

# Package ‘EcoIndR’

July 4, 2017

**Version** 1.1

**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)

**Encoding** latin1

**Depends** R (>= 3.1.1)

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

**Repository** CRAN

**NeedsCompilation** no

**Date/Publication** 2017-07-03 22:18:41 UTC

## R topics documented:

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|     |  |
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| DER | <i>DIFFERENTIATING SAMPLES USING RARITY, HETEROGENEITY, EVENNESS, TAXONOMIC, PHYLOGENETIC AND FUNCTIONAL DIVERSITY INDICES</i> |
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## 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 columns with the functional traits of the species. Each row is an unique species, genus, family, etc.

| Pos | Class       | Subclass    | Superorder   | Order          | Family        | Genus         | Species        | F1.1 | F0.1 | G3.1 | F2.1 |
|-----|-------------|-------------|--------------|----------------|---------------|---------------|----------------|------|------|------|------|
| 2   | Eurotatoria | Monogononta | Pseudotrocha | Plolima        | Asplanchnidae | Asplanchnopus | multiceps      |      |      |      |      |
| 4   | Eurotatoria | Monogononta | Pseudotrocha | Plolima        | Euchlanidae   | Beauchampella | eudactylota    |      |      |      |      |
| 3   | Eurotatoria | Monogononta | Pseudotrocha | Plolima        | Brachionidae  | Brachionus    | quadridentatus |      |      |      |      |
| 2   | Eurotatoria | Monogononta | Pseudotrocha | Plolima        | Notommatidae  | Cephalodella  | gibba          | 1    |      |      |      |
| 3   | Eurotatoria | Monogononta | Gnathotrocha | Flosculariacea | Conochilidae  | Conochilus    | dossuarius     |      |      |      | 16   |
| 4   | Eurotatoria | Monogononta | Pseudotrocha | Plolima        | Euchlanidae   | Dipleuchlanis | prospatula     |      |      |      |      |
| 4   | Eurotatoria | Monogononta | Pseudotrocha | Plolima        | Euchlanidae   | Euchlanis     | dapidula       | 4    | 1    | 23   | 6    |
| 4   | Eurotatoria | Monogononta | Pseudotrocha | Plolima        | Euchlanidae   | Euchlanis     | sp1            |      | 3    |      |      |
| 4   | Eurotatoria | Monogononta | Pseudotrocha | Plolima        | Brachionidae  | Keratella     | troopica       | 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., but always without duplicates.

**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 <i>TaxonFunc</i> ) that achieve a higher dispersion among samples in a polar coordinates system. |
| corr         | Character string specifying the correction method to use, in the function <code>dbFD</code> , 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 <code>dbFD</code> 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*

Leroy                      Leroy et al. (2012; 2013)

Rarity. This index is a novel contribution of this package, where  $S$  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.

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

#### *Heterogeneity indices*

|                              |   |
|------------------------------|---|
| In Shannon-Wiener            | Wiener, (1939; 1948; 1949)                |
| and log Shannon-Wiener       | Shannon (1948); Shannon and Weaver (1949) |
| Fisher's alpha               | Fisher et al. (1943)                      |
| Simpson                      | Simpson (1949)                            |
| Inverse Simpson              | Williams (1964)                           |
| Brillouin                    | Brillouin (1956)                          |
| Margalef                     | Margalef (1959)                           |
| Rényi entropy                | Rényi (1961)                              |
| Menhinick                    | Menhinick (1964)                          |
| McIntosh                     | McIntosh (1967)                           |
| Inverse Berger-Parker        | Berger and Parker (1970)                  |
| Hill- Rényi and Hill-Tsallis | Hill (1973)                               |
| Tsallis entropy              | Patil and Taillie (1982); Tsallis (1988)  |

#### *Evenness indices*

|                          |                         |
|--------------------------|-------------------------|
| Simpson                  | Simpson (1949)          |
| Pielou                   | Pielou (1966)           |
| McIntosh                 | McIntosh (1967)         |
| Hill-Rényi numbers       | Hill (1973)             |
| Heip                     | Heip (1974)             |
| Camargo                  | Camargo (1992)          |
| Smith and Wilson's Index | Smith and Wilson (1996) |

*Taxonomic diversity indices*

|                            |                                       |
|----------------------------|---------------------------------------|
| Taxonomic diversity        | Warwick and Clarke (1995; 1998; 2001) |
| and Taxonomic distinctness | Clarke and Warwick (1998)             |

*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*

|                           |                               |
|---------------------------|-------------------------------|
| Rao's quadratic entropy   | Botta-Dukát (2005)            |
| Functional group richness | Petchey and Gaston (2006)     |
| Functional richness       | Villéger et al. (2008)        |
| Functional evenness       | Villéger et al. (2008)        |
| Functional divergence     | Villéger et al. (2008)        |
| Functional dispersion     | Laliberté and Legendre (2010) |

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 ( $\alpha$ ). Degrees to radians angle conversion is carried out assuming that 1 degree = 0.0174532925 radians.

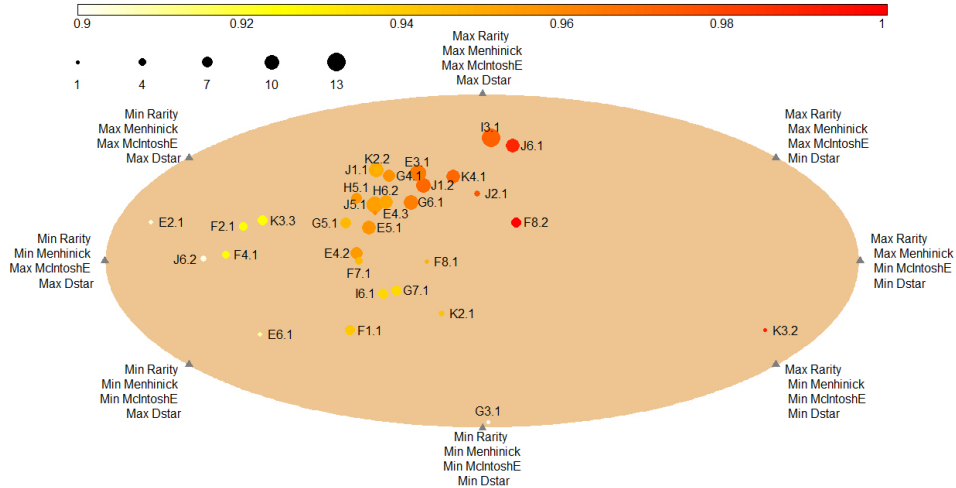
4. With the polar coordinates of the samples obtained for each combination, it is calculated the convex hull (alpha = 6) and the mean Euclidean distance, and the values are saved in a file.
5. The algorithm selects the combination of indices with the highest value of the mean between convex hull and 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 `lrr`, 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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