Package 'EcoIndR'

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Title Ecological Indicators

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Description Calculates several indices, such as of diversity, fluctuation, etc., and they are used to estimate ecological indicators.

License GPL (>= 2)

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Depends R (>= 3.1.1)

Suggests vegan, shape, Rarity, splancs, plotrix, FD, picante

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R topics documented:

DER	*DIFFERENTIATING SAMPLES USING RARITY, HETEROGENEITY, EVENNESS, TAXONOMIC, PHYLOGENETIC AND FUNCTIONAL DIVERSITY INDICES*

Description

An algorithm for differentiating samples on the basis of the rarity, heterogeneity, evenness, taxonomic/phylogenetic and functional diversity indices that better reflect the differences among assemblages.

Usage

```
DER(data, Samples, Species, Taxon, TaxonFunc=NULL, TaxonPhyl=NULL,
pos=NULL, varSize="Richness", varColor="Rarity", Index=NULL, corr="sqrt",
palette= "heat.colors", size=c(1,5),digitsS=0, digitsC=2, ncolor=100,
transparency=1, references=TRUE, a=1.5, q=2.5, ResetPAR=TRUE, PAR=NULL,
dbFD=NULL, LEGENDS=NULL, TEXT=NULL, COLOR=c("#EEC591FF", "black", "grey50"),
file1="Diversity indices.csv", file2="Polar coordinates.csv",
file3="Indices and area of the polygon.csv", na="NA", dec=",", row.names=FALSE)
```

Arguments

data
: Data file with the taxonomy, abundance of the species and functional traits (optional). The format of the file must be: an optional column with the position of labels' samples in the DER plot (blue column) in the same order as the variables with the species' abundance in the samples (red columns), the columns with the taxonomy of the species (as many as needed, green columns), the columns with the abundance of the species in each sample (red columns) and optionally the colums with the functional traits of the species. Each row is an unique species, genus, family, etc.

Pos	Class	Subclass	Superorder	Order	Family	Genus	Species	J1.1	K4.1	G3.1	F2.1
2	Eurotatoria	Monogononta	Pseudotrocha	Ploima	Asplanchnidae	Asplanchnopus	multiceps				
4	Eurotatoria	Monogononta	Pseudotrocha	Ploima	Euchlanidae	Beauchampiella	eudactylota				
3	Eurotatoria	Monogononta	Pseudotrocha	Ploima	Brachionidae	Brachionus	quadridentatus				
2	Eurotatoria	Monogononta	Pseudotrocha	Ploima	Notommatidae	Cephalodella	gibba	1			
3	Eurotatoria	Monogononta	Gnesiotrocha	Flosculariacea	Conochilidae	Conochilus	dossuarius				16
4	Eurotatoria	Monogononta	Pseudotrocha	Ploima	Euchlanidae	Diplleuchlanis	propatula				
4	Eurotatoria	Monogononta	Pseudotrocha	Ploima	Euchlanidae	Euchlanis	dapidula	4	1	23	6
4	Eurotatoria	Monogononta	Pseudotrocha	Ploima	Euchlanidae	Euchlanis	sp1		3		
4	Eurotatoria	Monogononta	Pseudotrocha	Ploima	Brachionidae	Keratella	tropica	2	10		5

Samples
: Variables with the abundance of the species in each sample: sampling sites, dates, etc.

Species
: Variable with the name of the species (without including the genus). It may be other node of the phylogenetic tree, such as the genus, family, etc., for genus level phylogenies, family level phylogenies, etc.

Taxon
: Variables with the taxonomy of the species (taxonomic diversity), as many levels as needed but without including the variable with the node of the argument *Species*.

TaxonFunc
: Optionally variables with the functional traits (functional diversity).

TaxonPhyl
: Optionally the name of the RData file of the class phylo with the phylogeny. The file must be in the working directory.

pos
: Optionally it is possible to indicate a column with the position of labels' samples in the DER plot. It must be as many as the number of samples and in the same order than the variables described in the argument *Samples*. Values of 1, 2, 3 and 4, respectively indicate positions below, to the left of, above and to the right of the specified coordinates.

varSize
: This variable defines the size of the bubble in the DER plot.

varColor
: This variable defines the color gradient of the bubbles in the DER plot.

Index	The four/five indices used in the DER algorithm. If it is NULL the algorithm select one, index of rarity, one of heterogeneity, one of evenness one of taxonomy and one of the functional group (if functional traits are provided in the argument *TaxonFunc*) that achieve a higher dispersion among samples in a polar coordinates system.
corr	Character string specifying the correction method to use, in the function dbFD, when the species-by-species distance matrix cannot be represented in a Euclidean space. Options are "sqrt" (default), "cailliez", "lingoes" or "none".
palette	The color gradient of the bubbles may be one of these palettes: "heat.colors", "terrain.colors", "gray.colors", "topo.colors" or "cm.colors", or any other option defined by the user.
size	Range of size of the bubbles. Two values: minimum and maximum size.
digitsS	Number of digits of the bubble size legend.
digitsC	Number of digits of the color legend.
ncolor	Gradient color of the color legend.
transparency	Transparency of the color gradient, from 0 to 1.
references	If it is TRUE the reference points are depicted on the DER plot.
a	Scale of Rényi diversity.
q	Scale of Tsallis diversity.
ResetPAR	If it is FALSE, the default condition of the function PAR of the package StatR is not placed and maintained those defined by the user in previous graphics.
PAR	It accesses the function PAR of the package StatR that allows to modify many different aspects of the graph.
dbFD	It accesses the function dbFD which allows to specify the arguments that calculates the functional diversity indices.
LEGENDS	It allows to modify the legend of the bubble size.
TEXT	It allows to modify the text of the labels in the bubbles.
COLOR	A vector with three values: color of the ellipse, color of the points in the legend of the size of the bubbles and color of the references points in the ellipse, respectively.
file1	CSV FILES. Filename with values of total abundance, richness and the rarity, heterogeneity, evenness, taxonomic, phylogenetic and functional diversity indices of each sample.
file2	CSV FILES. Filename with the polar coordinates of all samples considering the four/five selected indices.
file3	CSV FILES. Filename with the area of the convex hull (alpha=6) and Euclidean distance obtained in the polar coordinates system for all combinations of the indices.
na	CSV FILE. Text that is used in the cells without data.
dec	CSV FILE. It defines if the comma "," is used as decimal separator or the dot ".".
row.names	CSV FILE. Logical value that defines if identifiers are put in rows or a vector with a text for each of the rows.

Details

DER algorithm

The steps of DER algorithm are described below:

1. The function DER calculates the most often used indices (see below): a total of 39 indices that includes 2 of rarity, 14 of heterogeneity, 7 of evenness, 2 of taxonomic diversity, 8 of phylogenetic diversity and 6 of functional diversity. It is important to mention that the indices included in the groups of phylogenetic diversity and functional diversity, each explores a different facet of phylogenetic diversity (Kembel et al., 2010) and functional diversity (Laliberté et al., 2010), respectively.

Rarity indices

In the following equations *S* is the number of species (species richness), *s* is the number of samples, r_{ij} is the number of records of the species *i* in the sample *j*, *R* is the total number of records considering all the species in all samples, Q_i is the occurrence of species *i*, Q_{min} and Q_{max} are respectively the minimum and maximum occurrences in the species pool, *r* is the chosen rarity cutoff point (as a percentage of occurrence), w_i is the weight of the *ith* species in the assemblage, w_{min} and w_{max} the minimum and maximum weights respectively.

Leroy (Leroy et al., 2012; 2013)

$$w_i = \frac{1}{e^{\left(\frac{Q_i - Q_{min}}{rQ_{max}Q_{min}} * 0.97 + 1.05\right)^2}}$$

$$I_{RR} = \frac{\frac{\sum_{i=1}^{S} w_i}{S} - w_{min}}{w_{max} - w_{min}}$$

Rarity This index is a novel contribution of this package.

$$R = 1 - \frac{\sum_{i=1}^{S}\sum_{j=1}^{s}\frac{r_{ij}}{R}}{S}$$

Heterogeneity indices

In the following equations *S* is the number of species (species richness), p_i is the abundace's proportion of species *i*, *N* is the total number of individuals in the sample, n_i is the number of individuals of the species *i*, n_{max} is the number of individuals of the most abundant species, *a* and *q* are the orders of Rényi and Tsallis indices respectively and, finally, in Fisher's alpha the index is the α parameter.

log Shannon-Wiener (S.W.LOG2) and *ln Shannon-Wiener (S.W)* (Wiener, 1939; 1948; 1949; Shannon, 1948; Shannon & Weaver, 1949). See Spellerger & Fedor (2013) for an explanation of the dual use of the terms Shannon-Wiener and Shannon-Weaver to refer to this diversity index.

$$H = -\sum_{i=1}^{S} p_i log_2 p_i$$

$$H' = -\sum_{i=1}^{S} p_i ln p_i$$

Fisher's alpha (Fisher et al., 1943)

$$\alpha x, \frac{\alpha x^2}{2}, \frac{\alpha x3}{3}, ..., \frac{\alpha x^n}{n}$$

Simpson (Simpson, 1949)

$$D_1 = 1 - \sum_{i=1}^{S} p_i^2$$

Inverse Simpson (InvSimpson) Williams (1964)

$$D_2 = \frac{1}{\sum_{i=1}^{S} p_i^2}$$

Brillouin (Brillouin, 1956)

$$H_B = \frac{lnN! - \sum_{i=1}^{S} lnn_i!}{N}$$

Margalef (Margalef, 1959)

$$D_{Mg} = \frac{(S-1)}{lnN}$$

Rényi entropy (Rényi, 1961)

$$H_a = \frac{1}{(1-a)} log \sum_{i=1}^{S} p_i^a$$

Menhinick (Menhinick, 1964)

$$D_{Mn} = \frac{S}{\sqrt{N}}$$

McIntosh (McIntosh, 1967)

$$D_{Mc} = \frac{N - \sqrt{\sum_{i=1}^{S} n_i^2}}{N - \sqrt{N}}$$

Inverse Berger-Parker (InvB.P) (Berger & Parker, 1970)

$$D_{BP} = \frac{1}{\frac{n_{max}}{N}}$$

Hill numbers (Hill, 1973)

Hill-Rényi

$$N_a = e^{H_a}$$

Hill-Tsallis

$$N_q = (1 - (q-1)H_q)^{\frac{1}{(1-q)}}$$

where

a or q = 0 is species richness

a or q = 1 is Shannon's index (H')

a or q = 2 is Inverse Simpson's index (D_2)

a or q = Inf is Inverse Berger-Parker index (D_{BP})

Tsallis entropy (Patil & Taillie, 1982; Tsallis, 1988)

$$H_q = \frac{1}{(q-1)}(1 - \sum_{i=1}^{S} p_i^q)$$

Evenness indices

Annotations of the equations as mentioned for heterogeneity indices.

Simpson evenness (SimpsonE) (Simpson, 1949)

$$E_{D1} = \frac{D_1}{S}$$

Pielou (PielouE) (Pielou, 1966)

$$J' = \frac{H'}{lnS}$$

McIntosh evenness (McIntoshE) (McIntosh, 1967)

$$E_{Mc} = \frac{N - \sqrt{\sum_{i=1}^{S} n_i^2}}{N - \frac{N}{\sqrt{S}}}$$

Hill evenness (HillE) (Hill, 1973)

It is used Hill-Rényi numbers where in N_2 the value of a = 2 and in N_2 the value of a = 1

$$E_{2,1} = \frac{N_2}{N_1}$$

Heip evenness (HeipE) (Heip, 1974)

$$E_{Heip} = \frac{e^{H'} - 1}{S - 1}$$

Camargo (CamargoE) (Camargo, 1992)

$$E_{Camargo} = 1 - \sum_{i=1}^{S} \sum_{j=i'+1}^{S} \frac{|p_i - p_j|}{s}$$

Smith and Wilson's Index (Evar) (Smith and Wilson, 1996)

$$E_{var} = 1 - \left(\frac{2}{\pi}\right)\left(arctan\left(\frac{\sum\limits_{i=1}^{S}\left(lnn_i - \frac{\sum\limits_{j=1}^{S}n_j}{S}\right)^2}{S}\right)\right)$$

Taxonomic diversity indices

In the following equations summation goes over species *i* and *j*, ω are the taxonomic distances among taxa, *x* are species abundances, and *n* is the total abundance for a site.

Taxonomic diversity (D) (Clarke, 1995; 1998; 2001):

$$\Delta = \frac{\sum\sum_{i<j}\omega_{ij}x_ix_j}{n(n-1)/2}$$

Taxonomic distinctness (Dstar) (Clarke and Warwick, 1998):

$$\Delta^* = \frac{\sum\sum_{i<j}\omega_{ij}x_ix_j}{\sum\sum_{i<j}x_ix_j}$$

Phylogenetic diversity indices

Faith's phylogenetic diversity	Faith (1992)
Mean pairwise phylogenetic distance	Webb et al. (2008)
Mean nearest taxon distance	Webb et al. (2008)
Phylogenetic species richness	Helmus et al. (2007)
Phylogenetic species variability	Helmus et al. (2007)
Phylogenetic species evenness	Helmus et al. (2007)
Phylogenetic species clustering	Helmus et al. (2007)
Quadratic entropy	Rao (1982)

Functional diversity indices

In the following equations *S* is the number of species, where d_{ij} is the difference between the *i-th* and *j-th* species, p_i is the abundance's proportion of the species *i*, p_j is the abundance's proportion of the species *j*, *EW* is weighted evenness, dist(*i*, *j*) is the Euclidean distance between species *i* and *j*, the species involved is branch *l*, w_i is the relative abundance of the species *i*, PEW_l is the partial weighted evenness, g_k are the coordinates of the center of gravity of the *V* species forming the vertices of the convex hull, x_{ik} is the coordinate of species *i* on trait *k*, dG_i is the Euclidean distance of the center of gravity, $\bar{dG}$ is the mean distance of the *S* species to the center of gravity, Δd is the sum of abundance-weighted deviances and $\Delta|d|$ absolute abundance-weighted deviances.

Rao's quadratic entropy (Rao, 1982; Botta-Dukát, 2005):

$$Q = \sum_{i=1}^{S-1} \sum_{j=i+1}^{S-1} d_{ij} p_i p_j$$

$$d_{ij} = \sum_{k=1}^{n} \sum_{l=1}^{n} w_{kl}(X_{ik} - X_{jk})(X_{il} - X_{jl})$$

Functional group richness (FGR) Petchey and Gaston (2006)

Functional richness (FRic) is measured as the amount of functional space (convex hull volume) filled by the community (Villéger et al., 2008).

Functional evenness (FEve) (Villéger et al., 2008):

$$FEve = \frac{\sum_{l=1}^{S-1} min(PEW_l, \frac{1}{S-1}) - \frac{1}{S-1}}{1 - \frac{1}{S-1}}$$

$$PEW_l = \frac{EW_l}{\sum_{l=1}^{S} EW_l} \qquad EW_l = \frac{dis(i,j)}{w_i + w_j}$$

Functional divergence (FDiv) (Villéger et al., 2008):

$$FDiv = \frac{\Delta d + \bar{dG}}{\Delta|d| + \bar{dG}}$$

$$\Delta|d| = \sum_{i=1}^{S} w_i |dG_i - \bar{dG}| \qquad \Delta d = \sum_{i=1}^{S} w_i (dG_i - \bar{dG})$$

$$\bar{dG} = \frac{1}{S} \sum_{i=1}^{S} dG_i \qquad dG_i = \sqrt{\sum_{k=1}^{T} (x_{ik} - g_k)^2} \qquad g_k = \frac{1}{V} \sum_{i=1}^{V} x_{ik}$$

Functional dispersion (FDis) (Laliberté and Legendre, 2010):

$$FDisp = \frac{\sum a_j z_j}{\sum a_j} \qquad c = \frac{\sum a_j x_{ij}}{\sum a_j}$$

2. Each index is transformed to a scale range between 0 and 1 for all samples with the following

equation:

$$\frac{(index\,of\,the\,sample - min)}{(max - min)}$$

where *min* and *max* are the minimum and maximum values of the index considering all samples, respectively.

3. With the standardized values of the indices, the algorithm calculates the polar coordinates of all samples with all possible combinations among all groups of indices. Therefore, in each combination an index of each group of rarity, heterogeneity (species richness is included in this group), evenness, taxonomic/ phylogenetic diversity and functional diversity (if it is included functional traits in the analysis) is used for calculating the polar coordinates of all samples. In the group of taxonomic/phylogenetic diversity the user must use either taxonomy or a phylogenetic tree, so either taxonomic diversity or phylogenetic diversity indices are used in the algorithm. The X and Y polar coordinates for each sample are estimated using the following equations:

$$X = \sum_{i=1}^{4} |z_j| cos(\alpha) \quad Y = \sum_{i=1}^{4} |z_j| sin(\alpha)$$

where *z* is the standardized value of the index *j* of the four groups considered.

Each index is assigned an angle (α). Degrees to radians angle conversion is carried out assuming that 1 degree = 0.0174532925 radians.

4. With the polar coordinates of the samples obtained for each combination, it is calculated the convex hull (alpha = 6) and the mean Euclidean distance, and the values are saved in a file.

5. The algorithm selects the combination of indices with the highest value of the mean between convex hull and mean Euclidean distance among samples, therefore priority is given to maximize dispersion among samples (see Fig. 1). The polar coordinates of the selected combination are depicted on a diagram, where it is possible to see the differences in rarity, heterogeneity, evenness and taxonomic/phylogenetic diversity and/or functional diversity (if it is included) among assemblages.

6. Finally, DER function allows the user to select the four/five indices to be used in the diagram, so the algorithm of selecting the combination with the maximum dispersion among samples is not applied.
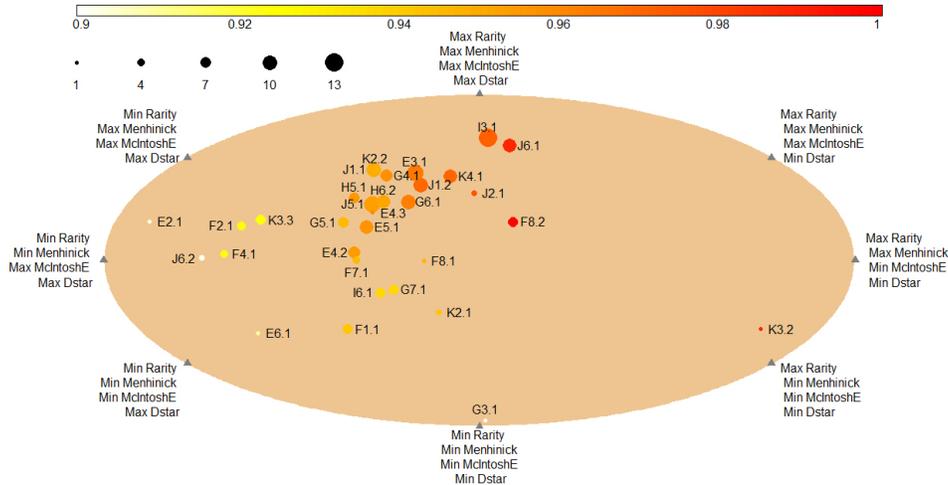
FUNCTIONS

The index Fisher alpha was estimated with the function fisher.alpha, the index Rényi with the function renyi, the index Tsallis with the function tsallis, the taxonomic diversity and taxonomic distinctness with the functions taxa2dist and taxondive, all of them of the package vegan (Oksanen et al., 2016). The ellipse is depicted with the function plotellipse of the package shape (Soetaert, 2016). The convex hull (alpha=6) was calculated with the function areapl of the package splancs (Bivand et al., 2016). The color legend of DER plot was depicted with the function color.legend of the package plotrix (Lemon et al., 2016). The rarity index of Leroy was calculated with the functions rWeights and Irr, both of the package Rarity (Leroy et al., 2012; 2103; Leroy, 2016). The functional diversity indices were calculated with the function dbFD of the package FD (Laliberté et al., 2015). The phylogenetic indices were calculated with the functions psv, psr, pse, psc, raoD, mntd, mpd and pd of the package picante (Kembel et al. 2010 2016)

EXAMPLE

The example without functional diversity is a dataset with the abundance of rotifers species in ponds (see table 1 in Mazuelos et al., 1993). In the argument *Index* were selected Rarity, Menhinick,

McIntoshE and Dstar, which are the indices selected by the algorithm when *Index=NULL* (default option). The sample G3.1 had the lowest values of the indices of rarity, heterogeneity, evenness and taxonomic diversity and the pond I3.1 the highest values for all indices.

Value

It is depicted a plot of polar coordinates estimated with the rarity, heterogeneity, evenness, taxonomic/phylogenetic and functional diversity indices, CSV files are saved with all the indices, the polar coordinates estimated with the indices specified in the argument *Index* or estimated by the algorithm, and the area of the convex hull and mean Euclidean distance obtained in the polar coordinates system for all combinations of the indices.

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Examples

```
#An example without functional diversity

data(Rotifers)

DER(data=Rotifers, Samples=c("J1.1","K4.1","G3.1","F2.1","K2.2","F8.2","F8.1",
"F1.1","F4.1","J2.1","E5.1","H5.1","K3.2","E4.2","I6.1","K2.1","J5.1","I3.1",
"K3.3","G5.1","E6.1","J1.2","J6.1","G7.1","G6.1","G4.1","E3.1","E4.3","E2.1",
"H6.2","F7.1","J6.2"), Species="Species", Taxon=c("Class","Subclass",
"Superorder","Order","Family","Genus"), pos="Pos", Index=c("Rarity","Menhinick",
"McIntoshE", "Dstar") )
```

Rotifers	*ABUNDANCE OF ROTIFERS IN PONDS*

Description

Abundance of species of rotifers in ponds of Doñana National Park (Spain), which were obtained from Table 1 of Mazuelos et al. (1993).

Usage

```
data(Rotifers)
```

Format

An data frame with 40 columns: position of the label of the pond in the DER plot, 7 columns with the taxonomy of the species and the rest of columns are the abundance of the species of rotifers in the ponds.

References

Mazuelos, N., Toja, J., & Guisande, C. (1993) Rotifers in ephemeral ponds of Doñana National Park. *Hidrobiologia*, 255/256: 429-434.

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