Package ‘foodweb’

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Version 1-0

Title visualisation and analysis of food web networks

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Depends rgl

Description Calculates twelve commonly-used, basic measures of food web network structure from binary, predator-prey matrices: species richness, connectance, total number of links, link density, number of trophic positions, predator:prey ratio, and fraction of carnivores, herbivores, top species and intermediate species. Employs food web language in the code and output, translates between a couple of common food web formats, can handle food webs consisting of multiple levels, and can automate the analysis for a large number of webs. The program produces 3-dimensional graphs of high quality that can be customized by the user.

License GPL (>= 2)

Collate 'functions.R' 'Asym2Sym.R' 'Calculations.R' 'Network.plot.R'

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NeedsCompilation no

R topics documented:

`analyse.list` *Calculate Network Parameters from Multiple, Binary, Predator-prey Matrices Whose Names Are Provided in a List*

Description

Calculates species richness, connectance, total number of links, link density, number of trophic positions, prey:predator ratio, and fraction of cannibals, herbivores, top species and intermediate species. If asymmetrical matrices are provided for analysis, they will be made symmetrical if species names have been provided in the first row and column. Absence of a species from the columns of a matrix is taken to mean that it does not consume any species. Absence of a species from the rows is taken to mean that it is not consumed by any species.

Usage

```
analyse.list(list, maxlevels=8, sym = c("FALSE", "TRUE"), output="Results.csv",
problem="Problem.csv", separator=",", sp.names = c("FALSE", "TRUE"))
```

Arguments

`list`	Full name of the file that contains the foodweb matrix file names. Individual matrix files should conform to standards of the files used in the function analyse.single(). See analyse.single() helpfile for details.
`maxlevels`	Optional. An integer indicating the maximum number of trophic levels expected to be represented in the food web matrix provided. Defaults to 8. Decreasing this number may make calculation faster.
`sym`	If TRUE, the matrix used for calculations is generated as output. This may be useful when the matrix provided was not symmetrical. The symmetrical matrix will be provided in a .csv file. Its name is that of the original matrix, followed by the suffix "-sym". Defaults to FALSE.
`output`	Optional. The full name of the output file in which results will be written. Defaults to Results.csv.
`problem`	Optional. The full name of the output file in which the names of food web matrix files with data other than zeroes and ones will be written. Defaults to Problem.csv.
`separator`	Optional. The character that separates values in the food web matrices provided. Defaults to comma.If separator="" is specified, the separator is 'white space', that is: one or more spaces, tabs, newlines or carriage returns separate the values. The matrices are imported via read.table(). Therefore, if you are having trouble, check that your matrices are read correctly by that function.
`sp.names`	Should be set to TRUE if species names are provided in the matrix files.

Value

A .csv file with the calculated network parameters of all the adequately formated matrices provided

Where problems in the matrices were found, a file with the name of the problematic matrix(ces) listed.

Optionally, binary, symmetrical, predator:prey matrices of each file provided can be generated as output.

Author(s)

Giselle Perdomo

References

Perdomo G., Sunnucks P. and Thompson R.M. (submitted). food web: an open-source program for the visualisation and analysis of compilations of complex food webs. Environmental Modelling and Software.

See Also

`analyse.single` `analyse.seq` `plotweb` `mat.2.list`

Examples

```
## Not run:
data(moss)
write.table(moss,file="Web1.csv", append=FALSE,sep=",", row.names=FALSE, col.names=FALSE)
write.table(moss[-(2:4), -(8:10)],file="Web2.csv", append=FALSE,sep=",",
row.names=FALSE, col.names=FALSE)
write.table(rbind("Web1.csv", "Web2.csv"), file="Mylist.csv", append=FALSE, sep=",",
row.names=FALSE, col.names=FALSE)
analyse.list(list="Mylist.csv", maxlevels=4, sp.names="FALSE")


## End(Not run)
```

`analyse.seq` *Calculate Network Parameters from Multiple, Binary, Predator-prey Matrices Contained in Files That Are Named Sequentially*

Description

Calculates species richness, connectance, total number of links, link density, number of trophic positions, prey:predator ratio, and fraction of cannibals, herbivores, top species and intermediate species. If asymmetrical matrices are provided for analysis, they will be made symmetrical if species names have been provided in the first row and column. Absence of a species from the columns of a matrix is taken to mean that it does not consume any species. Absence of a species from the rows is taken to mean that it is not consumed by any species.

Usage

```
analyse.seq(prefix, suffix, first, last, maxlevels=8,
sp.names = c("FALSE", "TRUE"), sym = c("FALSE", "TRUE"),
output="Results.csv", problem="Problem.csv", separator=",")
```

Arguments

`prefix`	Text preceding the number that forms the sequence of files to be read. For example, for files named Web1.csv, Web2.csv, Web3.csv, the prefix is Web
`suffix`	Text following the number that forms the sequence of files to be read. For example, for files named Web1.csv, Web2.csv, Web3.csv, the suffix is .csv
`first`	An integer. The first number in the sequence of files to be read.
`last`	An integer. Last number in the sequence of files to be read.
`maxlevels`	Optional. An integer indicating the maximum number of trophic levels expected to be represented in the food web matrix provided. Defaults to 8. Decreasing this number may make calculation faster.
`sym`	If TRUE, the matrix used for calculations is generated as output. This may be useful when the matrix provided was not symmetrical. The symmetrical matrix will be provided in a .csv file. Its name is that of the original matrix, followed by the suffix "-sym".
`output`	Optional. The full name of the output file in which results will be written. Defaults to Results.csv.
`problem`	Optional. The full name of the output file in which the names of food web matrix files with data other than zeroes and ones will be written. Defaults to Problem.csv.
`separator`	Optional. The character that separates values in the food web matrices provided. Defaults to comma. If separator="" is specified, the separator is 'white space', that is: one or more spaces, tabs, newlines or carriage returns separate the values. The matrices are imported via read.table(). Therefore, if you are having trouble, check that your matrices are read correctly by that function.
`sp.names`	Should be set to TRUE if species names are provided in the matrix files.

Value

A .csv file with the calculated network parameters of all the adequately formated matrices provided

Where problems in the matrices were found, a file with the name of the problematic matrix(ces) listed.

Optionally, binary, symmetrical, predator:prey matrices of each file provided can be generated as output.

Author(s)

Giselle Perdomo

References

Perdomo G., Sunnucks P. and Thompson R.M. (submitted). food web: an open-source program for the visualisation and analysis of compilations of complex food webs. Environmental Modelling and Software.

See Also

`analyse.single` `analyse.list` `plotweb` `mat.2.list`

Examples

```
## Not run:
data(moss)
write.table(moss,file="Web1.csv", append=FALSE,sep=",", row.names=FALSE, col.names=FALSE)
write.table(moss[-(2:4), -(8:10)],file="Web2.csv", append=FALSE,sep=",",
row.names=FALSE, col.names=FALSE)
analyse.seq(prefix="Web", suffix=".csv", first=1, last=2, maxlevels=4, sp.names="FALSE")

## End(Not run)
```

`analyse.single` *Calculate Network Parameters from One Binary Predator-prey Matrix*

Description

Calculates species richness, connectance, total number of links, link density, number of trophic positions, prey:predator ratio, and fraction of cannibals, herbivores, top species and intermediate species.

Usage

```
analyse.single(filename, omn = c("FALSE", "TRUE"), cann = c("FALSE", "TRUE"),
positions=c("FALSE", "TRUE"), matrix=c("FALSE", "TRUE"),
sp.names = c("FALSE", "TRUE"), maxlevels=8)
```

Arguments

`filename`	Full name of the comma-delimitted text file containing a binary, ordered predator-prey food web matrix. All species present in the food web must be represented, including basal resources. A zero denotes the absence of a trophic interaction. A one denotes that the species in the column consumes the species in the row. Column n must represent the same species as row n, unless an asymmetrical matrix is supplied. Asymmetrical matrices, i.e. matrices where basal resource species are not included in the columns and top predators are not included in the rows, will be turned into symmetrical matrices and ordered, prior to analysis. To do this, species names must be supplied in the first row and first column of the matrix. See matrix.

`omn`	A logical value. If TRUE, a list of omnivorous species will be generated as output: Omnivores.csv. Defaults to FALSE.
`cann`	Optional. A logical value. If TRUE, a list of cannibal species will be generated as output: Cannibals.csv. Defaults to FALSE.
`positions`	Optional.A logical value. If TRUE, a list indicating trophic positions of the food web and the species in them is generated: Trophic positions.csv. Defaults to FALSE.
`matrix`	Optional.A logical value. If TRUE, the matrix used for calculations is generated as output. This may be useful when the matrix provided was not symmetrical. Defaults to FALSE.
`sp.names`	A logical value. If TRUE, the first row and column will be considered to contain species names. These rows will not be used for calculations. Defaults to FALSE.
`maxlevels`	Optional. An integer indicating the maximum number of trophic levels expected to be represented in the food web matrix provided. Defaults to 8. Decreasing this number may make calculation faster.

Details

Basal species are those that do not consume others. Intermediate species are species that consume and are consumed by other species. Top species are those not consumed. Cannibals those that consume species from the same trophic position. Predator:prey ratio is calculated as the number of basal and intermediate species divided by the number of predatory and intermediate species. Connectance is calculated as the total number of links divided by the square of species richness. Species richness is the number of species in the food web. Link density is the number of links per species.

Value

A file in the current working directory is generated, containg the network parameters calculated. The name of the output file will be Results- followed by the name of the file provided for analysis. If omn, cann, positions and/or matrix were set to TRUE, the following files are also generated as output: Omnivores.csv, Cannibals.csv, Trophic positions.csv and/or Symmetrical matrix.csv, respectively (see Arguments section of this help page).

References

Perdomo G., Sunnucks P. and Thompson R.M. (submitted). food web: an open-source program for the visualisation and analysis of compilations of complex food webs. Environmental Modelling and Software.

See Also

`analyse.list` `analyse.seq` `plotweb` `mat.2.list`

Examples

```
## Not run:
data(moss)
```

```
write.table(moss,file="Myfoodweb.csv", append=FALSE,sep=",", row.names=FALSE, col.names=FALSE)
analyse.single(filename="Myfoodweb.csv")

## End(Not run)
```

`foodweb` *Visualisation and Analysis of Food Web Networks*

Description

Calculates twelve commonly-used, basic measures of food web network structure from binary, predator-prey matrices: species richness, connectance, total number of links, link density, number of trophic positions, predator:prey ratio, and fraction of cannibals, herbivores, top species and intermediate species. Employs food web language in the code and output, translates between a couple of common food web formats, can handle food webs consisting of multiple levels, and can automate the analysis for a large number of webs. The program produces 3-dimensional graphs of high quality that can be customized by the user.

Details

Package:	foodweb
Version:	1-0
Depends:	rgl
License:	GPL (>= 2)
Collate:	"functions.R" "Asym to Sym.R" "Calculations.R" "Network plot.R"

The package's contains 5 functions: analyse.single, analise.list, analyse.seq, mat.2.list and plotweb. See their helpfiles for more information on how to use them.

Author(s)

Giselle Perdomo

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References

Perdomo G., Sunnucks P. and Thompson R.M. (submitted). food web: an open-source program for the visualisation and analysis of compilations of complex food webs. Environmental Modelling and Software.

See Also

`analyse.single` `analyse.list` `analyse.seq` `plotweb` `mat.2.list`

`mat.2.list` *Transform a Binary Predator:prey Food Web Matrix into an Interaction List*

Description

Takes a matrix of zeroes and ones, where ones represent consumption of the species in the row by the species in the column, and transforms it into a list of trophic interactions (i.e. a list of the pairs of species where the value in the matrix was equal to zero).

Usage

```
mat.2.list(filename, output)
```

Arguments

`filename`	Name of the file in the current working directory that contains the predator:prey matrix. This file must NOT contain species names. The output is generated on the basis of the column and row numbers.
`output`	Full name of the file in which the list of interactions should be written. The file will be saved in the current working directory.

Value

A file containing the list of trophic interactions specified in the food web matrix.

Author(s)

Giselle Perdomo

References

Perdomo G., Sunnucks P. and Thompson R.M. (submitted). food web: an open-source program for the visualisation and analysis of compilations of complex food webs. Environmental Modelling and Software.

See Also

`analyse.single` `analyse.list` `analyse.seq` `plotweb`

`moss` *Predator:prey matrix of a moss-microarthropod food web.*

Description

Binary, symmetrical, ordered, predator:prey matrix. Column n represents the same species as row n. All species present in the food web are represented, including basal resources. Zeroes denote the absence of a trophic interaction. A one denotes that the species in the column consumes the species in the row.

Usage

```
moss
```

Format

A data frame with 103 columns and rows.

Source

Partial data for a publication that is in preparation. Perdomo, G; Thompson, R; Sunnucks, P. (unpublished data).

`plotweb` *Plot a Food Web Analysed Using the analyse.single() Function*

Description

Produces a three dimensional, coloured plot from data provided as a binary, ordered predator-prey matrix. The matrix needs to have been analysed with the function analyse.single() in order for this function to work.

Usage

```
plotweb(cols, radii)
```

Arguments

`cols`	a list of colours, one per trophic level in the food web. Any colour name found is colours() or colors() is allowed. See colours() and colors()
`radii`	a list of radii, one per trophic level in the food web.

Details

Angle of orientation of the plot can be manipulated by click, drag and drop operations directly on the graphics device. Zoom can be manipulated with the mouse wheel while the graphics device is active.

Value

A three dimensional plot of a food web network, as generated using plot3d of the package rgl.

Author(s)

Giselle Perdomo

References

Perdomo G., Sunnucks P. and Thompson R.M. (submitted). food web: an open-source program for the visualisation and analysis of compilations of complex food webs. Environmental Modelling and Software.

See Also

`analyse.single` `analyse.list` `analyse.seq` `mat.2.list`

Examples

```
## Not run:
data(moss)
write.table(moss, file = "moss.csv", append=FALSE, sep=",", col.names=FALSE, row.names=FALSE)
analyse.single(filename="moss.csv")
plotweb(col=c("red", "green", "blue", "yellow"), radii=c(5,10,12,12))

## End(Not run)
```

Index