Package ‘HyperG’

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Description

Implements various tools for storing and analyzing hypergraphs. Handles basic undirected, unweighted hypergraphs, and various ways of creating hypergraphs from a number of representations, and converting between graphs and hypergraphs.

Details

A hypergraph is implemented as a list containing (for now) a single element, \( M \), corresponding to the incidence matrix. It is an S3 object with class hypergraph and a plot method, summary and print methods. The package uses a sparse representation (from the Matrix package), so in principle it should allow for very large hypergraphs, although to date only relatively small hypergraphs have been investigated.

Index of help topics:

- `H2`: Two sections of a hypergraph.
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- `hypergraph.entropy`: Hypergraph Entropy
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- `hypergraph.union`: Unions and intersections of hypergraphs.
- `hypergraph_as_adjacency_matrix`: Adjacency Matrix of a Hypergraph.
- `hypergraph_as_edgelist`:
Introduction

A graph is a set of vertices, V, and a set of edges, E, each of which contains two vertices (or a single vertex, if self-loops are allowed). A hypergraph is a generalization of this, in which more than two vertices can be in a single hyper-edge. Multi-graphs are graphs in which E is not a set, but rather allows for duplicate edges. Hypergraphs are allowed to have duplicate hyper-edges.
This package is a simple implementation of hypergraphs built around the incidence matrix – a binary matrix in which the rows correspond to the hyper-edges, the columns to vertices, and a 1 in position (i,j) indicates that the vertex j is in the ith hyper-edge. There is currently no support for directed or weighted hypergraphs.

Various methods of manipulating hypergraphs, such as adding and removing edges and vertices are implemented, and for small hypergraphs the igraph package plot routine is used to plot the hypergraph and its hyper-edges. For hypergraphs with more than a few dozen vertices, it is recommended that the plot function be called with mark.groups=NULL. See igraph.plotting for more information.

There are utilities in this package for removing loops, duplicate hyper-edges, empty hyper-edges, and isolated vertices (ones that are not contained in any hyper-edge). Also, there is a function, reduce.hypergraph, which reduces the hypergraph down to its largest hyper-edges – that is, it removes hyper-edges that are subsets of other hyper-edges. It also has other ways to reduce the hypergraph, see the corresponding manual page.

There are also utilities for extracting information from the hypergraph. For example, simple statistics such as the number of vertices, hyper-edges, degrees of vertices, number of nodes per hyper-edge. Also global properties such as whether it is connected, if it has the Helly property or is conformal (see the manual pages for has.helly and is.conformal for more information on these topics).

Note

Some effort has been taken to avoid masking or redefining functions from the igraph package. While this results in awkward function names (“hypergraph” nearly everywhere) it does reduce the chances of hard-to-diagnose errors. I am considering adding aliases that replace “hypergraph” with “hg” or some such, but I’m not sure this is helpful. The two functions that are masked, is.simple and line.graph, first check whether their argument is an igraph graph, and if so calls the corresponding igraph function.

Author(s)

David J. Marchette
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References


See Also

igraph.
Examples

```r
h <- hypergraph_from_edgelist(list(1:2, 2:5, 3:7, c(1, 3, 5, 7, 9)))
hsize(h)
## 4
horder(h)
## 9
```

---

**as.bipartite**  
*Hypergraph as a bipartite graph.*

---

### Description

Converts a hypergraph (or graph) into a bipartite graph.

### Usage

```r
as.bipartite(h)
```

### Arguments

- `h`: a hypergraph or a graph.

### Details

This converts a hypergraph or a graph into a bipartite graph, by taking the incidence matrix and treating this as the incidence matrix of a bipartite graph. It uses `graph_from_incidence_matrix` to perform the conversion.

### Value

an `igraph` bipartite graph.

### Note

This works on graphs, resulting in the bipartite graph with edges as one type and vertices as another. This might not be what you want, for example if you think the graph is already bipartite, this will not return the graph, but will rather create a new bipartite graph from the vertices and edges.

### Author(s)

David J. Marchette <dmarchette@gmail.com>.

### See Also

- `graph_from_incidence_matrix`. 
Examples

```r
h <- hypergraph_from_edgelist(list(letters[1:3],
                                  letters[c(2,4,7)],
                                  letters[5:8]))
g <- as.bipartite(h)
```

---

**Convert between hypergraphs and graphs.**

**Description**

Convert a hypergraph to a graph or a graph to a hypergraph.

**Usage**

- `as.graph(h)`
- `hypergraph2graph(h)`
- `as.hypergraph(x, n, ...)`
- `graph2hypergraph(g, method = c("incidence", "adjacency",
                                    "neighborhood", "ego", "spectral"), ...)`

**Arguments**

- `h`: a hypergraph.
- `g`: a graph.
- `method`: see Details.
- `x`: a matrix, list or graph. See details.
- `n`: number of vertices if `x` is missing.
- `...`: arguments passed to various functions. See Details.

**Details**

For `as.graph` and `hypergraph2graph`, create a graph from the incidence matrix using the product of the transpose of the incidence matrix with the incidence matrix. `as.graph` is an alias of `hypergraph2graph`. This computes the 2-section of the hypergraph, in the terminology of Bretto.

The function `as.hypergraph()` returns a hypergraph defined by a graph, matrix (or edgelist). If a matrix is given, it is viewed as the incidence matrix of the hypergraph. If a list is given, it is interpreted as the hyper-edge list. If a graph is given, `graph2hypergraph` is called with the graph and the arguments passed in `...`. If `x` is NULL or missing, and `n>0` is given, an empty hypergraph on `n` nodes is returned. If all else fails, an empty hypergraph on no nodes is returned.

The `method` variable controls the method used for turning a graph into a hypergraph:

- `incidence`: use the incidence matrix of the graph.
adjacency - treat the adjacency matrix as the incidence matrix.
neighborhood, ego - Use the neighborhoods of the vertices. The arguments to ego are passed in the
dotted arguments.
spectral - The spectral embedding is performed, followed by Mclust. The arguments are passed to
hypergraph_from_spectral_clustering.

Value
An undirected igraph graph object.

Author(s)
David J. Marchette <dmarchette@gmail.com>

References

See Also
as.hypergraph, graph2hypergraph, hypergraph_from_spectral_clustering, ego, Mclust.

Examples
h <- hypergraph_from_edgelist(list(1:4,1:2,c(2,3,5),c(3,5:7)))
g <- as.graph(h)

ase (h) [1] 0.62377

ase (g) [1] 0.62377

adjacency spectral embedding.

Description
Using either adjacency or Laplacian spectral embedding, embed a graph into a lower dimensional
space.

Usage
ase(g, verbose = FALSE, adjust.diag = FALSE, laplacian = FALSE,
   normalize = FALSE, scale.by.values = FALSE, vectors = "u", d = 2)
lse(g,...)
hypergraph.spectrum(h, k=3)
Arguments

- **g,h** A graph (g) or hypergraph (h).
- **verbose** logical. Control output to terminal.
- **adjust.diag** logical. For adjacency embedding, whether to add degree/(n-1) to the diagonal of the adjacency matrix.
- **laplacian** logical. Use the Laplacian rather than the adjacency matrix.
- **normalize** logical. Whether to normalize by \(D^{1/2}\).
- **scale.by.values** logical. Whether to scale the eigen or singular vectors by the square root of the eigen or singular values.
- **vectors** character. "u", "v" or "uv" indicating which vectors to provide for the embedding.
- **d,k** dimension of the embedding.
- **...** arguments passed to ase.

Details

The **ase** is for graphs, and has the most control over the embedding, as indicated by the arguments. the **hypergraph.spectrum** computes the **svd** of the incidence matrix for the hypergraph h. ise is Laplacian spectral embedding, and is just a call to ase with laplacian=TRUE and adjust.diag=FALSE. For small hypergraphs (order or size < 3) the base svd function is used and k is ignored.

Value

- **ase** returns a matrix of points, with rows corresponding to vertices and columns to the embedding. There will be either d, or 2*d columns, depending on the value of the variable vectors. For "u" or "v" the dimension is d, for "uv" the dimension is 2*d. **hypergraph.spectrum** returns the singular value decomposition using the top k singular vectors and values.

Author(s)

- David J. Marchette <dmarclette@gmail.com>

References


See Also

- **svds**, **eigs**.
Examples

```r
g <- sample_gnp(10,.1)
ase(g)
```

```r
clique_hypergraph(g)
```

### clique_hypergraph

**Clique Hypergraph**

**Description**

Construct a clique hypergraph from a graph.

**Usage**

```r
clique_hypergraph(g)
```

**Arguments**

- `g` a graph.

**Details**

A clique hypergraph is one whose hyper-edge correspond to the maximal cliques of a given graph.

**Value**

A hypergraph.

**Warning**

The calculation of the maximal cliques of a graph can take a long time, and dense graphs may have many maximal cliques, so use this function with care.

**Author(s)**

David J. Marchette <dmarchette@gmail.com>

**References**


**See Also**

`max_cliques`

**Examples**

```r
g <- graph_from_literal(1-2-3-1, 3-4-5-3)
h <- clique_hypergraph(g)
```
**cluster_spectral**

**Spectral Graph Clustering**

**Description**

Use spectral embedding to embed a graph into a lower dimension, then cluster the points using model based clustering. This results in a clustering of the vertices.

**Usage**

```
cluster_spectral(g, verbose = FALSE, adjust.diag = FALSE, laplacian = FALSE,
                 normalize = FALSE, scale.by.values = FALSE, vectors = "u", d = 12, ...)
```

**Arguments**

- `g`: a graph.
- `verbose`: logical. Whether to print to the screen as it goes.
- `adjust.diag`: logical. Whether to set the diagonal of the adjacency matrix to `degree/(n-1)`. 
- `laplacian`: logical. Whether to use the Laplacian rather than the adjacency matrix.
- `normalize`: logical. Whether to normalize the matrix by `D^1/2`.
- `scale.by.values`: Whether to scale the embedding vectors by the eigen vectors.
- `vectors`: character. "u" or "v" or "uv". The latter is only appropriate for directed graphs.
- `d`: embedding dimension.
- `...`: arguments passed to `Mclust`.

**Details**

This first embeds the vertices into a d-dimensional space, using the adjacency matrix or the Laplacian. See `ase` for more information. It then applies `Mclust` to the resultant points to cluster.

**Value**

An object of class "Mclust".

**Author(s)**

David J. Marchette <dmarchette@gmail.com>

**References**

See Also

ase.

Examples

\[
P <- \text{rbind(c(.2,.05),c(.05,.1))}
ns <- \text{rep(50,2)}
\text{set.seed(451)}
g <- \text{sample_sbm(sum(ns),P,ns)}
\text{cluster_spectral(g)}
\]

---

dual                          Dual hypergraph.

Description

Construct the dual hypergraph of a hypergraph.

Usage

dual_hypergraph(h)

Arguments

h  a hypergraph.

Details

The dual hypergraph is a hypergraph whose nodes are the original hyper-edges, with hyper-edges indicating the original incidence. Essentially, the incidence matrix of the dual hypergraph is the transpose of the original incidence matrix.

Value

a hypergraph.

Author(s)

David J. Marchette <dmarchette@gmail.com>

References


Examples

\[
h <- \text{hypergraph_from_edgelist(list(1:4,2:5,4:6,c(1,3,7)))}
k <- \text{dual_hypergraph(h)}
\]
Description

Build a hypergraph by constructing hyperedges from balls around a set of points.

Usage

epsilon_hypergraph(x, epsilon, method = "Euclidean", reduce=FALSE, as.graph=FALSE)

Arguments

- **x**: a matrix of points.
- **epsilon**: radius of the balls. May be a vector.
- **method**: passed to dist to define the distance function.
- **reduce**: logical. Whether to reduce the hypergraph by removing redundant hyper-edges.
- **as.graph**: logical. Whether to return a graph instead of a hypergraph.

Details

Each point of x corresponds to a vertex in the hypergraph. For each point, a ball of radius epsilon is constructed, and all points in the ball form a hyper-edge in the graph. If epsilon is a vector, each ball may have a different radius, and if the length of epsilon is less than the number of points, they are repeated.

If reduce=TRUE redundant hyper-edges (those contained in other hyper-edges) are removed. If as.graph==TRUE, reduce is ignored and a graph is returned instead of a hypergraph.

Value

a hypergraph or graph.

Note

Because of symmetry (a is in the ball centered at b if and only if b is in the ball centered at a), the incidence matrix of an epsilon hypergraph is square and symmetric. It can thus be interpreted as an adjacency matrix, and it is this graph that is returned if as.graph==TRUE.

Author(s)

David J. Marchette <dmarchette@gmail.com>.

See Also

eknn_hypergraph, sample_geom_hypergraph, dist.
Examples

```r
set.seed(565)
x <- matrix(rnorm(100), ncol = 2)
h <- epsilon_hypergraph(x, epsilon = .25)
plot(h)
plot(h, layout = x)

epsilon <- runif(nrow(x), 0, .5)
k <- epsilon_hypergraph(x, epsilon = epsilon)
plot(k)
plot(k, layout = x)
```

---

equivalent.hypergraphs

**Equivalent Hypergraphs**

Description

Test whether two hypergraphs are equivalent. This is not an isomorphism test, merely a test that the incidence matrices are “the same” in the vertex/edge order in which they are presented.

Usage

```r
equivalent.hypergraphs(h1, h2, vertex.names = FALSE, edge.names = FALSE, strip.names = FALSE, method = c("any", "exact", "binary"))
as.binary.hypergraph(h)
```

Arguments

- `h, h1, h2`: Hypergraphs.
- `vertex.names`: Logical. Whether to ensure the vertex names are all the same.
- `edge.names`: Logical. Whether to ensure the hyper-edge names are all the same.
- `strip.names`: Logical. Whether to strip the row/column names from the incidence matrices (after ordering them) prior to the equivalence check.
- `method`: See Details.

Details

If either `vertex.names` or `edge.names` is TRUE, they are checked for equality, and the incidence matrices are reordered accordingly. The method "exact" checks for the matrices being exactly equal, while "binary" converts all non-zero entries to 1 before the check. The former is for future versions in the event that weighted or directed hypergraphs are implemented. If `strip.names` is TRUE, the row/column names are stripped from the matrices. If either `vertex.names` or `edge.names` is TRUE,
the matrices are first ordered according to the rows/columns as appropriate. Note that "binary" will always be TRUE if "exact" is TRUE, and that if "binary" is FALSE, then so will "exact" be.

The method "any" calls the code with strip.names=TRUE and all combinations of vertex.names and edge.names for the binary method, and returns the logical OR of these. Essentially, this tests that the matrices are "the same" under any reasonable interpretation (without checking for equivalence under any reordering except for lexicographic ordering of the row/column names).

Value

a logical in the case of equivalent.hypergraphs, a hypergraph in the case of as.binary.hypergraph.

Author(s)

David J. Marchette <dmarchette@gmail.com>

Examples

h1 <- hypergraph_from_edgelist(list(1:4,2:7,c(1,3,5,7),c(2,4,6)))
h2 <- hypergraph_from_edgelist(list(letters[1:4],letters[2:7],
  letters[c(1,3,5,7)],letters[c(2,4,6)]))
equivalent.hypergraphs(h1,h2)  ## TRUE
equivalent.hypergraphs(h1,h2,vertex.names=TRUE)  ## FALSE

H2

Two sections of a hypergraph.

Description

Two section of a hypergraph.

Usage

H2(h)

Arguments

h            a hypergraph.

Details

The 2-section of a hypergraph is the graph with vertices corresponding to hyper-edges, and edges corresponding to whether the hyper-edges intersect.

Value

a graph.
Author(s)

David J. Marchette <dmarchette@gmail.com>

References


Examples

```r
h <- hypergraph_from_edgelist(list(c(1,2,5),c(2,3,5),c(3,4),c(4,5)))
g <- H2(h)
## see Figure 7.11 of the reference.
```

---

<table>
<thead>
<tr>
<th>has.helly</th>
<th>Helly Property</th>
</tr>
</thead>
</table>

Description

Check whether a hypergraph has the Helly property.

Usage

```r
has.helly(h, strong=FALSE)
is.helly(h)
```

Arguments

- `h`: a hypergraph.
- `strong`: logical.

Details

An intersecting family is a collection of hyper-edges such that the intersection of any pair of hyper-edges in the family is non-empty. A hypergraph has the Helly property if each intersecting family has a non-empty intersection – there is at least one vertex in every hyper-edge. This is an implementation of the algorithm on page 32 of Bretto. The argument `strong` indicates whether the test should be for the strong Helly property or not. A hypergraph has the strong Helly property if every partial induced sub-hypergraph has the Helly property.

The function `is.helly` is an alias for a check for the non-strong Helly property.

Value

- `a logical`.

Note

Have not yet implemented the strong Helly property algorithm.
has.isolates

Author(s)

David J. Marchette <dmarchette@gmail.com>

References


Examples

```r
## Example from Bretto
h <- hypergraph_from_edgelist(list(1:5,
c(2,4,6,7),
c(4:6,8,9),
9:10))
has.helly(h)
```

```r
has.isolates Test for loops, isolates and empty hyper-edges.
```

Description

Tools to determine whether a hypergraph has degenerate elements such as loops (hyper-edges with a single vertex) isolated vertices (ones which appear in no hyper-edges) and empty hyper-edges.

Usage

```r
has.isolates(h)
has.loops(h)
has.empty.hyperedges(h)
```

Arguments

- `h` a hypergraph.

Value

returns a logical.

Author(s)

David J. Marchette <dmarchette@gmail.com>.

See Also

remove.isolates, remove.loops, remove.empty.hyperedges, reduce.hypergraph.
Examples

h <- hypergraph_from_edgelist(list(1:3,2:8,9))
has.loops(h) ## TRUE
has.isolates(h) ## FALSE
k <- hypergraph.add.vertices(h,10)
has.isolates(k) ## TRUE

hdegree

Degrees of a hypergraph.

Description

The degree of a vertex in a hypergraph is the number of hyper-edges containing the vertex.

Usage

hdegree(h)

plotDegreeDistribution(h, xlab="Degree", ylab="Density",
add.line=FALSE,
lty=2,lwd=1,line.col=1,
...)  

Arguments

h  a hypergraph. For plotDegreeDistribution it could also be a graph.
xlab,ylab axis labels.
add.line logical. Whether to add a regression line to the plot.
lty,lwd,line.col plotting controls for the line.
... arguments passed to plot.

Details

Returns a vector of the number of (hyper-)edges containing each vertex. The plot.hdegree.distributions plots the distribution of degrees on a log-log scale, optionally adding a regression line.

Value

a vector of degrees.

Author(s)

David J. Marchette <dmarchette@gmail.com>
horder

See Also
degree, degree.distribution.

Examples

```r
set.seed(452)
h <- sample_gnp_hypergraph(100, p=.1)
hdegree(h)
```

| horder | The number of vertices, edges and statistics of the hypergraph. |

Description

This returns the number of vertices and hyper-edges, and similar statistics, for a hypergraph.

Usage

```r
hnames(h)
horder(h)
hsize(h)
edge_orders(h)
```

Arguments

- `h`: a hypergraph.

Value

a named vector of vertices, or the names of the vertices. Order refers to the number of vertices, size to the number of hyper-edges. The `edge_orders` function returns the number of vertices in each of the hyper-edges. In a simple graph, this would always be 2.

Author(s)

David J. Marchette <dmarchette@gmail.com>

See Also
gorder, gsize, hrank.

Examples

```r
h <- hypergraph_from_edgelist(list(3:7,8:12,c(1,3,9)))
horder(h)
hsize(h)
hnames(h)
```
hypergraph.add.edges

Description

Add edges or vertices to a hypergraph.

Usage

hypergraph.add.edges(h, edges, verbose = FALSE)
add.hyperedges(h, edges, verbose = FALSE)
hypergraph.add.vertices(h, nv, names)

hypergraph.add.edges

Add edges or vertices to a hypergraph.
Arguments

h  A hypergraph.
edges  A list of edges to be added.
nv  Number of vertices to add.
names  Optional vector of names of the vertices.
verbose  logical. Whether to warn if new vertices are created.

Details

The edges can be indices or edge names. This is different than the graph call – see the *igraph* package help for that. If edges is NULL, or missing, `hypergraph.add.edges` adds a single empty hyper-edge to the hypergraph. `add.hyperedges` is an alias for `hypergraph.add.edges`.

Value

Returns a hypergraph (or graph) as appropriate.

Author(s)

David J. Marchette <dmarchette@gmail.com>

See Also

`add_vertices`, `add_edges`

Examples

```r
h <- hypergraph_from_edgelist(list(1:4,1:2,c(2,3,5),c(3,5:7))
h1 <- hypergraph.add.vertices(h,1,"8")
h2 <- hypergraph.add.edges(h,list(c(1,5,8),7:9))
```

---

**hypergraph.as.edgelist**

*Convert between hypergraphs and graphs.*

Description

Convert a hypergraph to a graph or a graph, matrix or list to a hypergraph.

Usage

```r
hyper_edges(h)
hypergraph.as.edgelist(h)
```

Arguments

h  a hypergraph.
The function `hypergraph_as_edgelist` is just an alias for `hyper_edges`.

A list of the hyperedges.

David J. Marchette <dmarchette@gmail.com>

See Also

`as_edgelist`

Examples

```r
h <- hypergraph_from_edgelist(list(1:4,1:2,c(2,3,5),c(3,5:7)))
hypergraph_as_edgelist(h)
```

The complement of a hypergraph is a hypergraph consisting of the hyper-edges that are not found in the original hypergraph.

A hypergraph.

David J. Marchette <dmarchette@gmail.com>
Delete edges or vertices of a hypergraph.

Description
Remove edges or vertices from a hypergraph.

Usage
hypergraph.delete.edges(h, edges)
delete.hyperedges(h, edges)
hypergraph.delete.vertices(h, v)

Arguments
h a hypergraph.
edges,v A vector of edges or vertices (indices) to remove.

Details
delete.hyperedges is an alias for hypergraph.delete.edges.

Value
a hypergraph

Author(s)
David J. Marchette <dmarchette@gmail.com>

See Also
delete.vertices, delete.edges.

Examples
h <- hypergraph_from_edgelist(list(1:3,3:7,7:8))
hypergraph.delete.vertices(h,3)
hypergraph.delete.vertices(h,7)
hypergraph.delete.edges(h,2)
hypergraph.entropy

Description

The hypergraph entropy, which is a sum of the suitably scaled eigenvalues of the hypergraph Laplacian.

Usage

hypergraph.entropy(h)

Arguments

h

a hypergraph.

Details

Bretto, page 9, defines hypergraph entropy as follows. Let \( L'(h) \) be the Laplacian of \( h \) divided by the sum of its diagonal. Then the \(|V| - 1 \) eigenvalues sum to 1, and the entropy is defined by \(-\sum(\lambda_i \log_2 \lambda_i)\).

Value

a number.

Author(s)

David J. Marchette <dmarchette@gmail.com>

References


See Also

hypergraph_laplacian_matrix.

Examples

```r
h <- hypergraph_from_edgelist(list(3:4,1:3,c(3,5,7:10),c(4,6),c(3,5,8)))
hypergraph.entropy(h)
## 2.802822
```
hypergraph.is.connected

Is the hypergraph connected?

Description

Uses the igraph is.connected function to determine if a hypergraph is connected.

Usage

hypergraph.is.connected(h)

Arguments

h       a hypergraph.

Details

First the hypergraph is converted to a graph. Then the resulting graph is passed to the igraph is.connected function.

Value

a logical.

Author(s)

David J. Marchette <dmarchette@gmail.com>

See Also

is.connected.

Examples

hypergraph.is.connected(hypergraph_from_edgelist(list(1:4,3:5)))
## TRUE
hypergraph.is.connected(hypergraph_from_edgelist(list(1:4,5:7)))
## FALSE
hypercgraf.union  

Unions and intersections of hypergraphs.

Description

Given two hypergraphs, compute their union or intersection.

Usage

hypergraph.union(h1, h2, reduce = TRUE)
hypergraph.disjoint.union(h1, h2)
hypergraph.intersection(h1, h2, strict = FALSE)

Arguments

h1, h2  
hypergraphs.
reduce  
logical. Whether to reduce the resultant hypergraph by removing edges that are subsets of other edges.
strict  
logical. See details.

Details

The disjoint union of two hypergraphs is a hypergraph on the disjoint union of the vertices. The vertices are renamed, if necessary, so that those in the first hypergraph are distinct from those in the second. All edges that occur in either hypergraph, with the vertices renamed, are retained. The (non-disjoint) union treats vertices with the same name (or if they are unnamed, the same index) as the same vertex, and produces the hypergraph containing all edges that are in either hypergraph. If reduce is TRUE, the hypergraph is reduced so that hyper-edges that are subsets of another edge are removed. For the intersection, only those edges that are in one of the hypergraphs are retained. Again, vertices with the same name are consider to be the same, and only these vertices are retained. If strict is true, the edges must be exactly the same. Otherwise, an edge in one hypergraph that is a subset of an edge in the other will be retained.

Value

a hypergraph.

Author(s)

David J. Marchette <dmarchette@gmail.com>

Examples

h1 <- hypergraph_from_edgelist(list(1:3, 3:5, 4:9, 2:6))
h2 <- hypergraph_from_edgelist(list(2:3, 3:5, 4:9, 2:6, c(3, 5, 10:11)))
hypergraph.disjoint.union(h1, h2)
hypergraph.union(h1, h2)
hypergraph.intersection(h1, h2)
hypergraph_as_adjacency_matrix

Adjacency Matrix of a Hypergraph.

Description

Returns the adjacency matrix, computed from the incidence matrix.

Usage

hypergraph_as_adjacency_matrix(h)

hadjacency(h)

Arguments

h a hypergraph.

Details

The adjacency matrix is a weighted adjacency matrix corresponding to \(\text{code}(t(M))\) diagonal of the matrix set to 0. hadjacency is an alias for the longer named function.

Value

a (sparse) matrix.

Author(s)

David J. Marchette <dmarchette@gmail.com>

See Also

as_adjacency_matrix, Matrix.

Examples

h <- hypergraph_from_edgelist(list(1:4,2:5))
hypergraph_as_adjacency_matrix(h)

# returns:
# 5 x 5 Matrix of class "dgeMatrix"
# 1 2 3 4 5
# 1 0 1 1 0
# 2 1 0 2 1
# 3 1 2 0 1
# 4 1 2 0 1
# 5 0 1 0 0
hypergraph_from_incidence_matrix

*Hypergraph construction.*

**Description**

Construct a hypergraph from a collection of hyper-edges.

**Usage**

```r
hypergraph_from_incidence_matrix(incidence_matrix)
hypergraph_from_edgelist(x,v)
hypergraph_from_membership(x)
hypergraph_from_fuzzy_clustering(z,threshold)
hypergraph_from_spectral_clustering(g,m,fuzzy=FALSE,threshold,...)
```

**Arguments**

- `incidence_matrix`: an sxn binary matrix corresponding to the s hyper-edges on n vertices.
- `x`: a list of hyper-edges, or a vector corresponding to which hyper-edge each node is in.
- `z`: a matrix of probabilities that is nxc where c is the number of clusters.
- `v`: optional vector of node names.
- `g`: a graph. Only used if `m` is missing.
- `m`: a communities object. See communities in the igraph package.
- `fuzzy`: logical.
- `threshold`: threshold on the probabilities if `fuzzy` is true. If not given, it defaults to the inverse of the number of communities.
- `...`: arguments passed to cluster_spectral if `g` is given and `m` is given.

**Details**

An edgelist is a list of hyper-edges. An incidence matrix is a binary matrix that is \( hsize(g) \times horder(h) \). A membership vector is the vector of node membership returned from a community detection or clustering algorithm. A hypergraph constructed from a membership vector has a disconnected component for each hyper-edge.

**Value**

a hypergraph.

**Author(s)**

David J. Marchette <dmarchette@gmail.com>
See Also

cluster_spectral, communities.

Examples

h <- hypergraph_from_edgelist(list(1:4,3:6))

h1 <- hypergraph_from_literal(1-2-3,3-a-b,c-1-4)
plot(h1)
hypergraph_laplacian_matrix

Laplacian Matrix

Description
The Laplacian of a hypergraph is D-A, where A is the (weighted) adjacency matrix, and D is the row-sums.

Usage
hypergraph_laplacian_matrix(h, normalize=FALSE)

Arguments
- `h`: a hypergraph.
- `normalize`: logical. Whether to normalize the Laplacian matrix.

Details
The Laplacian is D-A, where D is the row sums of the adjacency matrix A. If `normalize` is TRUE, then the normalized version is returned.

Value
a (sparse) matrix.

Author(s)
David J. Marchette <dmarchette@gmail.com>

See Also
- `laplacian_matrix`

Examples
```r
h <- hypergraph_from_edgelist(list(1:4,2:5,c(3,5,7,8,10),c(2,9),c(2:3,6,10)))
L <- hypergraph_laplacian_matrix(h)
Ln <- hypergraph_laplacian_matrix(h, normalize=TRUE)
```
Graph Incidence Matrix.

Description

Converts a graph to an incidence matrix. Not the bipartite version.

Usage

    incidence_matrix(g)
    hypergraph_as_incidence_matrix(h)

Arguments

- **g**: a graph or hypergraph.
- **h**: a hypergraph.

Details

An incidence matrix has \( g\text{order}(g) \) columns and \( g\text{size}(g) \) rows. \texttt{incidence_matrix} can be called on either a graph or a hypergraph. It calls \texttt{hypergraph_as_incidence_matrix} in the latter case.

Value

A sparse incidence matrix.

Author(s)

David J. Marchette <dmarchette@gmail.com>

Examples

    set.seed(2343)
    g <- sample_gnp(10,.1)
    h <- hypergraph_from_edgelist(list(1:3,4:5,c(3,5,7)))
Description

Computes the hypergraph induced by a subset of the vertices.

Usage

induced_hypergraph(h, v, simplify = TRUE)

Arguments

h       a hypergraph.
v       a vector of vertices.
simplify   logical.

Details

First the hypergraph is reduced to only those vertices in v. This results in it retaining only those hyper-edges containing any elements of v, as well as removing from the resultant hyper-edges any vertices not in v. If simplify is true, loops are then removed. This function always removes empty hyper-edges, so any hyper-edge which does not contain any elements of v is removed.

Value

a hypergraph.

Author(s)

David J. Marchette <dmarchette@gmail.com>

Examples

h <- hypergraph_from_edgelist(list(1:4,3:7,c(1,3,5)))
k <- induced_hypergraph(h,c(1,3,5))
is.conformal

Conformal Hypergraphs

Description
Tests whether a hypergraph is conformal.

Usage

\[
\text{is.conformal}(h) \quad \text{is.bi.conformal}(h)
\]

Arguments

- **h**: a hypergraph.

Details

A hypergraph \( h \) is conformal if all the maximal cliques of its 2-section are the maximal (by inclusion) edges of \( h \). The test uses a theorem (see the reference, Theorem 7.6.4) that says a hypergraph is conformal if and only if its dual is Helly. A hypergraph is bi-conformal if it and its dual are conformal.

Value

- a logical.

Author(s)

David J. Marchete <dmarchette@gmail.com>

References


See Also

- **is.helly**

Examples

\[
\begin{align*}
\text{h <- hypergraph_from_edgelist(list(1:4,3:6,5:10))} \\
\text{is.conformal(h)} \\
\quad \text{## TRUE} \\
\text{h <- hypergraph_from_edgelist(list(1:2,2:3,c(1,3)))} \\
\text{is.conformal(h)} \\
\quad \text{## FALSE}
\end{align*}
\]
is.empty.hypergraph  
*Is the hypergraph empty.*

**Description**

determines whether the hypergraph contains no hyper-edges.

**Usage**

```r
is.empty.hypergraph(h)
```

**Arguments**

- `h`  
a hypergraph.

**Value**

a logical.

**Author(s)**

David J. Marchette <dmarchette@gmail.com>

**Examples**

```r
h <- hypergraph_from_edgelist(list(1:3))
is.empty.hypergraph(h)
k <- hypergraph.delete.edges(h,1)
is.empty.hypergraph(k)
```

is.hypergraph  
*Is an object a hypergraph?*

**Description**

Check that an object is a hypergraph object.

**Usage**

```r
is.hypergraph(h)
```

**Arguments**

- `h`  
a hypergraph.
is.hypertree

Details
This only checks that the object’s class contains hypergraph.

Value
A logical.

Author(s)
David J. Marchette <dmarchette@gmail.com>

Examples

```r
h <- hypergraph_from_edgelist(list(1:4,1:2,c(2,3,5),c(3,5:7)))
g <- as.graph(h)
is.hypergraph(h)
is.hypergraph(g)
```

Description
Test if a hypergraph is a hypertree.

Usage

```r
is.hypertree(h, ...)
```

Arguments

- `h`: a hypergraph.
- `...`: arguments passed to the igraph `is_chordal` function.

Details
Uses Corollary 8.1.1 of the reference: a hypergraph is a hypertree if and only if it is Helly and it’s line graph is chordal.

Value
A logical.

Author(s)
David J. Marchette <dmarchette@gmail.com>.
References

See Also
is_chordal, line_graph, line.graph, has.helly.

Examples
h <- hypergraph_from_edgelist(list(1:3,2:4,4:5,c(2,4:5)))
is.helly(h)
g <- line.graph(h)
is_chordal(g)
is.hypertree(h)

is.simple Is a hypergraph simple/linear?

Description
Tests whether a hypergraph is simple or linear.

Usage
is.simple(h)
is.linear(h)

Arguments
h a hypergraph. Can be a graph for is.simple, in which case the igraph version is called.

Details
A hypergraph is simple if all its edges are distinct, non-empty, and if edge i is contained in edge j, then i=j. A hypergraph is linear if it is simple and the intersection of any two hyper-edges has at most one element.

Value
a logical.

Author(s)
David J. Marchette <dmarchette@gmail.com>.

References
Examples

```r
h <- hypergraph_from_edgelist(list(1:4,4:7,c(6,8:10),10:14))
is.linear(h) ## TRUE
is.simple(h) ## TRUE
```

Description

Tests whether a hypergraph is a star. Finds the minimal intersection set of the hyper-edges.

Usage

```r
is.star(h,type=c("weak","strong"))
intersection_set(h)
```

Arguments

- `h`: a hypergraph.
- `type`: see Details.

Details

A (weak) star hypergraph is one in which the intersection of all the hyper-edges is non-empty.

An intersection set is a set of vertices that is contained in every edge. The argument `type="strong"` for `is.star` indicates that the only vertices which are common between any pair of vertices are contained in the intersection set (or "hub") of the star hypergraph. So a hypergraph that is strongly star is weakly star, but not vice versa.

Value

- a logical, for `is.star`. A set of vertices (or NULL) that are contained in every hyper-edge. This would be the "hub" of the star.

Author(s)

David J. Marchette <dmarchette@gmail.com>.

References

Examples

```r
h <- hypergraph_from_edgelist(list(c(1:4,16),
    c(4:7,16),
    c(4:8:10,16),
    c(4,10:16),
    c(4,16)))
is.star(h)    ## TRUE
is.star(h,type='strong') ## FALSE
intersection_set(h) ## 4, 16
```

Description

Test if a graph is a tree or a forest.

Usage

```r
is.tree(g)
is.forest(g, strict=FALSE)
```

Arguments

- `g`: a graph.
- `strict`: logical.

Details

test whether an undirected graph `g` is a tree (connected, acyclic) or a forest (disjoint union of trees). The flag `strict` enforces the strict rule that a forest must contain more than a single tree. The default is to allow for single-tree forests, which is the convention.

Value

a logical.

Author(s)

David J. Marchette <dmarchette@gmail.com>

Examples

```r
g <- make_tree(10)
is.tree(g)
is.forest(g)
is.forest(g, strict=TRUE)
```
**kCores**

<table>
<thead>
<tr>
<th>kCores</th>
<th>K-Cores</th>
</tr>
</thead>
</table>

**Description**

Find all the k-cores in a hypergraph.

**Usage**

`kCores(h)`

**Arguments**

- `h` a hypergraph.

**Details**

A k-core in a hypergraph is a maximal subhypergraph where (a) no hyperedge is contained in another, and (b) each node is adjacent to at least k hyperedges in the subgraph.

The implementation is based on the algorithm by E. Ramadan, A. Tarafdar, A. Pothen, 2004.

The code is a direct copy of the code from the BioConductor package `hypergraph`, modified to work with the data structures used in this package.

**Value**

A vector of core numbers for each vertex.

**Author(s)**

David J. Marchette <dmarchette@gmail.com>

The implementation in the `hypergraph` package from which this function was taken was written by:

Li Long <li.long@isb-sib.ch>.

**References**


See also the BioConductor `hypergraph` package:

Examples

```r
## example from the hypergraph version
edges <- list(c("A", "C"),
               c("B", "C"),
               c("C", "E"),
               c("C", "F"),
               c("E", "D"),
               c("E", "F"),
               c("D", "G"),
               c("D", "H"),
               c("D", "J"),
               c("H", "G"),
               c("H", "J"),
               c("G", "J"),
               c("J", "M"),
               c("J", "K"),
               c("M", "K"),
               c("M", "O"),
               c("M", "N"),
               c("K", "N"),
               c("K", "F"),
               c("K", "I"),
               c("K", "L"),
               c("I", "I"),
               c("I", "L"),
               c("F", "L"),
               c("F", "Q"),
               c("Q", "R"),
               c("Q", "S"),
               c("R", "T"),
               c("S", "T"))

h <- hypergraph_from_edgelist(edges,v=union(unlist(edges),"U"))
kc <- kCores(h)
```

**knn_hypergraph**  
*K-Nearest Neighbor Hypergraph.*

**Description**

A hypergraph is constructed from data in which each hyper-edge corresponds to a vertex and its k-nearest neighbors.

**Usage**

```r
knn_hypergraph(x, k = 1, method = "Euclidean", reduce=FALSE,
               as.graph=FALSE)
```
Arguments

- **x**: a matrix of data points.
- **k**: the number of neighbors. May be a vector.
- **method**: distance type passed to `dist`.
- **reduce**: logical. Whether to remove redundant hyper-edges.
- **as.graph**: logical. Whether to return a graph instead of a hypergraph.

Details

Each vertex is in one-to-one correspondence with the points (rows) of `x`. For each vertex, the `k`-closest vertices and itself form a hyper-edge.

If `reduce=TRUE` redundant hyper-edges (those contained in other hyper-edges) are removed. If `as.graph=TRUE`, `reduce` is ignored and the incidence matrix is treated as an adjacency matrix, returning a (directed) `igraph` graph.

Value

- a hypergraph or graph.

Author(s)

David J. Marchette <dmarchette@gmail.com>

See Also

- `epsilon_hypergraph`, `dist`.

Examples

```r
set.seed(565)
x <- matrix(rnorm(100), ncol=2)
k <- knn_hypergraph(x, k=4)
plot(k)
plot(k, layout=x)
```

Description

Construct the line graph of a hypergraph.

Usage

- `line.graph(h)`
Arguments

h a hypergraph.

Details

The line graph of a hypergraph is essentially the same concept as the line graph of a graph: it is the graph whose vertices correspond to the hyper-edges, with an edge between two vertices if their corresponding hyper-edges intersect.

Value

a graph.

Note

If h is an igraph graph, the function igraph::line_graph will be called. line_graph is the only function that masks an igraph function, but I am assuming that the `_` version is preferred by igraph.

Author(s)

David J. Marchette <dmarchette@gmail.com>

References


See Also

line_graph.

Examples

h <- hypergraph_from_edgelist(list(1:3,2:4,4:5,c(2,4:5)))
g <- line_graph(h)

Description

Create an empty hypergraph.

Usage

make_empty_hypergraph(n)
**Arguments**

n  
a non-negative integer.

**Details**

Creates an empty hypergraph (no hyper-edges) on n nodes.

**Value**

a hypergraph.

**Author(s)**

David J. Marchette <dmarchette@gmail.com>

**Examples**

```r
h <- make_empty_hypergraph(4)
horder(h)
hsize(h)

h <- make_empty_hypergraph(0)
horder(h)
hsize(h)
```

---

### pendant  

**Pendant Vertices**

**Description**

Determine the set of pendant vertices.

**Usage**

pendant(h)

**Arguments**

h  
a hypergraph.

**Details**

A pendant vertex is one whose set of hyper-edges is a subset of the hyper-edges of another vertex. That is, if v is in hyper-edges 1 and 2, and w is in hyper-edges 1, 2 and 5, then v is pendant to w, and w is called a twin of v.
Value

- **vertices**: a vector of the pendant vertices
- **twins**: a list, each element of which is the set of twins of the corresponding pendant vertex

Author(s)

David J. Marchette <dmarchette@gmail.com>.

References


Examples

```r
h <- hypergraph_from_edgelist(list(1:4,2:5,c(4,6),c(7),c(3:5,8)))
pendant(h)
```

---

**plot.hypergraph**

Plot a hypergraph.

Description

Plot a hypergraph using the **igraph** plot function.

Usage

```r
## S3 method for class 'hypergraph'
plot(x, edge.color = NA,
    mark.groups=hypergraph_as_edgelist(h),
    layout,...)
```

Arguments

- **x**: a hypergraph.
- **edge.color**: color for the edges.
- **layout**: optional layout for the plot. If the hypergraph has a layout attribute, this will be used, unless layout is given. If it does not have a layout attribute and the layout is not provided, it uses the code from **igraph** to choose a layout.
- **mark.groups**: the groups correspond to the hyper-edges. Set this to NULL if you do not want the hyper-edge polygons to plot.
- **...**: optional arguments passed to plot.
Details

Plots the hypergraph, using the `igraph` plotting function applied to a graph converted from the hypergraph. For the example below, the plot will look something like:

![Hypergraph Plot](image)

Value

the layout is returned invisibly.

Author(s)

David J. Marchette <dmarchette@gmail.com>

See Also

`as.graph`, `plot.igraph`, `igraph.plotting`.

Examples

```r
h <- hypergraph_from_edgelist(list(3:7,8:12,c(1,3,9)))

plot(h)
```

print.hypergraph

Print a hypergraph to the console.

Description

Print method for hypergraphs.
Usage

```r
## S3 method for class 'hypergraph'
print(x, ...)
```

**Arguments**

- `x`: a hypergraph.
- `...`: ignored arguments.

**Value**

No return value, called for side effects only – prints to console.

**Author(s)**

David J. Marchette <dmarchette@gmail.com>

**Examples**

```r
h <- hypergraph_from_edgelist(list(3:7,8:12,c(1,3,9)))
print(h)
```

---

**reduce.hypergraph**

Remove redundant hyperedges and isolated vertices.

**Description**

Reduce a hypergraph by removing redundant edges, loops, or isolated vertices.

**Usage**

```r
reduce.hypergraph(h, method="inclusion")
simplify.hypergraph(h)
remove.isolates(h)
remove.loops(h)
remove.empty.hyperedges(h)
remove.loops(h)
```

**Arguments**

- `h`: a hypergraph
- `method`: character. See details.
Details

reduce.hypergraph removes redundant edges and/or reduces the hyper-edges: if the method is "inclusion" this removes hyper-edges that are contained in other hyper-edges; if the method is "intersection", it replaces the hypergraph with a new hypergraph whose edges are intersections of the original hypergraph’s hyper-edges – each pair of hyper-edges e1 and e2 with a non-empty intersection result in a hyper-edge corresponding to that intersection in the new hypergraph; if the method is "union" it removes edges that are contained in the union of the other edges, reducing to a hypegraph in which every hyper-edge contains at least one vertex which is contained in no other hyper-edge.

Isolates are vertices that are not in any hyper-edges, and loops are hyper-edges containing a single vertex. reduce.hypergraph will remove edges which contain no vertices, since the null set is a subset of any hyper-edge and hence is in the union of all other hyper-edges, so for either method such edges would be removed. simplify.hypergraph removes loops, isolates, and empty hyper-edges from a hypergraph. Isolates are removed after removing loops. This may reduce the order of the hypergraph, unlike the igraph simplify command, which only removes edges.

Value

a hypergraph.

Author(s)

David J. Marchette <dmarchette@gmail.com>

Examples

h <- hypergraph_from_edgelist(list(1:4,1:3,2:4,2:6))
reduce.hypergraph(h)

remove.redundant.vertices

Remove redundant vertices.

Description

Remove vertices whose removal does not disconnect the hypergraph.

Usage

remove.redundant.vertices(H, check.empty = TRUE)

Arguments

H a hypergraph.
check.empty logical. See details.
Details

This function was created with a binary term document hypergraph in mind. The idea is to remove words that appear in large documents, in order of decreasing degree, so long as the removal does not disconnect the graph. The argument check.empty is to ensure that removing a word does not result in an empty document. If this is set to FALSE, the resultant hypergraph may be much smaller than expected.

Value

a hypergraph.

Author(s)

David J. Marchette <dmarchette@gmail.com>

Examples

```r
edges <- list(letters[c(1:4,9)],
              letters[3:9],
              letters[c(3,6:9)],
              letters[c(3,5:9)],
              letters[2:9])
  h1 <- hypergraph_from_edgelist(edges)
  h <- remove.redundant.vertices(h1)
  # removed c, f, g, i

  h2 <- hypergraph_from_edgelist(list(letters[1:3],
                                     letters[3:5]))
  h <- remove.redundant.vertices(h2)
  ## h == h2
```

---

reorder_vertices

Reorder the vertices of a hypergraph.

Description

Return a hypergraph in which the vertices have been reordered so that they are in the given order as columns of the incidence matrix.

Usage

reorder_vertices(h, ord, decreasing=FALSE)

Arguments

- **h**: a hypergraph.
- **ord**: an ordering of the vertices.
- **decreasing**: if ord is not given, the order function is called on the names of the vertices as controlled by the decreasing variable.
sample_geom_hypergraph

Value

a hypergraph.

Author(s)

David J. Marchette <dmarchette@gmail.com>

See Also

order

Examples

h <- hypergraph_from_edgelist(list(3:7,8:12,c(1,3,9)))
k <- reorder_vertices(h)
hnames(h)
hnames(k)

h <- hypergraph_from_edgelist(list(letters[3:7],letters[8:12], LETTERS[c(1,3,9)]))
k <- reorder_vertices(h)
hnames(h)
hnames(k)

sample_geom_hypergraph

Construct a hypergraph from a random collection of points.

Description

A hypergraph defined by the relationships amongst a set of points.

Usage

sample_geom_hypergraph(n, m, d = 2, X, Y, radius, method = "Euclidean", thresh.method="leq", uniformly = FALSE)
plot_geom_hypergraph(h, pch = 20, cex = 3, col = "gray", plotY = TRUE, plot.circles = plotY, full.circles=TRUE, lty = 2, lcol = "black", ...)

Arguments

n The number of points to generate (ignored if X is provided). This corresponds to the number of vertices in the hypergraph.
m The number of nodes in the hypergraph (ignored if Y is provided). This corresponds to the number of hyper-edges in the hypergraph.
sample_geom_hypergraph

dimension of the points (ignored if both \(X\) and \(Y\) are provided).

\(radius\), \texttt{uniformly}

see Description.

\(X\)

see Description.

\(Y\)

see Description.

\texttt{method}

method passed to \texttt{dist}.

\texttt{thresh.method}

if this is 'leq' then hyper-edges are defined by whether the \(Y\) points are a distance less than or equal to the radius. If 'geq', then it is determined by greater than. Any other value will default to 'leq'.

\(h\)

a hypergraph generated by \texttt{sample_geom_hypergraph}.

\texttt{plotY}

logical. Whether to plot the \(Y\) variables defining the hypergraph.

\texttt{pch}, \texttt{cex}, \texttt{col}

parameters controling the plotting of \(Y\).

\texttt{plot.circles}, \texttt{full.circles}

logical. Whether to plot the circles defining the hyper-edges. If \texttt{full.circles} is \texttt{TRUE}, the plot limits are set so that the complete circles are plotted. Otherwise they may be clipped.

\texttt{lty}, \texttt{lcol}

parameters controling the plotting of the circles.

\ldots

parameters passed to \texttt{plot}.

Details

If either \(X\) or \(Y\) is missing, it is generated as a set of \(d\)-dimensional points in the unit cube, \(n\) points in \(X\), \(m\) points in \(Y\). If \(X\) is given, then \(n\) is ignored. Similarly with \(Y\) and \(m\). If both are given, then \(d\) is ignored. There is no checking that the provided \(X\) and/or \(Y\) matrices conform to the \(n, m, d\) values given in the call.

The inter-point distance matrix is computed using \texttt{dist} as \texttt{proxy::dist(Y,X,method=method)}. If \texttt{radius} is not provided, it is chosen uniformly at random from the unique values of the distance matrix if \texttt{uniformly} is \texttt{FALSE}, and uniformly from between the minimum and maximum distance if \texttt{uniformly} is \texttt{TRUE}. As a rule, one should not let this function choose the radius, but the code will do so if you wish. The matrix is then thresholded by the radius, resulting in a binary matrix which is then used as the \(m\times n\) incidence matrix for the hypergraph.

Value

a hypergraph. Additionally, the defining vectors \(X\) and \(Y\) and the radius are returned as named values of the hypergraph.

Note

If both \(X\) and \(Y\) are given, and \(R\) is not given, a random value for \(R\) is chosen randomly from the unique inter-point distances. If all three of these variables are provided, the hypergraph is not random.

Author(s)

David J. Marchette <dmarchette@gmail.com>
See Also
dist.

Examples

```r
set.seed(235)
h <- sample_geom_hypergraph(100,20,radius=0.2)
set.seed(3519)
Y <- matrix(runif(20),ncol=2)
X <- do.call(rbind,
    lapply(1:nrow(Y),function(i) cbind(rnorm(10,Y[i,1]),rnorm(10,Y[i,2]))))

h <- sample_geom_hypergraph(X=X,Y=Y,radius=0.2)
```

Description

Sample an Erdos-Renyi \( p \) hypergraph.

Usage

```r
sample_gnp_hypergraph(n, m, p, lambda)
```

Arguments

- \( n \) number of nodes.
- \( m, \lambda \) controls the number of hyper-edges. If \( m \) is not given, the number is drawn from a Poisson(\( \lambda \)), or, a Poisson(\( n \times p \)) if \( \lambda \) is not given.
- \( p \) Hyper-edge probability.

Details

This generates an ER hypergraph by using `rbinom` to generate a random \( m \times n \) matrix of Bernoulli random variables and treating this matrix as the incidence matrix for the hypergraph. If \( m \) is not given, and \( \lambda \) is, then \( m \) is drawn from a Poisson distribution with parameter \( \lambda \). If neither is given, the number of hyper-edges is drawn from a Poisson distribution with parameter \( n \times p \).

Value

a hypergraph.

Author(s)

David J. Marchette <dmarchette@gmail.com>
See Also

rbinom, rpois.

Examples

```r
set.seed(672)
  h <- sample_gnp_hypergraph(n=100, p=.1)
```

---

sample_k_uniform_hypergraph

*Random k-uniform and k-regular hypergraphs.*

---

Description

Randomly generate a hypergraph in which each hyper-edge contains k vertices, or each vertex is incident to k hyper-edges.

Usage

```r
sample_k_uniform_hypergraph(n, m, k, prob)
sample_k_regular_hypergraph(n, m, k, prob)
```

Arguments

- `n` the order of the hypergraph.
- `m` the size of the hypergraph.
- `k` the order of each hyper-edge.
- `prob` a vector of length n containing the probabilities for the vertices. This is passed to `sample`.

Details

A k-uniform hypergraph is one for which each hyper-edge contains exactly k vertices. A k-regular hypergraph is one for which each vertex has degree k. These are implemented through calls to `sample`.

Value

a hypergraph.

Note

For both of these functions m, the number of hyper-edges, must be provided. This is unlike the corresponding functions for graphs – all simple graphs are 2-uniform, and there are constraints on the values of k for which a graph can be k-regular, since the graphs are constrained to be 2-regular, i.e. all rows of the incidence matrix must contain 2 ones.
sample_sbm_hypergraph

Author(s)
David J. Marchette <dmarchette@gmail.com>.

See Also
sample.

Examples

set.seed(77)
h <- sample_k_uniform_hypergraph(20,5,3)
set.seed(73)
k <- sample_k_regular_hypergraph(20,5,3)

Description

A stochastic block model hypergraph.

Usage

sample_sbm_hypergraph(n,P,block.sizes,d,impurity=0,variable.size=FALSE, absolute.purity=TRUE)

Arguments

n number of vertices.
P A kxk probability matrix.
block.sizes vector of community sizes.
d size of a hyper-edge. See Details.
impurity See Details.
variable.size,absolute.purity logical. See Details.

Details

A stochastic block model is first generated using the function sample_sbm(n,P,block.sizes). The edges are augmented with vertices, resulting in a stochastic block model hypergraph, as discussed below.

The variable d corresponds to the number of vertices per edge. If it is a vector, it is recycled as necessary. If variable.size is TRUE, then d is used as the mean of a Poisson random variable to generate hyper-edge orders, to which 2 is added. So a d of 2 will result in hyper-edge orders with a mean of 4.
For each edge (say, edge k) in the graph, new vertices are added so that the number of vertices in
the (now hyper-)edge is \(d[k]\).

If impurity is 0, then for each edge the vertices are added in proportion to the block sizes, using
sample, so if one community has many more vertices than the others, it will tend to dominate in the
hyper-edges as well. However, it is guaranteed that hyper-edges between two distinct communities
have at least one vertex from each of those two communities, and hyper-edges within communities
are pure in the case of impurity=0; no hyper-edge will contain vertices from more than two
communities.

If impurity>0, then impurity of the vertices not in the original stochastic block model hypergraph
are replaced by random vertices. If absolute.purity is TRUE, these new vertices are sampled
from all other classes. Otherwise they are sample from vertices not in the original hyper-edge. If \(k\)
is 2, only the within community hyper-edges will contain impurities.

Value

a hypergraph.

Author(s)

David J. Marchette <dmarchette@gmail.com>

See Also

sample_gnp_hypergraph, sample_sbm.

Examples

```r
P <- rbind(c(0.1,0.01),c(0.01,0.1))
block.sizes <- c(50,50)
set.seed(55)
h <- sample_sbm_hypergraph(100,P=P,block.sizes=block.sizes,d=4)
range(edge_orders(h))
## should all be 4
set.seed(1233)
k <- sample_sbm_hypergraph(100,P=P,d=2,block.sizes=block.sizes,
variable.size=TRUE)
mean(edge_orders(k))
## should be approximately 4
set.seed(1235)
Q <- rbind(c(.2,.01,.01),
c(.01,.1,.05),
c(.01,.05,.2))
kk <- sample_sbm_hypergraph(300,P=Q,d=6,block.sizes=rep(100,3),
variable.size=TRUE,impurity=2)
```
subtree.hypergraph

Description

Construct a subtree hypergraph from a graph.

Usage

subtree.hypergraph(g, v)

Arguments

g  a graph.

v  a list of vertex sets. See details.

Details

A subtree hypergraph is a hypergraph on the vertices of the graph g, each of whose hyper-edges induces a subtree in g. If v is given, each element of the list must contain at least two elements. For each element of v, all paths between its first element and each of the other elements are computed, and the hyper-edge corresponds to all the vertices in these paths.

Value

a hypergraph.

Note

There are many possible subtree hypergraphs for a given graph. The default is to loop through the vertices in a particular way to generate a hypergraph. The intent is that the use should provide v, rather than using this admittedly arbitrary algorithm.

Author(s)

David J. Marchette <dmarchette@gmail.com>

References


Examples

g <- make_tree(20, mode='undirected')
Summary method for hypergraphs.

Usage

```r
## S3 method for class 'hypergraph'
summary(object, ...)
```

Arguments

- `object`: a hypergraph.
- `...`: ignored arguments.

Value

No return value, called for side effects only – prints to console.

Author(s)

David J. Marchette <dmarchette@gmail.com>

Examples

```r
h <- hypergraph_from_edgelist(list(3:7, 8:12, c(1, 3, 9)))
print(h)
summary(h)
```
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