Package 'econullnetr'

June 2, 2021

Type Package

Title Null Model Analysis for Ecological Networks

Version 0.2.1

Depends R (>= 2.10)

Imports reshape2, bipartite, gtools

Suggests igraph, knitr, readr, rmarkdown, testthat, vdiffr

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BugReports https://github.com/ivaughan/econullnetr/issues

Description Tools for using null models to analyse ecological
networks (e.g. food webs, flower-visitation networks, seed-dispersal
networks) and detect resource preferences or non-random interactions among
network nodes. Tools are provided to run null models, test for and plot
preferences, plot and analyse bipartite networks, and export null model
results in a form compatible with other network analysis packages. The
underlying null model was developed by Agusti et al. (2003) Molecular
Ecology <doi:10.1046/j.1365-294X.2003.02014.x> and the full application to
ecological networks by Vaughan et al. (2018) econullnetr: an R package
using null models to analyse the structure of ecological networks and
identify resource selection. Methods in Ecology & Evolution,
<doi:10.1111/2041-210X.12907>.

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LazyData TRUE

RoxygenNote 7.1.1

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

Date/Publication 2021-06-02 08:10:05 UTC

R topics documented:

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bipartite_stats	*Test for significant differences in a range of network metrics between the observed and null bipartite networks*

Description

Acts as a wrapper for the bipartite package's [networklevel](#), [grouplevel](#) and [specieslevel](#) functions, allowing a wide range of measures to be calculated (Dormann *et al*., 2008, 2009; Dorman 2011). These are calculated both for the observed network and across the iterations of the null model, allowing for simple tests of whether the observed values differ from those expected by chance.

Usage

```
bipartite_stats(
  nullnet,
  signif.level = 0.95,
  index.type,
  indices,
  prog.count = TRUE,
  ...
)
```

Arguments

`nullnet`	An object of class 'nullnet' from `generate_null_net`
`signif.level`	An optional value specifying the threshold used for testing for 'significant' deviations from the null model. Defaults to 0.95
`index.type`	String specifying which function to call from the `bipartite` package: `specieslevel`, `grouplevel` or `networklevel`, according to the level at which the statistics are required. For `specieslevel`, statistics are calculated for both 'higher' and 'lower' levels i.e. `level = "both"` and cannot be changed: adding a `level` argument will produce an error: statistics from higher and lower levels are easily separated in the output from `bipartite_stats`.
`indices`	Vector listing the bipartite network statistics to calculate. All indices are currently supported, with the exception of the dependence matrix: if `ALL` is specified, it will default to `ALLBUTD`.
`prog.count`	A logical value specifying whether the progress count should be shown. Defaults to `TRUE`.
`...`	Other arguments that may be supplied to `bipartite`'s `specieslevel`, `grouplevel` or `networklevel` functions.

Details

Allows most of the network metrics in the `bipartite` package to be calculated for an observed bipartite network and compared to the distribution of those network metrics across the iterations of the null model. This indicates whether the observed network differs from the structure of the network that could be expected if consumers simply used resources in proportion to their relative abundance.

The user sets the significance level (default = 95% confidence limits), and the metrics selected are classified into those that are higher, lower or consistent with the null model at that significance level. Significance is determined by comparing the observed value of the statistic to the 1-alpha/2 percentiles from the frequency distribution, with 'significant' values falling outside the confidence interval (Manly 2006).

Value

Returns one or more data frames according to the level at which the statistics are calculated (`specieslevel`, `grouplevel` or `networklevel`). If `index.type = "networklevel"` or `index.type = "grouplevel"` a single data frame is returned, listing the chosen network statistics and with the following column headings:

`Observed` Value of the statistic for the observed network

`Null` Mean value of the statistic across the iterations of the null model

`Lower.CL` Lower confidence limit for the metric

`Upper.CL` Upper confidence limit for the network metric

`Test` Whether the value of the statistic with the observed network is significantly **higher** than expected under the null model, **lower** or consistent with the null model (**ns**)

`SES` The standardised effect size for the difference between the observed network and the null model (see Gotelli & McCabe 2002 for details)

If `index.type = "specieslevel"`, a list comprising two data frames for each statistic, representing the `higher` and `lower` levels in the network. Each data frame has the same format as for `networklevel` except that the rows are individual nodes (species) in the network. See examples for how to call the individual data frames.

References

Dormann, C.F., Gruber B. & Frund, J. (2008). Introducing the bipartite package: analysing ecological networks. *R news*, **8**, 8–11.

Dormann, C.F., Frund, J., Bluthgen, N. & Gruber, B. (2009). Indices, graphs and null models: analyzing bipartite ecological networks. *Open Ecology Journal* **2**, 7–24.

Dormann, C.F. (2011) How to be a specialist? Quantifying specialisation in pollination networks. *Network Biology*, **1**, 1-20.

Gotelli, N.J. & McCabe, D.J. (2002) Species co-occurrence: a meta-analysis of J.M. Diamond's assembly rules model. *Ecology*, **83**, 2091–2096.

Manly, B.F.J. (2006) *Randomization, Bootstrap and Monte Carlo Methods in Biology* (3rd edn). Chapman & Hall, Boca Raton.

Vaughan, I.P., Gotelli, N.J., Memmott, J., Pearson, C.E., Woodward, G. & Symondson, W.O.C. (2018) econullnetr: an R package using null models to analyse the structure of ecological networks and identify resource selection. *Methods in Ecology and Evolution*, **9**, 728–733.

See Also

generate_null_net, plot_bipartite, networklevel, grouplevel, specieslevel

Examples

```
set.seed(1234)
sil.null <- generate_null_net(Silene[, 2:7], Silene.plants[, 2:6], sims = 10,
                              c.samples = Silene[, 1],
                              r.samples = Silene.plants[, 1])
# Network-level analysis
net.stats <- bipartite_stats(sil.null, index.type = "networklevel",
                             indices = c("linkage density",
                             "weighted connectance", "weighted nestedness",
                             "interaction evenness"), intereven = "sum")
net.stats

# Group-level analysis
grp.stats <- bipartite_stats(sil.null, index.type = "grouplevel",
                             indices = c("generality",
                             "vulnerability", "partner diversity"),
                             logbase = 2)
grp.stats

# Species-level statistics
spp.stats <- bipartite_stats(sil.null, index.type = "specieslevel",
                             indices = c("degree", "normalised degree",
                             "partner diversity"), logbase = exp(1))
```

```
spp.stats # Show all data frames of results
spp.stats$normalised.degree # Select one statistic
spp.stats$normalised.degree$lower # Select one statistic at one level
```

Broadstone *Part of the highly-resolved food web from Broadstone Stream, UK*

Description

Part of the highly-resolved macroinvertebrate food web from Broadstone Stream in south-east England (see Woodward *et al*., 2005 for full details of the web). This data frame contains data collected in August 1996, with 19 macroinvertebrate taxa. Predation was determined via visual gut contents analysis, with identification of hard parts allowing counts of the number of individual prey organisms each individual predator consumed. There are three accompanying data sets:

1. `Broadstone.prey` Gives the total abundance of each prey taxon from 30 Surber samples collected at the same time as the interaction data.

2. `Broadstone.fl` Specifies 'forbidden' links which are not allowed in the null model.

3. `Broadstone.nodes` The abundance and mean body mass for each taxon in the food web in a format for use alongside a `generate_null_model` object with the `cheddar` package (Hudson *et al*., 2013). Body size is taken from cheddar's 'BroadstoneStream' data set.

Usage

```
Broadstone
```

Format

A data frame with 319 rows and 20 columns. Each row represents the gut contents of an individual predator. There are 20 columns in total, with the first column (`Predator`) indicating the predator taxon (seven taxa in total) and the remaining 19 columns indicating the number of individuals eaten of each of the 19 potential prey taxa.

Source

Woodward, G., Speirs, D.C. & Hildrew, A.G. (2005) Quantification and resolution of a complex, size-structured food web. *Advances in Ecological Research*, **36**, 84–135.

Broadstone.fl	*'Forbidden' links to accompany the* Broadstone *data set*

Description

Networks often contain 'forbidden links', where interactions are not possible between two taxa due to factors such as large differences in body size, spatio-temporal mismatches or specialised flower morphology in flower visitation networks. Broadstone.fl summarises the forbidden links in the Broadstone food web, estimated from the interactions observed from a complete year's sampling (Table 3 in Woodward *et al.* 2005). This table is illustrative, and should not be considered a definitive list.

Usage

    Broadstone.fl

Format

A data frame with 20 columns and seven rows, one row for each of the seven predator taxa. The first column (Predator) lists the seven taxa, whilst the remaining 19 columns are the invertebrate taxa in the food web: each element indicates whether the predator can consume that taxon (1) or whether the link is 'forbidden' (0).

Source

Woodward, G., Speirs, D.C. & Hildrew, A.G. (2005) Quantification and resolution of a complex, size-structured food web. *Advances in Ecological Research*, **36**, 84–135.

Broadstone.nodes	*Abundance and body mass data to accompany the* Broadstone *data set*

Description

Provides additional information about each macroinvertebrate taxon in the Broadstone food web for use alongside null model results in the foodweb package cheddar (Hudson *et al.* 2013).

Usage

    Broadstone.nodes

Format

A data frame with three columns and 19 rows:

node The name of the macroinvertebrate taxon (node) in the network

M The mean body mass of an individual of the taxon, from cheddar's `BroadstoneStream` object

N The total abundance of each taxon from the 30 Surber samples (see `Broadstone.prey` for details)

Broadstone.prey	*Macroinvertebrate abundance data to accompany the* Broadstone *data frame*

Description

The abundance of the 19 macroinvertebrate taxa present in the Broadstone food web in August 1996 (see Woodward *et al*. 2005 for full details). The values are the total number of individuals collected from 30 Surber samples.

Usage

```
Broadstone.prey
```

Format

A data frame with 19 columns and one row, with each column name representing one taxon. Names match those in `Broadstone`.

Source

Woodward, G., Speirs, D.C. & Hildrew, A.G. (2005) Quantification and resolution of a complex, size-structured food web. *Advances in Ecological Research*, **36**, 84–135.

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econullnetr	*econullnetr: tools for using null models to analyse the structure of ecological networks and identify resource selection*

Description

econullnetr provides a set of functions for running null models, analysing and plotting the results, and exporting the outputs for use with other network packages in R.

References

Vaughan, I.P., Gotelli, N.J., Memmott, J., Pearson, C.E., Woodward, G. & Symondson, W.O.C. (2018) econullnetr: an R package using null models to analyse the structure of ecological networks and identify resource selection. *Methods in Ecology and Evolution*, **9**, 728–733.

---

expand_matrix   *Expand a summarised interaction matrix*

Description

A simple function for converting interaction matrices that are summarised at (typically) species-level to individual-level matrices, ready for use with generate_null_net. This is only applicable to the special (but common) case where one individual = one interaction (e.g. many pollination networks, ant-seed networks). Data can be stored either with consumers as columns and resources as rows or vice versa. Taxon names for each row in the matrix could either be stored as the row names of the matrix or data frame (as used, for example, by the bipartite package), or as a column containing the names in a data frame.

Usage

```
expand_matrix(X, r.names = rownames(X), MARGIN = 1)
```

Arguments

X	A matrix or data frame representing the interaction matrix. This should only include the interaction data (i.e. counts of different interactions) and no additional columns for taxon names, covariates, etc
r.names	An optional object of identical length to the number of rows in X listing the taxon names. In many situations these may be the row names of X (the default). Alternatively r.names can be use to specify a column in a data frame containing the names or a separate vector.
MARGIN	Similar to apply, an integer value indicating whether the data are arranged in rows or columns. MARGIN = 1 (the default) indicates that each column relates to one consumer taxon (the format typically used for bipartite networks), whilst MARGIN = 2 indicates that each row is one consumer taxon, with column names being the resources.

Value

A data frame where each row represents the interaction observed between an individual consumer and one resource species. The first column is named Consumer and records which taxon each indidual belongs to. The remaining columns represent the resources: one column for each taxon.

Examples

```
# Toy example representing a typical bipartite format.
  bp.inter <- matrix(c(1, 2, 2, 0, 5, 3, 3, 0, 2), nrow = 3, byrow = FALSE,
                     dimnames = list(c("A", "B", "C"),
                                      c("sp1", "sp2", "sp3")))
 bp.inter
 expand_matrix(bp.inter)
```

```
# Use a simplified version of the Silene data set, pooling data
# across the 11 visits.
  int.summ <- aggregate(Silene[, 3:7], by = list(Silene$Insect), sum)
  colnames(int.summ)[1] <- "taxon"
  expand_matrix(int.summ[, -1], r.names = int.summ$taxon, MARGIN = 2)
```

---

generate_edgelist   *Export null modelling results*

Description

Exports the observed network alongside the mean interaction strengths calculated from the null model and the significance test results in a standard format that can be imported into other network analysis packages e.g. `igraph` (Csardi & Nepusz 2006) or `cheddar` (Hudson *et al.* 2013). This provides access to a wide range of plotting and analysis tools, especially for non-bipartite networks.

Usage

```
generate_edgelist(
  nullnet,
  signif.level = 0.95,
  export.null = FALSE,
  edge.cols = c("#67A9CF", "#F7F7F7", "#EF8A62")
)
```

Arguments

nullnet   An object of class nullnet from `generate_null_net`

signif.level   An optional value specifying the threshold used for testing for 'significant' deviations from the null model. Defaults to 0.95

export.null   An optional logical value specifying whether export should be limited to those interactions that were present in the observed network or should include any additional interactions present across iterations of the null network. Depending upon the data and any forbidden links specified, additional interactions may be present in the modelled networks. Defaults to FALSE (only observed interactions are exported).

edge.cols   An optional character vector of length three specifying potential colours for network links when used with a suitable plotting function: in sequence, these should represent i) interactions that are weaker than expected, ii) consistent with the null model and iii) stronger than expected. The default is a colour-blind friendly blue, white and red scheme, using Colorbrewer's Red-Blue colour scheme (Brewer 2017).

Value

A data frame where each row represents the interaction observed between a pair of consumer and resource species, and with the following column headings:

`Consumer` Name of the consumer species (node)

`Resource` Name of the resource species (node)

`Observed` Strength of the observed interaction

`Null` Mean strength of the interaction across the iterations of the null model

`SES` The standardised effect size for the interaction

`Test` Whether the observed interaction is significantly **stronger** than expected under the null model, **weaker** or consistent with the null model **ns**

References

Brewer, C.A. (2017) https://colorbrewer2.org/

Csardi, G. & Nepusz, T. (2006) The igraph software package for complex network research. *Inter-Journal, Complex Systems*, **1695**.

Vaughan, I.P., Gotelli, N.J., Memmott, J., Pearson, C.E., Woodward, G. & Symondson, W.O.C. (2018) econullnetr: an R package using null models to analyse the structure of ecological networks and identify resource selection. *Methods in Ecology and Evolution*, **9**, 728–733.

See Also

generate_null_net

Examples

```
set.seed(1234)
bs.null <- generate_null_net(Broadstone, Broadstone.prey,
                             data.type = "counts", sims = 10,
                             r.weights = Broadstone.fl)
BS.export <- generate_edgelist(bs.null, signif.level = 0.95,
                               edge.cols = c("#67A9CF", "black", "#EF8A62"))

if (requireNamespace("igraph", quietly = TRUE)) {
 net.1 <- igraph::graph_from_edgelist(as.matrix(BS.export[, c("Resource",
                                                             "Consumer")]),
                                      directed = TRUE)

 # Add in the null modelling results
 igraph::E(net.1)$obs.str <- BS.export$Observed
 igraph::E(net.1)$test.res <- BS.export$Test
 igraph::E(net.1)$edge.cols <- BS.export$edge.col

 igraph::plot.igraph(net.1, layout = igraph::layout_in_circle,
                     edge.color = igraph::E(net.1)$edge.cols,
                     edge.width = sqrt(igraph::E(net.1)$obs.str),
                     edge.arrow.size = .4)
}
```

---

generate_null_net *Null models for ecological networks*

Description

Uses the algorithm of Agusti *et al.* (2003) to specify and run a null model for an ecological network based upon interaction data and independent estimates of resource abundance (see Vaughan *et al.*, 2018 for full details). Typically, network nodes represent species, and the following documentation uses the term species in place of node, but this need not be the case.

Usage

```
generate_null_net(
  consumers,
  resources,
  sims = 100,
  data.type = "names",
  maintain.d = NULL,
  summary.type = "sum",
  c.samples = NULL,
  r.samples = NULL,
  r.weights = NULL,
  prog.count = TRUE
)
```

Arguments

consumers   A matrix or data frame containing the interaction data. The first column should contain the name of the consumer species, with the remaining column names listing the resources (the names must be identical and in the same order as in `resources`). Each row represents one individual, with the elements in the matrix indicating whether a resource was used or how much was used (see Details).

resources   A matrix or data frame containing the relative abundances of the different resources (e.g. density of different prey species or abundance of different flower species). May either have one row, if all data came from the same location and/or time, or have the same number of rows as there are sampling stratum codes in `r.samples` and `c.samples` (e.g. the set of time points or plot names), if the data are subdivided across sampling times/sites. Resource names (column names) in `resources` and `consumers` must be identical and in the same order.

sims   Number of iterations of the null model. The default value is 100, but this should generally be increased to estimate meaningful confidence limits.

data.type   An optional string specifying the type of interaction data. One of three options: `"names"` (the default), `"counts"` or `"quantities"`. See Details for a full explanation and examples.

maintain.d   When `data.type` = "counts" or "quantities", a string indicating whether
                  the degree of each individual consumer (i.e. the number of different resource
                  species it interacted with) should be maintained when allocating individual re-
                  sources/quantities. Default is FALSE.

summary.type   An optional string indicating how the interactions should be summarised at the
                  species level: one of "sum" (the default), indicating that the interactions be-
                  tween a consumer and resource species will be summed across all individuals,
                  or "mean", indicating that the mean value per individual of a consumer species
                  will be calculated.

c.samples   An optional vector that specifies names for subdivisions of the interaction data
                  when data on interactions and resource abundance were collected across a se-
                  ries of subdivisions (e.g. at different sites or time points). If suddivisions were
                  present, they should be specified for both c.samples and r.samples. The sam-
                  ple names must be identical in c.samples and r.samples (although c.samples
                  is likely to be much longer than r.samples due to >1 individual consumer per
                  subdivision)

r.samples   An optional vector specifying the sample names for the resource abundance data
                  (resources), and corresponding to the names used in c.samples. Must have
                  the name number of entries as there are rows in resources. Not needed when
                  resources contains a single row/c.samples is absent.

r.weights   An optional data frame or matrix specifying weights to be applied to rows in
                  resources: all entries must be in the range 0–1. The first column should contain
                  the consumer species names, one entry for each species, within the remaining
                  columns listing all species present in resources (names must be identical and
                  in the same order as in resources). Mainly used to specify forbidden links by
                  specifying zero values for forbidden links and ones for the remaining entries.
                  Only one table is supplied, which then applies across all subdivisions of the data
                  (if present).

prog.count   A logical value specifying whether the progress count should be shown. De-
                  faults to TRUE.

Details

A basic call to `generate_null_net` only needs two arguments: consumers and resources, but
it is recommended that sims is also specified to run a larger number of iteration of the null model
(e.g. 1000). It is important to ensure that species names are consistent throughout and that the
resource species used as column names in resources, consumers and (optionally) r.weights are
in the same order (both consumers and r.weights should be one column wider than resources,
because they include an extra column at the start to list the consumer species).

The same species can appear as both a consumer and a resource e.g. when a species is both predator
and prey in a food web. Interactions can be excluded from the modelled networks by specifying
forbidden links with r.weights, based either on existing data/literature or hypothesed choices,
generating the network that would be created if those choices were made. Placing limits on the
feasible range of resources with which a consumer interacts should lead to more realistic networks:
great white sharks not feeding on zooplankton in a marine food web, for example.

The interactions between individual consumers and the resources may be recorded in a range of dif-
ferent ways depending upon the empirical data that are available, and these differences are handled

by using the optional `data.type` argument. Three types of data can be specified:

1. `data.type = "names"` (the default value). This is the most common type of data, recording one or more resource species with which an interaction occurred, but without any attempt to quantify the strength of the interaction. For data of this type, `resources` should simply comprise 1s and 0s, indicating whether an interaction was present or absent respectively: row sums may equal one or be >1 if individual consumers can interact with multiple resources.

2. `data.type = "counts"`. These data record the number of times an individual consumer interacted with different resource species e.g. the number of times different flower species were visited by an individual pollinator during a 5 minute observation period. When modelling count data there is a choice of whether the total number of interactions (an individual's row sum) can be distributed across all potential resources, which may result in interactions with a different number of resource species (i.e. a change in an individual's degree) or whether the degree is held constant for each individual. This is determined by the additional `maintain.d` argument: `maintain.d = FALSE` (the default) does not constrain an individual's degree, whereas `maintain = TRUE` does.

3. `data.type = "quantities"`. Quantitative data are obtained from each individual, such as the proportion of a predator's gut contents derived from different prey. The data in `consumers` can be represented by either proportions (so that the row sum for an individual = 1) or in the native units (so the total <> 1). As for count data, the degree can be free or fixed at the individual consumer level by using the `maintain.d` argument.

For data types 2 and 3, it does not matter what units are used (e.g. each row does not need to add up to one). The row total will be maintained, so the results are returned in the same units as the original data.

One problem that may arise in specifying the null model is in situations where an interaction is recorded with a particular resource, but that resource was not actually detected in the abundance data (i.e. abundance = 0). This may occur, for example, when a predator eats a rare species that was missed during concomitant sampling of prey abundance: in effect, the predator's 'sampling' was more comprehensive. The implication of this is that the resource species will not be sampled in the null model – a potential source of bias. `generate_null_net` will issue a warning if it detects this situation. Possible corrective actions include removing that resource species altogether or replacing its zero abundance with a small constant.

Value

Returns an object of class "nullnet", which is a list containing the following components:

`rand.data` Data frame containing the results from all of the iterations of the null model

`obs.interactions` Interaction matrix summarising the observed interactions (from `consumers`)

`n.iterations` The value of `sims` i.e. the number of interations of the null model

References

Agusti, N., Shayler, S.P., Harwood, J.D., Vaughan, I.P., Sunderland, K.D. & Symondson, W.O.C. (2003) Collembola as alternative prey sustaining spiders in arable ecosystems: prey detection within predators using molecular markers. *Molecular Ecology*, **12**, 3467–3475.

Davey, J.S., Vaughan, I.P., King, R.A., Bell, J.R., Bohan, D.A., Bruford, M.W., Holland, J.M. & Symondson, W.O.C. (2013) Intraguild predation in winter wheat: prey choice by a common epigeal carabid consuming spiders. *Journal of Applied Ecology*, **50**, 271–279.

King, R.A, Vaughan, I.P., Bell, J.R., Bohan, D.A, & Symondson, W.O.C. (2010) Prey choice by carabid beetles feeding on an earthworm community analysed using species- and lineage-specific PCR primers. *Molecular Ecology*, **19**, 1721–1732.

Pearson, C.E., Symondson, W.O.C., Clare, E.L., Ormerod, S.J., Iparraguirre Bolanos, E. & Vaughan, I.P. (2018) The effects of pastoral intensification on the feeding interactions of generalist predators in streams. *Molecular Ecology*, **27**, 590-602.

Vaughan, I.P., Gotelli, N.J., Memmott, J., Pearson, C.E., Woodward, G. & Symondson, W.O.C. (2018) econullnetr: an R package using null models to analyse the structure of ecological networks and identify resource selection. *Methods in Ecology and Evolution*, **9**, 728–733.

See Also

[test_interactions](), [plot_preferences]()

Examples

```
null.1 <- generate_null_net(Silene[, 2:7], Silene.plants[, 2:6], sims = 10,
  data.type = "names", summary.type = "sum", c.samples = Silene[, 1],
  r.samples = Silene.plants[, 1])
```

---

plot_bipartite	*Plot a bipartite network, colour coding individual links according to whether they are stronger or weaker than expected under the null model*

Description

Acts as a wrapper for the `bipartite` package's [plotweb]() function (Dormann *et al.*, 2008), colour coding the links in the familiar bipartite plots according to whether they are stronger, weaker or consistent with the null model.

Usage

```
plot_bipartite(
  nullnet,
  signif.level = 0.95,
  edge.cols = c("#67A9CF", "#F7F7F7", "#EF8A62"),
  ...
)
```

Arguments

nullnet	An object of class "nullnet" from generate_null_net
signif.level	An optional value specifying the threshold used for testing for 'significant' deviations from the null model. Defaults to 0.95
edge.cols	An optional character vector of length three specifying the colours for links in the bipartite plot: they should represent interactions that are weaker than expected, consistent with the null model and stronger than expected in that order. The default is a colourblind friendly blue, white and red scheme, using colorbrewer's Red-Blue colour scheme (Brewer 2017).
...	Other arguments to be supplied to bipartite's plotweb function.

Details

Extensive options can be passed to [plotweb](#) to customise the network plot beyond the colour coding of the links. See the appropriate help file in the bipartite package for details.

Value

No return value, called for side effects.

References

Brewer, C.A. (2017) <https://colorbrewer2.org/>

Dormann, C.F., Gruber B. & Frund, J. (2008). Introducing the bipartite package: analysing ecological networks. *R news*, **8**, 8-11.

Vaughan, I.P., Gotelli, N.J., Memmott, J., Pearson, C.E., Woodward, G. & Symondson, W.O.C. (2018) econullnetr: an R package using null models to analyse the structure of ecological networks and identify resource selection. *Methods in Ecology and Evolution*, **9**, 728–733.

See Also

[generate_null_net](#), [bipartite_stats](#), [plotweb](#)

Examples

```
# Run the null model
set.seed(1234)
sil.null <- generate_null_net(Silene[, 2:7], Silene.plants[, 2:6], sims = 10,
                              c.samples = Silene[, 1],
                              r.samples = Silene.plants[, 1])

# Basic plot
plot_bipartite(sil.null)

# With alternative colour scheme and nodes width in the lower level proportional
#  to mean floral abundance
mean.abunds <- colMeans(Silene.plants[, 2:6])
plot_bipartite(sil.null, signif.level = 0.95, edge.cols = c("#67a9cf",
```

```
                  "#F7F7F7", "#ef8a62"), low.abun = mean.abunds,
                  abuns.type = "independent", low.abun.col = "black",
                  high.abun.col = "black", high.lablength = 0, low.lablength = 0)
```

---

plot_preferences   *Plot the resource preferences of a consumer*

Description

Takes a 'nullnet' object from running a null model with generate_null_net and plots the observed and expected link strengths for every resource for a selected consumer species (node in the network). There are two styles of plot: the default is a dot plot based on [dotchart](), whilst the alternative is a bar plot based on [barplot](). There are arguments in plot_preferences to set some of the graphical parameters, but see the respective help files for [dotchart]() and [barplot]() for further options to customise the plots.

Usage

```
plot_preferences(
  nullnet,
  node,
  signif.level = 0.95,
  style = "dots",
  type = "counts",
  res.col = c("#67A9CF", "#F7F7F7", "#EF8A62"),
  res.order = NULL,
  l.cex = 1,
  p.cex = 1,
  ...
)
```

Arguments

nullnet	An object of class nullnet from generate_null_net
node	A string specifying the consumer node (species) whose preferences will be plotted
signif.level	An optional value specifying the threshold used for testing for 'significant' deviations from the null model. Defaults to 0.95
style	An optional string to set whether a dotchart or bar chart is plotted. The default (style = "dots") is a Cleveland dot plot, whilst the alternative (style = "bars") is a bar chart of the type used by King *et al.* (2010) and Davey *et al.* (2013).
type	Optional string to specify how preferences are displayed. The default (type = "counts") is the total number of interactions or mean interaction strength, depending upon which one was requested in the original call to [generate_null_net]()

using the summary.type argument. The alternative is the standardised effect size (type = "SES"). With type = "counts", confidence limits will be drawn, whilst for the standardised effect size, dashed lines are added at +2 and -2, which is approximately equivalent to a 5% significance level: fill colours for type = "SES" are based on the estimated confidence limits, rather than the +2/-2 thresholds.

res.col   An optional character vector of length three specifying the colours with which to fill the dots or bars representing interactions that are weaker than expected, consistent with the null model and stronger than expected (in that order). The default is a red-blue colour scheme.

res.order   An optional data frame used to set the order in which the resource species are plotted. Should have two columns: the first listing the resource species (names must be identical to those used by generate_null_net) and the second the plotting order (bars will be plotted in ascending order)

l.cex   An optional numeric value to set the size of the labels when using style = "dots". Ignored when style = "bars", as barplot's cex.names argument can be used.

p.cex   An optional numeric value to set the size of the points when when using style = "dots".

...   Other arguments to control basic plotting functions in R, such as lwd, xlab, ylab, main, xlim and ylim.

Details

Plots the preferences for individual consumer species. The bar plot format follows the basic style of King *et al.* (2010; Figure 3) and Davey *et al.* (2013; Figure 3).

Value

No return value, called for side effects.

References

Brewer, C.A. (2017) <https://colorbrewer2.org/>

Davey, J.S., Vaughan, I.P., King, R.A., Bell, J.R., Bohan, D.A., Bruford, M.W., Holland, J.M. & Symondson, W.O.C. (2013) Intraguild predation in winter wheat: prey choice by a common epigeal carabid consuming spiders. *Journal of Applied Ecology*, **50**, 271–279.

King, R.A, Vaughan, I.P., Bell, J.R., Bohan, D.A, & Symondson, W.O.C. (2010) Prey choice by carabid beetles feeding on an earthworm community analysed using species- and lineage-specific PCR primers. *Molecular Ecology*, **19**, 1721–1732.

Vaughan, I.P., Gotelli, N.J., Memmott, J., Pearson, C.E., Woodward, G. & Symondson, W.O.C. (2018) econullnetr: an R package using null models to analyse the structure of ecological networks and identify resource selection. *Methods in Ecology and Evolution*, **9**, 728–733.

See Also

[generate_null_net](), [plot_bipartite]()

Examples

```
null.1 <- generate_null_net(WelshStreams[, 2:18], WelshStreams.prey[, 2:17],
                          sims = 10, c.samples = WelshStreams[, 1],
                          r.samples = WelshStreams.prey[, 1])

# Basic plots, showing the dot and bar plot styles. Increased lower margin
#   on the bar plot so that names fit
plot_preferences(null.1, "Dinocras", signif.level = 0.95, type = "counts",
               xlab = "Num. of visits", p.cex = 1.2, lwd = 2)

op <- par(mar = c(9, 4, 4, 2) + 0.1)
plot_preferences(null.1, "Dinocras", style = "bars", signif.level = 0.95,
               type = "counts", ylab = "Num. of visits")
par(op)

# Same results, this time showing the standardised effect sizes
plot_preferences(null.1, "Rhyacophila", signif.level = 0.95,
               type = "SES", xlab = "SES")

op <- par(mar = c(9, 4, 4, 2) + 0.1)
plot_preferences(null.1, "Rhyacophila", signif.level = 0.95, style = "bars",
               type = "SES", ylab = "SES")
par(op)
```

Silene   *Flower visitation network from an arable field in the UK*

Description

A flower visitation network from an arable field site in the UK, notable for the presence of small-flowered catchfly *Silene gallica*, a rare arable weed species in the UK. Flower visitors and floral abundance were sampled on 11 occasions in the summer of 2002, with all insect flower visitors (31 taxa) recorded on the flower species where they were observed. Gibson *et al*. (2006) provide full details of the data and analysis of the results.

Usage

```
Silene
```

Format

A data frame with 128 rows and seven columns, one row for each individual pollinator. The first column (Visit) represents the sampling occasion on which the pollinator was collected (V1–V11), the second column (Insect) represents the flower visitor taxon, and the remaining five columns are the five flower species, which were either visited (1) or not (0) by each insect.

Source

Gibson, R.H., Nelson, I.L., Hopkins, G.W., Hamlett, B.J. & Memmott, J. (2006) Pollinator webs, plant communities and the conservation of rare plants: arable weeds as a case study. *Journal of Applied Ecology*, **43**, 246–257.

Silene.plants	*Flower abundance data to accompany the* Silene *visitation network*

Description

Floral abundance data for the five flower species recorded in the Silene flower visitation network (see `Silene`) for full details.

Usage

```
Silene.plants
```

Format

A data frame with 11 rows and six columns. Each row represents the floral abundance on one sampling occasion. The first column (`Visit`) lists the codes for the sampling visit (V1–V11), whilst the remaining five variables represent the abundance of each of the flower species.

Source

Gibson, R.H., Nelson, I.L., Hopkins, G.W., Hamlett, B.J. & Memmott, J. (2006) Pollinator webs, plant communities and the conservation of rare plants: arable weeds as a case study. *Journal of Applied Ecology*, **43**, 246–257.

---

test_interactions	*Compare observed interaction strengths in a network to those estimated from a null model*

Description

Takes the result of running a null model with `generate_null_net` and tests whether the observed interactions between consumer species and resource species differ those expected under the null model.

Usage

```
test_interactions(nullnet, signif.level = 0.95)
```

Arguments

nullnet   An object of class "nullnet" from generate_null_net

signif.level   An optional value specifying the threshold used for testing for 'significant' de-
                 viations from the null model. Defaults to 0.95

Details

Statistical significance is determined for each consumer-resource interaction according to whether
the observed interaction strength falls outside the confidence limits calculated across the iterations
of the null model. Confidence limits are calculated as the 1 – alpha/2 percentiles from the frequency
distribution (Manly 2006).

The observed and expected interactions strengths are also compared by calculating the standardised
effect size (Gotelli & McCabe 2002):

$$(observed link strength - expected link strength)/standard deviation of the link strength across the iterations of the nu$$

test_interactions will issue warnings when:

1. The number of iterations of the null model was small <100, as the confidence intervals are
   unlikely to be reliable

2. The number of tests >50, due to the increasing risk of Type I errors (incorrectly denoting an
   interaction as significantly different from the null model). Many networks will contain many
   more than 100 potential interactions, so the significance of individual interactions should be
   treated with caution. Some form of false discovery rate correction may be valuable (e.g. the
   local false discovery rate; Gotelli & Ulrich 2010).

Value

Returns a data frame listing all possible consumer and resource species combinations with the
following column headings:

Consumer The name of the consumer species

Resource The name of the resource species

Observed The 'strength' of the observed interaction (e.g. total number of interactions summed
          across the individual consumers)

Null The mean strength of the interaction across the iterations of the null model

Lower Lower confidence limit for the interaction strength

Upper Upper confidence limit for the interaction strength

Test Whether the observed interaction is significantly **stronger** than expected under the null model,
      weaker or consistent with the null model (**ns**)

SES The standardised effect size for the interaction

References

Gotelli, N.J. & McCabe, D.J. (2002) Species co-occurrence: a meta-analysis of J. M. Diamond's assembly rules model. *Ecology*, **83**, 2091–2096.

Gotelli, N.J. & Ulrich, W. (2010) The empirical Bayes approach as a tool to identify non-random species associations. *Oecologia*, **162**, 463–477.

Manly, B.F.J. (2006) *Randomization, Bootstrap and Monte Carlo Methods in Biology* (3rd edn). Chapman & Hall, Boca Raton.

Vaughan, I.P., Gotelli, N.J., Memmott, J., Pearson, C.E., Woodward, G. & Symondson, W.O.C. (2018) econullnetr: an R package using null models to analyse the structure of ecological networks and identify resource selection. *Methods in Ecology and Evolution*, **9**, 728–733.

See Also

generate_null_net, plot_preferences

Examples

```
null.1 <- generate_null_net(WelshStreams[, 2:18], WelshStreams.prey[, 2:17],
                            sims = 10, c.samples = WelshStreams[, 1],
                            r.samples = WelshStreams.prey[, 1])
test_interactions(null.1, 0.95)
```

WelshStreams	*Part of the food web from upland streams in south Wales, UK*

Description

Part of a food web from upland streams in south Wales, UK, comprising 85 individuals of two macroinvertebrate predator species (the caddisfly *Rhyacophila dorsalis* and the stonefly *Dinocras cephalotes*). Data were collected in Dec 2013 from six streams spread across an agricultural intensity gradient as part of a wider study (Pearson *et al*. 2018). The data comprise presence or absence of predation by each predator on 16 potential prey taxa determined using next generation sequencing of predator gut contents. There are three accompanying data sets:

1. WelshStreams.prey, which gives the mean abundance of each prey taxon in each of the six streams (counts of individuals from 3–min kick samples)

2. WelshStreams.fl which specifies forbidden links (one forbidden link for each predator species, ruling out cannibalism)

3. WelshStreams.order which ranks the 16 prey taxa in taxonomic order according to the Centre for Ecology and Hydrology's Coded Macroinvertebrate List. This is used for plotting the results.

Usage

```
WelshStreams
```

Format

A data frame with 85 rows and 18 variables. Each row represents the gut contents of an individual predator. The first column Stream indicates which of the six streams each predator was collected from, whilst the second column indicates which genus the predator belonged to (*Dinocras* or *Rhyacophila*). The remaining 16 columns represent the potential prey taxa, which were either predated (1) or not (0) by each individual predator.

Source

Pearson, C.E., Symondson, W.O.C., Clare, E.L., Ormerod, S.J., Iparraguirre Bolanos, E. & Vaughan, I.P. (2018) The effects of pastoral intensification on the feeding interactions of generalist predators in streams. *Molecular Ecology*, **27**, 590-602.

WelshStreams.fl   *'Forbidden' links to accompany the upland streams food web*

Description

A table specifying trophic links that are allowed when modelling part of the food web from upland Welsh stream containing the two macroinvetebrate predators *Rhyacophila dorsalis* and *Dinocras cephalotes* (see WelshStreams). There is one forbidden link for each predator species, preventing cannibalism from being included in the null model: this is because the method used to screen predator gut contents for prey (next generation sequencing) cannot distinguish between predator and prey of the same species. Both predators are generalists, so all other trophic links are permitted.

Usage

```
WelshStreams.fl
```

Format

A data frame with 2 rows and 17 columns, each row representing one of the two predator genera. The first column (Predator) indicates the predator genus, whilst columns 2–17 indicate which of the 16 potential prey taxa can be consumed (1) or are forbidden (0).

Source

Pearson, C.E., Symondson, W.O.C., Clare, E.L., Ormerod, S.J., Iparraguirre Bolanos, E. & Vaughan, I.P. (2018) The effects of pastoral intensification on the feeding interactions of generalist predators in streams. *Molecular Ecology*, **27**, 590-602.

WelshStreams.order   *Additional data to assist with plotting outputs from* WelshStreams

---

Description

The rank order of 16 prey taxa in WelshStreams on the Centre for Ecology and Hydrology's Coded Macroinvertebrate List https://www.ceh.ac.uk/services/coded-macroinvertebrates-list. This is used primarily for controlling the order in which prey taxa are plotted with plot_preferences.

Usage

```
WelshStreams.order
```

Format

A data frame with 16 rows and two columns:

Taxon The names of each prey taxon

CEH The rank order of the taxa based on the Centre for Ecology and Hydrology's Coded Macroinvertebrate List

Source

Pearson, C.E., Symondson, W.O.C., Clare, E.L., Ormerod, S.J., Iparraguirre Bolanos, E. & Vaughan, I.P. (2018) The effects of pastoral intensification on the feeding interactions of generalist predators in streams. *Molecular Ecology*, **27**, 590-602.

WelshStreams.prey   *Macroinvertebrate abundance to accompany part of the food web from upland streams in south Wales, UK*

Description

The abundance of 16 potential macroinvertebrate prey taxa to accompany the food web data in WelshStreams.

Usage

```
WelshStreams.prey
```

Format

A data frame with 6 rows and 17 variables. Each row represents the abundance of individual macroinvertebrate taxa in each of the six streams. Column 1 contains the stream codes, whilst columns 2–17 represent the abundance of each macroinvertebrate taxon summed across three 1-minute kick-samples in each stream.

Source

Pearson, C.E., Symondson, W.O.C., Clare, E.L., Ormerod, S.J., Iparraguirre Bolanos, E. & Vaughan, I.P. (2018) The effects of pastoral intensification on the feeding interactions of generalist predators in streams. *Molecular Ecology*, **27**, 590-602.

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