

R documentation

of all in ‘man’

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`convert.to.graph.list` *Convert to a list of igraph objects*

Description

Convert to a list of igraph objects

Usage

```
convert.to.graph.list(list1)
```

Arguments

`list1` List produced by the function `create.fw.list`

Value

Returns a list of igraph objects.

Examples

```
data(mg1)
graph_list1 <- convert.to.graph.list(mg1)
```

convert2adjacency	<i>Converts all matrices to adjacency matrices (0 and 1 values for interaction)</i>
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Description

Converts all matrices to adjacency matrices (0 and 1 values for interaction)

Usage

```
convert2adjacency(list1)
```

Arguments

list1 List with the interaction matrices

Value

A list of adjacency matrices.

Examples

```
data(mg1)
mg2 <- convert2adjacency(mg1)
```

create.fw.list	<i>Download dataset from database</i>
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Description

Download dataset from database

Usage

```
create.fw.list(
  db,
  folder = NULL,
  type = NULL,
  ecosyst = FALSE,
  ref = FALSE,
  spatial = FALSE,
  code = FALSE
)
```

Arguments

db	Database: eb (EcoBase), gw (GlobalWeb), wl (Web of Life) and mg (Mangal)
folder	Folder in the working directory to get the dataset files (db=gw and wl)
type	If db=mg the user should provide the type of interactions to be downloaded
ecosyst	Getting ecosystem information (only for db=gw, db=eb)
ref	references information
spatial	get spatial info (only for db=wl, db=eb and db=mg)
code	To get the food web code

Value

A list of matrices

Examples

```
#mg2 <- create.fw.list(db="mg", ref=TRUE, spatial=TRUE)
```

dd.fw

Derive and plot the degree distribution

Description

Derive and plot the degree distribution

Usage

```
dd.fw(list1, log = TRUE, cumulative = TRUE)
```

Arguments

list1	List with the interaction matrices
log	Log-log scale
cumulative	Show cumulative degree distribution

Value

A plot with the degree distribution for the full dataset

Examples

```
data(mg1)
dd.fw(mg1, log=TRUE, cumulative=TRUE)
```

<code>exponent.removal</code>	<i>Computes de probability of removal of each node in the food web base on a exponential function</i>
-------------------------------	---

Description

Computes de probability of removal of each node in the food web base on a exponential function

Usage

```
exponent.removal(fw, i_index)
```

Arguments

<code>fw</code>	Food web matrix to be attacked, a data frame.
<code>i_index</code>	Parameter, between 0 and 1 defining the probability of attacking hubs.

Examples

```
data(mg1)
graph_list1 <- convert.to.graph.list(mg1)
#Create a vector with the values for the Intentionality Index (I)
i_index <- seq(from = 0, to = 1, by =0.01)
i_index <- head(i_index,-1)
fw1 <- graph_list1[[1]]
prob_exp <- exponent.removal(fw1, i_index)
```

<code>fw.metrics</code>	<i>Derives structural metrics to each food web matrix</i>
-------------------------	---

Description

Derives structural metrics to each food web matrix

Usage

```
fw.metrics(list1)
```

Arguments

<code>list1</code>	List with the interaction matrices
--------------------	------------------------------------

Value

A list of vectors with each metric.

Examples

```
data(mg1)
metric_mg1 <- fw.metrics(mg1)
```

is.adjacency.matrix	<i>Check which matrices are adjacency matrices (0 and 1 values for interaction)</i>
---------------------	---

Description

Check which matrices are adjacency matrices (0 and 1 values for interaction)

Usage

```
is.adjacency.matrix(list1)
```

Arguments

list1	List with the interaction matrices
-------	------------------------------------

Value

Information on whether each matrix is an adjacency matrix.

Examples

```
data(mg1)
is.adjacency.matrix(mg1)
```

is.sq.matrix	<i>Check which matrices are square matrices (same number of columns and rows)</i>
--------------	---

Description

Check which matrices are square matrices (same number of columns and rows)

Usage

```
is.sq.matrix(list1)
```

Arguments

list1	List with the interaction matrices
-------	------------------------------------

Value

Information on whether each matrix is square (same number of columns and rows).

Examples

```
data(mg1)
is.sq.matrix(mg1)
```

iterate

Iterate through species-removal robustness assessments in food webs

Description

Iterate through species-removal robustness assessments in food webs

Usage

```
iterate(
  fw_to_attack,
  probs_of_fw,
  alpha1,
  iter,
  i_index,
  plot = FALSE,
  export_plot = FALSE,
  plot_name = NULL
)
```

Arguments

fw_to_attack	Food web matrix to be attacked, a matrix.
probs_of_fw	Vector with the probability of attack to each node.
alpha1	Percentage of secondary extinctions after a primary extinction.
iter	Number of iterations to simulate.
i_index	Parameter, between 0 and 1 defining the probability of attacking hubs.
plot	Plot the results of the simulation (TRUE/FALSE).
export_plot	Should plots be exported to the working directory (TRUE/FALSE)
plot_name	Plot file naming.

Value

A list of vectors with each metric.

Examples

```
data(mg1)
graph_list1 <- convert.to.graph.list(mg1)
#Create a vector with the values for the Intentionality Index (I)
i_index <- seq(from = 0, to = 1, by =0.01)
i_index <- head(i_index,-1)
fw1 <- graph_list1[[1]]
prob_exp <- exponent.removal(fw1, i_index)
it1 <- iterate(fw_to_attack=fw1, prob_exp, alpha1=50, iter=10, i_index, plot = TRUE)
```

mg1	<i>Mangal dataset (herbivory and predation types only)</i>
-----	--

Description

Mangal dataset (herbivory and predation types only)

Usage

```
mg1
```

Format

An object of class `list` of length 3.

Author(s)

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References

<https://mangal-wg.github.io/rmangal/articles/rmangal.html>

Examples

```
data(mg1)
```

pl.removal	<i>Computes de probability of removal of each node in the food web base on a power-law function</i>
------------	---

Description

Computes de probability of removal of each node in the food web base on a power-law function

Usage

```
pl.removal(fw, i_index)
```

Arguments

fw	Food web matrix to be attacked, a data frame.
i_index	Parameter, between 0 and 1 defining the probability of attacking hubs.

Examples

```
data(mg1)
graph_list1 <- convert.to.graph.list(mg1)
#Create a vector with the values for the Intentionality Index (I)
i_index <- seq(from = 0, to = 1, by =0.01)
i_index <- head(i_index,-1)
fw1 <- graph_list1[[1]]
prob_pl <- pl.removal(fw1, i_index)
```

rect2square	<i>Convert rectangular matrices to square matrices (same number of columns and rows)</i>
-------------	--

Description

Convert rectangular matrices to square matrices (same number of columns and rows)

Usage

```
rect2square(list1, is.gw = FALSE)
```

Arguments

list1	List with the interaction matrices
is.gw	Was the dataset downloaded from Globalweb? (TRUE/FALSE)

Value

A list of square matrices.

Examples

```
data(mg1)
mg3 <- rect2square(mg1)
```

remove.non.numeric	<i>Remove matrices with non-numeric values</i>
--------------------	--

Description

Remove matrices with non-numeric values

Usage

```
remove.non.numeric(list1)
```

Arguments

list1	List with the interaction matrices
-------	------------------------------------

Value

A list of matrices.

Examples

```
data(mg1)
mg4 <- remove.non.numeric(mg1)
```

`remove.repeated.names` *Remove food web matrices with repeated names, whether in columns or rows*

Description

Remove food web matrices with repeated names, whether in columns or rows

Usage

```
remove.repeated.names(list1)
```

Arguments

`list1` List with the interaction matrices

Value

A list of matrices.

Examples

```
data(mg1)
mg5 <- remove.repeated.names(mg1)
```

`robustness` *Conducts species-removal robustness assessments on food webs*

Description

Conducts species-removal robustness assessments on food webs

Usage

```
robustness(fw_to_attack, probs_of_fw, alpha1)
```

Arguments

`fw_to_attack` Food web matrix to be attacked, a data frame.
`probs_of_fw` Vector with the probability of attack to each node.
`alpha1` Percentage of secondary extinctions after a primary extinction.

Examples

```
data(mg1)
graph_list1 <- convert.to.graph.list(mg1)
#Create a vector with the values for the Intentionality Index (I)
i_index <- seq(from = 0, to = 1, by =0.01)
i_index <- head(i_index,-1)
fw1 <- graph_list1[[1]]
prob_exp <- exponent.removal(fw1, i_index)
r1 <- robustness(fw1, prob_exp, alpha1=50)
```

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