



Apéro technique 23/06/2015

# Calcul d'indices de diversité fonctionnelle

**Sébastien VILLÉGER**

[sebastien.villeger@umontpellier.fr](mailto:sebastien.villeger@umontpellier.fr)

<http://villeger.sebastien.free.fr/publications>



CNRS

Laboratoire Biodiversité Marine et ses usages  
Montpellier, France



# Biodiversity



Assemblages of  
species



-> biodiversity indices to describe/compare assemblages

# Biodiversity



Assemblages of  
species



-> biodiversity indices to describe/compare assemblages

**Taxonomic diversity based only on species names**

Strawberry ≠ banana ≠ grapes ≠ apple ≠ pear ≠ orange

# Biodiversity



Assemblages of  
species



-> **biodiversity indices to describe/compare assemblages**

Taxonomic diversity based only on species names

**Functional diversity based on species biological attributes**

e.g. size, color, origin, nutritional value...

**Environment -> Functional Diversity -> Ecosystem services**

# Steps in functional ecology

1) Defining the ecological question

2) Collecting abundance of species in assemblages

		Regional pool of species			
		Sp a	Sp b	...	Sp N
Local Assemblages	As 1	Presence, abundance, biomass			
	As 2				
	...				
	As C				

# Steps in functional ecology

- 1) Defining the ecological question
- 2) Collecting abundance of species in assemblages
- 3) Selecting relevant functional traits

**Regional pool of species**

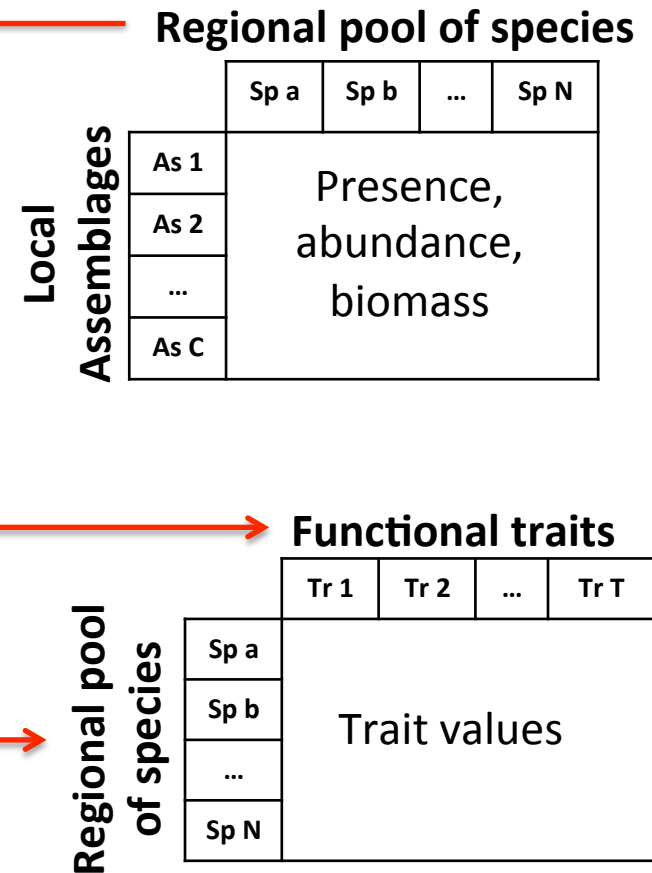
		Sp a	Sp b	...	Sp N
Local Assemblages	As 1	Presence, abundance, biomass			
	As 2				
	...				
	As C				

**Functional traits**

		Tr 1	Tr 2	...	Tr T
Local Assemblages					

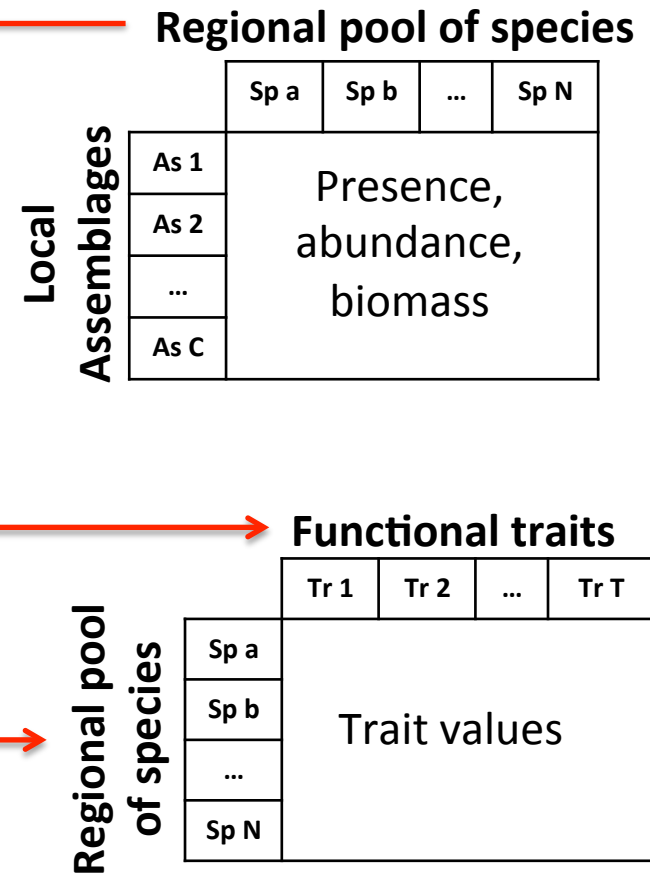
# Steps in functional ecology

- 1) Defining the ecological question
- 2) Collecting abundance of species in assemblages
- 3) Selecting relevant functional traits
- 4) Measuring functional traits on all species



# Steps in functional ecology

- 1) Defining the ecological question
- 2) Collecting abundance of species in assemblages
- 3) Selecting relevant functional traits
- 4) Measuring functional traits on all species



**5) Building a functional space for all species**

**6) Computing functional diversity within and/or between assemblages**

**7) Testing observed indices values against null hypotheses**





# Computing functional space

		Functional traits			
		Tr 1	Tr 2	...	Tr T
Regional pool of species	Sp a	Trait values			
	Sp b				
	...				
	Sp N				

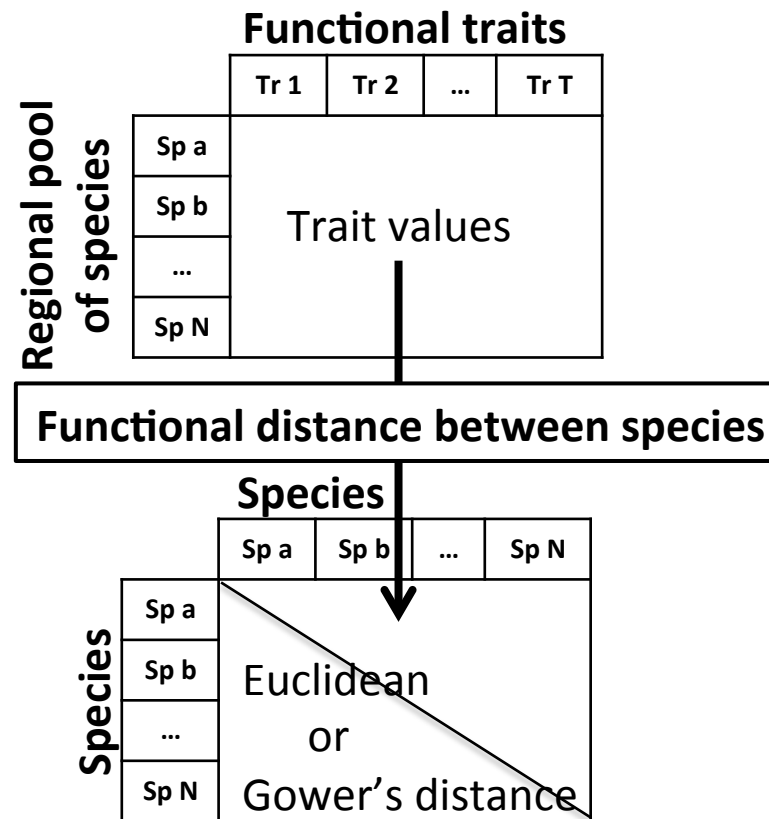
**Be careful with type of variable** after importing traits values to R !

Quantitative : Continuous variable -> `as.numeric`

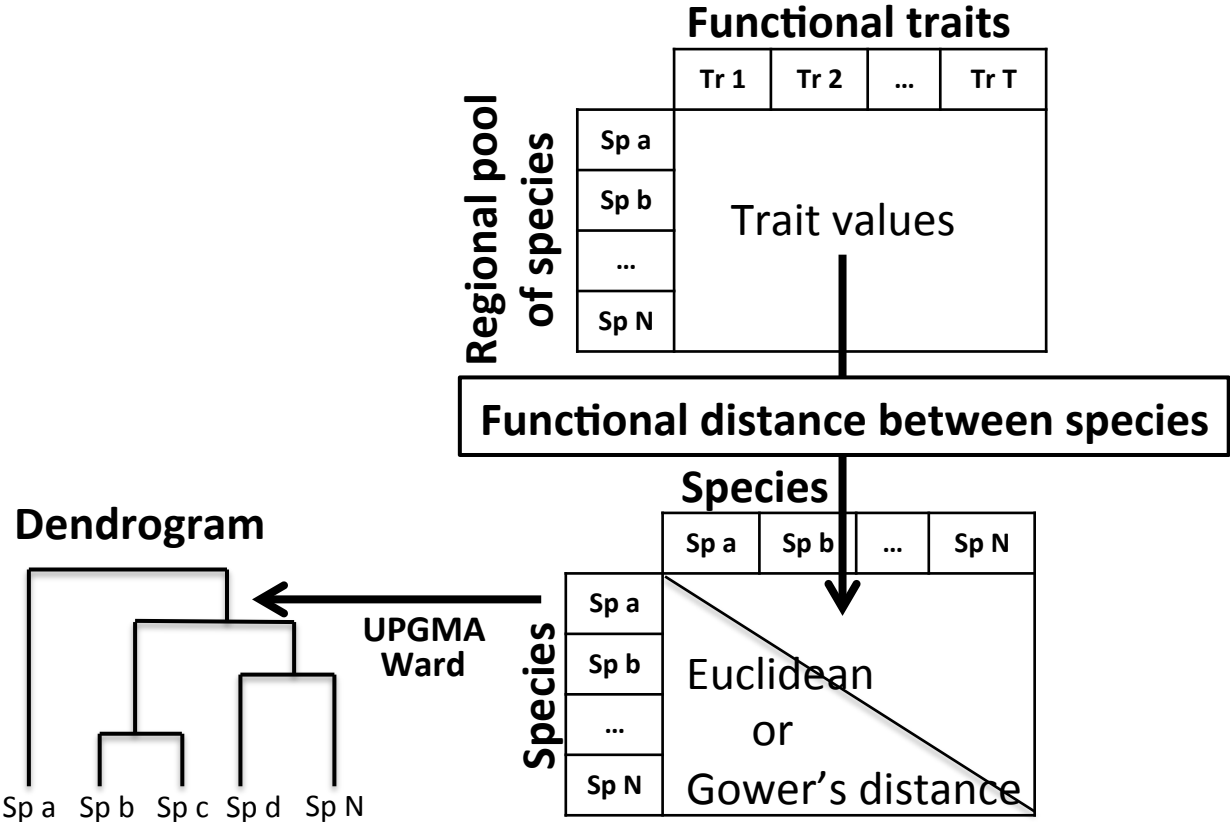
Semi-quantitative : Ordered categories -> `as.ordered`

Qualitative: Unordered categories -> `as.factor`

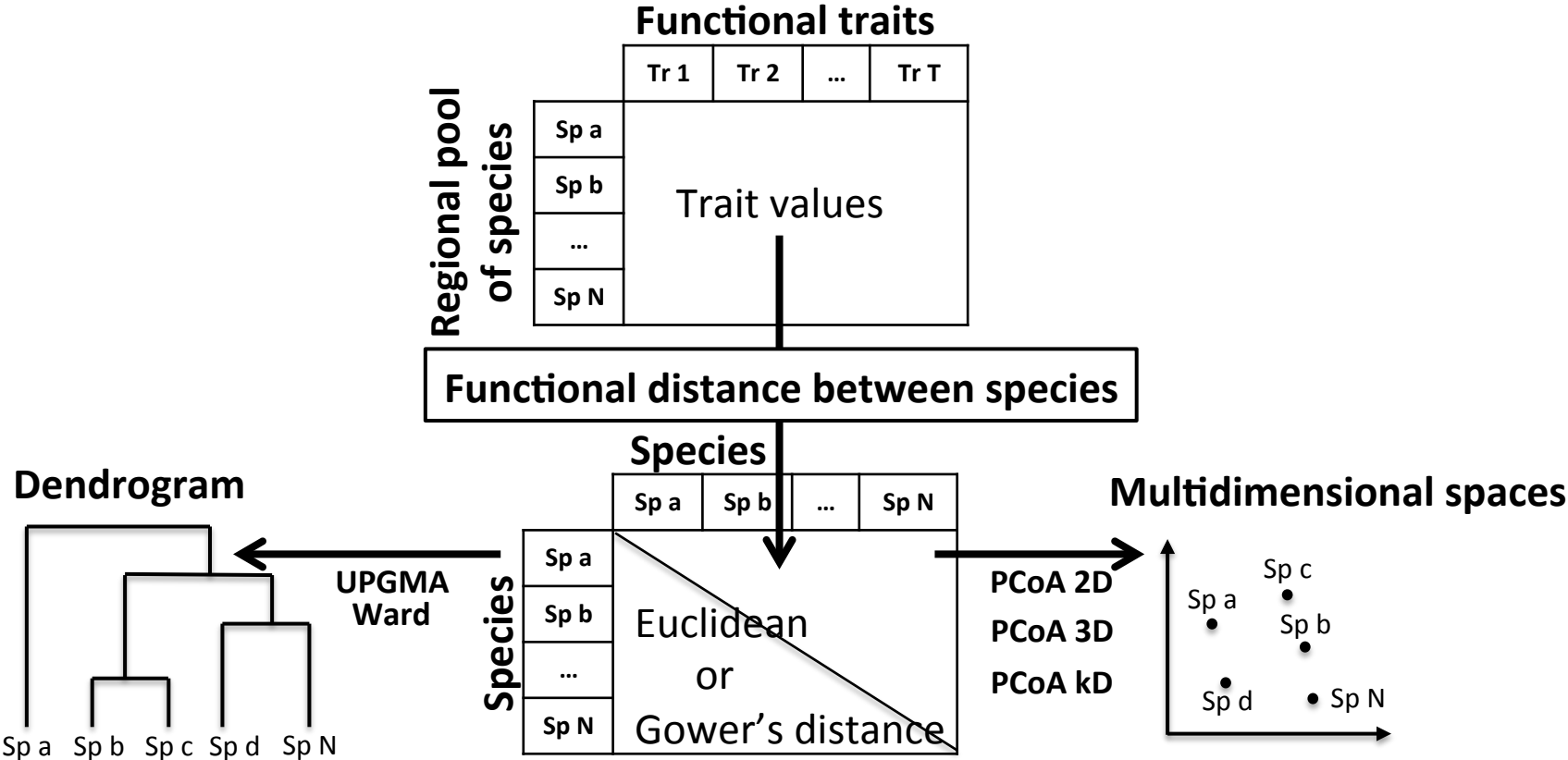
# Computing functional space



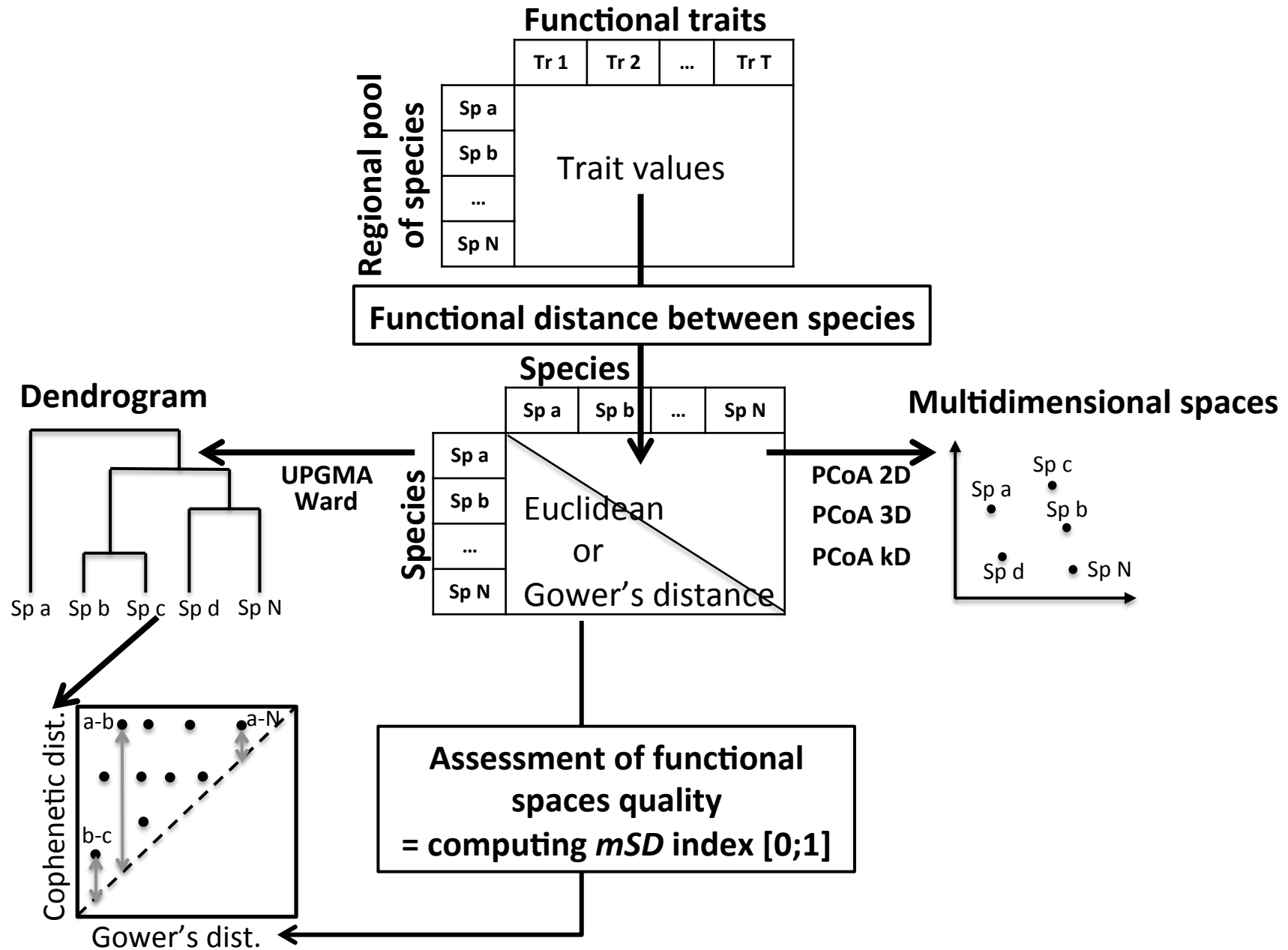
# Computing functional space



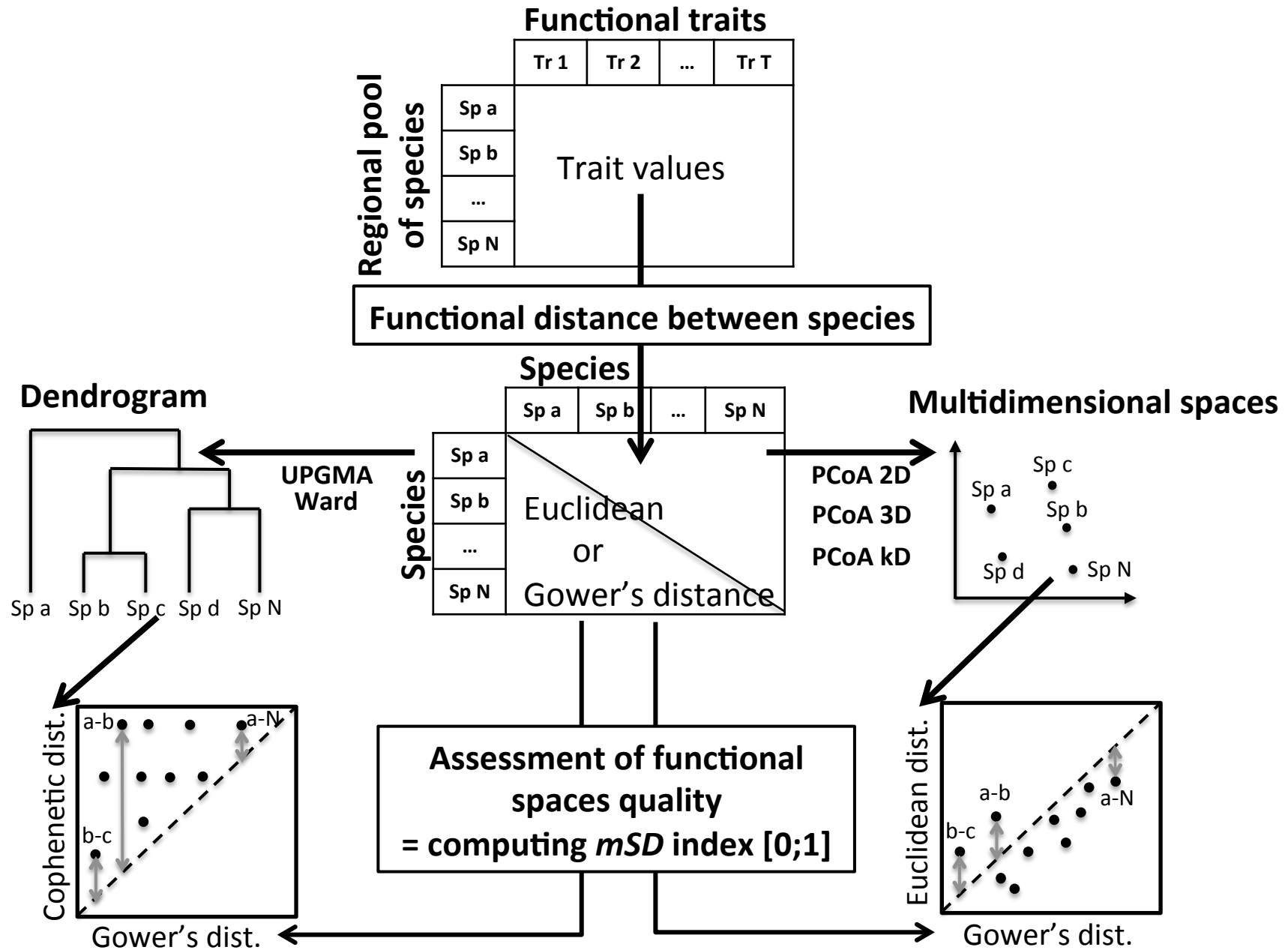
# Computing functional space



# Computing functional space



# Computing functional space



# Computing functional space

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



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

Eva Maire<sup>1</sup>, Gaël Grenouillet<sup>2</sup>, Sébastien Brosse<sup>2</sup> and Sébastien Villéger<sup>1\*</sup>



Appendix S1 = R function *qual\_funct\_space*

**Inputs :** **mat\_funct**= matrix with functional traits values for all species  
**nbdim**= value (maximum number of dimensions to consider)  
**metric**="Gower" or "Euclidean" (to compute functional distance between species)

# Computing functional space

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



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**Inputs :** **mat\_func**= matrix with functional traits values for all species  
**nbdim**= value (maximum number of dimensions to consider)  
**metric**="Gower" or "Euclidean" (to compute functional distance between species)

### **Outputs :**

\$mSD = a vector with mSD values for spaces of 2 to k dimensions + best dendrogram  
\$ details\_func\_space = a list with intermediate results (e.g. outputs of PCoA)

+ 1 jpeg file with illustration of functional spaces quality



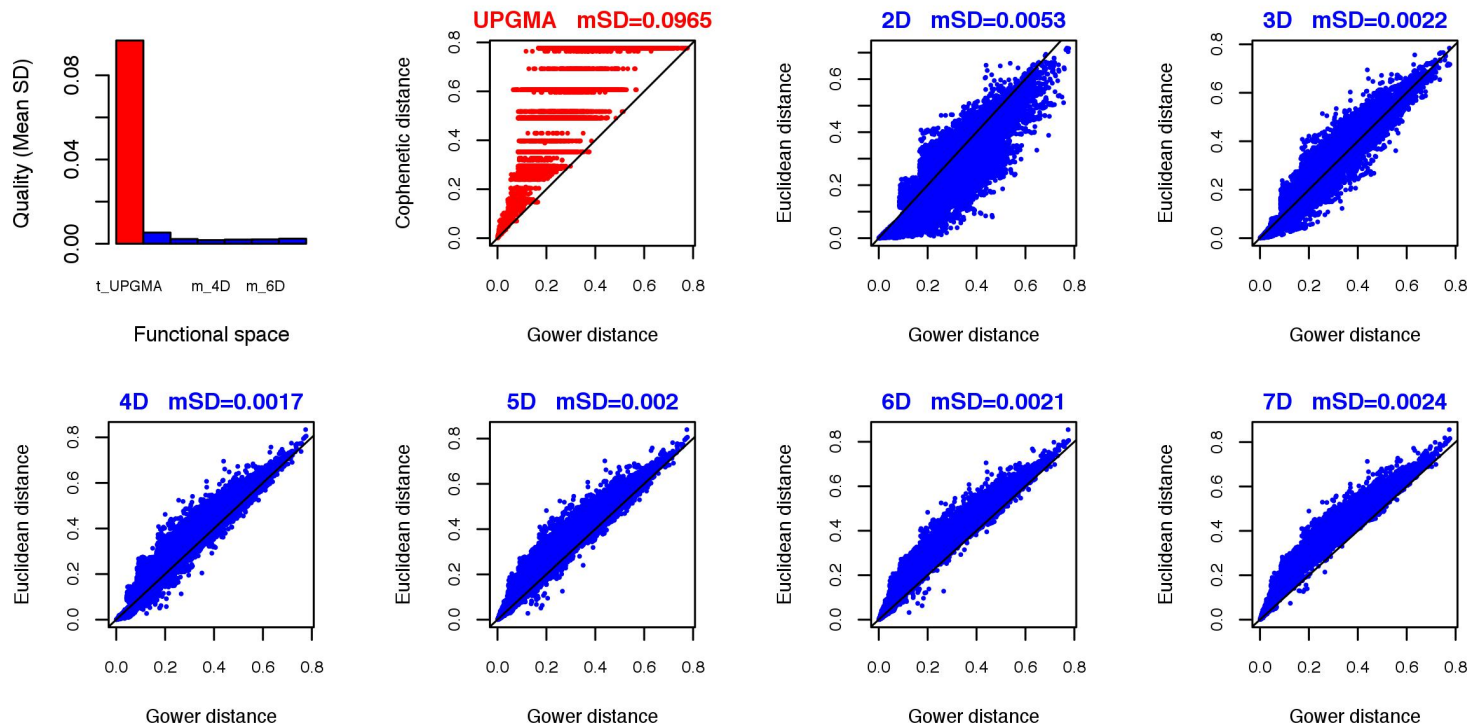
# Computing functional space

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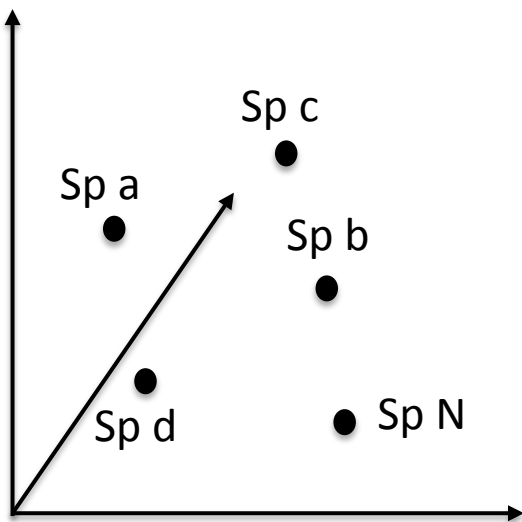
# Computing functional diversity within assemblages

Abundance of species in all assemblages

Regional pool of species

		Sp a	Sp b	...	Sp N
Local Assemblages	As 1	Presence, abundance, biomass			
	As 2				
	...				
	As C				

“Best” multidimensional functional space with all species



Functional diversity within each assemblage

# Computing functional diversity within assemblages

## A functional approach reveals community responses to disturbances

David Mouillot<sup>1,2</sup>, Nicholas A.J. Graham<sup>2</sup>, Sébastien Villéger<sup>1,3</sup>, Norman W.H. Mason<sup>4</sup>,  
and David R. Bellwood<sup>2,5</sup>

Mouillot et al. 2013, *Trends in Ecology and Evolution*

R function: *FDchange* (coord, abundances)

-> designed to assess change in FD facets following a disturbance

Inputs : “abund” = species abundances before/after disturbance (matrix 2xS)

“coord” = species coordinates in a D-dimensional functional space (matrix SxD)



# Computing functional diversity within assemblages

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**Inputs** : “abund” = species abundances before/after disturbance (matrix 2xS)

“coord” = species coordinates in a D-dimensional functional space (matrix SxD)

**Outputs** : **\$FId** = a table (Dx3) with aggregated traits values on each functional axis

**\$FD** = a table (7x3) with 7 multivariate indices values

**\$details** = a list with details about FD indices computation



# Computing functional diversity within assemblages

How using *FDchange* function to compute FD indices on any set of communities ?

```
# abund_sp = abundance of species in N communities
```

```
id_comm<-row.names(abund_sp) # ID of communities
```

```
# coord_sp = coordinates of species in a functional space (e.g. output of qual_funct_space)
```

```
nm_axes<-c("PC1", "PC2", "PC3") # names of functional axes (here 3D)
```

```
# names of the multivariate FD indices of interest for the study
```

```
nm_FDind<-c("FRic", "FEve", "FDiv", "FSpe", "FOri") # 'FDis', "FEnt" not computed
```

```
# matrix to store FD indices values for the N communities
```

```
funct_div<-matrix(NA, length(id_comm), length(c(nm_axes, nm_FDind)),  
  dimnames=list(id_comm, c(nm_axes, nm_FDind)))
```

```
# loop on communities
```

```
for (k in id_comm)
```

```
{
```

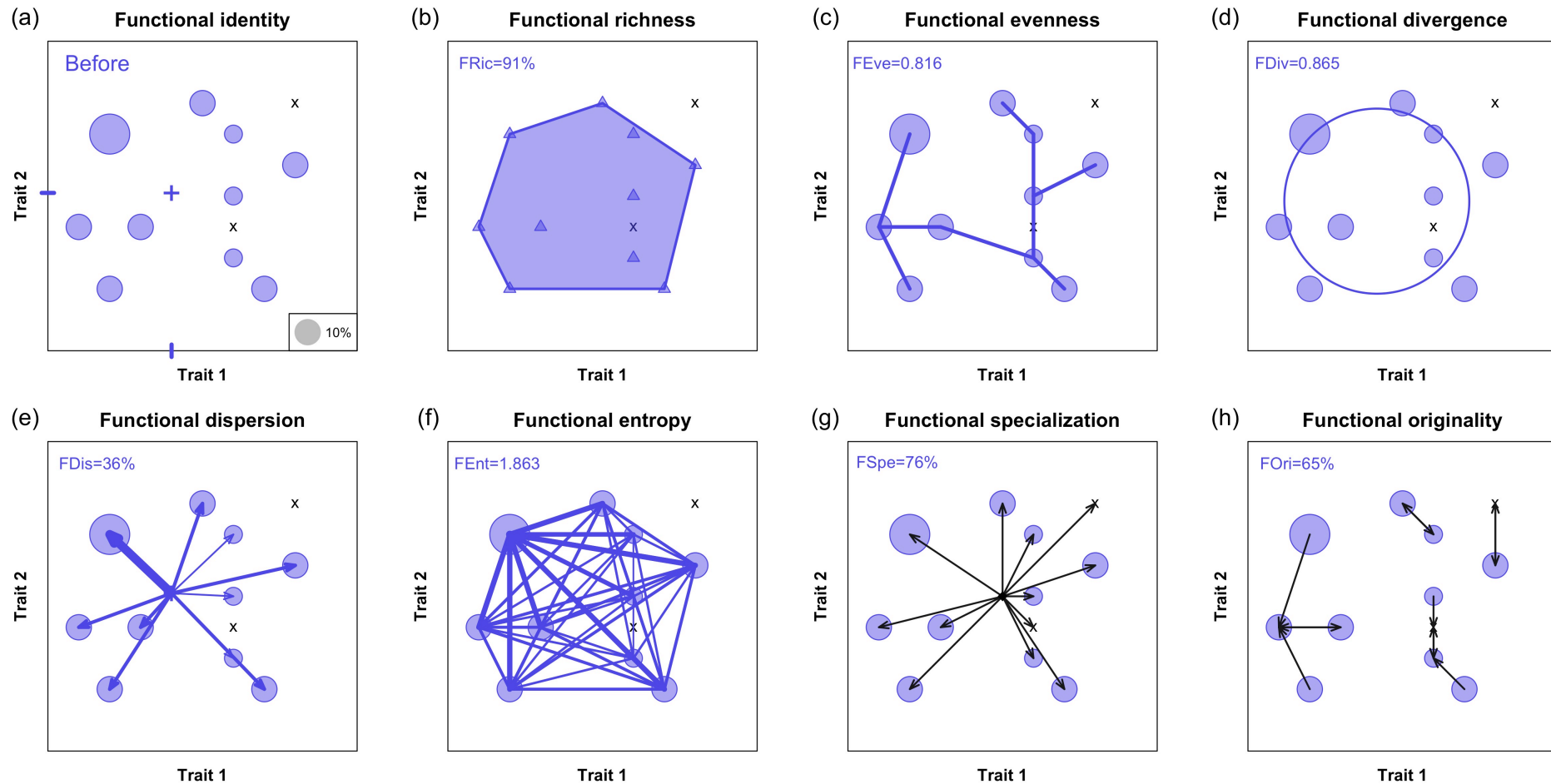
```
  FD_k<-FDchange(abundances=rbind(Before=abund_sp[k,], After=abund_sp[k,]) ,  
    coord=coord_sp)
```

```
  funct_div[k,]<-c( FD_k$FId[1, nm_axes], FD_k$FD[nm_FDind,1] )
```

```
} # end of k
```

# Computing functional diversity within assemblages

## Complementary facets of functional diversity



-> Graphical function in prep.

## Computing functional dissimilarity between assemblages

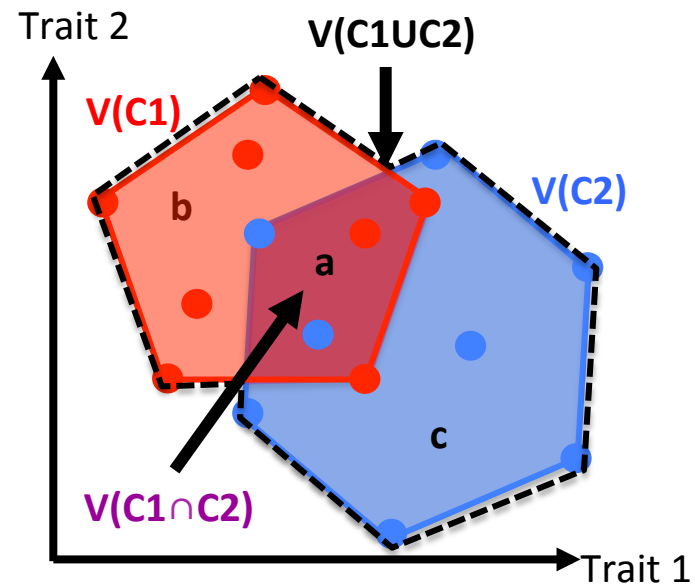


Dissimilarity based on functional composition (i.e. only species traits values)

# Computing functional dissimilarity between assemblages



Dissimilarity based on functional composition (i.e. only species traits values)





# Computing functional dissimilarity between assemblages



Dissimilarity based on functional composition (i.e. only species traits values)

*Global Ecology and Biogeography, (Global Ecol. Biogeogr.) (2013) 22, 671–681*



**Decomposing functional  $\beta$ -diversity reveals that low functional  $\beta$ -diversity is driven by low functional turnover in European fish assemblages**

Sébastien Villéger\*, Gaël Grenouillet and Sébastien Brosse

# Computing functional dissimilarity between assemblages



Dissimilarity based on functional composition (i.e. only species traits values)



## Package 'betapart'

February 19, 2015

**Type** Package

**Title** Partitioning beta diversity into turnover and nestedness components

**Version** 1.3

**Date** 2013-12-12

**Author** Andres Baselga, David Orme, Sebastien Villeger, Julien De Bortoli and Fabien Leprieur

# Computing functional dissimilarity between assemblages



Dissimilarity based on functional composition (i.e. only species traits values)

**R function: *functional.beta.pair* -> Works with up to 5-dimensions**



## Usage

```
functional.beta.pair(x, traits, index.family="sorensen")
```

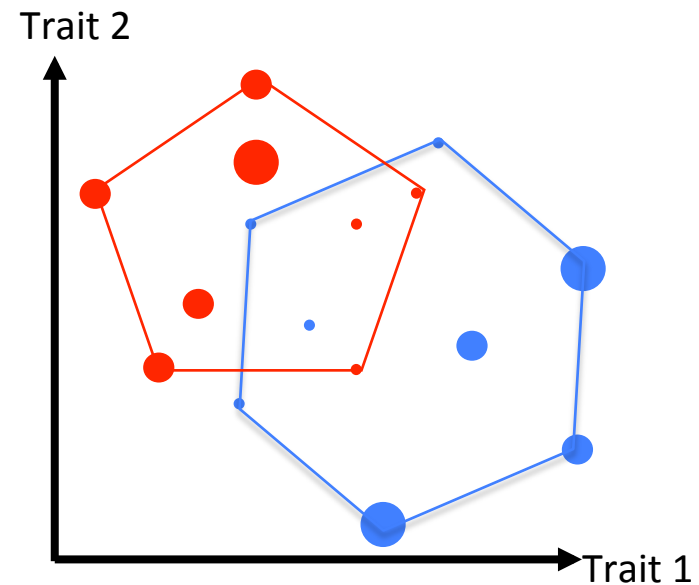
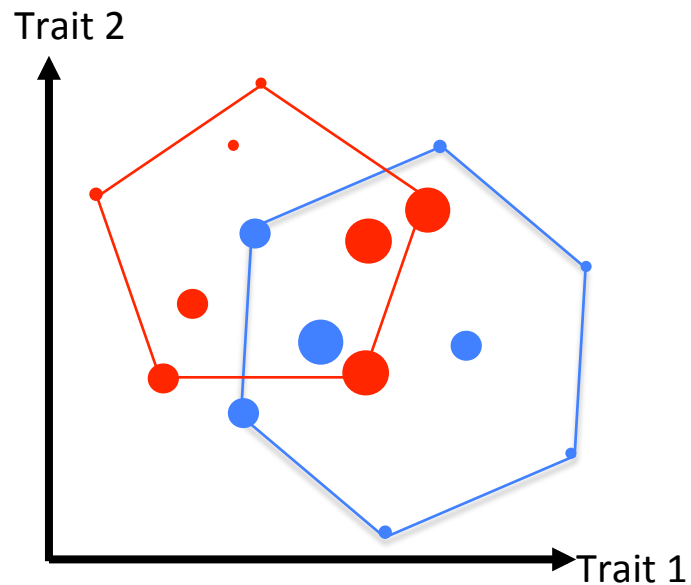
## Arguments

x	data frame, where rows are sites and columns are species. Alternatively x can be a <code>functional.betapart</code> object derived from the <code>functional.betapart.core</code> function
traits	if x is not a <code>functional.betapart</code> object, a data frame, where rows are species and columns are functional space dimensions (i.e. quantitative traits or synthetic axes after PCoA). Number of species in each site must be strictly higher than number of dimensions.
index.family	family of dissimilarity indices, partial match of "sorensen" or "jaccard".

# Computing functional dissimilarity between assemblages



Dissimilarity based on functional structure (i.e. including species abundances)



# Computing functional dissimilarity between assemblages



Dissimilarity based on functional structure (i.e. including species abundances)

## Low Functional $\beta$ -Diversity Despite High Taxonomic $\beta$ Diversity among Tropical Estuarine Fish Communities

Sébastien Villéger<sup>1\*</sup>, Julia Ramos Miranda<sup>2</sup>, Domingo Flores Hernandez<sup>2</sup>, David Mouillot<sup>3,4</sup>

Villéger et al. 2012, *PLoS ONE*



Multiplicative decomposition of Rao's Quadratic entropy

-> R function: ***betaQmult***(functdist, abundances)



# An “all inclusive” R package

*Ecology*, 91(1), 2010, pp. 299–305  
© 2010 by the Ecological Society of America

## A distance-based framework for measuring functional diversity from multiple traits

ETIENNE LALIBERTÉ<sup>1,3</sup> AND PIERRE LEGENDRE<sup>2</sup>

### Package ‘FD’

February 19, 2015

**Type** Package

**Title** Measuring functional diversity (FD) from multiple traits, and  
other tools for functional ecology

**Version** 1.0-12

**Date** 2014-19-08

**Author** Etienne Laliberté, Pierre Legendre, Bill Shipley



R function: *dbFD*

# FD indices accounting for intraspecific variability

**Package ‘hypervolume’** [Blonder et al. 2014, \*Global Ecology and Biogeography\*](#)

June 3, 2015

**Type** Package

**Title** High-Dimensional Kernel Density Estimation and Geometry Operations

**Version** 1.3.0

**Date** 2015-06-01

**Author** Benjamin Blonder

**Package ‘cati’** [Taudière & Violle 2015, \*Ecography\*](#)

May 29, 2015

**Type** Package

**Title** Community Assembly by Traits: Individuals and Beyond

**Version** 0.99

**Date** 2015-05-28

**Author** Adrien Taudiere, Cyrille Violle with contribution by Francois Munoz

ME  CI

[sebastien.villeger@umontpellier.fr](mailto:sebastien.villeger@umontpellier.fr)

<http://villeger.sebastien.free.fr/publications>



