Package ‘netassoc’

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R topics documented:

netassoc-package .......................................................... 1
makenetwork ................................................................. 2
plot_netassoc_network ..................................................... 4

Index

netassoc-package Inference of species associations from co-occurrence data

Description

Infers species associations from local and regional-scale co-occurrence data (species x site matrices). The resulting network can be analyzed using functions from the igraph network package.
**makenetwork**

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**References**
Morueta-Holme, N., Blonder, B., et al. IN PREPARATION.

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**Description**

Infers a species association network by determining which co-occurrence patterns between species are more or less likely than expected under a null model of community assembly. Steps taken are:

1) obtaining input data and trimming to eliminate species that do not occur in any site
2) resampling a set of null community matrices from the expectation with the same richness and abundance as the observed community
3) calculating species co-occurrence scores for each pair of species within the observed matrix and all resampled null matrices
4) calculating standardized effect sizes for species’ co-occurrence scores
5) thresholding effect sizes to retain only significant associations
6) converting matrix of scores to association network

The resulting network can be analyzed using functions from the igraph network package.

**Usage**

```r
makenetwork(obs, nul, whichmethod = "pearson", kappa = 2, numnulls = 1000, plot = FALSE, verbose = TRUE)
```

**Arguments**

- **obs**: A m x n community matrix describing the abundance of m species at n sites. Represents the observed data.
- **nul**: A m x n community matrix describing the abundance of m species at n sites. Represents the regional null expectation data.
- **whichmethod**: Method used to calculate co-occurrence score between abundance vectors of species across sites. Can be either ‘pearson’ or ‘spearman’, as per arguments in cor
- **kappa**: Threshold value determining the minimum absolute standardized effect size to be retained in the network. Set to zero to retain all associations.
- **numnulls**: Number of resamples of the nul matrix used to assemble null communities. Larger values produce more accurate results.
- **plot**: If TRUE, plots all intermediate matrices calculated by the algorithm. Can be used to visualize input.
- **verbose**: If TRUE, prints status updates and progress bars during calculations.
Details
Full explanation of the algorithm is provided in the referenced paper.

Value
A list with the following components:

- `matrix_sp_site_obs`  
The trimmed obs matrix
- `matrix_sp_site_null`  
The trimmed null matrix
- `matrix_sp_sp_obs`  
The observed co-occurrence scores between species
- `matrix_sp_sp_null_mean`  
The mean null co-occurrence scores between species
- `matrix_sp_sp_null_sd`  
The s.d. null co-occurrence scores between species
- `matrix_sp_sp_ses_all`  
The raw standardized effect size co-occurrence scores between species
- `matrix_sp_sp_ses_thresholded`  
The thresholded standardized effect size co-occurrence scores between species
- `network_all`  
An igraph object representing the association network
- `network_pos`  
An igraph object representing an association network including only positive associations
- `network_neg`  
An igraph object representing an association network including only negative associations

Note
Warnings may be generated when calculating co-occurrence scores using the cor function in cases where a pair of species co-occur identically at all sites. These warnings can be ignored.

References

Examples
```r
# generate random data
set.seed(1)
nsp <- 10
nsi <- 5
m_obs <- floor(matrix(rgamma(nsp*nsi, shape=5), ncol=nsi, nrow=nsp))
m_nul <- floor(matrix(rexp(nsp*nsi, rate=0.05), ncol=nsi, nrow=nsp))
n <- makenetwork(m_obs, m_nul, numnulls=50, plot=TRUE)
```

# extract network
n$network_all

# example statistics
degree(n$network_all)

plot_netassoc_network   Plots species association network

Description

Draws a network of species associations. By default edge widths are proportional to association strength and edge color reflects association type (blue, positive; red, negative).

Usage

plot_netassoc_network(network, layout = layout.auto(network),
vertex.label = V(network)$name,
vertex.color = NA,
vertex.shape = "none",
vertex.label.color = "black",
vertex.label.family = "sans",
edge.width = NULL,
edge.color = NULL,
edge.arrow.size = 0.05,
vertex.label.cex = 0.5,
...
)

Arguments

- **network**: An igraph object corresponding to the association network
- **layout**: Graphical layout. See igraph::layout.
- **vertex.label**: String labels for species.
- **edge.width**: Edge widths for links between species.
- **edge.color**: Edge colors for links between species.
- **vertex.color**: Vertex colors for species.
- **vertex.label.color**: Vertex label colors for species.
- **vertex.shape**: Vertex shape for species.
- **edge.arrow.size**: Edge arrow size for links between species.
- **vertex.label.cex**: Vertex label expansion factor for species.
- **vertex.label.family**: Vertex shape font family for species.
- **...**: Other arguments to be passed to plot.igraph.
Examples

# generate random data
set.seed(1)
nsp <- 10
nsi <- 5
m_obs <- floor(matrix(rgamma(nspsnsi, shape=5), ncol=nsi, nrow=nsi))
m_nul <- floor(matrix(rexp(nspsnsi, rate=0.05), ncol=nsi, nrow=nsi))

n <- makenetwork(m_obs, m_nul, numnulls=50, plot=TRUE)

# plot
plot_netassoc_network(n$network_all)

# plot using circular layout
plot_netassoc_network(n$network_all, layout=layout.circle(n$network_all))
Index

*Topic package
  netassoc-package, 1

cor, 2

makenetwork, 2

netassoc (netassoc-package), 1
netassoc-package, 1

plot.igraph, 4
plot_netassoc_network, 4