Package 'backbone'

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Type Package

Title Extracts the Backbone from Graphs

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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>).

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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()`, `sdsm()`, and `fdsm()`.
- For non-projection weighted networks: `global()`, `disparity()`.
- 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

References

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

`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 with a non-zero weight. It yields a backbone that perserves edges whose weights are significantly *stronger* than expected in the chosen null model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker) is performed for each every pair of nodes. It yields a backbone that contains positive edges for edges whose weights are significantly *stronger*, and negative edges for edges whose weights are significantly *weaker*, than expected in the chosen null model. *NOTE: Before v2.0.0, all significance tests were two-tailed and zero-weight edges were evaluated.*

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 *Suggest a backbone model*

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 <= s <= 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 sparisfication 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

Examples

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

---

bicm *Bipartite Configuration Model*

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 Bij is the *approximate* probability that Mij = 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 sdsm() 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 Ri and the *j*th column's fitness Rj, the entry Bij in the probability matrix can be computed as Ri x Rj/(1+(Ri x Rj)).

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,
  signed = FALSE,
  mtc = "none",
  class = "original",
  narrative = FALSE
)
```

Arguments

W	A 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)
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 with a non-zero weight. It yields a backbone that perserves edges whose weights are significantly *stronger* than expected in the chosen null model. When signed = TRUE, a two-tailed test (is the weight stronger or weaker) is performed for each every pair of nodes. It yields a backbone that contains positive edges for edges whose weights are significantly *stronger*, and negative edges for edges whose weights are significantly *weaker*, than expected in the chosen null model. *NOTE: Before v2.0.0, all significance tests were two-tailed and zero-weight edges were evaluated.*

If W is an unweighted bipartite graph, any rows and columns that contain only zeros or only ones are removed, then the global threshold 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(0,10,10,10,10,75,0,0,0,0,
                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 <- 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

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,
  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)
`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*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 give row and column vertex degrees.

When signed = FALSE, a one-tailed test (is the weight stronger) is performed for each edge with a non-zero weight. It yields a backbone that perserves edges whose weights are significantly *stronger* than expected in the chosen null model. When signed = TRUE, a two-tailed test (is the weight stronger or weaker) is performed for each every pair of nodes. It yields a backbone that contains positive edges for edges whose weights are significantly *stronger*, and negative edges for edges whose weights are significantly *weaker*, than expected in the chosen null model. *NOTE: Before v2.0.0, all significance tests were two-tailed and zero-weight edges were evaluated.*

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, and the confidence that a given p-value is less than the desired alpha level. Because these p-values are proportions (i.e., the proportion of times an edge is weaker/stronger in the projection of a random bipartite graphs), evaluating the statistical significance of an edge is equivalent to comparing a proportion (the p-value) to a known proportion (alpha). When trials = NULL, the power.prop.test function is used to estimate the required number of trials to make such a comparison with a alpha type-I error rate, (1-alpha) power, and when the riskiest p-value being evaluated is at least 5% smaller than alpha. When any mtc correction is applied, for simplicity this estimation is based on a conservative Bonferroni correction.

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,.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,
  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)
`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 with a non-zero weight. It yields a backbone that perserves edges whose weights are significantly *stronger* than expected under the null model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker) is performed for each every pair of nodes. It yields a backbone that contains positive edges for edges whose weights are significantly *stronger*, and negative edges for edges whose weights are significantly *weaker*, than expected in the chosen null model. *NOTE: Before v2.0.0, all significance tests were two-tailed and zero-weight edges were evaluated.*

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,
  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)
`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 with a non-zero weight. It yields a backbone that perserves edges whose weights are significantly *stronger* than expected under the null model. When `signed = TRUE`, a two-tailed test (is the weight stronger or weaker) is performed for each every pair of nodes. It yields a backbone that contains positive edges for edges whose weights are significantly *stronger*, and negative edges for edges whose weights are significantly *weaker*, than expected in the chosen null model. *NOTE: Before v2.0.0, all significance tests were two-tailed and zero-weight edges were evaluated.*

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,
  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)
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 with a non-zero weight. It yields a backbone that perserves edges whose weights are significantly *stronger* than expected under the null model. When signed = TRUE, a two-tailed test (is the weight stronger or weaker) is performed for each every pair of nodes. It yields a backbone that contains positive edges for edges whose weights are significantly *stronger*, and negative edges for edges whose weights are significantly *weaker*, than expected in the chosen null model. *NOTE: Before v2.0.0, all significance tests were two-tailed and zero-weight edges were evaluated.*

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(
  W,
  upper = 0,
  lower = NULL,
```

```
  keepzeros = TRUE,
  class = "original",
  narrative = FALSE
)
```

Arguments

W	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 in the backbone if its weight exceeds upper. If a lower threshold is also specified, it returns a signed backbone in which edge weights are set to 1 if above the given upper threshold, set to -1 if below the given lower threshold, and set to 0 otherwise.

If W is an unweighted bipartite graph, any rows and columns that contain only zeros or only ones are removed, then 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

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

Examples

```
W <- matrix(sample(0:5, 100, replace = TRUE), 10) #Random weighted graph
diag(W) <- 0
W
global(W, narrative = TRUE)  #Keep all non-zero edges
global(W, upper = 4, lower = 2, narrative = TRUE)  #Signed with specified thresholds
```

```
global(W, upper = function(x)mean(x),  #Above-average --> positive edges
         lower = function(x)mean(x), narrative = TRUE)  #Below-average --> negative edges
```

`osdsm` *Extract backbone using the Ordinal Stochastic Degree Sequence Model*

Description

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

Usage

```
osdsm(
  B,
  alpha = 0.05,
  trials = NULL,
  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)
`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.

Details

The osdsm 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 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 with a non-zero weight. It yields a backbone that perserves edges whose weights are significantly *stronger* than expected in the chosen null model. When signed = TRUE, a two-tailed test (is the weight stronger or weaker) is performed for each every pair of nodes. It yields a backbone that contains positive edges for edges whose weights are significantly *stronger*, and negative edges for edges whose weights are significantly *weaker*, than expected in the chosen null model. *NOTE: Before v2.0.0, all significance tests were two-tailed and zero-weight edges were evaluated.*

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, and the confidence that a given p-value is less than the desired alpha level. Because these p-values are proportions (i.e., the proportion of times an edge is weaker/stronger in the projection of a random bipartite graphs), evaluating the statistical significance of an edge is equivalent to comparing a proportion (the p-value) to a known proportion (alpha). When trials = NULL, the power.prop.test function is used to estimate the required number of trials to make such a comparison with a alpha type-I error rate, (1-alpha) power, and when the riskiest p-value being evaluated is at least 5% smaller than alpha. When any mtc correction is applied, for simplicity this estimation is based on a conservative Bonferroni correction.

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

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

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,
  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)
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 sdsm 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 network where both the row vertex degrees and column vertex degrees are *approximately* fixed at their values in B. It uses the Bipartite Configuration Model bicm to compute probabilities for the Poisson binomial distribution.

When signed = FALSE, a one-tailed test (is the weight stronger) is performed for each edge with a non-zero weight. It yields a backbone that perserves edges whose weights are significantly *stronger* than expected in the chosen null model. When signed = TRUE, a two-tailed test (is the weight stronger or weaker) is performed for each every pair of nodes. It yields a backbone that contains

positive edges for edges whose weights are significantly *stronger*, and negative edges for edges whose weights are significantly *weaker*, than expected in the chosen null model. *NOTE: Before v2.0.0, all significance tests were two-tailed and zero-weight edges were evaluated.*

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

sdsm: 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

sdsm: 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 <- sdsm(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 = "original",
  normalize,
  filter,
  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
`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. There are 10 options for assigning an edge's score; when `escore =`

- `random`: a random number drawn from a uniform distribution

- `betweenness`: edge betweenness
- `triangles`: number of triangles that include the edge
- `jaccard`: jaccard coefficient of the neighborhoods of an edge's endpoints, or alternatively, triangles normalized by the size of the union of the endpoints neighborhoods
- `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. There are three options; when `normalize =`

- `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. There are three options; when `filter =`

- `threshold`: Edges with scores more important than `s` are retained in the backbone
- `proportion`: Specifies the proportion of most important 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"`)

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::sbm.game(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(escore = "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: Sparsificiation threshold, $0 < s < 1$; larger values yield sparser graphs
`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.

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::sbm.game(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 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.

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::sbm.game(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(escore = "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: Sparsificiation threshold, $0 < s < 1$; smaller values yield sparser graphs
`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.

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::sbm.game(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: Sparsificiation threshold, $0 < s < 1$; larger values yield sparser graphs
`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.

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::sbm.game(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 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.

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: 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

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 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.

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::sbm.game(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: Sparsificiation threshold, 0 < s < 1; larger values yield sparser graphs
`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.

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::sbm.game(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(escore = "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 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.

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: 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

Examples

```
U <- igraph::sbm.game(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: Sparsificiation threshold, 0 < s < 1; larger values yield sparser graphs
`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.

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: 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

Examples

```
U <- igraph::sbm.game(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(escore = "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 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.

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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