

# Package ‘FWebs’

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**Type** Package

**Title** FWebs

**Version** 0.1.1

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

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**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)
```

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`convert2adjacency` *Converts all matrices to adjacency matrices (0 and 1 values for interaction)*

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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 (0: no interaction; 1: interaction).

**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>
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---

**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>
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---

**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 (number of nodes, number of links, link density, connectance, compartmentalization, maximum trophic level).

**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)
```

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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)**

Frederico Mestre <fmestre@uevora.pt>

**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)
```

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

### 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 (not simetrical).

### Examples

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



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