \frac{b+c}{a+b+c}$$

a= number of categories common to obs *i* and *j*
b= number of categories exclusive to the obs *i*
c= number of categories exclusive to the obs *j*

Species	red	blue	green
Obs 1	0	1	1
Obs 2	1	0	0
Obs 3	0	1	0

$$D_{1,2} = \frac{2+1}{0+2+1} = 1$$

$$D_{1,3} = \frac{1+1}{1+1+1} = 0.66$$

$$D_{2,3} = \frac{1+1}{0+1+1} = 1$$

The question of the distance

If all traits are fuzzy variables = **Manly's distance**

$$D_{ij} = \left. 1 - \sum_{m=1}^{M} p_{im} p_{jm} \middle/ \sqrt{\sum_{m=1}^{M} p_{im}^2 \sum_{m=1}^{M} p_{jm}^2} \right.$$

M= number of categories
p_{im} = proportion of the category m for the obs i
p_{jm} = proportion of the category m for the obs j

Obs	auto	insect	wind
Obs 1	0.3	0.3	0.4
Obs 2	0	0.5	0.5
Obs 3	0.8	0	0.2

$$D_{1,2} = 1 - \frac{(0.3\times0.5 + 0.4\times0.5)}{\sqrt{(0.3^2 + 0.3^2 + 0.4^2)\times(0.5^2 + 0.5^2)}} = 0.15$$

$$D_{1,3} = 1 - \frac{(0.3\times0.8 + 0.4\times0.2)}{\sqrt{(0.3^2 + 0.3^2 + 0.4^2)\times(0.8^2 + 0.2^2)}} = 0.33$$

$$D_{2,3} = 1 - \frac{(0.5\times0.2)}{\sqrt{(0.5^2 + 0.5^2)\times(0.8^2 + 0.2^2)}} = 0.82$$

Pavoine, S., & Dolédec, S. (2005). The apportionment of quadratic entropy: a useful alternative for partitioning diversity in ecological data. Environmental and Ecological Statistics, 12(2), 125-138.

4. Type of traits & distances

The question of the distance

But if you have different types of traits in your trait matrix?

The Gower's distance

$$D_{ij} = \sqrt{1 - \frac{\sum_{k=1}^{n} s_{ijk}\delta_{ijk}w_k}{\sum_{k=1}^{n} \delta_{ijk}w_k}}$$

n is the number of variables (traits).
s_{ijk} is the similarity between species i and j for the trait k.
$\delta_{ijk} = 0$ if information is missing for at least one species and 1 if the information is availbale for the two species.
w_k is the variable weights.

The question of the distance

The only distance capable to handle ordinal and strict categorical traits

Obs	Trait 1	Trait 2
Obs 1	A	C
Obs 2	B	D
Obs 3	B	E

$$D_{12} = \sqrt{1 - \frac{(0)+(0)}{(2)}} = 1$$

$$D_{13} = \sqrt{1 - \frac{(0)+(0)}{(2)}} = 1$$

$$D_{23} = \sqrt{1 - \frac{(1)+(0)}{(2)}} = 0.5$$

The question of the distance

Pavoine et al. (2009) propose to use the Gower's distance formula as a framework to create a generalized index of dissimilarity for functional traits.

Research

Oikos 118: 391–402, 2009
doi: 10.1111/j.1600-0706.2008.16668.x,

Subject Editor: Owen Petchey. Accepted 30 September 2008

On the challenge of treating various types of variables: application for improving the measurement of functional diversity

Sandrine Pavoine, Jeanne Vallet, Anne-Béatrice Dufour, Sophie Gachet and Hervé Daniel

Sandrine Pavoine

4. Type of traits & distances

The question of the distance

Pavoine et al. (2009) propose to use the Gower's distance formula as a framework to create a generalized index of dissimilarity for functional traits.

- Identify the most adapted distance for each type of trait
- Standardize each distance to obtain dissimilarities bounded between 0 and 1
- Average distance matrices of each trait to obtain a global functional dissimilarity distance (= the Gower's distance)
- Provide simple and intuitive tools to evaluate: (1) correlation between distances and (2) contribution of the distances to the global distance.

The question of the distance

Examples of standardization

For continuous variables:

$$d_{ij} = \sqrt{\frac{1}{n} \sum\nolimits_{k=1}^{n} (z_{ik} - z_{jk})^2}$$

$$z_{ik} = \frac{x_{ik}}{R_k}$$

R is the range of the variable k

For ordinal variables:

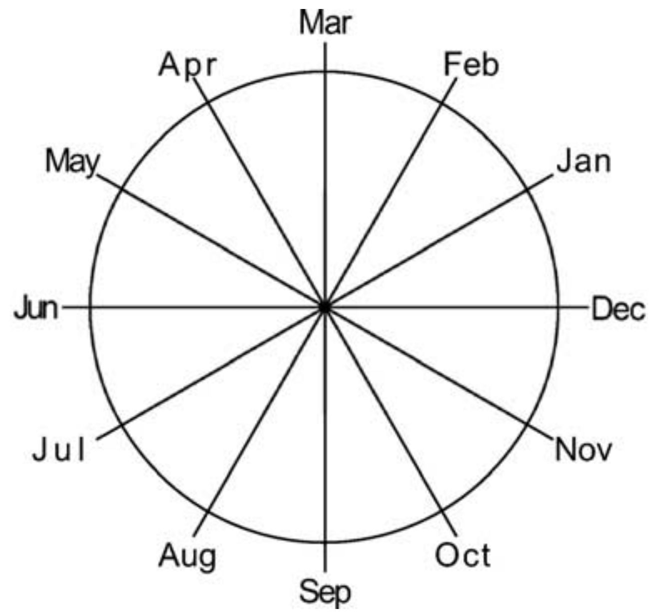
$$d_{ij} = \sqrt{\frac{1}{n} \sum\nolimits_{k=1}^{n} |z_{ik} - z_{jk}|}$$

4. Type of traits & distances

The question of the distance

The "tricky" case of circular traits

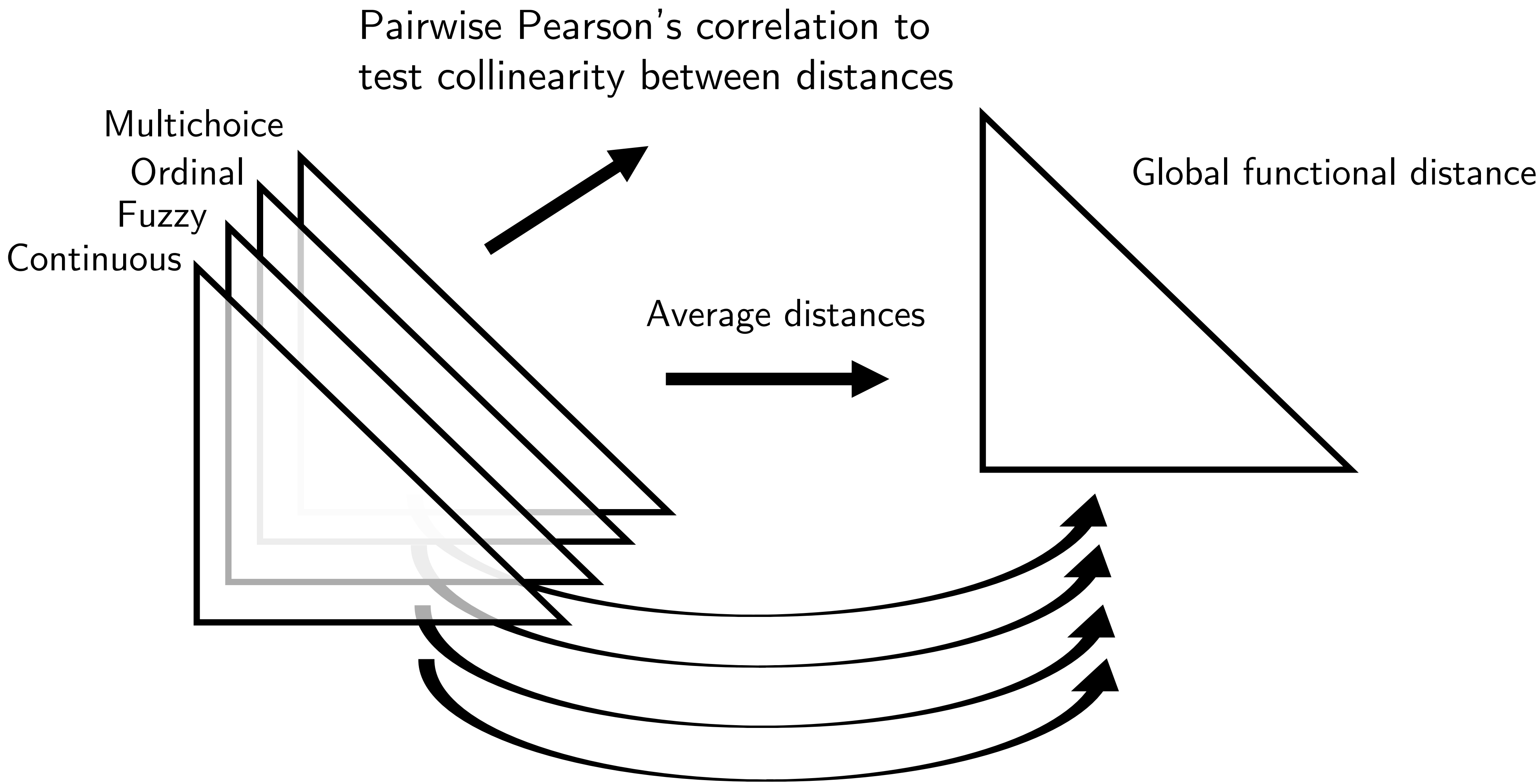
Obs	Trait
Obs 1	March
Obs 2	June
Obs 3	December



The maximum distance is a time lag of 6 months and not 12

4. Type of traits & distances

The question of the distance

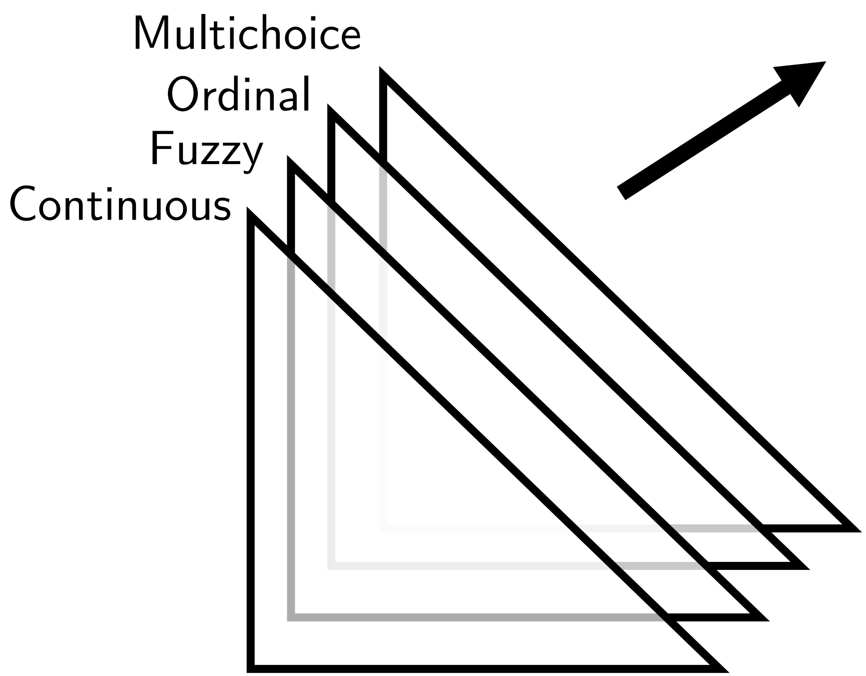


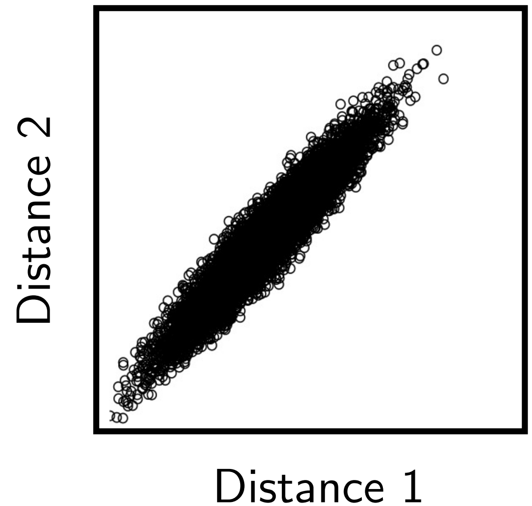
Contribution = Pearson's correlation between each distance and the global distance.

4. Type of traits & distances

The question of the distance

Pairwise Pearson's correlation to test collinearity between distances



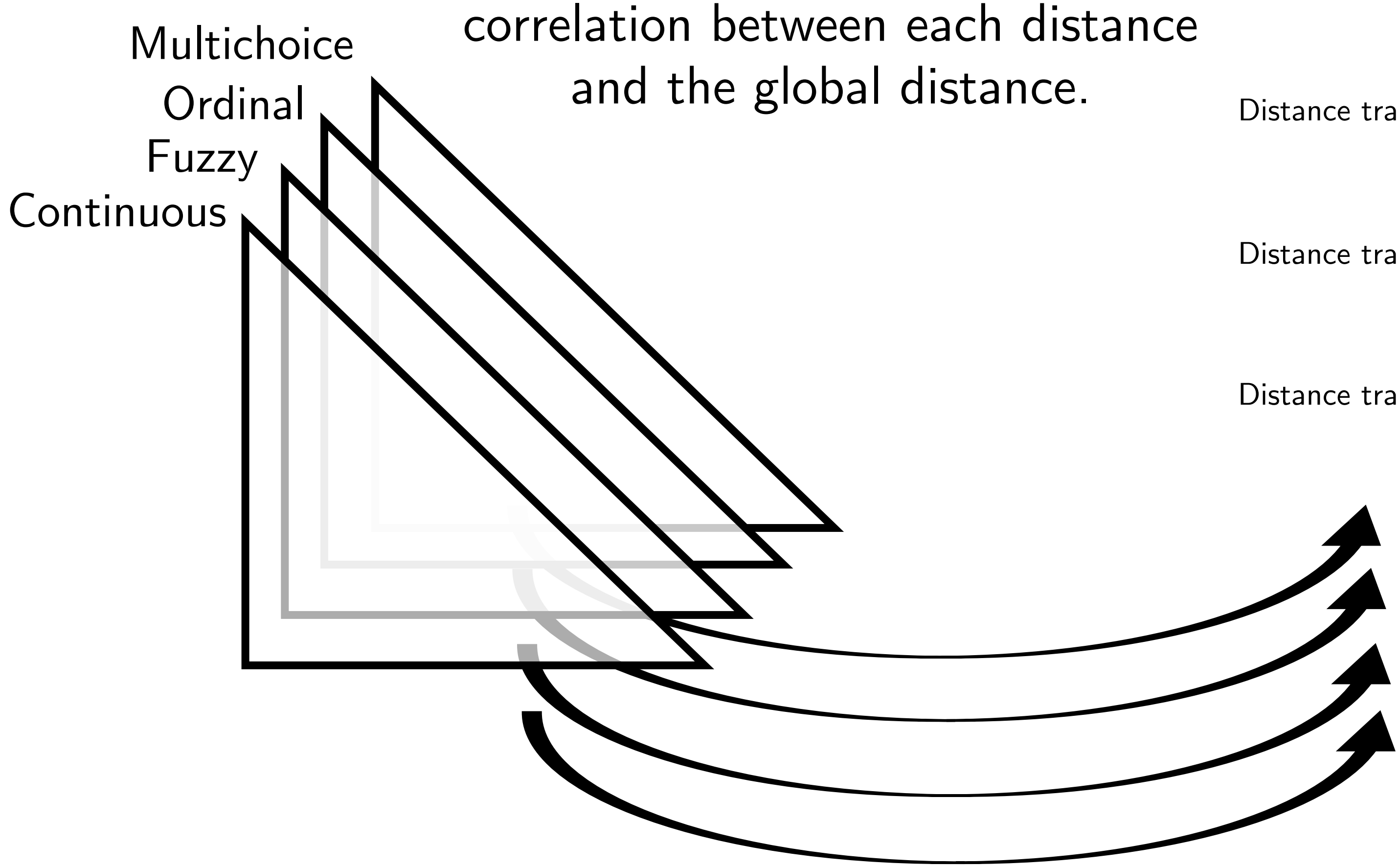


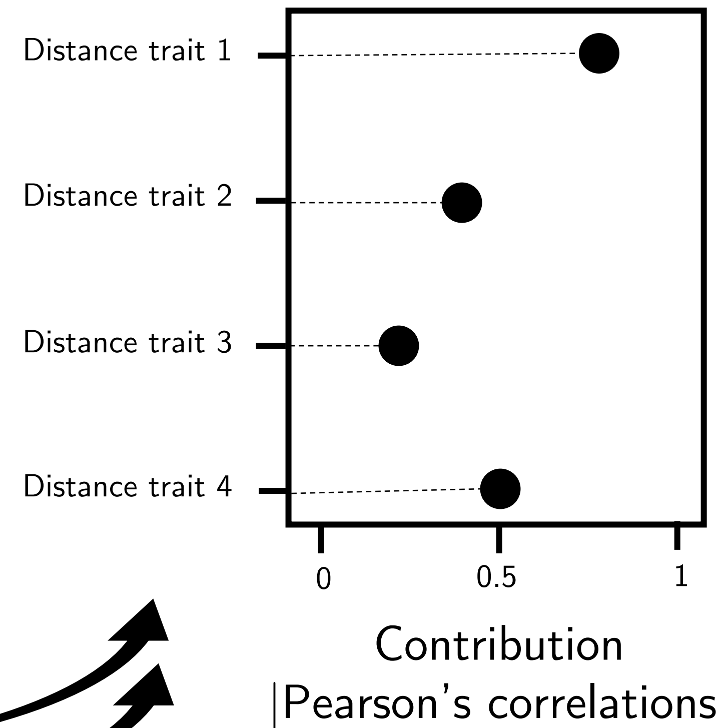
If some pairs of distances are highly correlated ($|r>0.7|$), one of the two can be removed.

4. Type of traits & distances

The question of the distance

Contribution = Pearson's correlation between each distance and the global distance.





The question of the distance

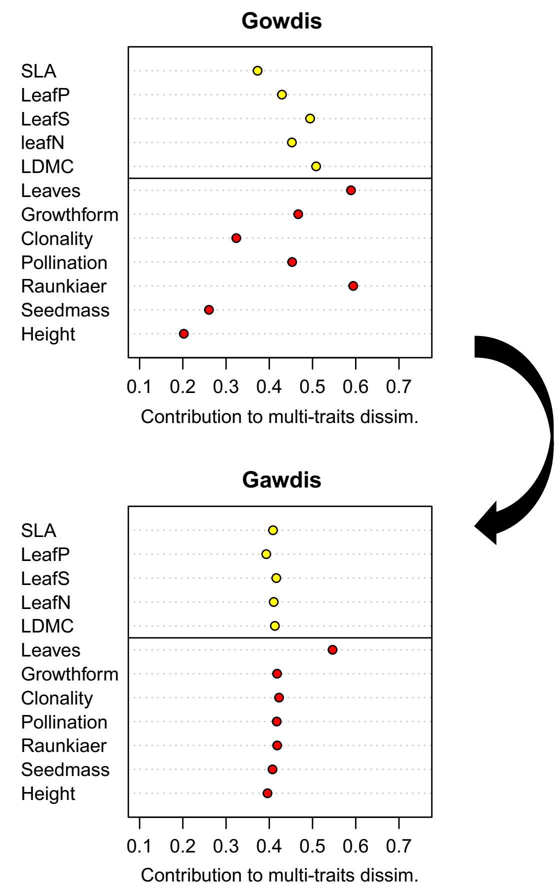
The new method *Gawdis* to rebalance the contributions of the traits to the global functional dissimilarity matrix.

APPLICATION

Methods in Ecology and Evolution BRITISH ECOLOGICAL SOCIETY

Towards a more balanced combination of multiple traits when computing functional differences between species

Francesco de Bello[1,2] | Zoltán Botta-Dukát[3] | Jan Lepš[2,4] | Pavel Fibich[2,5]



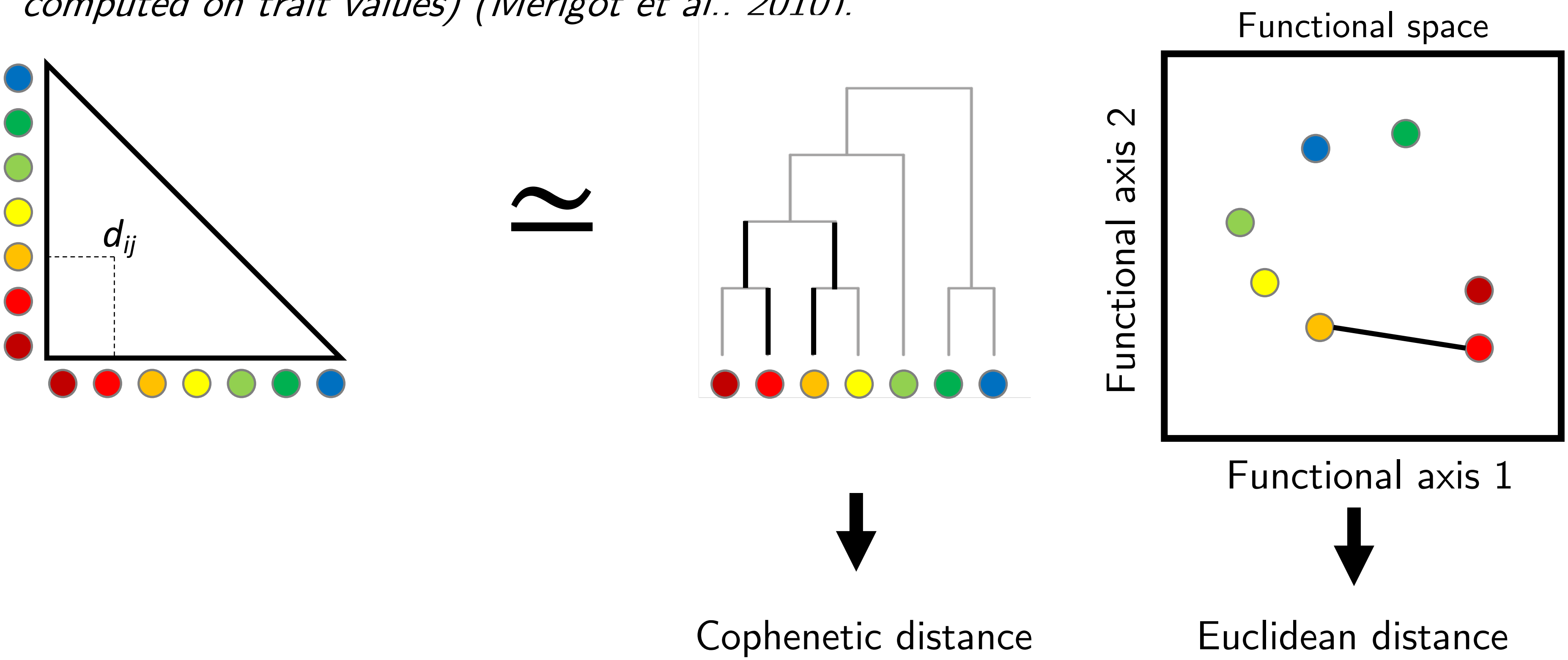
Based genetic analyses that explores several sets of weights of traits in the global distance and select to new weights that will cause the minimal standard deviation of correlations.

Implemented for the Gower's distance but not the framework of Pavoine et al. 2009.

4. Type of traits & distances

Assessing the reliability of the functional space with the original matrix ?

"A functional space of high quality is a functional space where distance between each pair of species is congruent with the initial functional distance (i.e. Gower's or Euclidean distance computed on trait values) (Mérigot et al.. 2010)."



Maire, E. et al. (2015). How many dimensions are needed to accurately assess functional diversity? A pragmatic approach for assessing the quality of functional spaces. *Global Ecology and Biogeography*, *24*(6), 728-740. Mérigot, B et al. (2010). On goodness-of-fit measure for dendrogram-based analyses. Ecology, 91(6), 1850-1859.

4. Type of traits & distances

Assessing the reliability of the functional space with the original matrix ?

Compute the Pearson's correlation between the original distance matrix and the distance within the new space.

$r = 1$ when the functional space (tree or hypervolume) perfectly represents the initial distance.

$r = 0$ and $r < 0$ when pairs of species are poorly represented in the functional space, i.e. when species with similar trait values are far in the functional space or alternatively when species with different trait values are close in the functional space.

4. Type of traits & distances

Assessing the reliability of the functional space with the original matrix ?

Mean squared deviation

$$mSD = \frac{\sum_{i=1}^{S-1}\sum_{j=i+1}^{S}\left(x_{ij} - y_{ij}^{st}\right)^2}{\frac{S\times(S-1)}{2}}$$

mSD	Mean squared deviation index
S	the number of species
x_{ij}	distance between species i and j in the original matrix
y_{ij}^{st}	standardized distance between species i and j in the new spaces matrix

$$y_{ij}^{st} = \frac{y_{ij}}{max\left(y_{ij}\right)} \times max\left(x_{ij}\right)$$

4. Type of traits & distances

Assessing the reliability of the functional space with the original matrix ?

mSD $= 0$ when the functional space (tree or hypervolume) perfectly represents the initial distance.

mSD > 0 when pairs of species are poorly represented in the functional space, i.e. when species with similar trait values are far in the functional space or alternatively when species with different trait values are close in the functional space.

4. Type of traits & distances

Which traits ?

« All traits that are important for the functions of interest and no traits that are functionally uninformative ».

From Petchey, O. L., & Gaston, K. J. (2006). Functional diversity: back to basics and looking forward. Ecology letters, 9(6), 741-758.

Biology should prevail but...

4. Type of traits & distances

How many traits ?

The best combinations of traits or (PC) dimensions that maximize the correlation or minimize mSD between the functional space and the original distance. According to Maire et al; 2015, functional spaces having at least four dimensions have the highest quality.

Global Ecology and Biogeography, (Global Ecol. Biogeogr.) (2015) **24**, 728–740

MACROECOLOGICAL METHODS

How many dimensions are needed to accurately assess functional diversity? A pragmatic approach for assessing the quality of functional spaces

Eva Maire[1], Gaël Grenouillet[2], Sébastien Brosse[2] and Sébastien Villéger[1]*

For Hull and probabilistic hypervolume, we also need to limit the number of dimensions due to computations times.

4. Type of traits & distances

...and if you want to do it for a single trait?

Possibility to calculate the mean and the dispersion for a single trait

	Body size	Diet	Abundance	Relative Abundance
Obs1	1	Herbivores	5	0.25
Obs2	2	Carnivores	10	0.5
Obs3	3	Carnivores	3	0.15
Obs4	4	Herbivores	2	0.1

4. Type of traits & distances

…and if you want to do it for a single trait?

	Body size	Diet	Abundance	Relative Abundance
Obs1	1	Herbivores	5	0.25
Obs2	2	Carnivores	10	0.5
Obs3	3	Carnivores	3	0.15
Obs4	4	Herbivores	2	0.1

For body size:

Community weighted mean (CWM)

$$\sum_{i=1}^{S} p_i x_i = 1\times 0.25 + 2\times0.5 + 3\times0.15 + 4\times0.1 = 2.1$$

Community weighted dispersion (CWD)

$$\sqrt{\sum_{i=1}^{S} p_i (x_i - \bar{x})^2} = \sqrt{0.25\times(1 - 2.1)^2 \ldots} = 0.88$$

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C., & Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PloS one*, *2*(3), e296.

4. Type of traits & distances

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Obs3	3	Carnivores	3	0.15
Obs4	4	Herbivores	2	0.1

For Diet:

Dummy variables

	Body size	Herbivores	Carnivores	Abundance	Relative Abundance
Obs1	1	1	0	5	0.25
Obs2	2	0	1	10	0.5
Obs3	3	0	1	3	0.15
Obs4	4	1	0	2	0.1

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C., & Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PloS one*, *2*(3), e296.

4. Type of traits & distances

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	Body size	Herbivores	Carnivores	Abundance	Relative Abundance
Obs1	1	1	0	5	0.25
Obs2	2	0	1	10	0.5
Obs3	3	0	1	3	0.15
Obs4	4	1	0	2	0.1

For herbivores (here handled as quantitative variables):

Community weighted mean (CWM)

$$\sum_{i=1}^{S} p_i x_i = 1\times 0.25 + 0\times 0.5 + 1\times 0.15 + 0\times 0.1 = 0.35$$

Community weighted dispersion (CWD)

$$\sqrt{\sum_{i=1}^{S} p_i (x_i - \bar{x})^2} = \sqrt{0.25\times(1-0.35)^2 \ldots} = 0.47$$

Moretti, M., De Cáceres, M., Pradella, C., Obrist, M. K., Wermelinger, B., Legendre, P., & Duelli, P. (2010). Fire-induced taxonomic and functional changes in saproxylic beetle communities in fire sensitive regions. Ecography, 33(4), 760-771.

6. Trait-based community assembly & null models

Trait-based community assembly

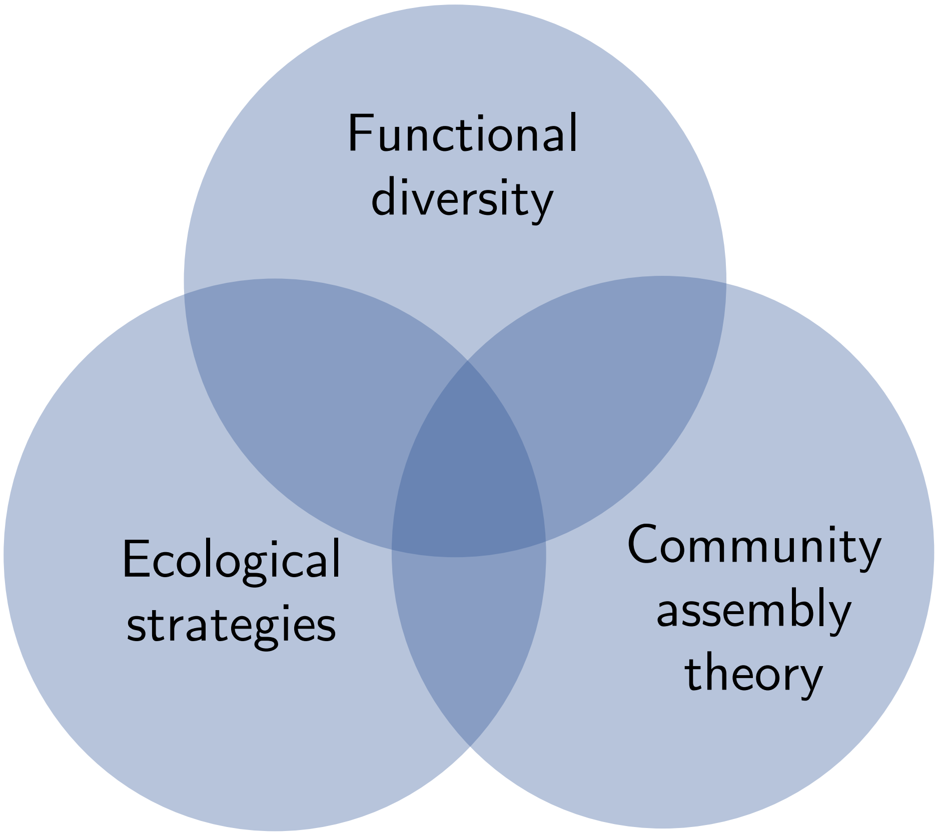
Ana SANTOS (Monday, 25th)

Island community-assembly rules

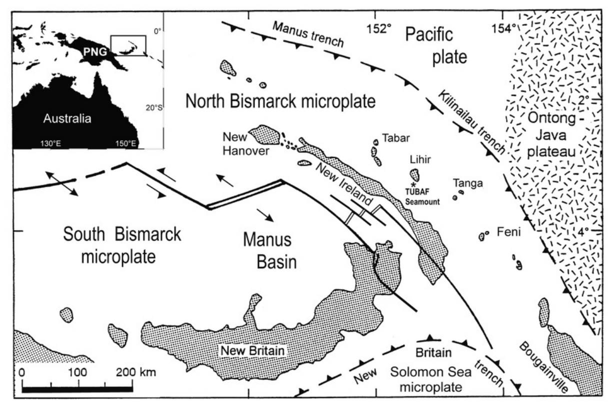
Ackerly, D. D., & Cornwell, W. K. (2007). A trait-based approach to community assembly: partitioning of species trait values into within-and among-community components. *Ecology letters*, *10*(2), 135-145.

6. Trait-based community assembly & null models

Trait-based community assembly



Assembly rules encompass all ecological processes favouring or limiting the species co-occurrence at "local" scales [Interaction (e.g. competition, predation, mutualism) and environmental conditions.



Ackerly, D. D., & Cornwell, W. K. (2007). A trait-based approach to community assembly: partitioning of species trait values into within-and among-community components. *Ecology letters*, *10*(2), 135-145.

Diamond, J. M. 1975. Assembly of species communities. In: Cody, M. L. and Diamond, J. M. (eds), Ecology and evolution of communities. Harvard Press, pp. 342-444.

6. Trait-based community assembly & null models

Two key processes:

1. Habitat filtering → role of abiotic factors

2. Competitive exclusion → role of biotic factors

6. Trait-based community assembly & null models

1. Habitat filtering:

Is FD of my community lower than expect by chance ?

No → My community is a random assortment of species from the pool. No association between traits and local conditions.

Yes → Some ecological filters constrain species co-occurring in my community to share some functional attributes (i.e. selection of species with similar ecological features).

6. Trait-based community assembly & null models

1. Competitive exclusion:

Is FD of my community higher than expect by chance ?

No → My community is a random assortment of species from the pool. No association between traits and local conditions.

Yes → High functional differentiation among co-occuring species in my community which is consistent with the hypothesis of limiting similarity (i.e. the results of past competitions).

Null Models in process inferences

Null models are pattern-generating models that deliberately exclude a mechanism of interest, and allow for randomization tests of ecological and biogeographic data.

For Trait-based community assembly : To detect and to test the signature of species interactions (e.g. competitive exclusion) and habitat filters.

Null Models in process inferences

Four steps:

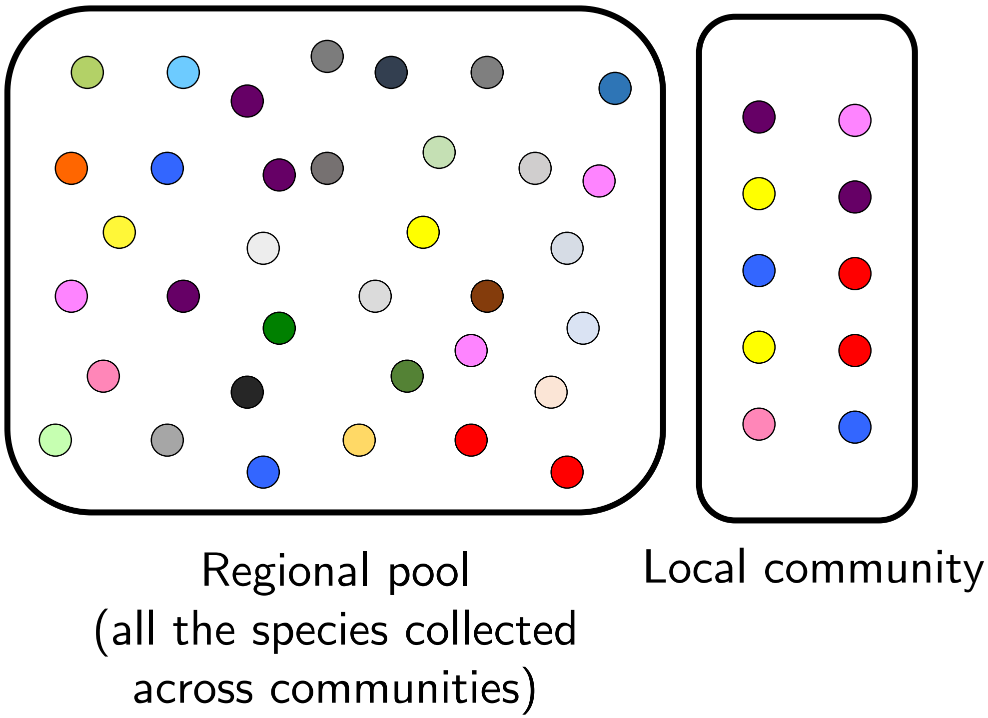
1. Calculate an index with the data (Richness, Dispersion, Regularity);
2. Exclude the mechanism of interest using some rules (here we will break the association between trait and co-occurrence).
3. Calculate the index for the new data n times;
4. Compare the true index with the n recalculated. The position of the true index reveals the probability that it is important (p-value).

Null Models in process inferences

Can a model without the excluded mechanism still reveal the same patterns?

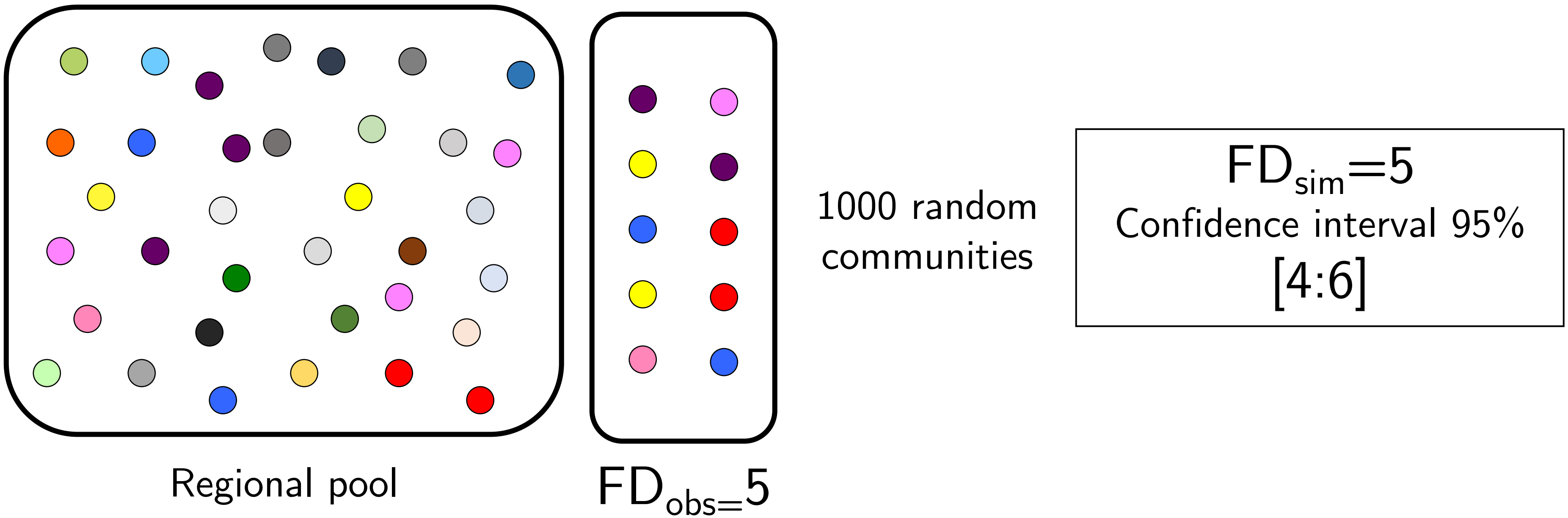
- **Yes**: the mechanism is not important;
- **No**: the mechanism is crucial;
- **Sort of**: the mechanism is part of the equation but not alone. (in this case we have to extract more variables to evaluate the combination of important variables)

Null Models in process inferences



6. Trait-based community assembly & null models

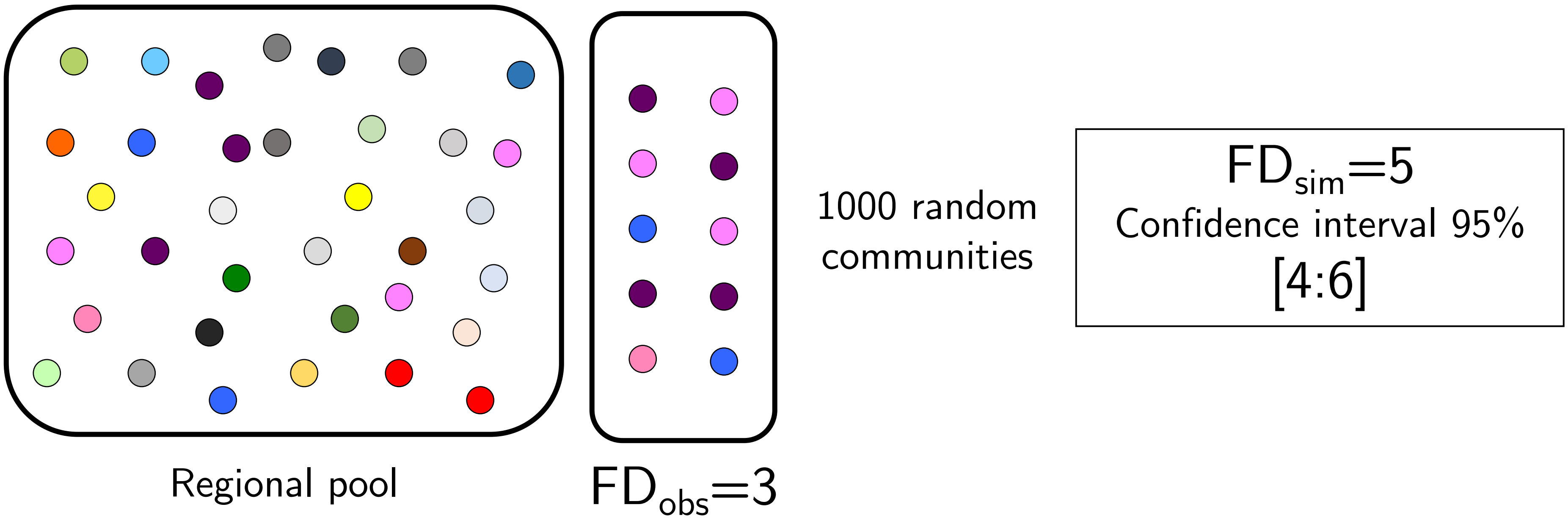
Null Models in process inferences



Results: The local FD is not significantly lower or higher than expected by random

Meaning: The observed FD is due to a random selection of species from the regional pool

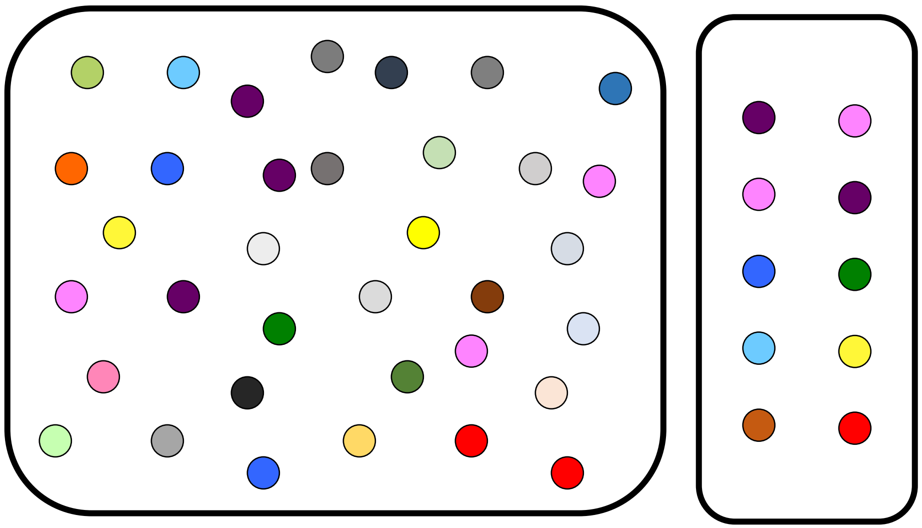
Null Models in process inferences



Results: The local FD observed is significantly lower than expected by random

Meaning: Trait convergence resulting from habitat filtering. The FD lower than expected indicates that ecological filters constrain coexisting species to share some similar traits.

Null Models in process inferences



Regional pool

$FD_{obs}=8$

1000 random communities

$FD_{sim}=5$

Confidence interval 95%

[4:6]

Results: The local FD observed is significantly higher than expected by random

Meaning: Functional differentiation among co-existing species which is consistent with the hypothesis of limiting similarity.

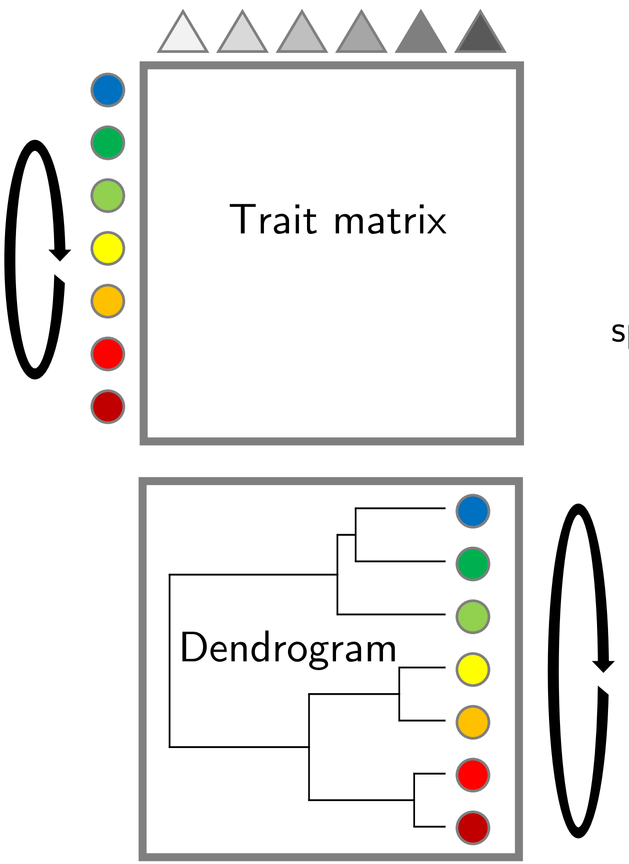
Null Models in process inferences

Standardized effect size

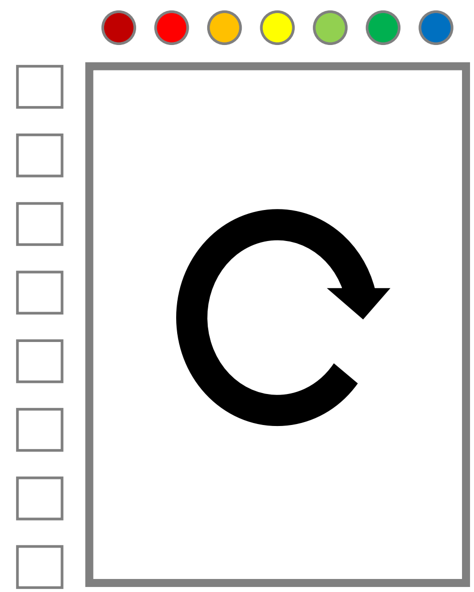
$$SES = \frac{(FD_{obs} - \mu_{null})}{\sigma_{null}}$$

- Index to measure the deviation from the null expectation. SES can be read in a standard normal distribution :
  - SES < -1.96 significantly lower than excepted
  - SES > 1.96 significantly higher than expected

Null Models in process inferences



Reassign randomly species names at the rows or at the tips

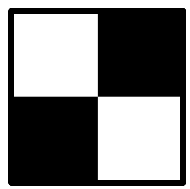


Randomisation of the presence and/or abundances of the species within the community matrix by imposing constrains (e.g. species frequency and species richness unchanged)

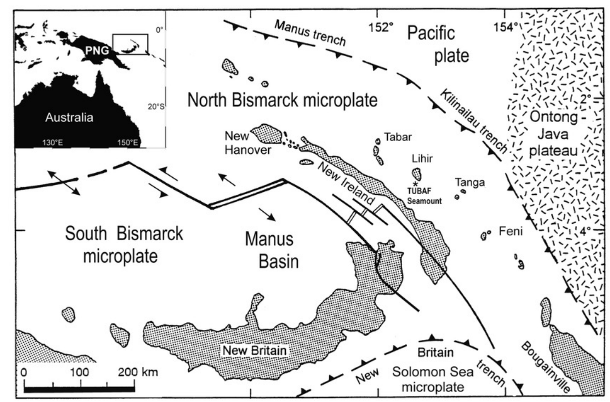
6. Trait-based community assembly & null models

Diamond, J. M. 1975. Assembly of species communities. In: Cody, M. L. and Diamond, J. M. (eds), Ecology and evolution of communities. Harvard Press, pp. 342-444.

	$s1$	$s2$
I1	0	1
I2	1	0



Checkerboard

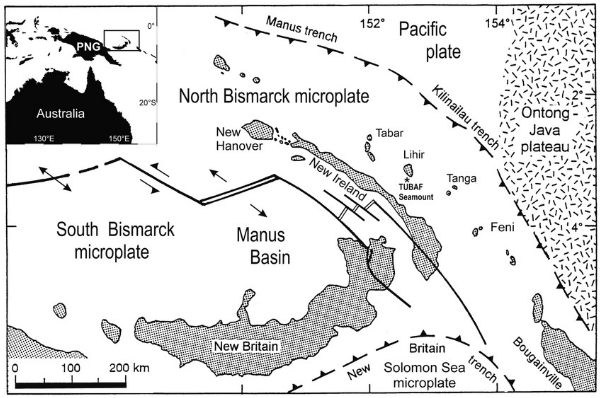


6. Trait-based community assembly & null models

Diamond, J. M. 1975. Assembly of species communities. In: Cody, M. L. and Diamond, J. M. (eds), Ecology and evolution of communities. Harvard Press, pp. 342-444.

	$s1$	$s2$	$s3$
I1	0	1	0
I2	1	0	1
I3	1	0	1
I4	1	0	0

5 Checkerboards



6. Trait-based community assembly & null models

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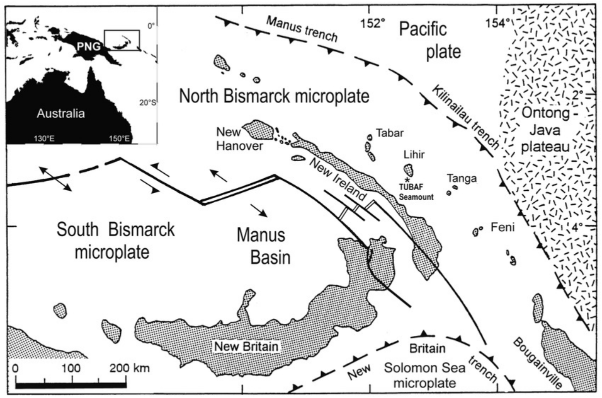

	$s1$	$s2$	$s3$
I1	1	0	0
I2	1	1	0
I3	0	1	1
I4	0	1	0

	$s1$	$s2$	$s3$
I1	1	0	0
I2	1	1	0
I3	1	1	0
I4	0	1	0

	$s1$	$s2$	$s3$
I1	0	0	1
I2	0	1	1
I3	1	1	0
I4	0	0	1

	$s1$	$s2$	$s3$
I1	0	0	1
I2	0	1	1
I3	1	0	1
I4	0	0	1

[...]

Null Models in process inferences

Gotelli, N. J. (2000). Null model analysis of species co-occurrence patterns. *Ecology*, *81*(9), 2606-2621.

Gotelli, N. J., & Entsminger, G. L. (2003). Swap algorithms in null model analysis. *Ecology*, *84*(2), 532-535.

Miklós, I., & Podani, J. (2004). Randomization of presence-absence matrices: comments and new algorithms. *Ecology*, *85*(1), 86-92.

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Hardy, O. J. (2008). Testing the spatial phylogenetic structure of local communities: statistical performances of different null models and test statistics on a locally neutral community. Journal of ecology, 96(5), 914-926.

5. Study cases and R packages

Azorean Arthropods

5. Study cases and R packages

BIODIVERSITY RESEARCH

WILEY Diversity and Distributions A Journal of Conservation Biogeography

Functional traits of indigenous and exotic ground-dwelling arthropods show contrasting responses to land-use change in an oceanic island, Terceira, Azores

François Rigal[1,2,3] | Pedro Cardoso[1,2,4] | Jorge M. Lobo[5] | Kostas A. Triantis[1,2,6] | Robert J. Whittaker[7,8] | Isabel R. Amorim[1,2] | Paulo A. V. Borges[1,2]

[1]Azorean Biodiversity Group, cE3c – Centre for Ecology, Evolution and Environmental Changes, Angra do Heroísmo, Azores, Portugal

[2]Departamento de Ciências e Engenharia do Ambiente, Universidade dos Açores, Angra do Heroísmo, Azores, Portugal

[3]CNRS-Université de Pau et des Pays de l'Adour, Institut des Sciences Analytiques et de Physico-Chimie pour l'Environnement et les Materiaux, MIRA, Environment and Microbiology Team, UMR 5254, BP 1155, Pau, France

[4]Finnish Museum of Natural History, University of Helsinki, Helsinki, Finland

[5]Departament of Biogeography and Global Change, Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain

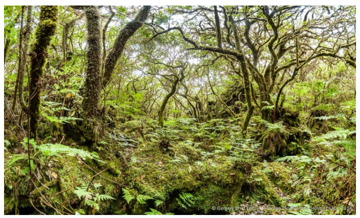
[6]Department of Ecology and Taxonomy, Faculty of Biology, National and Kapodistrian University of Athens, Athens, Greece

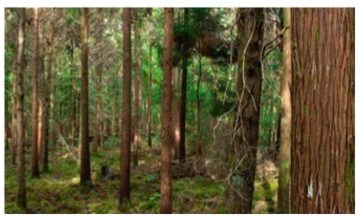
[7]Conservation Biogeography and Macroecology Programme, School of Geography and the Environment, University of Oxford, Oxford, UK

[8]Center for Macroecology, Evolution and Climate, Department of Biology, University of Copenhagen, Copenhagen, Denmark

5. Study cases and R packages

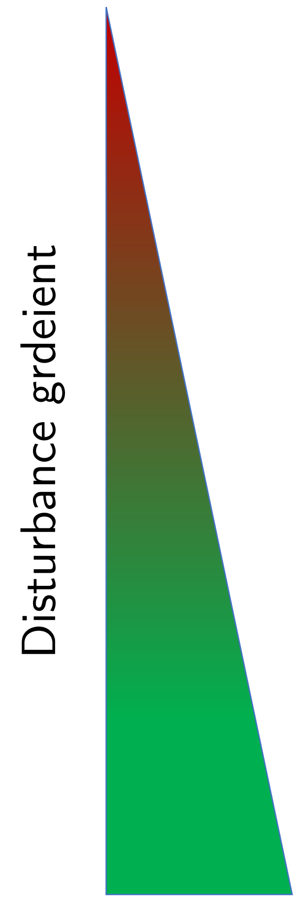
Azorean Arthropods


1- Native forest (NAT)

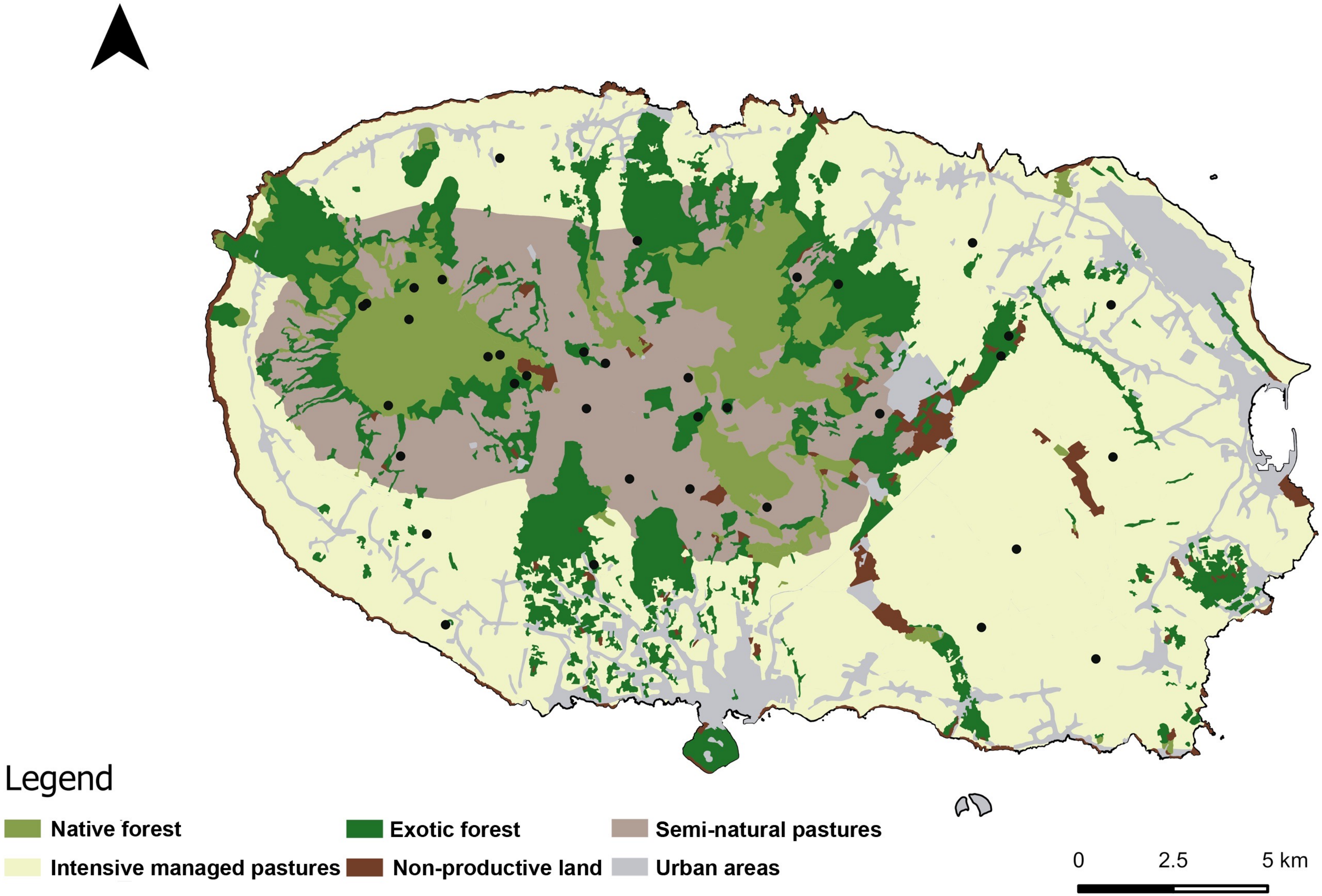

2- Exotic forest (EXO)


3- Semi-natural pastures (SEM)


4- Intensive-managed pastures (INT)

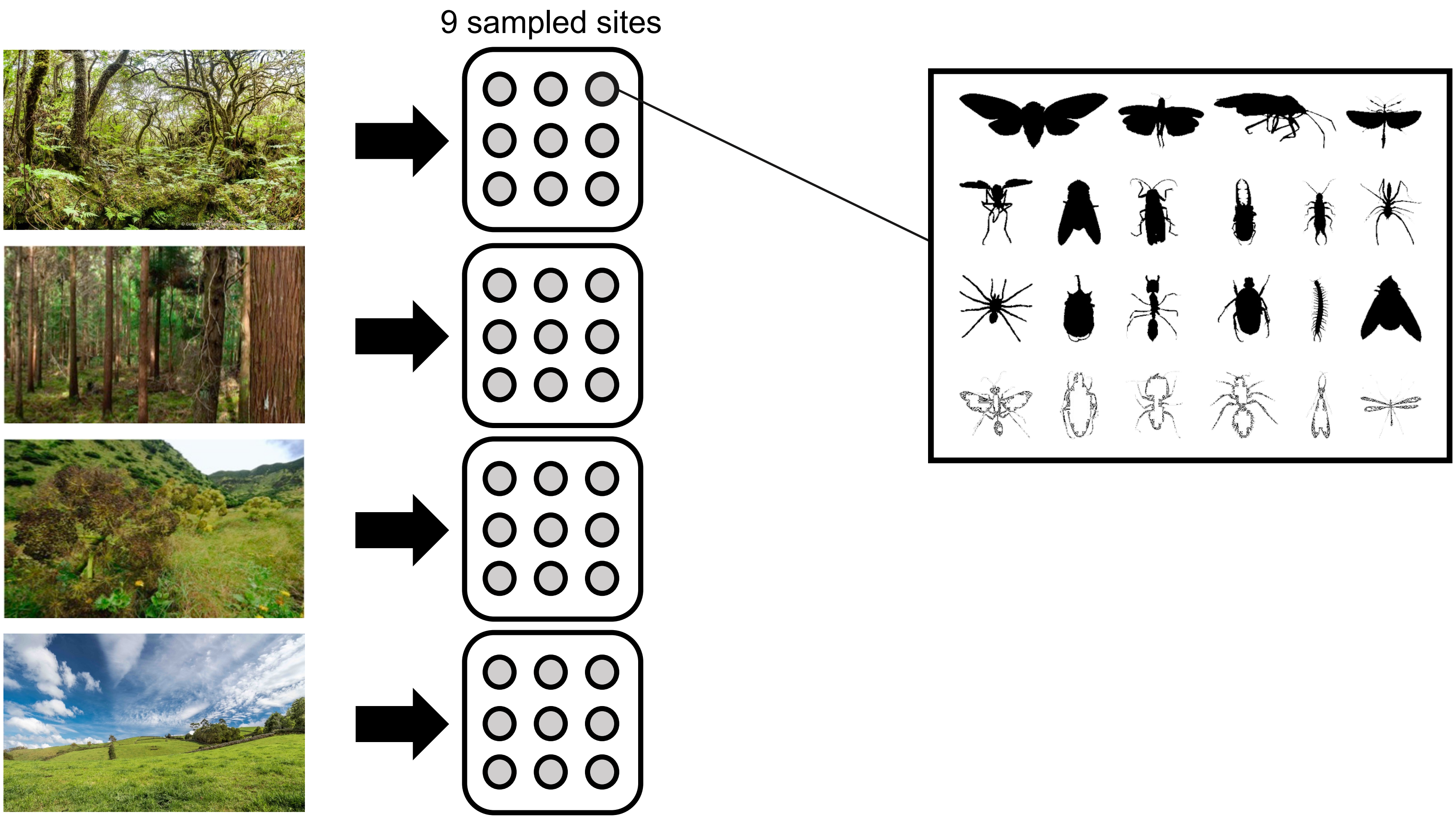


5. Study cases and R packages



5. Study cases and R packages

Azorean Arthropods



5. Study cases and R packages

Azorean Arthropods

9 sites x 4 habitats = 36 sites

20,800 soil-arthropod specimens collected and 202 (morpho) species identified representing 20 orders, 76 families and 161 genera.
86 indigenous (endemics +native endemics) and 116 exotics.

Community tables = 36 sites (rows) x 202 species (columns)

Trait matrix wit body size, dispersal abilities and a set of functional traits related to resource use were collected.

- Body size was measured on the individuals sampled in this study.
- The others traits were collected from an extensive literature search, including manuscripts with the first descriptions of the species, first species records for the Azores, brief notes and ecological studies.

Azorean Arthropods

Traits	Attributes (abbreviations)	Definition	Ecological relevance
Body size	Absolute body length in mm	Defined as mean body length measured from up to 10 individuals per species. Males and females were incorporated when clear distinction was available. Measures recorded using digital photography *via* a stereoscopic microscope	Body size is related to many life-history traits such as growth rate, fecundity/clutch size, foraging ability, dispersal and life span
Dispersal abilities	High dispersal ability (Hdisp[a]) versus low dispersal ability (Ldisp)	Based on the presence of active wings for coleopteran and Hemipteran, ballooning for spiders and based on descriptions of flying ability for endemics and general guides for the other species. Species subsequently classified as possessing either high or low dispersal ability	Dispersal abilities condition potential colonization/recolonization
Type of food	Plants (FoodPl); Animals (FoodAni); Fungi (FoodFg); Detritus (FoodDet)	Refers to the main food consumed by species during their adult stages except for Lepidoptera, where traits were assigned by reference to the larvae	Species can co-occur in the same site but differ in their feeding strategies and resource use. Feeding guilds can also react differently to land-use changes, such as herbivores being sensitive to change in plant diversity and biomass and predators such as spiders reacting to changes of habitat architecture (Pearce & Venier, 2006; Scherber et al., 2010)
Way of getting food	High active search (GetHact[a]) versus low active search (GetLact)	Refers to the mobility of the species in getting their food. Species classified as having active search or low active search such as species with ambush tactics or using traps	Land-use changes can impact the architecture at microscale and reduce potential foraging sites selected by low active search species and affect their feeding opportunities
Mode of ingestion	Chewing and cutting (IngCC); Piercing and sucking (IngPS); extra-intestinal digestion and sucking (IngEDS)	Defined as the way nutrients are ingested	Mode of ingestion can be related to host specificity. For instance, land-use changes may alter the kind of plants available and consequently alter the availability of resources for chewing and sucking species
Period of activity	Day (ActDay); Night (ActNig); Twilight (ActTwi)	Classified as species being active during the day, during the twilight or during the night or to a combination of those periods	Species can co-occur in the same sites but have separated temporal niches. Circadian activities also play important roles in species interaction (e.g., prey–predator). Land-use changes may promote high proportion of open microhabitats, which are less favourable for species with day activity

5. Study cases and R packages

5. Study cases and R packages

`vegan` (Diversity indices and null models)

`FD` (FD indices mainly based on the framework of Villeger et al. 2008)

`entropart` (FD indices based on the Hill numbers)

`picante` (Indices for PD but can be implemented for FD, null models)

`phytools/ape` (Useful to manipulate trees)

`ade4` (Compute the Pavoine's framework for the Gower's distance)

`BAT` (Diversity indices for FD and many other stuffs)

Methods in Ecology and Evolution

British Ecological Society

Methods in Ecology and Evolution 2014 doi: 10.1111/2041-210X.12310

APPLICATION

BAT – Biodiversity Assessment Tools, an R package for the measurement and estimation of alpha and beta taxon, phylogenetic and functional diversity

Pedro Cardoso[1,2]*, François Rigal[2] and José C. Carvalho[2,3]

APPLICATION

Methods in Ecology and Evolution BRITISH ECOLOGICAL SOCIETY

Functional diversity metrics using kernel density *n*-dimensional hypervolumes

Stefano Mammola[1,2] | Pedro Cardoso[2]

Villéger, S. et al. (2008). New multidimensional functional diversity indices for a multifaceted framework in functional ecology. Ecology, 89(8), 2290-2301.