**Package ‘ComEcoPaCR’**

**Title**

Community Ecology Parameter Calculator in R

**Description**

ComEcoPaCR provides following types of calculation:

* Species richness and species diversity (number of species, species richness indices, species diversity indices), evenness (for specific diversity indices).
* Abundance and prediction of relative abundance based on Broken stick model, number of singletons and doubletons, dominance classification based on the Tischler's categories,
* Quantitative and qualitative similarity indices for group of samples

**Abstract**

Quantitative analysis of ecological data is substantial for recent ecological research. We developed a package Community Ecology Parameter Calculator in R (ComEcoPaCR) with a focus on basic taxocoenosis parameters. The recent version of the package ComEcoPaCR includes in functions which offer more user-friendly settings and provide both tabular and graphical outputs. These functions calculate and visualize species richness and abundance of samples, structure of species in the sample (dominance and frequency), species richness indices (Margalef and Menhinick index), species diversity indices and evenness for the indices (Shannon index, Simpson and Brillouin index), and calculate similarity of samples (Jaccard and Renkonen index, Sørensen coefficient and Bray-Curtis index). The package will be extended in the future for other important parameters and functions such as richness estimates, species accumulation curves and other popular analyses.

*Keywords: ComEcoPaCR, R package, abundance, dominance, species richness, diversity indices, similarity of samples, community ecology analysis*

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# read.eco - Uploading the dataset

**Description**

Uploading the dataset, performing basic analyses for the loaded table, creating table attributes

**Usage**

read.eco(first.col=2, na2null=T, attrib=T)

**Arguments**

first.col = the first column of samples (to skip non-relevant columns)

na2null = converting NA values to null

attrib = creating attributes

**Examples**

x<-read.eco()

**Details**

The function read.eco appeals to users to copy the dataset from the spreadsheet. With uploaded dataset is worked from the user's specified column (first.col=2). This function also automatically converts NA values to null (na2null=T) and writes out attributes of the uploaded dataset.

# Sn.eco – Species richness and abundance

**Descriptions**

Calculation of species richness and abundance

**Usage**

sn.eco(x, first.col = 2, table = T, graph = T)

**Arguments**

x = data

first.col = integer, the first column for the analysis

table = logical, if TRUE table will be creating (T) or uncreating (F)

graph = logical, if TRUE graphical output will be drawn

**Examples**

sn.eco(x)

**Details**

The function sn.eco provides the calculations of species richness and abundance for uploaded dataset (x). With dataset is worked from the user's specified column (first.col=2). This function provides tabular (table=T) and graphical outputs (graph=T).

# mm.eco - Margalef's and Menhinick's index

**Description**

Calculation of species richness indices (Margalef's and Menhinick's index)

**Usage**

mm.eco(x, first.col=2, table=1, graph=1)

**Arguments**

x = data

first.col = integer, the first column for the analysis

table = logical, if TRUE table will be creating (T) or uncreating (F)

graph = logical, if TRUE graphical output will be drawn

**Examples**

mm.eco(x)

mm\_index.eco(x, table = 2, graph = 2)

mm\_index.eco(x, table = 3, graph = 3)

**Details**

The function mm.eco provides the calculations of Margalef's (DMg) and Menhinick's (DMm) index for uploaded dataset (x). With dataset is worked from the user's specified column (first.col=2). This function returns tabular (table=T) and graphical outputs (graph=T). Users can set the outputs as:

1 = table and graph are made for both indices

2 = table and graph are made only for Margalef's index

3 = table and graph are made only for Menhinick's index

**References**

Clifford H.T. & Stephenson W., 1975: An introduction to numerical classification. Academic Press: New York, San Francisco, ISBN 978-0-12-176750-1.

Magurran A.E., 2013: Measuring Biological Diversity. Wiley-Blackwell: Malden, Oxford, Carlton, ISBN 978-1-118-68792-5.

Whittaker R., 1977: Evolution of species diversity in land communities. Evolutionary Biology 10: 1–67.

# shannon.eco - Shannon index and evenness for Shannon index

**Descriptions**

Calculation and graphical visualization of Shannon index and evenness for Shannon index

**Usage**

shannon.eco(x, first.col=2, table=1, graph=T, arrow=T)

**Arguments**

x = data

first.col = integer, the first column for the analysis

table = creating table

graph = logical, if TRUE graphical output will be drawn graph

arrows = logical, if TRUE arrows will be drawn

log\_base = used base of logarithm

**Examples**

shannon.eco(x)

shannon.eco(x, table = 2, arrow = F)

shannon.eco(x, table = 3)

**Details**

The function shannon.eco provides the calculations of Shannon index (H'), maximal (Hmax) and minimal (Hmin) diversity values and evennesses for Shannon index (Even1, Even2) for every sample in the uploaded dataset (x). Formula for Even1 is , for Even2 is . With dataset is worked from the user's specified column (first.col=2). This function provides tabular (table=T) and graphical outputs (graph=T), where it is possible to set arrows showing the maximal and minimal values (arrows=T) of diversity. Users can set the tabular outputs as:

1 = calculations for Shannon indices, maximal and minimal diversity values and evennesses for Shannon index

2 = calculations for Shannon indices, maximal and minimal diversity values

3 = calculations only for evennesses for Shannon index

In this function you can also set base for logarithm used in Shannon index formula, where:

1 = base is equal to Euler's number, which means that is used natural logarithm

2 = base is equal to two, which means that is used binary logarithm

**References**

Hurlbert S., 1971: The Nonconcept of Species Diversity: A Critique and Alternative Parameters. Ecology 52(4): 577–586.

Magurran A.E., 2013: Measuring Biological Diversity. Wiley-Blackwell: Malden, Oxford, Carlton, ISBN 978-1-118-68792-5.

Pielou E.C., 1969: An introduction to mathematical ecology. Wiley-Interscience: New York, ISBN 978-0-471-68918-8.

Pielou E.C., 1975: Ecological Diversity. Wiley-Interscience: New York, ISBN 0-471-68925-4.

Shannon C. & Weaver W., 1964: The Mathematical Theory of Communication. The University of Illinois press: Urbana, ISBN 978-0-252-72548-7.

# simpson.eco - Simpson index and evenness for Simpson index

**Descriptions**

Calculation and graphical visualization of Simpson's index and evenness for Simpson's index

**Usage**

simpson.eco(x, first.col = 2, table = T, graph = T)

**Arguments**

x = data

first.col = integer, the first column for the analysis

table = logical, if TRUE table will be creating (T) or uncreating (F)

graph = logical, if TRUE graphical output will be drawn graph

**Examples**

simpson.eco(x)

**Details**

The function simpson.eco provides the calculations of Simpson's index (D) in reciprocal (Dr) and complementary (Dc) variant and evenness for this specific index for every sample in the uploaded dataset (x). With dataset is worked from the user's specified column (first.col=2).

This function returns tabular (table=T) and graphical outputs (graph=T).

**References**

Krebs C.J., 1999: Ecological Methodology. 2nd ed. Benjamin Cummings: Menlo Park, ISBN 978-0-321-02173-1.

Magurran A.E., 2013: Measuring Biological Diversity. Wiley-Blackwell: Malden, Oxford, Carlton, ISBN 978-1-118-68792-5.

Smith B. & Wilson J.B., 1996: A Consumer’s Guide to Evenness Indices. Oikos 76(1): 70–82.

Southwood T. & Henderson P., 2000: Ecological Methods 3rd ed. Blackwell Science: USA, ISBN 978-0-632-05477-0.

# brillouin.eco - Brillouin index and evenness for Brillouin index

**Descriptions**

Calculation and graphical visualization of Brillouin index and evenness for Brillouin index

**Usage**

brillouin.eco(x, first.col = 2, table = T, graph = T)

**Arguments**

x = data

first.col = integer, the first column for the analysis

table = logical, if TRUE table will be creating (T) or uncreating (F)

graph = logical, if TRUE graphical output will be drawn graph

**Examples**

brillouin.eco(x)

**Details**

The function brillouin.eco provides the calculations of Brillouin index (HB), maximal diversity value (Hbmax) and evenness for Brillouin index for every sample in the uploaded dataset (x). With dataset is worked from the user's specified column (first.col=2). This function returns tabular (table=T) and graphical outputs (graph=T).

**References**

Krebs C.J., 2014: Ecological Methodology. 3rd ed. (in prep).

Pielou E.C., 1966: The measurement of diversity in different types of biological collections. Journal of Theoretical Biology 13: 131–144.

# broks.eco - Broken stick model

**Descriptions**

Prediction of distribution of species relative abundance based on Broken stick model

**Usage**

broks.eco(x, first.col = 2, table=T, graph = T)

**Arguments**

x = data

first.col = integer, the first column for the analysis

table = logical, if TRUE table will be creating (T) or uncreating (F)

graph = logical, if TRUE graphical output will be drawn graph

**Examples**

broks.eco(x)

**Details**

The function broks.eco predicts distribution of species relative abundance based on Broken stick model calculation. With uploaded dataset (x) is worked from the user's specified column (first.col=2). This function returns tabular (table=T) and graphical outputs (graph=T).

**References**

MacArthur R.H., 1957: On the Relative Abundance of Species. Proceedings of the National Academy of Sciences 43(3): 293–295.

Magurran A.E., 2013: Measuring Biological Diversity. Wiley-Blackwell: Malden, Oxford, Carlton, ISBN 978-1-118-68792-5.

May R., 1975: Patterns of species abundance and diversity. Ecology and Evolution of Communities: 81–120.

# dominance.eco - Dominance

**Description**

Tischler's dominance classes analyses

**Usage**

dominance.eco(x, first.col = 2, table = 1, graph = 1, pos\_leg = 11)

**Arguments**

x = data

first.col = integer, the first column for the analysis

table = creating specific table

graph = creating specific graph

posl\_leg = legend setting

**Examples**

dominance.eco(x)

dominance.eco(x, table = 2, graph = 2)

dominance.eco(x, table = 3, graph = 3)

**Details**

The function dominance.eco provides Tischler's dominance classes analyses (Sr, R, Sd, D, E) for uploaded dataset (x). With uploaded dataset is worked from the user's specified column (first.col=2). This function returns tabular (table=T) and graphical outputs (graph=T), where it is feasible to set a position of the legend (pos\_leg=11). There are three possible displays of results:

1 = the table and the graph show results of calculations in absolute and relative variant

2 = the table and the graph show results of calculations only in absolute variant

3 = the table and the graph show results of calculations only in relative variant

**References**

Tischler W., 1949: Grundzüge der terrestrischen Tierökologie. Friedrich Vieweg und Sohn: Braunschweig, ISBN 978-3-663-00636-7.

# single\_double.eco - Singletons and doubletons

**Descriptions**

Calculation and graphical visualization of singletons and doubletons

**Usage**

single\_double.eco(x, first.col = 2, table = 1, graph = 1, pos\_leg = 8.5)

**Arguments**

x = data

first.col = integer, the first column for the analysis

table = creating specific table

graph = creating specific graph

posl\_leg = legend setting

**Examples**

single\_double.eco(x)

single\_double.eco(x, table = 2, graph = 2)

single\_double.eco(x, table = 3, graph = 3)

**Details**

The function single\_double.eco provides the number of singletons (F1) and doubletons (F2) for uploaded dataset (x). With uploaded dataset is worked from the user's specified column (first.col=2). This function returns tabular (table=T) and graphical outputs (graph=T), where it is feasible to set a position of the legend (pos\_leg=8.5). There are three possible displays of results:

1 = the table and the graph show number of singletons and doubletons in terms of number of samples and abundance

2 = the table and the graph show number of singletons and doubletons only in terms of number of samples

3 = the table and the graph show number of singletons and doubletons only in terms of abundance

# jac\_ren.eco - Jaccard a Renkonen index

**Descriptions**

Calculation and graphical visualization of Jaccard and Renconen index

**Usage**

jac\_ren.eco(x, first.col=2, table=T, graph=T, txt=T, txs=1)

**Arguments**

x = data

first.col = integer, the first column for the analysis

table = logical, if TRUE table will be creating (T) or uncreating (F)

graph = logical, if TRUE graphical output will be drawn graph

txt = insertion of values of calculations into graph

txs = size of inserted values

**Examples**

jac\_ren.eco(x)

**Details**

The function jac\_ren.eco provides the calculations of Jaccard index and Renkonen similarity index for samples in uploaded dataset (x). With uploaded dataset is worked from the user's specified column (first.col=2). This function returns tabular (table=T) and graphical outputs (graph=T), where it is feasible to insert values of calculations (txt=T). Setting the size of inserted values is also possible (txs=1).

**References**

Magurran A.E., 2013: Measuring Biological Diversity. Wiley-Blackwell: Malden, Oxford, Carlton, ISBN 978-1-118-68792-5.

Renkonen O., 1938: Statisch-okologische Untersuchungen uber die terrestrische Kaferwelt der finnischen Bruchmoore. Annales Zoologici Societatis Zoologicae-Botanicae Fennicae Vanamo 6: 1–231.

Sepkoski J., 1988: Alpha, beta, or gamma: where does all the diversity go? Paleobiology 14(3): 221–234.

# soren.eco - Sørensen and Bray-Curtis index

**Descriptions**

Calculation and graphical visualization of Sørensen and Bray-Curtis index

**Usage**

soren.eco(x, first.col=2, table=T, graph=T, txt=T, txs=1)

**Arguments**

x = data

first.col = integer, the first column for the analysis

table = logical, if TRUE table will be creating (T) or uncreating (F)

graph = logical, if TRUE graphical output will be drawn graph

txt = values insertion into graph

txs = size of inserted values

**Examples**

soren.eco(x)

**Details**

The function soren.eco provides the calculations of Sørensen and Bray-Curtis index for samples in uploaded dataset (x). With uploaded dataset is worked from the user's specified column (first.col=2). This function returns tabular (table=T) and graphical outputs (graph=T), where it is feasible to insert values of calculations (txt=T). Setting the size of inserted values is also possible (txs=1).

**References**

Bray J.R. & Curtis J.T., 1957: An Ordination of the Upland Forest Communities of Southern Wisconsin. Ecological Monographs 27(4): 325–349.

Czekanowski J., 1913: Zarys Metod Statystycnck. E. Wendego.: Warsaw.

Magurran A.E., 2013: Measuring Biological Diversity. Wiley-Blackwell: Malden, Oxford, Carlton, ISBN 978-1-118-68792-5.

Sørensen T., 1948: A method of establishing groups of equal amplitude in plant sociology based on similarity of species content and its application to analyses of the vegetation on Danish commons. Kongelige Danske Videnskabernes Selskab, Biologiske Skrifter 5: 1–34.

Southwood T. & Henderson P., 2000: Ecological Methods 3rd ed. Blackwell Science: USA, ISBN 978-0-632-05477-0.