

Package ‘FWebs’

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Type Package

Title FWebs

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Description This package allows downloading food web matrices from several online databases. It also provides the tools to process these matrices and derive basic structural metrics and degree distribution.

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

Imports methods, Hmisc, stringr, NetIndices, RCurl, XML, ggplot2, igraph, plyr, random-coloR, rmangal, sf, sp, magrittr

Depends R (>= 3.5.0)

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<code>convert.to.graph.list</code>	<i>Convert to a list of igraph objects</i>
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Description

Convert to a list of igraph objects

Usage

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

Arguments

<code>list1</code>	List produced by the function <code>create.fw.list</code>
--------------------	---

Value

Returns a list of igraph objects.

Examples

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

<code>convert2adjacency</code>	<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

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

Value

A list of adjacency matrices.

Examples

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

create.fw.list*Download datasets from online database*

Description

Download datasets from online database

Usage

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

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)
ecosyst	Getting ecosystem information (only for db=gw, db=eb)
ref	references information
spatial	get spatial info (only for)
code	To get the food web code
mangal_types	If db=mg the user should provide the type of interactions to be downloaded; if 'db=all' all mangal interaction types are used

Value

Returns a list that might have the following elements (depending on use options): 1. list of interaction matrices, 2. Reference data frame with FW code, first author of original publication, year of publication, full reference (if db='mg': FW code, type of interaction matrix, original ID in mangal, first author of original publication, year of publication); 3. Study site location (for db=wl, db=eb and db=mg); 4. FW code.

Examples

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

dd.fw	<i>Derive and plot the degree distribution</i>
-------	--

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)
```

exponent.removal	<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

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_exp <- exponent.removal(fw1, i_index)
```

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

Description

Derives structural metrics to each food web matrix

Usage

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

Arguments

list1 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)
```

<code>is.sq.matrix</code>	<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)
```

<code>iterate</code>	<i>Iterate through species-removal robustness assessments in food webs</i>
----------------------	--

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

Mangal dataset (herbivory and predation types only)

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)
```

<code>pl.removal</code>	<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

<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_pl <- pl.removal(fw1, i_index)
```

<code>rect2square</code>	<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

<code>list1</code>	List with the interaction matrices
<code>is.gw</code>	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	<i>Remove food web matrices with repeated names, whether in columns or rows</i>
-----------------------	---

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

<code>fw_to_attack</code>	Food web matrix to be attacked, a data frame.
<code>probs_of_fw</code>	Vector with the probability of attack to each node.
<code>alpha1</code>	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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