Methods in
Ecology and Evolution

Tutorial

Quantifying the relevance of intraspecific trait variability for functional diversity

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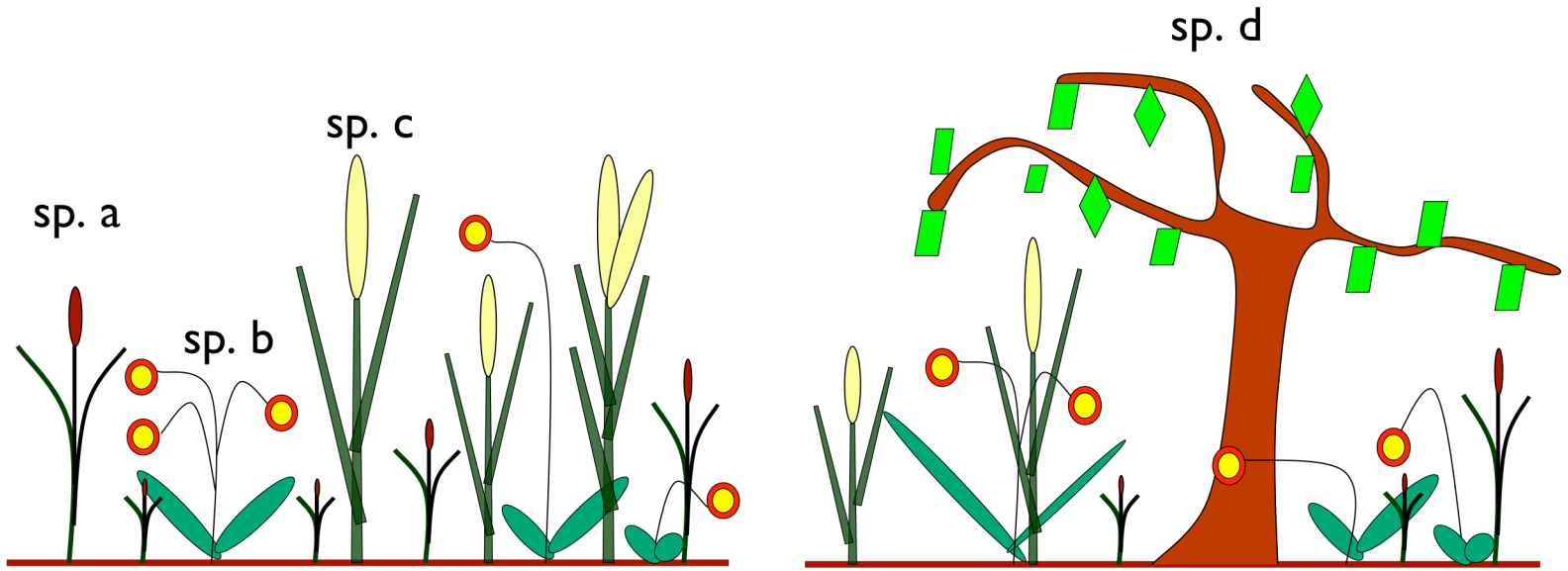
Intraspecific trait variability is a crucial, often neglected, component of functional diversity (i.e. the extent of trait dissimilarity in a given ecological community).

e.g. traits = plant height, n° of leaves, n° of flowers...



How much trait variability is due to intraspecific variation within and across communities ?

Two new methods proposed

1. Quantifying the extent of within- vs. between-species functional diversity (FD) within different communities

2. Decomposing the effects of species turnover and intraspecific trait variability in FD across communities

Present TUTORIAL:

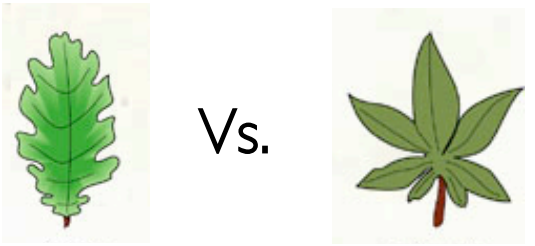
Use of the R functions designed for the first method

1. Quantifying the extent of within- vs. between-species functional diversity (FD) within different communities

2. Decomposing the effects of species turnover and intraspecific trait variability in FD across communities

Within each community (plot) the functional trait diversity can be partitioned into effects due to:

Between species FD: *extent of trait dissimilarity in a community because of differentiation between coexisting species*



Within species FD: *extent of trait dissimilarity in a community because of intraspecific trait variability*

APPROACH: decomposition of total community trait variance

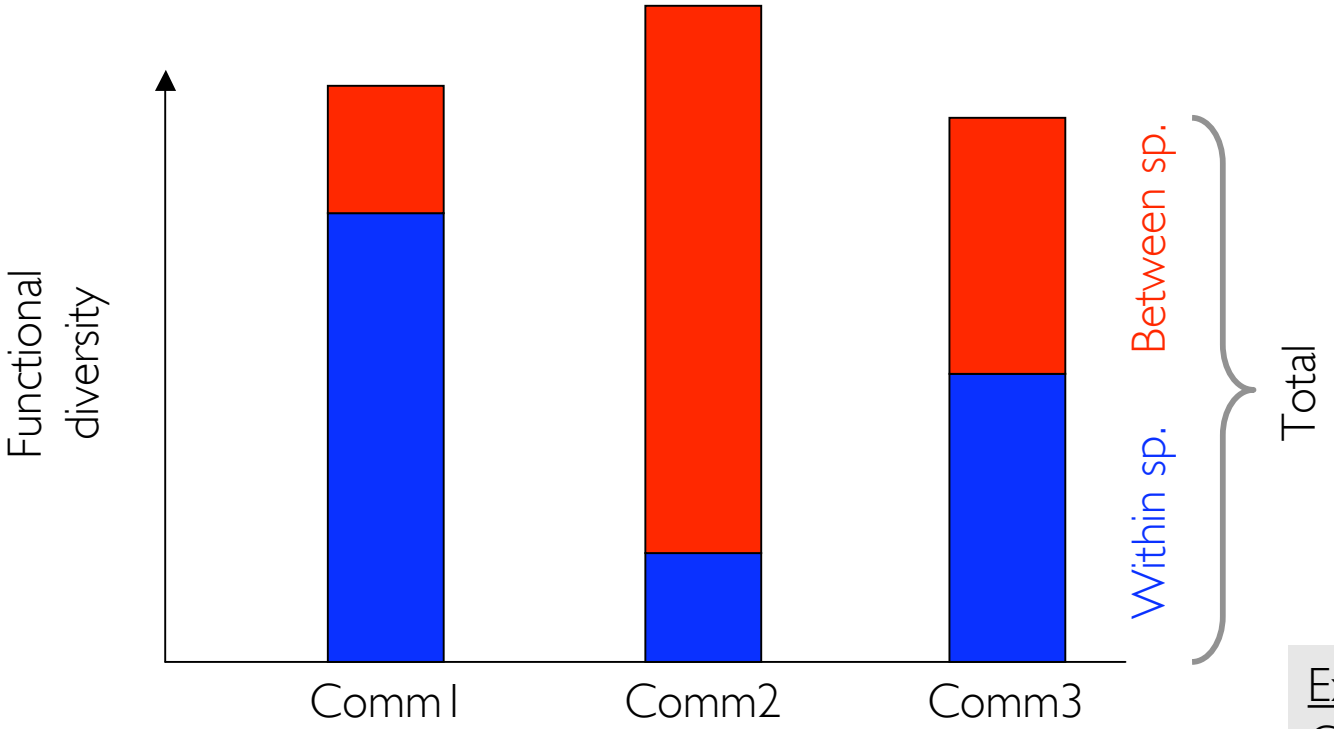
Total diversity = Between species div. + Within species div.

ADVANTAGES

- Take into account different type of species abundances
- Similar to the decomposition with the Rao quadratic entropy
- Similar to PERMANOVA and other existing mathematical tools
- Use with single and multiple traits

Total diversity = Between species div. + Within species div.

Calculated for each community (plot) separately!!



Example:
Comm2 has lowest within species diversity, but highest between species and total diversity

Method overview

Total diversity = Between species div. + Within species div.

3 possible ways to calculate the "weight" of each species
(see Eqn. 3 in the paper)

R scripts
(in the paper Appendix)

1 all species have the same contribution
(i.e. **1/nsp**, nsp=number of species in a plot)

2 species contribution is given by their abundance
in classic relevés (cover, biomass etc..)

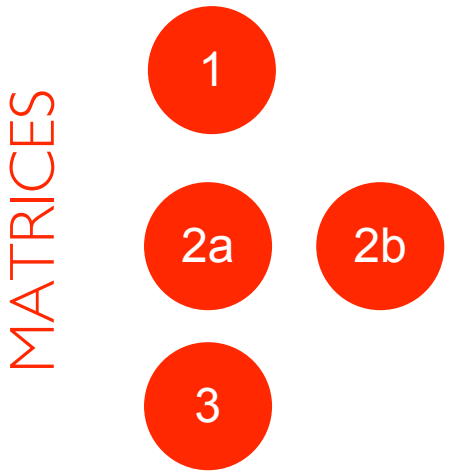
RaoRel.r

3 species contribution is given by the number of
individuals sampled for trait measurements

RaoAdo.r

Preparing the data for R

3 matrices needed (FOR EACH COMMUNITY/PLOT):



Trait values for different individuals

Individual identity
(with and without species abundances)

Trait dissimilarity
(computed from the first matrix)

Preparing the data for R

3 matrices needed (FOR EACH COMMUNITY/PLOT):

The following examples are based on virtual data as used in the Appendix example

The R functions are applicable to your real data when formatted as shown in the virtual examples

1

TRAIT X INDIVIDUAL

For each trait (e.g. plant height, leaf area etc..), a vector with the trait value for different individuals within each species

Example: for plant height, 6 individuals were measured for species 1, 8 individuals for species 2, 10 for species 3 and 16 for species 4.

Species	Trait value (e.g. height in cm)
ind1 for Sp1	1
ind2 for Sp1	2
ind3 for Sp1	3
ind4 for Sp1	4
ind5 for Sp1	5
ind6 for Sp1	6
ind1 for Sp2	2
ind2 for Sp2	3
ind3 for Sp2	4
ind4 for Sp2	5
ind5 for Sp2	6
ind6 for Sp2	7
ind7 for Sp2	8
ind8 for Sp2	9
ind1 for Sp3	1
ind2 for Sp3	2
ind3 for Sp3	3
ind4 for Sp3	4
ind5 for Sp3	5
ind6 for Sp3	6
ind7 for Sp3	7
ind8 for Sp3	8
ind9 for Sp3	9
ind10 for Sp3	10
ind1 for Sp4	4
ind2 for Sp4	6
ind3 for Sp4	8
ind4 for Sp4	10
ind5 for Sp4	12
ind6 for Sp4	14
ind7 for Sp4	16
ind8 for Sp4	18
ind9 for Sp4	2
ind10 for Sp4	4
ind11 for Sp4	6
ind12 for Sp4	8
ind13 for Sp4	10
ind14 for Sp4	12
ind15 for Sp4	14
ind16 for Sp4	16

Matrix

2a

SPECIES IDENTITY

This matrix denotes species identity of each individual collected, as a dummy code.

MATRIX FOR EACH COMMUNITY SAMPLED

Species	Sp1	Sp2	Sp3	Sp4
ind1 for Sp1	1	0	0	0
ind2 for Sp1	1	0	0	0
ind3 for Sp1	1	0	0	0
ind4 for Sp1	1	0	0	0
ind5 for Sp1	1	0	0	0
ind6 for Sp1	1	0	0	0
ind1 for Sp2	0	1	0	0
ind2 for Sp2	0	1	0	0
ind3 for Sp2	0	1	0	0
ind4 for Sp2	0	1	0	0
ind5 for Sp2	0	1	0	0
ind6 for Sp2	0	1	0	0
ind7 for Sp2	0	1	0	0
ind8 for Sp2	0	1	0	0
ind1 for Sp3	0	0	1	0
ind2 for Sp3	0	0	1	0
ind3 for Sp3	0	0	1	0
ind4 for Sp3	0	0	1	0
ind5 for Sp3	0	0	1	0
ind6 for Sp3	0	0	1	0
ind7 for Sp3	0	0	1	0
ind8 for Sp3	0	0	1	0
ind9 for Sp3	0	0	1	0
ind10 for Sp3	0	0	1	0
ind1 for Sp4	0	0	0	1
ind2 for Sp4	0	0	0	1
ind3 for Sp4	0	0	0	1
ind4 for Sp4	0	0	0	1
ind5 for Sp4	0	0	0	1
ind6 for Sp4	0	0	0	1
ind7 for Sp4	0	0	0	1
ind8 for Sp4	0	0	0	1
ind9 for Sp4	0	0	0	1
ind10 for Sp4	0	0	0	1
ind11 for Sp4	0	0	0	1
ind12 for Sp4	0	0	0	1
ind13 for Sp4	0	0	0	1
ind14 for Sp4	0	0	0	1
ind15 for Sp4	0	0	0	1
ind16 for Sp4	0	0	0	1

Matrix

2b

SPECIES IDENTITY with ABUNDANCE

Sometimes species abundances in the community are available (i.e. measured independently via classic relevés or plot record).

For computation purposes we allocate species abundance measured in the community/plot to all individuals of that particular species.

Example: the abundance could be estimated by species biomass (species 1= 10 g, species 2=20 g, species 3 = 30 g, species 4 = 40 g)

Species	Sp1	Sp2	Sp3	Sp4
ind1 for Sp1	10	0	0	0
ind2 for Sp1	10	0	0	0
ind3 for Sp1	10	0	0	0
ind4 for Sp1	10	0	0	0
ind5 for Sp1	10	0	0	0
ind6 for Sp1	10	0	0	0
ind1 for Sp2	0	20	0	0
ind2 for Sp2	0	20	0	0
ind3 for Sp2	0	20	0	0
ind4 for Sp2	0	20	0	0
ind5 for Sp2	0	20	0	0
ind6 for Sp2	0	20	0	0
ind7 for Sp2	0	20	0	0
ind8 for Sp2	0	20	0	0
ind1 for Sp3	0	0	30	0
ind2 for Sp3	0	0	30	0
ind3 for Sp3	0	0	30	0
ind4 for Sp3	0	0	30	0
ind5 for Sp3	0	0	30	0
ind6 for Sp3	0	0	30	0
ind7 for Sp3	0	0	30	0
ind8 for Sp3	0	0	30	0
ind9 for Sp3	0	0	30	0
ind10 for Sp3	0	0	30	0
ind1 for Sp4	0	0	0	40
ind2 for Sp4	0	0	0	40
ind3 for Sp4	0	0	0	40
ind4 for Sp4	0	0	0	40
ind5 for Sp4	0	0	0	40
ind6 for Sp4	0	0	0	40
ind7 for Sp4	0	0	0	40
ind8 for Sp4	0	0	0	40
ind9 for Sp4	0	0	0	40
ind10 for Sp4	0	0	0	40
ind11 for Sp4	0	0	0	40
ind12 for Sp4	0	0	0	40
ind13 for Sp4	0	0	0	40
ind14 for Sp4	0	0	0	40
ind15 for Sp4	0	0	0	40
ind16 for Sp4	0	0	0	40

TRAIT X INDIVIDUAL

Species	Trait value (e.g. height in cm)
ind1 for Sp1	1
ind2 for Sp1	2
ind3 for Sp1	3
ind4 for Sp1	4
ind5 for Sp1	5
ind6 for Sp1	6
ind1 for Sp2	2
ind2 for Sp2	3
ind3 for Sp2	4
ind4 for Sp2	5
ind5 for Sp2	6
ind6 for Sp2	7
ind7 for Sp2	8
ind8 for Sp2	9
ind1 for Sp3	1
ind2 for Sp3	2
ind3 for Sp3	3
ind4 for Sp3	4
ind5 for Sp3	5
ind6 for Sp3	6
ind7 for Sp3	7
ind8 for Sp3	8
ind9 for Sp3	9
ind10 for Sp3	10
ind1 for Sp4	4
ind2 for Sp4	6
ind3 for Sp4	8
ind4 for Sp4	10
ind5 for Sp4	12
ind6 for Sp4	14
ind7 for Sp4	16
ind8 for Sp4	18
ind9 for Sp4	2
ind10 for Sp4	4
ind11 for Sp4	6
ind12 for Sp4	8
ind13 for Sp4	10
ind14 for Sp4	12
ind15 for Sp4	14
ind16 for Sp4	16

Matrix 1

EUCLIDIAN DISTANCE*

TRAIT DISSIMILARITIES between individuals

Matrix 3

Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39
ind1 for Sp1																																							
ind2 for Sp1	1																																						
ind3 for Sp1	2	1																																					
ind4 for Sp1	3	2	1																																				
ind5 for Sp1	4	3	2	1																																			
ind6 for Sp1	5	4	3	2	1																																		
ind1 for Sp2	1	0	1	2	3	4																																	
ind2 for Sp2	2	1	0	1	2	3	1																																
ind3 for Sp2	3	2	1	0	1	2	2	1																															
ind4 for Sp2	4	3	2	1	0	1	3	2	1																														
ind5 for Sp2	5	4	3	2	1	0	4	3	2	1																													
ind6 for Sp2	6	5	4	3	2	1	5	4	3	2	1																												
ind7 for Sp2	7	6	5	4	3	2	6	5	4	3	2	1																											
ind8 for Sp2	8	7	6	5	4	3	7	6	5	4	3	2	1																										
ind1 for Sp3	0	1	2	3	4	5	1	2	3	4	5	6	7	8																									
ind2 for Sp3	1	0	1	2	3	4	0	1	2	3	4	5	6	7	1																								
ind3 for Sp3	2	1	0	1	2	3	1	0	1	2	3	4	5	6	2	1																							
ind4 for Sp3	3	2	1	0	1	2	2	1	0	1	2	3	4	5	3	2	1																						
ind5 for Sp3	4	3	2	1	0	1	3	2	1	0	1	2	3	4	4	3	2	1																					
ind6 for Sp3	5	4	3	2	1	0	4	3	2	1	0	1	2	3	5	4	3	2	1																				
ind7 for Sp3	6	5	4	3	2	1	5	4	3	2	1	0	1	2	6	5	4	3	2	1																			
ind8 for Sp3	7	6	5	4	3	2	6	5	4	3	2	1	0	1	7	6	5	4	3	2	1																		
ind9 for Sp3	8	7	6	5	4	3	7	6	5	4	3	2	1	0	8	7	6	5	4	3	2	1																	
ind10 for Sp3	9	8	7	6	5	4	8	7	6	5	4	3	2	1	9	8	7	6	5	4	3	2	1																
ind1 for Sp4	3	2	1	0	1	2	2	1	0	1	2	3	4	5	3	2	1	0	1	2	3	4	5	6															
ind2 for Sp4	5	4	3	2	1	0	4	3	2	1	0	1	2	3	5	4	3	2	1	0	1	2	3	4	2														
ind3 for Sp4	7	6	5	4	3	2	6	5	4	3	2	1	0	1	7	6	5	4	3	2	1	0	1	2	4	2													
ind4 for Sp4	9	8	7	6	5	4	8	7	6	5	4	3	2	1	9	8	7	6	5	4	3	2	1	0	6	4	2												
ind5 for Sp4	11	10	9	8	7	6	10	9	8	7	6	5	4	3	11	10	9	8	7	6	5	4	3	2	8	6	4	2											
ind6 for Sp4	13	12	11	10	9	8	12	11	10	9	8	7	6	5	13	12	11	10	9	8	7	6	5	4	10	8	6	4	2										
ind7 for Sp4	15	14	13	12	11	10	14	13	12	11	10	9	8	7	15	14	13	12	11	10	9	8	7	6	12	10	8	6	4	2									
ind8 for Sp4	17	16	15	14	13	12	16	15	14	13	12	11	10	9	17	16	15	14	13	12	11	10	9	8	14	12	10	8	6	4	2								
ind9 for Sp4	1	0	1	2	3	4	0	1	2	3	4	5	6	7	1	0	1	2	3	4	5	6	7	8	2	4	6	8	10	12	14	16							
ind10 for Sp4	3	2	1	0	1	2	2	1	0	1	2	3	4	5	3	2	1	0	1	2	3	4	5	6	0	2	4	6	8	10	12	14	2						
ind11 for Sp4	5	4	3	2	1	0	4	3	2	1	0	1	2	3	5	4	3	2	1	0	1	2	3	4	2	0	2	4	6	8	10	12	4	2					
ind12 for Sp4	7	6	5	4	3	2	6	5	4	3	2	1	0	1	7	6	5	4	3	2	1	0	1	2	4	2	0	2	4	6	8	10	6	4	2				
ind13 for Sp4	9	8	7	6	5	4	8	7	6	5	4	3	2	1	9	8	7	6	5	4	3	2	1	0	6	4	2	0	2	4	6	8	8	6	4	2			
ind14 for Sp4	11	10	9	8	7	6	10	9	8	7	6	5	4	3	11	10	9	8	7	6	5	4	3	2	8	6	4	2	0	2	4	6	10	8	6	4	2		
ind15 for Sp4	13	12	11	10	9	8	12	11	10	9	8	7	6	5	13	12	11	10	9	8	7	6	5	4	10	8	6	4	2	0	2	4	12	10	8	6	4	2	
ind16 for Sp4	15	14	13	12	11	10	14	13	12	11	10	9	8	7	15	14	13	12	11	10	9	8	7	6	12	10	8	6	4	2	0	2	14	12	10	8	6	4	2

*for multiple traits, the traits needs to be normalized first (see details in the paper)

Running the R functions

REQUIREMENTS:

- Basic knowledge of R
- Having installed the package ade4
- Add the R functions to the specified working directory
-(having read the paper)

R functions

1. Data set for a VIRTUAL example (as in the Appendix)

```
> tind
 [1]  1  2  3  4  5  6  2  3  4  5  6  7  8  9  1
[16]  2  3  4  5  6  7  8  9 10  4  6  8 10 12 14
[31] 16 18  2  4  6  8 10 12 14 16
>
```

TRAIT X INDIVIDUAL
object tind
as for matrix 1 before

Matrix 1

Species	Trait value (e.g. height in cm)
ind1 for Sp1	1
ind2 for Sp1	2
ind3 for Sp1	3
ind4 for Sp1	4
ind5 for Sp1	5
ind6 for Sp1	6
ind1 for Sp2	2
ind2 for Sp2	3
ind3 for Sp2	4
ind4 for Sp2	5
ind5 for Sp2	6
ind6 for Sp2	7
ind7 for Sp2	8
ind8 for Sp2	9
ind1 for Sp3	1
ind2 for Sp3	2
ind3 for Sp3	3
ind4 for Sp3	4
ind5 for Sp3	5
ind6 for Sp3	6
ind7 for Sp3	7
ind8 for Sp3	8
ind9 for Sp3	9
ind10 for Sp3	10
ind1 for Sp4	4
ind2 for Sp4	6
ind3 for Sp4	8
ind4 for Sp4	10
ind5 for Sp4	12
ind6 for Sp4	14
ind7 for Sp4	16
ind8 for Sp4	18
ind9 for Sp4	2
ind10 for Sp4	4
ind11 for Sp4	6
ind12 for Sp4	8
ind13 for Sp4	10
ind14 for Sp4	12
ind15 for Sp4	14
ind16 for Sp4	16

NOTE

In the Appendix the object tind is built artificially by the commands:

```
> tind1<-c(1:6)
> tind2<-c(2:9)
> tind3<-c(1:10)
> tind4<-c(c(tind2*2), c(tind2*2)-2)
> tind<-c(tind1, tind2, tind3, tind4)
```

or INSTEAD IMPORT YOUR REAL MATRIX 1

Running the R functions

R functions

I bis. VIRTUAL data set for the example

```
> indxsp
      [,1] [,2] [,3] [,4]
 [1,]    1    0    0    0
 [2,]    1    0    0    0
 [3,]    1    0    0    0
 [4,]    1    0    0    0
 [5,]    1    0    0    0
 [6,]    1    0    0    0
 [7,]    0    1    0    0
 [8,]    0    1    0    0
 [9,]    0    1    0    0
[10,]    0    1    0    0
[11,]    0    1    0    0
[12,]    0    1    0    0
[13,]    0    1    0    0
[14,]    0    1    0    0
[15,]    0    0    1    0
[16,]    0    0    1    0
[17,]    0    0    1    0
[18,]    0    0    1    0
[19,]    0    0    1    0
[20,]    0    0    1    0
[21,]    0    0    1    0
[22,]    0    0    1    0
[23,]    0    0    1    0
[24,]    0    0    1    0
[25,]    0    0    0    1
[26,]    0    0    0    1
[27,]    0    0    0    1
[28,]    0    0    0    1
[29,]    0    0    0    1
[30,]    0    0    0    1
[31,]    0    0    0    1
[32,]    0    0    0    1
[33,]    0    0    0    1
[34,]    0    0    0    1
[35,]    0    0    0    1
[36,]    0    0    0    1
[37,]    0    0    0    1
[38,]    0    0    0    1
[39,]    0    0    0    1
[40,]    0    0    0    1
>
```

SPECIES IDENTITY

object indxsp (without relative abundance)

as matrix 2a before

Matrix

2a

Species	Sp1	Sp2	Sp3	Sp4
Sp1	1	0	0	0
Sp1	1	0	0	0
Sp1	1	0	0	0
Sp1	1	0	0	0
Sp1	1	0	0	0
Sp1	1	0	0	0
Sp2	0	1	0	0
Sp2	0	1	0	0
Sp2	0	1	0	0
Sp2	0	1	0	0
Sp2	0	1	0	0
Sp2	0	1	0	0
Sp2	0	1	0	0
Sp2	0	1	0	0
Sp3	0	0	1	0
Sp3	0	0	1	0
Sp3	0	0	1	0
Sp3	0	0	1	0
Sp3	0	0	1	0
Sp3	0	0	1	0
Sp3	0	0	1	0
Sp3	0	0	1	0
Sp3	0	0	1	0
Sp3	0	0	1	0
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1
Sp4	0	0	0	1

Running the R functions

R functions

I bis. VIRTUAL data set for the example

```
> indxsp
      [,1] [,2] [,3] [,4]
 [1,]    1    0    0    0
 [2,]    1    0    0    0
 [3,]    1    0    0    0
 [4,]    1    0    0    0
 [5,]    1    0    0    0
 [6,]    1    0    0    0
 [7,]    0    1    0    0
 [8,]    0    1    0    0
 [9,]    0    1    0    0
[10,]    0    1    0    0
[11,]    0    1    0    0
[12,]    0    1    0    0
[13,]    0    1    0    0
[14,]    0    1    0    0
[15,]    0    0    1    0
[16,]    0    0    1    0
[17,]    0    0    1    0
[18,]    0    0    1    0
[19,]    0    0    1    0
[20,]    0    0    1    0
[21,]    0    0    1    0
[22,]    0    0    1    0
[23,]    0    0    1    0
[24,]    0    0    1    0
[25,]    0    0    0    1
[26,]    0    0    0    1
[27,]    0    0    0    1
[28,]    0    0    0    1
[29,]    0    0    0    1
[30,]    0    0    0    1
[31,]    0    0    0    1
[32,]    0    0    0    1
[33,]    0    0    0    1
[34,]    0    0    0    1
[35,]    0    0    0    1
[36,]    0    0    0    1
[37,]    0    0    0    1
[38,]    0    0    0    1
[39,]    0    0    0    1
[40,]    0    0    0    1
>
```

NOTE

In the Appendix the object indxsp is built artificially by the commands:

```
> indxsp<-matrix(0, 40, 4)
> indxsp[1:6, 1]=1
> indxsp[7:14, 2]=1
> indxsp[15:24, 3]=1
> indxsp[25:40, 4]=1
>
```

or INSTEAD IMPORT YOUR MATRIX 2

R functions

2a. Calculate trait dissimilarity, open and run the RaoRel.r function

3

Trait Euclidian distances

Matrix

Matrix

SPECIES IDENTITY

object indxsp

2a

```
> d<-as.matrix(dist(tind))
>
> source("RaoRel.r")
> library(ade4)
> Raotind<-RaoRel(sample=indxsp, dfunc=d^2/2,
dphyl=NULL, weight=F, Jost=F, structure=NULL)
>
```

Note that to obtain the equivalence between the Rao index and Variance, the trait dissimilarity needs to be squared and divided by 2 (see paper)

Running the R functions

R functions

2b. Alternatively a matrix considering species abundance (as matrix 2b before) can be used with RaoRel.r

Matrix

2b

SPECIES IDENTITY
object indxspp (with abundance)

```
> Raotindp<-RaoRel(sample=indxspp, dfunc=d^2/2,
dphyl=NULL, weight=T, Jost=F, structure=NULL)
>
```

Note the option "weight" needs to be specified otherwise the species abundance is not taken into account

Species	Sp1	Sp2	Sp3	Sp4
ind1 for Sp1	10	0	0	0
ind2 for Sp1	10	0	0	0
ind3 for Sp1	10	0	0	0
ind4 for Sp1	10	0	0	0
ind5 for Sp1	10	0	0	0
ind6 for Sp1	10	0	0	0
ind1 for Sp2	0	20	0	0
ind2 for Sp2	0	20	0	0
ind3 for Sp2	0	20	0	0
ind4 for Sp2	0	20	0	0
ind5 for Sp2	0	20	0	0
ind6 for Sp2	0	20	0	0
ind7 for Sp2	0	20	0	0
ind8 for Sp2	0	20	0	0
ind1 for Sp3	0	0	30	0
ind2 for Sp3	0	0	30	0
ind3 for Sp3	0	0	30	0
ind4 for Sp3	0	0	30	0
ind5 for Sp3	0	0	30	0
ind6 for Sp3	0	0	30	0
ind7 for Sp3	0	0	30	0
ind8 for Sp3	0	0	30	0
ind9 for Sp3	0	0	30	0
ind10 for Sp3	0	0	30	0
ind1 for Sp4	0	0	0	40
ind2 for Sp4	0	0	0	40
ind3 for Sp4	0	0	0	40
ind4 for Sp4	0	0	0	40
ind5 for Sp4	0	0	0	40
ind6 for Sp4	0	0	0	40
ind7 for Sp4	0	0	0	40
ind8 for Sp4	0	0	0	40
ind9 for Sp4	0	0	0	40
ind10 for Sp4	0	0	0	40
ind11 for Sp4	0	0	0	40
ind12 for Sp4	0	0	0	40
ind13 for Sp4	0	0	0	40
ind14 for Sp4	0	0	0	40
ind15 for Sp4	0	0	0	40
ind16 for Sp4	0	0	0	40

Running the R functions

R functions

3. Run function RaoAdo.r

Matrix

2a

SPECIES IDENTITY
object indxsp
no species abundances!

```
> source("RaoAdo.r")
> RaoPerm<-RaoAdo(sample=indxsp, dfunc=d^2/2,
dphyl=NULL, weight=T, Jost=F, structure=NULL)
>
```

Note the option "weight" needs to be specified
This way the weight of each species corresponds to the number of individuals sampled

The objects created by the functions RaoRel.r and RaoAdo.r (i.e. Raoind, Raoindp and RaoPerm; see previous pages) are LISTS where different results are stored (under "xxx$FD")

Example with the Raoind object

```
> names(Raotind$FD)
[1] "Mean_Alpha"      "Alpha"           "Gamma"           "Beta_add"
[5] "Beta_prop"       "Pairwise_samples"
>
```

```
> names(Raotind$FD)
[1] "Mean_Alpha"      "Alpha"           "Gamma"           "Beta_add"
[5] "Beta_prop"       "Pairwise_samples"
>
```

Gamma= TOTAL community diversity (within species + between species)

Mean alpha = overall community WITHIN species FD
Alpha = trait diversity within each species

Beta_add = community BETWEEN species FD
Beta_prop = proportion accounted by community BETWEEN species FD

```
> names(Raotind$FD)
[1] "Mean_Alpha"       "Alpha"            "Gamma"            "Beta_add"
[5] "Beta_prop"        "Pairwise_samples"
> witRao<-Raotind$FD$Mean_Alpha
> witRao
[1] 9.604167
> betRao<-Raotind$FD$Beta_add
> betRao
[1] 5.671875
> totRao<-Raotind$FD$Gamma
> totRao
[1] 15.27604
> (betRao+witRao)==totRao
[1] TRUE
> Raotind$FD$Beta_prop
[1] 37.12922
> Raotind$FD$Alpha
[1]  2.916667  5.250000  8.250000 22.000000
>
```

Total diversity = Between species div. + Within species div.

IT WORKS!

```
> names(Raotind$FD)
[1] "Mean_Alpha"       "Alpha"            "Gamma"            "Beta_add"
[5] "Beta_prop"        "Pairwise_samples"
> witRao<-Raotind$FD$Mean_Alpha
> witRao
[1] 9.604167
> betRao<-Raotind$FD$Beta_add
> betRao
[1] 5.671875
> totRao<-Raotind$FD$Gamma
> totRao
[1] 15.27604
> (betRao+witRao)==totRao
[1] TRUE
> Raotind$FD$Beta_prop
[1] 37.12922
> Raotind$FD$Alpha
[1]  2.916667  5.250000  8.250000 22.000000
>
```

The between-species FD is lower (37%) than the within species (63%)

```
> names(Raotind$FD)
[1] "Mean_Alpha"       "Alpha"            "Gamma"            "Beta_add"
[5] "Beta_prop"        "Pairwise_samples"
> witRao<-Raotind$FD$Mean_Alpha
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[1] 9.604167
> betRao<-Raotind$FD$Beta_add
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[1] TRUE
> Raotind$FD$Beta_prop
[1] 37.12922
> Raotind$FD$Alpha
[1]  2.916667  5.250000  8.250000 22.000000
>
```
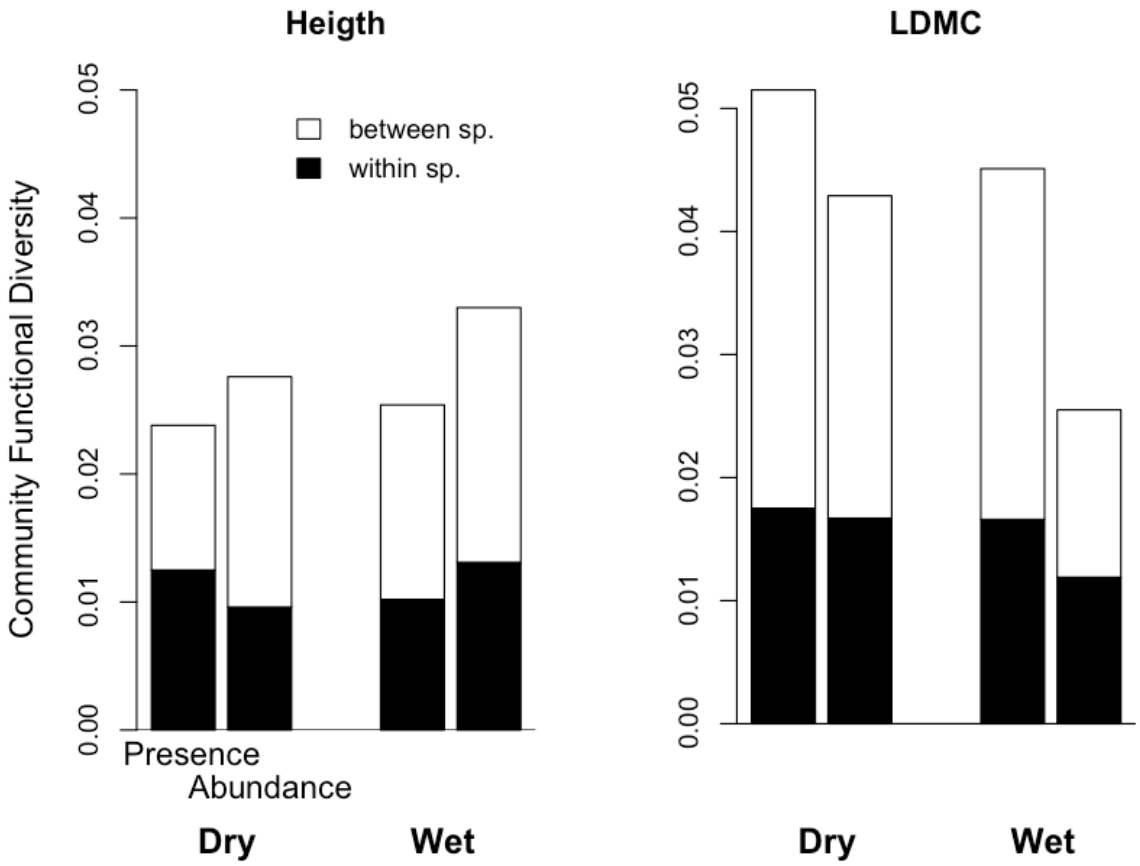

Species	Trait value (e.g. height in cm)
ind1 for Sp1	1
ind2 for Sp1	2
ind3 for Sp1	3
ind4 for Sp1	4
ind5 for Sp1	5
ind6 for Sp1	6
ind1 for Sp2	2
ind2 for Sp2	3
ind3 for Sp2	4
ind4 for Sp2	5
ind5 for Sp2	6
ind6 for Sp2	7
ind7 for Sp2	8
ind8 for Sp2	9
ind1 for Sp3	1
ind2 for Sp3	2
ind3 for Sp3	3
ind4 for Sp3	4
ind5 for Sp3	5
ind6 for Sp3	6
ind7 for Sp3	7
ind8 for Sp3	8
ind9 for Sp3	9
ind10 for Sp3	10
ind1 for Sp4	4
ind2 for Sp4	6
ind3 for Sp4	8
ind4 for Sp4	10
ind5 for Sp4	12
ind6 for Sp4	14
ind7 for Sp4	16
ind8 for Sp4	18
ind9 for Sp4	2
ind10 for Sp4	4
ind11 for Sp4	6
ind12 for Sp4	8
ind13 for Sp4	10
ind14 for Sp4	12
ind15 for Sp4	14
ind16 for Sp4	16

The within species trait variance is highest for species 4



Example from the paper

1. The within species effect on community FD is NOT negligible
2. It changes across traits (height and LDMC), while considering species abundances and across different environmental conditions (e.g. dry vs. wet meadows)

Methods in
Ecology and Evolution

Tutorial

Quantifying the relevance of intraspecific trait variability for functional diversity

For more information, questions & suggestions:

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