

Package ‘backbone’

July 29, 2025

Type Package

Title Extracts the Backbone from Graphs

Version 2.1.5

Description An implementation of methods for extracting an unweighted unipartite graph (i.e. a backbone) from an unweighted unipartite graph, a weighted unipartite graph, the projection of an unweighted bipartite graph, or the projection of a weighted bipartite graph (Neal, 2022 <[doi:10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)>).

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Encoding UTF-8

RoxygenNote 7.3.2

Depends R (>= 2.10)

Imports igraph, Matrix, methods, stats, Rcpp, utils,

Suggests knitr, rmarkdown, tinytest

LinkingTo Rcpp

VignetteBuilder knitr

URL <https://www.zacharyneal.com/backbone>,
<https://github.com/zpneal/backbone>

BugReports <https://github.com/zpneal/backbone/issues>

NeedsCompilation yes

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Repository CRAN

Date/Publication 2025-07-29 15:20:02 UTC

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backbone

backbone: Extracts the Backbone from Graphs

Description

Provides methods for extracting from an unweighted and sparse subgraph (i.e., a backbone) that contains only the most "important" edges in a weighted bipartite projection, a non-projection weighted network, or an unweighted network.

Available backbone extraction functions include:

- For weighted bipartite projections of weighted bipartite networks: [osdsm\(\)](#).
- For weighted bipartite projections of binary bipartite networks: [fixedfill\(\)](#), [fixedrow\(\)](#), [fixedcol\(\)](#), [sdsd\(\)](#), and [fdsm\(\)](#).
- For non-projection weighted networks: [global\(\)](#), [disparity\(\)](#), [mlf\(\)](#), [lans\(\)](#).

- For unweighted networks: `sparsify()`, `sparsify.with.skeleton()`, `sparsify.with.gspar()`, `sparsify.with.lspar()`, `sparsify.with.simmelian()`, `sparsify.with.jaccard()`, `sparsify.with.meetmin()`, `sparsify.with.geometric()`, `sparsify.with.hypergeometric()`, `sparsify.with.localdegree()`, `sparsify.with.quadrilateral()`.
- For all networks: `backbone.suggest()` will examine the data and suggest an appropriate backbone function

The package also includes some utility functions:

- `fastball()` - Fast marginal-preserving randomization of binary matrices
- `bicm()` - Compute probabilities under the bipartite configuration model

For additional documentation and background on the package functions, see `vignette("backbone")`.

For updates, papers, presentations, and other backbone news, please see www.rbackbone.net

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References

Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

See Also

Useful links:

- <https://www.zacharyneal.com/backbone>
- <https://github.com/zpneal/backbone>
- Report bugs at <https://github.com/zpneal/backbone/issues>

backbone.extract

Extracts a backbone network from a backbone object

Description

`backbone.extract` returns a binary or signed adjacency matrix containing the backbone that retains only the significant edges.

Usage

```
backbone.extract(
  bb.object,
  signed = FALSE,
  alpha = 0.05,
  mtc = "none",
  class = bb.object$class,
  narrative = FALSE
)
```

Arguments

bb.object	backbone: backbone S3 class object.
signed	boolean: TRUE for a signed backbone, FALSE for a binary backbone (see details)
alpha	real: significance level of hypothesis test(s)
mtc	string: type of Multiple Test Correction to be applied; can be any method allowed by p.adjust .
class	string: the class of the returned backbone graph, one of c("matrix", "sparseMatrix", "igraph", "edgelist"), converted via tomatrix .
narrative	boolean: TRUE if suggested text & citations should be displayed.

Details

The "backbone" S3 class object is composed of (1) the weighted graph as a matrix, (2) upper-tail p-values as a matrix, (3, if signed = TRUE) lower-tail p-values as a matrix, (4, if present) node attributes as a dataframe, and (5) several properties of the original graph and backbone model

When signed = FALSE, a one-tailed test (is the weight stronger?) is performed for each edge. The resulting backbone contains edges whose weights are significantly *stronger* than expected in the null model. When signed = TRUE, a two-tailed test (is the weight stronger or weaker?) is performed for each edge. The resulting backbone contains positive edges for those whose weights are significantly *stronger*, and negative edges for those whose weights are significantly *weaker*, than expected in the null model.

Value

backbone graph: Binary or signed backbone graph of class given in parameter class.

Examples

```
#A binary bipartite network of 30 agents & 75 artifacts; agents form three communities
B <- rbind(cbind(matrix(rbinom(250,1,.8),10),
  matrix(rbinom(250,1,.2),10),
  matrix(rbinom(250,1,.2),10)),
  cbind(matrix(rbinom(250,1,.2),10),
  matrix(rbinom(250,1,.8),10),
  matrix(rbinom(250,1,.2),10)),
  cbind(matrix(rbinom(250,1,.2),10),
```

```

matrix(rbinom(250,1,.2),10),
matrix(rbinom(250,1,.8),10))

backbone.object <- fixedrow(B, alpha = NULL)
bb <- backbone.extract(backbone.object, alpha = 0.05)

```

backbone.suggest	<i>Suggest a backbone model</i>
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Description

`backbone.suggest` suggests and optionally runs an appropriate backbone model for a graph object.

Usage

```
backbone.suggest(G, s = NULL)
```

Arguments

G	graph: A graph represented in an object of class matrix, sparse Matrix , dataframe, or igraph .
s	numeric: If provided, a backbone is extracted using this value as the significance level or sparsification parameter.

Value

If `s == NULL`: `NULL`, but a message is displayed with a suggested model. If $0 \leq s \leq 1$: A binary backbone graph in the same class as `G`, obtained by extracting the backbone at the `s` significance level (if a statistical model is suggested) or using sparsification parameter `s` (if a sparsification model is suggested). The code used to perform the extraction, and suggested manuscript text are displayed.

References

Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

Examples

```

M <- matrix(runif(100),10,10) #A random weighted, directed graph
backbone <- backbone.suggest(M)
backbone <- backbone.suggest(M, s = 0.05)

```

bicm	<i>Bipartite Configuration Model</i>
------	--------------------------------------

Description

bicm estimates cell probabilities under the bipartite configuration model

Usage

```
bicm(M, fitness = FALSE, tol = 1e-08, max_steps = 200, ...)
```

Arguments

M	matrix: a binary matrix
fitness	boolean: FALSE returns a matrix of probabilities, TRUE returns a list of row and column fitnesses only
tol	numeric, tolerance of algorithm
max_steps	numeric, number of times to run loglikelihood_prime_bicm algorithm
...	optional arguments

Details

Given a binary matrix **M**, the Bipartite Configuration Model (BiCM; Saracco et. al. 2015) returns a valued matrix **B** in which B_{ij} is the *approximate* probability that $M_{ij} = 1$ in the space of all binary matrices with the same row and column marginals as **M**. The BiCM yields the closest approximations of the true probabilities compared to other estimation methods (Neal et al., 2021), and is used by [sdsbm\(\)](#) to extract the backbone of a bipartite projection using the stochastic degree sequence model.

Matrix **M** is "conforming" if no rows and no columns contain only zeros or only ones. If **M** is conforming, then `bicm()` is faster. Additionally, if `fitness = TRUE`, then `bicm()` returns a list of row and column fitnesses, which requires less memory. Given the i th row's fitness R_i and the j th column's fitness R_j , the entry B_{ij} in the probability matrix can be computed as $R_i \times R_j / (1 + (R_i \times R_j))$.

Matrix **M** is "non-conforming" if any rows or any columns contain only zeros or only ones. If **M** is non-conforming, then `bicm()` is slower and will only return a probability matrix.

Value

a matrix of probabilities or a list of fitnesses

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:10.1371/journal.pone.0269137

bicm: Saracco, F., Di Clemente, R., Gabrielli, A., & Squartini, T. (2015). Randomizing bipartite networks: The case of the World Trade Web. *Scientific Reports*, 5, 10595. doi:10.1038/srep10595

Examples

```
M <- matrix(c(0,0,1,0,1,0,1,0,1),3,3) #A binary matrix
bicm(M)
```

disparity

Extract backbone using the Disparity Filter

Description

disparity extracts the backbone of a weighted network using the Disparity Filter.

Usage

```
disparity(
  W,
  alpha = 0.05,
  missing.as.zero = FALSE,
  signed = FALSE,
  mtc = "none",
  class = "original",
  narrative = FALSE
)
```

Arguments

W	A positively-weighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a three-column dataframe; (3) an igraph object.
alpha	real: significance level of hypothesis test(s)
missing.as.zero	boolean: should missing edges be treated as edges with zero weight and tested for significance
signed	boolean: TRUE for a signed backbone, FALSE for a binary backbone (see details)
mtc	string: type of Multiple Test Correction to be applied; can be any method allowed by p.adjust .
class	string: the class of the returned backbone graph, one of c("original", "matrix", "Matrix", "igraph", "edgelist"). If "original", the backbone graph returned is of the same class as W.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Details

The disparity function applies the disparity filter (Serrano et al., 2009), which compares an edge's weight to its expected weight if a node's total degree was uniformly distributed across all its edges. The graph may be directed or undirected, however the edge weights must be positive.

When `signed = FALSE`, a one-tailed test (is the weight stronger?) is performed for each edge. The resulting backbone contains edges whose weights are significantly *stronger* than expected in the null model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker?) is performed for each edge. The resulting backbone contains positive edges for those whose weights are significantly *stronger*, and negative edges for those whose weights are significantly *weaker*, than expected in the null model.

If `W` is an unweighted bipartite graph, then the disparity filter is applied to its weighted bipartite projection.

Value

If `alpha != NULL`: Binary or signed backbone graph of class `class`.

If `alpha == NULL`: An S3 backbone object containing (1) the weighted graph as a matrix, (2) upper-tail p-values as a matrix, (3, if `signed = TRUE`) lower-tail p-values as a matrix, (4, if present) node attributes as a dataframe, and (5) several properties of the original graph and backbone model, from which a backbone can subsequently be extracted using `backbone.extract()`.

References

- package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:10.1371/journal.pone.0269137
- disparity filter: Serrano, M. A., Boguna, M., & Vespignani, A. (2009). Extracting the multiscale backbone of complex weighted networks. *Proceedings of the National Academy of Sciences*, 106, 6483-6488. doi:10.1073/pnas.0808904106

Examples

```
#A network with heterogeneous (i.e. multiscale) weights
net <- matrix(c(0,10,10,10,10,10,75,0,0,0,0,
               10,0,1,1,1,0,0,0,0,0,0,
               10,1,0,1,1,0,0,0,0,0,0,
               10,1,1,0,1,0,0,0,0,0,0,
               10,1,1,1,0,0,0,0,0,0,0,
               75,0,0,0,0,0,100,100,100,100,
               0,0,0,0,0,100,0,10,10,10,
               0,0,0,0,0,100,10,0,10,10,
               0,0,0,0,0,100,10,10,0,10,
               0,0,0,0,0,100,10,10,10,0),10)

net <- igraph::graph_from_adjacency_matrix(net, mode = "undirected", weighted = TRUE)
plot(net, edge.width = sqrt(igraph::E(net)$weight)) #A stronger clique & a weaker clique

strong <- igraph::delete_edges(net, which(igraph::E(net)$weight < mean(igraph::E(net)$weight)))
plot(strong) #A backbone of stronger-than-average edges ignores the weaker clique
```



```
bb <- disparity(net, alpha = 0.05, narrative = TRUE) #A disparity backbone...
plot(bb) #...preserves edges at multiple scales
```

fastball

Randomize a binary matrix using the fastball algorithm

Description

fastball randomizes a binary matrix, preserving the row and column sums

Usage

```
fastball(M, trades = 5 * nrow(M))
```

Arguments

M	matrix: a binary matrix (see details)
trades	integer: number of trades; the default is 5R trades (approx. mixing time)

Details

Given a matrix M, fastball randomly samples a new matrix from the space of all matrices with the same row and column sums as M.

Value

matrix: A random binary matrix with same row sums and column sums as M.

References

fastball: Godard, Karl and Neal, Zachary P. 2022. fastball: A fast algorithm to sample bipartite graphs with fixed degree sequences. *Journal of Complex Networks* doi:[10.1093/comnet/cnac049](https://doi.org/10.1093/comnet/cnac049)

Examples

```
M <- matrix(rbinom(200,1,0.5),10,20) #A random 10x20 binary matrix
Mrand <- fastball(M) #Random matrix with same row and column sums
```

fdsm

*Extract backbone using the Fixed Degree Sequence Model***Description**

fdsm extracts the backbone of a bipartite projection using the Fixed Degree Sequence Model.

Usage

```
fdsm(
  B,
  alpha = 0.05,
  trials = NULL,
  missing.as.zero = FALSE,
  signed = FALSE,
  mtc = "none",
  class = "original",
  narrative = FALSE,
  progress = TRUE,
  ...
)
```

Arguments

B	An unweighted bipartite graph, as: (1) an incidence matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
alpha	real: significance level of hypothesis test(s)
trials	numeric: the number of bipartite graphs generated to approximate the edge weight distribution. If NULL, the number of trials is selected based on alpha (see details)
missing.as.zero	boolean: should missing edges be treated as edges with zero weight and tested for significance
signed	boolean: TRUE for a signed backbone, FALSE for a binary backbone (see details)
mtc	string: type of Multiple Test Correction to be applied; can be any method allowed by p.adjust .
class	string: the class of the returned backbone graph, one of c("original", "matrix", "Matrix", "igraph", "edgelist"). If "original", the backbone graph returned is of the same class as B.
narrative	boolean: TRUE if suggested text & citations should be displayed.
progress	boolean: TRUE if the progress of Monte Carlo trials should be displayed.
...	optional arguments

Details

The `fdsm` function compares an edge's observed weight in the projection $B \times t(B)$ to the distribution of weights expected in a projection obtained from a random bipartite network where both the row vertex degrees and column vertex degrees are *exactly* fixed at their values in B . It uses the `fastball()` algorithm to generate random bipartite matrices with given row and column vertex degrees.

When `signed = FALSE`, a one-tailed test (is the weight stronger?) is performed for each edge. The resulting backbone contains edges whose weights are significantly *stronger* than expected in the null model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker?) is performed for each edge. The resulting backbone contains positive edges for those whose weights are significantly *stronger*, and negative edges for those whose weights are significantly *weaker*, than expected in the null model.

The p-values used to evaluate the statistical significance of each edge are computed using Monte Carlo methods. The number of trials performed affects the precision of these p-values. This precision impacts the confidence that a given edge's p-value is less than the desired alpha level, and therefore represents a statistically significant edge that should be retained in the backbone. When `trials = NULL`, `trials.needed()` is used to estimate the required number of trials to evaluate the statistical significance of an edge's p-values.

Value

If `alpha != NULL`: Binary or signed backbone graph of class `class`.

If `alpha == NULL`: An S3 backbone object containing (1) the weighted graph as a matrix, (2) upper-tail p-values as a matrix, (3, if `signed = TRUE`) lower-tail p-values as a matrix, (4, if present) node attributes as a dataframe, and (5) several properties of the original graph and backbone model, from which a backbone can subsequently be extracted using `backbone.extract()`.

References

- package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:10.1371/journal.pone.0269137
- fdsm: Neal, Z. P., Domagalski, R., and Sagan, B. (2021). Comparing Alternatives to the Fixed Degree Sequence Model for Extracting the Backbone of Bipartite Projections. *Scientific Reports*. doi:10.1038/s41598021032383
- fastball: Godard, Karl and Neal, Zachary P. 2022. fastball: A fast algorithm to sample bipartite graphs with fixed degree sequences. *Journal of Complex Networks* doi:10.1093/comnet/cnac049

Examples

```
#A binary bipartite network of 30 agents & 75 artifacts; agents form three communities
B <- rbind(cbind(matrix(rbinom(250,1,.8),10),
                    matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.2),10)),
          cbind(matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.8),10),
                    matrix(rbinom(250,1,.2),10)),
          cbind(matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.2),10)))
```

```

matrix(rbinom(250,1,.8),10)))

P <- B%*%t(B) #An ordinary weighted projection...
plot(igraph::graph_from_adjacency_matrix(P, mode = "undirected",
                                         weighted = TRUE, diag = FALSE)) #...is a dense hairball

bb <- fdsm(B, alpha = 0.05, trials = 1000, narrative = TRUE, class = "igraph") #An FDSM backbone...
plot(bb) #...is sparse with clear communities

```

fixedcol

Extract backbone using the Fixed Column Model

Description

fixedcol extracts the backbone of a bipartite projection using the Fixed Column Model.

Usage

```

fixedcol(
  B,
  alpha = 0.05,
  missing.as.zero = FALSE,
  signed = FALSE,
  mtc = "none",
  class = "original",
  narrative = FALSE
)

```

Arguments

B	An unweighted bipartite graph, as: (1) an incidence matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
alpha	real: significance level of hypothesis test(s)
missing.as.zero	boolean: should missing edges be treated as edges with zero weight and tested for significance
signed	boolean: TRUE for a signed backbone, FALSE for a binary backbone (see details)
mtc	string: type of Multiple Test Correction to be applied; can be any method allowed by p.adjust .
class	string: the class of the returned backbone graph, one of c("original", "matrix", "Matrix", "igraph", "edgelist"). If "original", the backbone graph returned is of the same class as B.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Details

This `fixedcol` function compares an edge's observed weight in the projection $B * t(B)$ to the distribution of weights expected in a projection obtained from a random bipartite graph where the *column* vertex degrees are fixed but the row vertex degrees are allowed to vary.

When `signed = FALSE`, a one-tailed test (is the weight stronger?) is performed for each edge. The resulting backbone contains edges whose weights are significantly *stronger* than expected in the null model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker?) is performed for each edge. The resulting backbone contains positive edges for those whose weights are significantly *stronger*, and negative edges for those whose weights are significantly *weaker*, than expected in the null model.

Value

If `alpha != NULL`: Binary or signed backbone graph of class `class`.

If `alpha == NULL`: An S3 backbone object containing (1) the weighted graph as a matrix, (2) upper-tail p-values as a matrix, (3, if `signed = TRUE`) lower-tail p-values as a matrix, (4, if present) node attributes as a dataframe, and (5) several properties of the original graph and backbone model, from which a backbone can subsequently be extracted using `backbone.extract()`.

References

- package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:10.1371/journal.pone.0269137
- fixedcol: Neal, Z. P., Domagalski, R., and Sagan, B. (2021). Comparing Alternatives to the Fixed Degree Sequence Model for Extracting the Backbone of Bipartite Projections. *Scientific Reports*, 11, 23929. doi:10.1038/s41598021032383

Examples

```
#A binary bipartite network of 30 agents & 75 artifacts; agents form three communities
B <- rbind(cbind(matrix(rbinom(250,1,.8),10),
                    matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.2),10)),
           cbind(matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.8),10),
                    matrix(rbinom(250,1,.2),10)),
           cbind(matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.8),10)))

P <- B%*%t(B) #An ordinary weighted projection...
plot(igraph::graph_from_adjacency_matrix(P, mode = "undirected",
                                         weighted = TRUE, diag = FALSE)) #...is a dense hairball

bb <- fixedcol(B, alpha = 0.05, narrative = TRUE, class = "igraph") #A fixedcol backbone...
plot(bb) #...is sparse with clear communities
```

fixedfill

*Extract backbone using the Fixed Fill Model***Description**

fixedfill extracts the backbone of a bipartite projection using the Fixed Fill Model.

Usage

```
fixedfill(
  B,
  alpha = 0.05,
  missing.as.zero = FALSE,
  signed = FALSE,
  mtc = "none",
  class = "original",
  narrative = FALSE
)
```

Arguments

B	An unweighted bipartite graph, as: (1) an incidence matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
alpha	real: significance level of hypothesis test(s)
missing.as.zero	boolean: should missing edges be treated as edges with zero weight and tested for significance
signed	boolean: TRUE for a signed backbone, FALSE for a binary backbone (see details)
mtc	string: type of Multiple Test Correction to be applied; can be any method allowed by p.adjust .
class	string: the class of the returned backbone graph, one of c("original", "matrix", "Matrix", "igraph", "edgelist"). If "original", the backbone graph returned is of the same class as B.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Details

The fixedfill function compares an edge's observed weight in the projection $B * t(B)$ to the distribution of weights expected in a projection obtained from a random bipartite graph where the number of edges present (i.e., the number of cells *filled* with a 1) is equal to the number of edges in B. When B is large, this function may be impractically slow and may return a backbone object that contains NaN values.

When `signed = FALSE`, a one-tailed test (is the weight stronger?) is performed for each edge. The resulting backbone contains edges whose weights are significantly *stronger* than expected in the null model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker?) is performed for each edge. The resulting backbone contains positive edges for those whose weights are significantly *stronger*, and negative edges for those whose weights are significantly *weaker*, than expected in the null model.

Value

If `alpha != NULL`: Binary or signed backbone graph of class `class`.

If `alpha == NULL`: An S3 backbone object containing (1) the weighted graph as a matrix, (2) upper-tail p-values as a matrix, (3, if `signed = TRUE`) lower-tail p-values as a matrix, (4, if present) node attributes as a dataframe, and (5) several properties of the original graph and backbone model, from which a backbone can subsequently be extracted using `backbone.extract()`.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:10.1371/journal.pone.0269137

fixedfill: Neal, Z. P., Domagalski, R., and Sagan, B. (2021). Comparing Alternatives to the Fixed Degree Sequence Model for Extracting the Backbone of Bipartite Projections. *Scientific Reports*, 11, 23929. doi:10.1038/s41598021032383

Examples

```
#A binary bipartite network of 30 agents & 75 artifacts; agents form three communities
B <- rbind(cbind(matrix(rbinom(250,1,.8),10),
  matrix(rbinom(250,1,.2),10),
  matrix(rbinom(250,1,.2),10)),
  cbind(matrix(rbinom(250,1,.2),10),
  matrix(rbinom(250,1,.8),10),
  matrix(rbinom(250,1,.2),10)),
  cbind(matrix(rbinom(250,1,.2),10),
  matrix(rbinom(250,1,.2),10),
  matrix(rbinom(250,1,.8),10)))

P <- B*%t(B) #An ordinary weighted projection...
plot(igraph::graph_from_adjacency_matrix(P, mode = "undirected",
  weighted = TRUE, diag = FALSE)) #...is a dense hairball

bb <- fixedfill(B, alpha = 0.05, narrative = TRUE, class = "igraph") #A fixedfill backbone...
plot(bb) #...is sparse with clear communities
```

fixedrow

Extract backbone using the Fixed Row Model

Description

`fixedrow` extracts the backbone of a bipartite projection using the Fixed Row Model.

Usage

```
fixedrow(
  B,
  alpha = 0.05,
  missing.as.zero = FALSE,
  signed = FALSE,
  mtc = "none",
  class = "original",
  narrative = FALSE
)
```

Arguments

B	An unweighted bipartite graph, as: (1) an incidence matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
alpha	real: significance level of hypothesis test(s)
missing.as.zero	boolean: should missing edges be treated as edges with zero weight and tested for significance
signed	boolean: TRUE for a signed backbone, FALSE for a binary backbone (see details)
mtc	string: type of Multiple Test Correction to be applied; can be any method allowed by p.adjust .
class	string: the class of the returned backbone graph, one of c("original", "matrix", "Matrix", "igraph", "edgelist"). If "original", the backbone graph returned is of the same class as B.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Details

The `fixedrow` function compares an edge's observed weight in the projection $B * t(B)$ to the distribution of weights expected in a projection obtained from a random bipartite graph where the *row* vertex degrees are fixed but the column vertex degrees are allowed to vary.

When `signed = FALSE`, a one-tailed test (is the weight stronger?) is performed for each edge. The resulting backbone contains edges whose weights are significantly *stronger* than expected in the null model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker?) is performed for each edge. The resulting backbone contains positive edges for those whose weights are significantly *stronger*, and negative edges for those whose weights are significantly *weaker*, than expected in the null model.

Value

If `alpha != NULL`: Binary or signed backbone graph of class `class`.

If `alpha == NULL`: An S3 backbone object containing (1) the weighted graph as a matrix, (2) upper-tail p-values as a matrix, (3, if `signed = TRUE`) lower-tail p-values as a matrix, (4, if present)

node attributes as a dataframe, and (5) several properties of the original graph and backbone model, from which a backbone can subsequently be extracted using `backbone.extract()`.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:10.1371/journal.pone.0269137

Neal, Z. P., Domagalski, R., and Sagan, B. (2021). Comparing Alternatives to the Fixed Degree Sequence Model for Extracting the Backbone of Bipartite Projections. *Scientific Reports*, 11, 23929. doi:10.1038/s41598021032383

Examples

```
#A binary bipartite network of 30 agents & 75 artifacts; agents form three communities
B <- rbind(cbind(matrix(rbinom(250,1,.8),10),
                    matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.2),10)),
          cbind(matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.8),10),
                    matrix(rbinom(250,1,.2),10)),
          cbind(matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.8),10)))

P <- B%*%t(B) #An ordinary weighted projection...
plot(igraph::graph_from_adjacency_matrix(P, mode = "undirected",
                                         weighted = TRUE, diag = FALSE)) #...is a dense hairball

bb <- fixedrow(B, alpha = 0.05, narrative = TRUE, class = "igraph") #A fixedrow backbone...
plot(bb) #...is sparse with clear communities
```

global

Compute global threshold backbone

Description

global extracts the backbone of a weighted network using a global threshold

Usage

```
global(
  G,
  upper = 0,
  lower = NULL,
  keepzeros = TRUE,
  class = "original",
  narrative = FALSE
)
```

Arguments

G	A weighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix , or dataframe; (2) an edgelist in the form of a three-column dataframe; (3) an igraph object.
upper	real, FUN, or NULL: upper threshold value or function that evaluates to an upper threshold value.
lower	real, FUN, or NULL: lower threshold value or function that evaluates to a lower threshold value.
keepzeros	boolean: TRUE if zero-weight edges in W should be excluded from (i.e. also be zero in) the backbone
class	string: the class of the returned backbone graph, one of c("original", "matrix", "Matrix", "igraph", "edgelist"). If "original", the backbone graph returned is of the same class as W.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Details

The global function retains a edge with weight W if $W > \text{upper}$. If a lower threshold is also specified, it returns a signed backbone in which an edge's weight is set to 1 if $W > \text{upper}$, is set to -1 if $W < \text{lower}$, and is set to 0 otherwise. The default is an unsigned backbone containing all edges with non-zero weights.

If G is an unweighted bipartite graph, the global threshold is applied to its weighted bipartite projection.

Value

Binary or signed backbone graph of class given in parameter class.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

model: Neal, Z. P. (2014). The backbone of bipartite projections: Inferring relationships from co-authorship, co-sponsorship, co-attendance, and other co-behaviors. *Social Networks*, 39, 84-97. doi:[10.1016/j.socnet.2014.06.001](https://doi.org/10.1016/j.socnet.2014.06.001)

Examples

```
G <- matrix(sample(0:5, 100, replace = TRUE), 10) #Random weighted graph
diag(G) <- 0
G
global(G, narrative = TRUE) #Keep all non-zero edges
global(G, upper = 4, lower = 2, narrative = TRUE) #Signed with specified thresholds
global(G, upper = function(x)mean(x), #Above-average --> positive edges
       lower = function(x)mean(x), narrative = TRUE) #Below-average --> negative edges
```

lans

*Extract backbone using Locally Adaptive Network Sparsification***Description**

lans extracts the backbone of a weighted network using Locally Adaptive Network Sparsification

Usage

```
lans(
  W,
  alpha = 0.05,
  missing.as.zero = FALSE,
  signed = FALSE,
  mtc = "none",
  class = "original",
  narrative = FALSE
)
```

Arguments

W	A positively-weighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a three-column dataframe; (3) an igraph object.
alpha	real: significance level of hypothesis test(s)
missing.as.zero	boolean: should missing edges be treated as edges with zero weight and tested for significance
signed	boolean: TRUE for a signed backbone, FALSE for a binary backbone (see details)
mtc	string: type of Multiple Test Correction to be applied; can be any method allowed by p.adjust .
class	string: the class of the returned backbone graph, one of c("original", "matrix", "Matrix", "igraph", "edgelist"). If "original", the backbone graph returned is of the same class as W.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Details

The lans function applies Locally Adaptive Network Sparsification (LANS; Foti et al., 2011), which compares an edge's fractional weight to the cumulative distribution function for the fractional edge weights of all edges connected to a given node. The graph may be directed or undirected, however the edge weights must be positive.

When signed = FALSE, a one-tailed test (is the weight stronger?) is performed for each edge. The resulting backbone contains edges whose weights are significantly *stronger* than expected in the null

model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker?) is performed for each edge. The resulting backbone contains positive edges for those whose weights are significantly *stronger*, and negative edges for those whose weights are significantly *weaker*, than expected in the null model.

If `W` is an unweighted bipartite graph, then LANS is applied to its weighted bipartite projection.

Value

If `alpha != NULL`: Binary or signed backbone graph of class `class`.

If `alpha == NULL`: An S3 backbone object containing (1) the weighted graph as a matrix, (2) upper-tail p-values as a matrix, (3, if `signed = TRUE`) lower-tail p-values as a matrix, (4, if present) node attributes as a dataframe, and (5) several properties of the original graph and backbone model, from which a backbone can subsequently be extracted using `backbone.extract()`.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:10.1371/journal.pone.0269137

lans: Foti, N. J., Hughes, J. M., and Rockmore, D. N. (2011). Nonparametric Sparsification of Complex Multiscale Networks. *PLOS One*, 6, e16431. doi:10.1371/journal.pone.0016431

Examples

```
#Simple star from Foti et al. (2011), Figure 2
net <- matrix(c(0,2,2,2,2,
               2,0,1,1,0,
               2,1,0,0,1,
               2,1,0,0,1,
               2,0,1,1,0),5,5)
net <- igraph::graph_from_adjacency_matrix(net, mode = "undirected", weighted = TRUE)
plot(net, edge.width = igraph::E(net)$weight^2)

bb <- lans(net, alpha = 0.05, narrative = TRUE) #The LANS backbone
plot(bb)
```

logit

Logit-based probabilities for SDSM

Description

logit estimates cell probabilities under the logit model

Usage

```
logit(M)
```

Arguments

M matrix

Details

Given a matrix **M**, the logit model returns a valued matrix **B** in which B_{ij} is the *approximate* probability that $M_{ij} = 1$ in the space of all binary matrices with the same row and column marginals as **M**.

The Bipartite Configuration Model (BiCM), which is available using [bicm](#) is faster and yields slightly more accurate probabilities (Neal et al., 2021). Therefore, it is the default used in [sds](#). However, the BiCM it requires the assumption that any cell in **M** can take a value of 0 or 1.

In contrast, the logit model allows constraints on specific cells. If **M** represents a bipartite graph, these constraints are equivalent to structural 0s (an edge that can never be present) and structural 1s (an edge that must always be present). To impose such constraints, **M** should be binary, except that structural 0s are represented with $M_{ij} = 10$, and structural 1s are represented with $M_{ij} = 11$.

Value

a matrix of probabilities

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

logit model: Neal, Z. P. (2014). The backbone of bipartite projections: Inferring relationships from co-authorship, co-sponsorship, co-attendance and other co-behaviors. *Social Networks*, 39, 84-97. doi:[10.1016/j.socnet.2014.06.001](https://doi.org/10.1016/j.socnet.2014.06.001)

logit model with constraints: Neal, Z. P. and Neal, J. W. (2024). Stochastic Degree Sequence Model with Edge Constraints (SDSM-EC) for Backbone Extraction. *Proceedings of the 12th International Conference on Complex Networks and their Applications*. Springer.

Examples

```
M <- matrix(c(0,0,1,0,1,0,1,0,1),3,3) #A binary matrix
logit(M)
M <- matrix(c(0,10,1,0,1,0,1,0,11),3,3) #A binary matrix with structural values
logit(M)
```

mlf

Extract backbone using the Marginal Likelihood Filter

Description

mlf extracts the backbone of a weighted network using the Marginal Likelihood Filter

Usage

```
mlf(
  W,
  alpha = 0.05,
  missing.as.zero = FALSE,
  signed = FALSE,
  mtc = "none",
  class = "original",
  narrative = FALSE
)
```

Arguments

<code>W</code>	An integer-weighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a three-column dataframe; (3) an igraph object.
<code>alpha</code>	real: significance level of hypothesis test(s)
<code>missing.as.zero</code>	boolean: should missing edges be treated as edges with zero weight and tested for significance
<code>signed</code>	boolean: TRUE for a signed backbone, FALSE for a binary backbone (see details)
<code>mtc</code>	string: type of Multiple Test Correction to be applied; can be any method allowed by p.adjust .
<code>class</code>	string: the class of the returned backbone graph, one of c("original", "matrix", "Matrix", "igraph", "edgelist"). If "original", the backbone graph returned is of the same class as <code>W</code> .
<code>narrative</code>	boolean: TRUE if suggested text & citations should be displayed.

Details

The `mlf` function applies the marginal likelihood filter (MLF; Dianati, 2016), which compares an edge's weight to its expected weight in a graph that preserves the total weight and preserves the degree sequence *on average*. The graph may be directed or undirected, however the edge weights must be positive integers.

When `signed = FALSE`, a one-tailed test (is the weight stronger?) is performed for each edge. The resulting backbone contains edges whose weights are significantly *stronger* than expected in the null model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker?) is performed for each edge. The resulting backbone contains positive edges for those whose weights are significantly *stronger*, and negative edges for those whose weights are significantly *weaker*, than expected in the null model.

If `W` is an unweighted bipartite graph, then the MLF is applied to its weighted bipartite projection.

Value

If `alpha != NULL`: Binary or signed backbone graph of class `class`.

If `alpha == NULL`: An S3 backbone object containing (1) the weighted graph as a matrix, (2) upper-tail p-values as a matrix, (3, if `signed = TRUE`) lower-tail p-values as a matrix, (4, if present) node attributes as a dataframe, and (5) several properties of the original graph and backbone model, from which a backbone can subsequently be extracted using `backbone.extract()`.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

mlf: Dianati, N. (2016). Unwinding the hairball graph: Pruning algorithms for weighted complex networks. *Physical Review E*, 93, 012304. doi:[10.1103/PhysRevE.93.012304](https://doi.org/10.1103/PhysRevE.93.012304)

Examples

```
#A network with heterogeneous weights
net <- matrix(c(0,10,10,10,10,75,0,0,0,0,
               10,0,1,1,1,0,0,0,0,0,
               10,1,0,1,1,0,0,0,0,0,
               10,1,1,0,1,0,0,0,0,0,
               10,1,1,1,0,0,0,0,0,0,
               75,0,0,0,0,0,100,100,100,100,
               0,0,0,0,0,100,0,10,10,10,
               0,0,0,0,0,100,10,0,10,10,
               0,0,0,0,0,100,10,10,0,10,
               0,0,0,0,0,100,10,10,10,0),10)

net <- igraph::graph_from_adjacency_matrix(net, mode = "undirected", weighted = TRUE)
plot(net, edge.width = sqrt(igraph::E(net)$weight)) #A stronger clique & a weaker clique

strong <- igraph::delete_edges(net, which(igraph::E(net)$weight < mean(igraph::E(net)$weight)))
plot(strong) #A backbone of stronger-than-average edges ignores the weaker clique

bb <- mlf(net, alpha = 0.05, narrative = TRUE) #An MLF backbone...
plot(bb) #...preserves edges at multiple scales
```

osdsm	<i>Extract backbone using the Ordinal Stochastic Degree Sequence Model</i>
-------	--

Description

osdsm extracts the backbone of a bipartite projection using the Ordinal Stochastic Degree Sequence Model.

Usage

```
osdsm(
  B,
  alpha = 0.05,
```

```

    trials = NULL,
    missing.as.zero = FALSE,
    signed = FALSE,
    mtc = "none",
    class = "original",
    narrative = FALSE,
    progress = TRUE,
    ...
)

```

Arguments

B	An ordinally weighted bipartite graph, as: (1) an incidence matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a three-column dataframe; (3) an igraph object.
alpha	real: significance level of hypothesis test(s)
trials	integer: the number of bipartite graphs generated to approximate the edge weight distribution. If NULL, the number of trials is selected based on alpha (see details)
missing.as.zero	boolean: should missing edges be treated as edges with zero weight and tested for significance
signed	boolean: TRUE for a signed backbone, FALSE for a binary backbone (see details)
mtc	string: type of Multiple Test Correction to be applied; can be any method allowed by p.adjust .
class	string: the class of the returned backbone graph, one of c("original", "matrix", "Matrix", "igraph", "edgelist"). If "original", the backbone graph returned is of the same class as B.
narrative	boolean: TRUE if suggested text & citations should be displayed.
progress	boolean: TRUE if the progress of Monte Carlo trials should be displayed.
...	optional arguments

Details

The `osdsm` function compares an edge's observed weight in the projection $B \times t(B)$ to the distribution of weights expected in a projection obtained from a random bipartite network where both the rows and the columns contain approximately the same number of each value. The edges in B must be integers, and are assumed to represent an ordinal-level measure such as a Likert scale that starts at 0.

When `signed = FALSE`, a one-tailed test (is the weight stronger?) is performed for each edge. The resulting backbone contains edges whose weights are significantly *stronger* than expected in the null model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker?) is performed for each edge. The resulting backbone contains positive edges for those whose weights are significantly *stronger*, and negative edges for those whose weights are significantly *weaker*, than expected in the null model.

The p-values used to evaluate the statistical significance of each edge are computed using Monte Carlo methods. The number of `trials` performed affects the precision of these p-values. This precision impacts the confidence that a given edge's p-value is less than the desired alpha level, and therefore represents a statistically significant edge that should be retained in the backbone. When `trials = NULL`, `trials.needed()` is used to estimate the required number of trials to evaluate the statistical significance of an edges' p-values.

Value

If `alpha != NULL`: Binary or signed backbone graph of class `class`.

If `alpha == NULL`: An S3 backbone object containing (1) the weighted graph as a matrix, (2) upper-tail p-values as a matrix, (3, if `signed = TRUE`) lower-tail p-values as a matrix, (4, if present) node attributes as a dataframe, and (5) several properties of the original graph and backbone model, from which a backbone can subsequently be extracted using `backbone.extract()`.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

osdsm: Neal, Z. P. (2017). Well connected compared to what? Rethinking frames of reference in world city network research. *Environment and Planning A*, 49, 2859-2877. doi:[10.1177/0308518X16631339](https://doi.org/10.1177/0308518X16631339)

Examples

```
#A weighted binary bipartite network of 20 agents & 50 artifacts; agents form two communities
B <- rbind(cbind(matrix(sample(0:3, 250, replace = TRUE, prob = ((1:4)^2)),10),
  matrix(sample(0:3, 250, replace = TRUE, prob = ((4:1)^2)),10)),
  cbind(matrix(sample(0:3, 250, replace = TRUE, prob = ((4:1)^2)),10),
  matrix(sample(0:3, 250, replace = TRUE, prob = ((1:4)^2)),10)))

P <- B%*%t(B) #An ordinary weighted projection...
plot(igraph::graph_from_adjacency_matrix(P, mode = "undirected",
  weighted = TRUE, diag = FALSE)) #...is a dense hairball

bb <- osdsm(B, alpha = 0.05, narrative = TRUE, #An oSDSM backbone...
  class = "igraph", trials = 100)
plot(bb) #...is sparse with clear communities
```

pb

Poisson binomial distribution function

Description

pb computes the poisson binomial distribution function using the refined normal approximation.

Usage

```
pb(k, p, lowertail = TRUE)
```

Arguments

k	numeric: value where the pdf should be evaluated
p	vector: vector of success probabilities
lowertail	boolean: If TRUE return both upper & lower tail probabilities, if FALSE return only upper tail probability

Details

The Refined Normal Approximation (RNA) offers a close approximation when `length(p)` is large (Hong, 2013).

Value

vector, length 2: The first value (if `lower = TRUE`) is the lower tail probability, the probability of observing `k` or fewer successes when each trial has probability `p` of success. The second value is the upper tail probability, the probability of observing `k` or more successes when each trial has probability `p` of success.

References

Hong, Y. (2013). On computing the distribution function for the Poisson binomial distribution. *Computational Statistics and Data Analysis*, 59, 41-51. doi:10.1016/j.csda.2012.10.006

Examples

```
pb(50,runif(100))
```

sdsm

Extract backbone using the Stochastic Degree Sequence Model

Description

sdsm extracts the backbone of a bipartite projection using the Stochastic Degree Sequence Model.

Usage

```
sdsm(
  B,
  alpha = 0.05,
  missing.as.zero = FALSE,
  signed = FALSE,
  mtc = "none",
  class = "original",
  narrative = FALSE,
  ...
)
```

Arguments

B	An unweighted bipartite graph, as: (1) an incidence matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
alpha	real: significance level of hypothesis test(s)
missing.as.zero	boolean: should missing edges be treated as edges with zero weight and tested for significance
signed	boolean: TRUE for a signed backbone, FALSE for a binary backbone (see details)
mtc	string: type of Multiple Test Correction to be applied; can be any method allowed by p.adjust .
class	string: the class of the returned backbone graph, one of c("original", "matrix", "Matrix", "igraph", "edgelist"). If "original", the backbone graph returned is of the same class as B.
narrative	boolean: TRUE if suggested text & citations should be displayed.
...	optional arguments

Details

The `sdsbm` function compares an edge's observed weight in the projection $B \times t(B)$ to the distribution of weights expected in a projection obtained from a random bipartite network where both the row vertex degrees and column vertex degrees are *approximately* fixed at their values in B.

When `signed = FALSE`, a one-tailed test (is the weight stronger?) is performed for each edge. The resulting backbone contains edges whose weights are significantly *stronger* than expected in the null model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker?) is performed for each edge. The resulting backbone contains positive edges for those whose weights are significantly *stronger*, and negative edges for those whose weights are significantly *weaker*, than expected in the null model.

The bipartite network B may contain some edges that are *required* in the null model (i.e., structural 1s); these edges should have a weight of 11 (i.e., $B_{ik} = 11$). This network may also contain some edges that are *prohibited* in the null model (i.e., structural 0s); these edges should have a weight of 10 (i.e., $B_{ik} = 10$). When B contains required or prohibited edges, cellwise probabilities are computed using [logit](#) following Neal et al. (2024). Otherwise, cellwise probabilities are computed using the faster and more accurate Bipartite Configuration Model with [bicm](#) (Neal et al. 2021).

Value

If `alpha != NULL`: Binary or signed backbone graph of class `class`.

If `alpha == NULL`: An S3 backbone object containing (1) the weighted graph as a matrix, (2) upper-tail p-values as a matrix, (3, if `signed = TRUE`) lower-tail p-values as a matrix, (4, if present) node attributes as a dataframe, and (5) several properties of the original graph and backbone model, from which a backbone can subsequently be extracted using [backbone.extract\(\)](#).

References

- package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:10.1371/journal.pone.0269137
- sdsbm: Neal, Z. P. (2014). The backbone of bipartite projections: Inferring relationships from co-authorship, co-sponsorship, co-attendance, and other co-behaviors. *Social Networks*, 39, 84-97. doi:10.1016/j.socnet.2014.06.001
- bicm: Neal, Z. P., Domagalski, R., and Sagan, B. (2021). Comparing Alternatives to the Fixed Degree Sequence Model for Extracting the Backbone of Bipartite Projections. *Scientific Reports*, 11, 23929. doi:10.1038/s41598021032383
- logit: Neal, Z. P. and Neal, J. W. (2024). Stochastic Degree Sequence Model with Edge Constraints (SDSM-EC) for Backbone Extraction. *Proceedings of the 12th International Conference on Complex Networks and their Applications*. Springer.

Examples

```
#A binary bipartite network of 30 agents & 75 artifacts; agents form three communities
B <- rbind(cbind(matrix(rbinom(250,1,.8),10),
                    matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.2),10)),
           cbind(matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.8),10),
                    matrix(rbinom(250,1,.2),10)),
           cbind(matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.2),10),
                    matrix(rbinom(250,1,.8),10)))

P <- B*%t(B) #An ordinary weighted projection...
plot(igraph::graph_from_adjacency_matrix(P, mode = "undirected",
                                         weighted = TRUE, diag = FALSE)) #...is a dense hairball

bb <- sdsbm(B, alpha = 0.05, narrative = TRUE, class = "igraph") #An SDSM backbone...
plot(bb) #...is sparse with clear communities
```

sparsify

Extract the backbone from a network using a sparsification model

Description

A generic function to extract the backbone of an undirected, unipartite network using a sparsification model described by a combination of an edge scoring metric, a edge score normalization, and an edge score filter.

Usage

```
sparsify(
  U,
  s,
```

```

    escore,
    normalize,
    filter,
    symmetrize = TRUE,
    umst = FALSE,
    class = "original",
    narrative = FALSE
)

```

Arguments

U	An unweighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
s	numeric: Sparsification parameter
escore	string: Method for scoring edges' importance
normalize	string: Method for normalizing edge scores
filter	string: Type of filter to apply
symmetrize	boolean: TRUE if the result should be symmetrized
umst	boolean: TRUE if the backbone should include the union of minimum spanning trees, to ensure connectivity
class	string: the class of the returned backbone graph, one of c("original", "matrix", "Matrix", "igraph", "edgelist"). If "original", the backbone graph returned is of the same class as U.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Details

The escore parameter determines how an unweighted edge's importance is calculated. Unless noted below, scores are symmetric and larger values represent more important edges.

- random: a random number drawn from a uniform distribution
- betweenness: edge betweenness
- triangles: number of triangles that include the edge
- jaccard: jaccard similarity coefficient of the neighborhoods of an edge's endpoints, or alternatively, triangles normalized by the size of the union of the endpoints neighborhoods
- dice: dice similarity coefficient of the neighborhoods of an edge's endpoints
- quadrangles: number of quadrangles that include the edge
- quadrilateral embeddedness: geometric mean normalization of quadrangles
- degree: degree of neighbor to which an edge is adjacent (asymmetric)
- meetmin: triangles normalized by the smaller of the endpoints' neighborhoods' sizes
- geometric: triangles normalized by the product of the endpoints' neighborhoods' sizes
- hypergeometric: probability of the edge being included at least as many triangles if edges were random, given the size of the endpoints' neighborhoods (smaller is more important)

The `normalize` parameter determines whether edge scores are normalized.

- `none`: no normalization is performed
- `rank`: scores are normalized by neighborhood rank, such that the strongest edge in a node's neighborhood is ranked 1 (asymmetric)
- `embeddedness`: scores are normalized using the maximum Jaccard coefficient of the top k -ranked neighbors of each endpoint, for all k

The `filter` parameter determines how edges are filtered based on their (normalized) edge scores.

- `threshold`: Edges with scores $\geq s$ are retained in the backbone
- `proportion`: Specifies the approximate proportion of edges to retain in the backbone
- `degree`: Retains each node's d 's most important edges, where d is the node's degree (requires that `normalize = "rank"`)
- `disparity`: Applies the disparity filter using `disparity()`

Using `escore == "degree"` or `normalize == "rank"` can yield an asymmetric network. When `symmetrize == TRUE` (default), after applying a filter, the network is symmetrized by such that $i \rightarrow j$ if $i \rightarrow j$ or $i \leftarrow j$.

Specific combinations of `escore`, `normalize`, `filter`, and `umst` correspond to specific sparsification models in the literature, and are available via the following wrapper functions: `sparsify.with.skeleton()`, `sparsify.with.gspar()`, `sparsify.with.lspar()`, `sparsify.with.simmelian()`, `sparsify.with.jaccard()`, `sparsify.with.meetmin()`, `sparsify.with.geometric()`, `sparsify.with.hypergeometric()`, `sparsify.with.localdegree()`, `sparsify.with.quadrilateral()`. See the documentation for these wrapper functions for more details and the associated citation.

Value

An unweighted, undirected, unipartite graph of class `class`.

References

Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:10.1371/journal.pone.0269137

Examples

```
U <- igraph::sample_sbm(60, matrix(c(.75,.25,.25,.25,.75,.25,.25,.25,.75),3,3), c(20,20,20))
plot(U) #A hairball
sparse <- sparsify(U, s = 0.6, escore = "jaccard", normalize = "rank",
  filter = "degree", narrative = TRUE)
plot(sparse) #Clearly visible communities
```

sparsify.with.geometric

Extract Goldberg and Roth's (2003) Geometric backbone

Description

sparsify.with.geometric is a wrapper for `sparsify()` that extracts the geometric backbone described by Goldberg and Roth (2003). It is equivalent to `sparsify(escape = "geometric", normalize = "none", filter = "threshold", umst = FALSE)`.

Usage

```
sparsify.with.geometric(U, s, class = "original", narrative = FALSE)
```

Arguments

U	An unweighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
s	numeric: Sparsification threshold, $0 < s < 1$; larger values yield sparser graphs
class	string: the class of the returned backbone graph, one of <code>c("original", "matrix", "Matrix", "igraph", "edgelist")</code> . If "original", the backbone graph returned is of the same class as U.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Value

An unweighted, undirected, unipartite graph of class class.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

model: Goldberg, D. S., & Roth, F. P. (2003). Assessing experimentally derived interactions in a small world. *Proceedings of the National Academy of Sciences*, 100, 4372-4376. doi:[10.1073/pnas.0735871100](https://doi.org/10.1073/pnas.0735871100)

Examples

```
U <- igraph::sample_sbm(60, matrix(c(.75,.25,.25,.25,.75,.25,.25,.25,.75),3,3), c(20,20,20))
plot(U) #A hairball
sparse <- sparsify.with.geometric(U, s = 0.25, narrative = TRUE)
plot(sparse) #Clearly visible communities
```

sparsify.with.gspar *Extract Satuluri et al's (2011) G-spar backbone*

Description

sparsify.with.gspar is a wrapper for `sparsify()` that extracts the G-spar backbone described by Satuluri et al. (2011). It is equivalent to `sparsify(escore = "jaccard", normalize = "none", filter = "proportion", umst = FALSE)`.

Usage

```
sparsify.with.gspar(U, s, class = "original", narrative = FALSE)
```

Arguments

U	An unweighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
s	numeric: Proportion of edges to retain, $0 < s < 1$; smaller values yield sparser graphs
class	string: the class of the returned backbone graph, one of <code>c("original", "matrix", "Matrix", "igraph", "edgelist")</code> . If "original", the backbone graph returned is of the same class as U.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Value

An unweighted, undirected, unipartite graph of class class.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

model: Satuluri, V., Parthasarathy, S., & Ruan, Y. (2011, June). Local graph sparsification for scalable clustering. In *Proceedings of the 2011 ACM SIGMOD International Conference on Management of data* (pp. 721-732). doi:[10.1145/1989323.1989399](https://doi.org/10.1145/1989323.1989399)

Examples

```
U <- igraph::sample_sbm(60, matrix(c(.75,.25,.25,.25,.75,.25,.25,.25,.75),3,3), c(20,20,20))
plot(U) #A hairball
sparse <- sparsify.with.gspar(U, s = 0.4, narrative = TRUE)
plot(sparse) #Clearly visible communities
```

sparsify.with.hypergeometric

Extract Goldberg and Roth's (2003) Hypergeometric backbone

Description

sparsify.with.hypergeometric is a wrapper for `sparsify()` that extracts the hypergeometric backbone described by Goldberg and Roth (2003). It is equivalent to `sparsify(escape = "hypergeometric", normalize = "none", filter = "threshold", umst = FALSE)`.

Usage

```
sparsify.with.hypergeometric(U, s, class = "original", narrative = FALSE)
```

Arguments

U	An unweighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
s	numeric: Sparsification threshold, $0 < s < 1$; smaller values yield sparser graphs
class	string: the class of the returned backbone graph, one of <code>c("original", "matrix", "Matrix", "igraph", "edgelist")</code> . If "original", the backbone graph returned is of the same class as U.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Value

An unweighted, undirected, unipartite graph of class class.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:10.1371/journal.pone.0269137

model: Goldberg, D. S., & Roth, F. P. (2003). Assessing experimentally derived interactions in a small world. *Proceedings of the National Academy of Sciences*, 100, 4372-4376. doi:10.1073/pnas.0735871100

Examples

```
U <- igraph::sample_sbm(60, matrix(c(.75,.25,.25,.25,.75,.25,.25,.25,.75),3,3), c(20,20,20))
plot(U) #A hairball
sparse <- sparsify.with.hypergeometric(U, s = 0.3, narrative = TRUE)
plot(sparse) #Clearly visible communities
```

sparsify.with.jaccard *Extract Goldberg and Roth's (2003) Jaccard backbone*

Description

sparsify.with.jaccard is a wrapper for `sparsify()` that extracts the jaccard backbone described by Goldberg and Roth (2003). It is equivalent to `sparsify(escore = "jaccard", normalize = "none", filter = "threshold", umst = FALSE)`.

Usage

```
sparsify.with.jaccard(U, s, class = "original", narrative = FALSE)
```

Arguments

U	An unweighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
s	numeric: Sparsification threshold, $0 < s < 1$; larger values yield sparser graphs
class	string: the class of the returned backbone graph, one of <code>c("original", "matrix", "Matrix", "igraph", "edgelist")</code> . If "original", the backbone graph returned is of the same class as U.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Value

An unweighted, undirected, unipartite graph of class class.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

model: Goldberg, D. S., & Roth, F. P. (2003). Assessing experimentally derived interactions in a small world. *Proceedings of the National Academy of Sciences*, 100, 4372-4376. doi:[10.1073/pnas.0735871100](https://doi.org/10.1073/pnas.0735871100)

Examples

```
U <- igraph::sample_sbm(60, matrix(c(.75,.25,.25,.25,.75,.25,.25,.25,.75),3,3), c(20,20,20))
plot(U) #A hairball
sparse <- sparsify.with.jaccard(U, s = 0.3, narrative = TRUE)
plot(sparse) #Clearly visible communities
```

sparsify.with.localdegree

Extract Hamann et al.'s (2016) Local Degree backbone

Description

sparsify.with.localdegree is a wrapper for `sparsify()` that extracts the local degree backbone described by Hamann et al. (2016). It is equivalent to `sparsify(escore = "degree", normalize = "rank", filter = "degree", umst = FALSE)`.

Usage

```
sparsify.with.localdegree(U, s, class = "original", narrative = FALSE)
```

Arguments

U	An unweighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
s	numeric: Sparsification exponent, $0 < s < 1$; smaller values yield sparser graphs
class	string: the class of the returned backbone graph, one of <code>c("original", "matrix", "Matrix", "igraph", "edgelist")</code> . If "original", the backbone graph returned is of the same class as U.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Value

An unweighted, undirected, unipartite graph of class class.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. [doi:10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

model: Hamann, M., Lindner, G., Meyerhenke, H., Staudt, C. L., & Wagner, D. (2016). Structure-preserving sparsification methods for social networks. *Social Network Analysis and Mining*, 6, 22. [doi:10.1007/s1327801603322](https://doi.org/10.1007/s1327801603322)

Examples

```
U <- igraph::as.undirected(igraph::sample_pa(60, m = 3), mode = "collapse")
plot(U) #A hairball
sparse <- sparsify.with.localdegree(U, s = 0.3, narrative = TRUE)
plot(sparse) #Clearly visible hubs
```

sparsify.with.lspar *Extract Satuluri et al's (2011) L-spar backbone*

Description

sparsify.with.lspar is a wrapper for [sparsify\(\)](#) that extracts the L-spar backbone described by Satuluri et al. (2011). It is equivalent to `sparsify(escore = "jaccard", normalize = "rank", filter = "degree", umst = FALSE)`.

Usage

```
sparsify.with.lspar(U, s, class = "original", narrative = FALSE)
```

Arguments

U	An unweighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
s	numeric: Sparsification exponent, $0 < s < 1$; smaller values yield sparser graphs
class	string: the class of the returned backbone graph, one of <code>c("original", "matrix", "Matrix", "igraph", "edgelist")</code> . If "original", the backbone graph returned is of the same class as U.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Value

An unweighted, undirected, unipartite graph of class class.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](#)

model: Satuluri, V., Parthasarathy, S., & Ruan, Y. (2011, June). Local graph sparsification for scalable clustering. In Proceedings of the 2011 ACM SIGMOD International Conference on Management of data (pp. 721-732). doi:[10.1145/1989323.1989399](#)

Examples

```
U <- igraph::sample_sbm(60, matrix(c(.75,.25,.25,.25,.75,.25,.25,.25,.75),3,3), c(20,20,20))
plot(U) #A hairball
sparse <- sparsify.with.lspar(U, s = 0.6, narrative = TRUE)
plot(sparse) #Clearly visible communities
```

sparsify.with.meetmin *Extract Goldberg and Roth's (2003) MeetMin backbone*

Description

sparsify.with.meetmin is a wrapper for `sparsify()` that extracts the meetmin backbone described by Goldberg and Roth (2003). It is equivalent to `sparsify(escore = "meetmin", normalize = "none", filter = "threshold", umst = FALSE)`.

Usage

```
sparsify.with.meetmin(U, s, class = "original", narrative = FALSE)
```

Arguments

U	An unweighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
s	numeric: Sparsification threshold, $0 < s < 1$; larger values yield sparser graphs
class	string: the class of the returned backbone graph, one of <code>c("original", "matrix", "Matrix", "igraph", "edgelist")</code> . If "original", the backbone graph returned is of the same class as U.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Value

An unweighted, undirected, unipartite graph of class class.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

model: Goldberg, D. S., & Roth, F. P. (2003). Assessing experimentally derived interactions in a small world. *Proceedings of the National Academy of Sciences*, 100, 4372-4376. doi:[10.1073/pnas.0735871100](https://doi.org/10.1073/pnas.0735871100)

Examples

```
U <- igraph::sample_sbm(60, matrix(c(.75,.25,.25,.25,.75,.25,.25,.25,.75),3,3), c(20,20,20))
plot(U) #A hairball
sparse <- sparsify.with.meetmin(U, s = 0.5, narrative = TRUE)
plot(sparse) #Clearly visible communities
```

sparsify.with.quadrilateral

Extract Nocaj et al.'s (2015) Quadrilateral Simmelian backbone

Description

sparsify.with.quadrilateral is a wrapper for `sparsify()` that extracts the quadrilateral Simmelian backbone described by Nocaj et al. (2015). It is equivalent to `sparsify(escape = "quadrilateral embeddedness", normalize = "embeddedness", filter = "threshold", umst = TRUE)`.

Usage

```
sparsify.with.quadrilateral(U, s, class = "original", narrative = FALSE)
```

Arguments

U	An unweighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
s	numeric: Sparsification exponent, $0 < s < 1$; larger values yield sparser graphs
class	string: the class of the returned backbone graph, one of <code>c("original", "matrix", "Matrix", "igraph", "edgelist")</code> . If "original", the backbone graph returned is of the same class as U.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Value

An unweighted, undirected, unipartite graph of class class.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

model: Nocaj, A., Ortmann, M., & Brandes, U. (2015). Untangling the hairballs of multi-centered, small-world online social media networks. *Journal of Graph Algorithms and Applications*, 19, 595-618. doi:[10.7155/jgaa.00370](https://doi.org/10.7155/jgaa.00370)

Examples

```
U <- igraph::sample_sbm(60, matrix(c(.75,.25,.25,.25,.75,.25,.25,.25,.75),3,3), c(20,20,20))
plot(U) #A hairball
sparse <- sparsify.with.quadrilateral(U, s = 0.5, narrative = TRUE)
plot(sparse) #Clearly visible communities in a connected graph
```

sparsify.with.simmelian

Extract Nick et al's (2013) Simmelian backbone

Description

sparsify.with.simmelian is a wrapper for `sparsify()` that extracts the simmelian backbone described by Nick et al. (2013). It is equivalent to `sparsify(escore = "triangles", normalize = "embeddedness", filter = "threshold", umst = FALSE)`.

Usage

```
sparsify.with.simmelian(U, s, class = "original", narrative = FALSE)
```

Arguments

U	An unweighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
s	numeric: Sparsification threshold, $0 < s < 1$; larger values yield sparser graphs
class	string: the class of the returned backbone graph, one of <code>c("original", "matrix", "Matrix", "igraph", "edgelist")</code> . If "original", the backbone graph returned is of the same class as U.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Value

An unweighted, undirected, unipartite graph of class `class`.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](https://doi.org/10.1371/journal.pone.0269137)

model: Nick, B., Lee, C., Cunningham, P., & Brandes, U. (2013, August). Simmelian backbones: Amplifying hidden homophily in facebook networks. In Proceedings of the 2013 IEEE/ACM international conference on advances in social networks analysis and mining (pp. 525-532). doi:[10.1145/2492517.2492569](https://doi.org/10.1145/2492517.2492569)

Examples

```
U <- igraph::sample_sbm(60, matrix(c(.75,.25,.25,.25,.75,.25,.25,.25,.75),3,3), c(20,20,20))
plot(U) #A hairball
sparse <- sparsify.with.simmelian(U, s = 0.5, narrative = TRUE)
plot(sparse) #Clearly visible communities
```

sparsify.with.skeleton

Extract Karger's (1999) skeleton backbone

Description

sparsify.with.skeleton is a wrapper for [sparsify\(\)](#) that extracts the skeleton backbone described by Karger (1999), which preserves a specified proportion of random edges. It is equivalent to `sparsify(escape = "random", normalize = "none", filter = "proportion", umst = FALSE)`.

Usage

```
sparsify.with.skeleton(U, s, class = "original", narrative = FALSE)
```

Arguments

U	An unweighted unipartite graph, as: (1) an adjacency matrix in the form of a matrix or sparse Matrix ; (2) an edgelist in the form of a two-column dataframe; (3) an igraph object.
s	numeric: Proportion of edges to retain, $0 < s < 1$; smaller values yield sparser graphs
class	string: the class of the returned backbone graph, one of <code>c("original", "matrix", "Matrix", "igraph", "edgelist")</code> . If "original", the backbone graph returned is of the same class as U.
narrative	boolean: TRUE if suggested text & citations should be displayed.

Value

An unweighted, undirected, unipartite graph of class class.

References

package: Neal, Z. P. (2022). backbone: An R Package to Extract Network Backbones. *PLOS ONE*, 17, e0269137. doi:[10.1371/journal.pone.0269137](#)

model: Karger, D. R. (1999). Random sampling in cut, flow, and network design problems. *Mathematics of Operations Research*, 24, 383-413. doi:[10.1287/moor.24.2.383](#)

Examples

```
U <- igraph::erdos.renyi.game(60, .5)
plot(U) #A dense graph
sparse <- sparsify.with.skeleton(U, s = 0.25, narrative = TRUE)
plot(sparse) #A sparser graph
```


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