Package ‘BiRewire’

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Title High-performing routines for the randomization of a bipartite graph (or a binary event matrix), undirected and directed signed graph preserving degree distribution (or marginal totals)
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Description Fast functions for bipartite network rewiring through N consecutive switching steps (See References) and for the computation of the minimal number of switching steps to be performed in order to maximise the dissimilarity with respect to the original network. Includes functions for the analysis of the introduced randomness across the switching steps and several other routines to analyse the resulting networks and their natural projections. Extension to undirected networks and directed signed networks is also provided. Starting from version 1.9.7 a more precise bound (especially for small network) has been implemented. Starting from version 2.2.0 the analysis routine is more complete and a visual monitoring of the underlying Markov Chain has been implemented. Starting from 3.6.0 the library can handle also matrices with NA (not for the directed signed graphs).
License GPL-3
Depends igraph, slam, tsne, Matrix
Suggests RUnit, BiocGenerics
Author Andrea Gobbi [aut], Francesco Iorio [aut], Giuseppe Jurman [cbt], Davide Albanese [cbt], Julio Saez-Rodriguez [cbt].
URL http://www.ebi.ac.uk/~iorio/BiRewire
biocViews Network
NeedsCompilation yes

R topics documented:

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BiRewire-package

The BiRewire package

Description

R package for computationally-efficient rewiring of bipartite graphs (or randomisation of 0-1 tables with prescribed marginal totals), undirected and directed signed graphs (dsg). The package provides useful functions for the analysis and the randomisation of large biological datasets that can be encoded as 0-1 tables, hence modeled as bipartite graphs by considering a 0-1 table as an incidence matrix, and for data that can be encoded as directed signed graphs such as pathways and signaling networks. Large collections of such randomised tables can be used to approximate null models, preserving event-rates both across rows and columns, for statistical significance tests of combinatorial properties of the original dataset. The package provides an interface to a sampler routine useful for generating correctly such collections. Moreover a visual monitoring for the Markov Chain underlying the switching algorithm has been implemented. Since version 3.6.0 the SA can be performed also using matrices with NAs. In this case the positions of the NAs are preserved as the degree distribution. This extension is limited when the tables are provided instead of the graphs and does not work for the dsg.

Details

Summary:

Package: BiRewire
Version: 3.6.0
Date: 2017-02-27
Require: slam, igraph, tsne, Matrix, R>=2.10
URL: http://www.ebi.ac.uk/~iorio/BiRewire
License: GPL-3

Author(s)

Andrea Gobbi [aut], Davide Albanese [cbt], Francesco Iorio [cbt], Giuseppe Jurman [cbt].
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References


birewire.analysis.bipartite

Analysis of Jaccard similarity trends across switching steps.

Description

This function performs a sequence of max.iter switching steps on the input bipartite graph g and compute the Jaccard similarity between g (the initial network) and its rewired version each step switching steps. This procedure is performed n.networks times and a simple explorative plot, with mean and CI, is visualized if display is set to true.

Usage

birewire.analysis.bipartite(incidence, step=10, max.iter="n",accuracy=0.00005, verbose=TRUE,MAXITER_MUL=10,exact=FALSE,n.networks=50,display=TRUE)

Arguments

incidence Incidence matrix of the initial bipartite graph g (can be extracted from an igraph bipartite graph using the get.incidence function). Since 3.6.0 this matrix can contain also NAs and the position of such entries will be preserved by the SA;

step 10 (default): the interval (in terms of switching steps) at which the Jaccard index between g and the its current rewired version is computed;
max.iter  "n" (default) the number of switching steps to be performed (or if exact=TRUE the number of successful switching steps). If equal to "n" then this number is considered equal to the analytically derived lower bound presented in Gobbi et al. (see References): \( N = \frac{e}{2(1 - d)} \ln \left( \frac{(e - de)}{\delta} \right) \) if exact is FALSE, \( N = \frac{e(1 - d)}{2} \ln \left( \frac{(e - de)}{\delta} \right) \) otherwise, where \( e \) is the number of edges of \( g \) and \( d \) its edge density. This bound is much lower than the empirical one proposed in Milo et al. 2003 (see References);

accuracy  0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;

verbose  TRUE (default). When TRUE a progression bar is printed during computation;

MAXITER_MUL  10 (default). If exact=TRUE in order to prevent a possible infinite loop the program stops anyway after MAXITER_MUL*max.iter iterations;

exact  FALSE (default). If TRUE the program performs max.iter switching steps, otherwise the program will count also the not-performed switching steps;

n.networks  50 (default), the number of independent rewiring process starting from the same initial graph from which the mean value and the CI is computed.

display  TRUE (default). If TRUE two explorative plots are displayed summarizing the trend of the Jaccard index in terms of mean and confidence interval.

Details

This function performs max.iter switching steps (see references). In particular, at each step two edges are randomly selected from the current version of \( g \). Let these two edges be \((a, b)\) and \((c, d)\) (where \( a \) and \( c \) belong to the first class of nodes whereas \( b \) and \( d \) belong to the second one), with \( a \neq c \) and \( b \neq d \).

If the \((a, d)\) and \((c, b)\) edges are not already present in the current current version of \( g \) then \((a, d)\) and\((c, b)\) replace \((a, b)\) and \((c, d)\).

At each step number of switching steps the function computes the Jaccard index between the original graph \( g \) and its current version.

This procedure is perfomed n.networks times and if display is set to TRUE, two explorative plots showing the mean value of the Jaccard Index over the SS and its CI are displayed.

Value

A list containing a data.frame data collecting all the Jacard index computed (each row is a run of the SA), and the analytically derived lower bound \( N \) of switching steps to be performed by the switching algorithm in order to provide the revired version of \( g \) with the maximal level of achievable randomness (in terms of dissimilarity from the initial \( g \)).

Author(s)

Andrea Gobbi

Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>

Special thanks to:
Davide Albanese

References


Examples

```r
library(BiRewire)
g <- graph.bipartite(rep(0:1,length=10), c(1:10))
##get the incidence matrix of g
m<-as.matrix(get.incidence(graph=g))
## set parameters
step=1
max=100*length(E(g))
## perform two different analysis using two different maximal number of switching steps
scores<-birewire.analysis.bipartite(m,step,max,n.networks=10)
scores2<-birewire.analysis.bipartite(m,step,"n",n.networks=10)
```

birewire.analysis.dsg  Analysis of Jaccard similarity trends across switching steps.

Description

This function performs a sequence of max.iterpos (and max.iterpos) switching steps on the positive (and negative) part of the input dsg g and computes the Jaccard similarity between g (the initial network) and its rewired version each step switching steps. This procedure is performed n.networks times and a simple explorative plot, with mean and CI, is visualized if display is set to TRUE. The plot shows the trend of the Jaccad Index relative to the positive (and negative) part of g.

Usage

```r
birewire.analysis.dsg(dsg, step=10, max.iter.pos='n', max.iter.neg='n', accuracy=0.00005, verbose=TRUE, MAXITER_MUL=10, exact=FALSE, n.networks=50, display=TRUE)
```
Arguments

dsg
The initial dsg object (see birewire.induced.bipartite). Note that the dsg must contain a list of two incidence matrices and not igraph bipartite graphs.

step
10 (default): the interval (in terms of switching steps) at which the Jaccard index between g and the its current rewired version is computed;

max.iter.pos
"n" (default) the number of switching steps to be performed (or if exact==TRUE the number of successful switching steps) for the positive part of g. See birewire.rewire.bipartite for more details;

max.iter.neg
"n" (default) the same of max.iter.p but relative to the negative part;

accuracy
0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;

verbose
TRUE (default). When TRUE a progression bar is printed during computation;

MAXITER_MUL
10 (default). If exact==TRUE in order to prevent a possible infinite loop the program stops anyway after MAXITER_MUL*max.iter iterations;

exact
FALSE (default). If TRUE the program performs max.iter switching steps, otherwise the program will count also the not-performed switching steps;

n.networks
50 (default), the number of independent rewiring process starting from the same initial graph from which the mean value and the CI is computed.

display
TRUE (default). If TRUE two explorative plots are displayed summarizing the trend of the Jaccard index in terms of mean and confidence interval.

Details

This procedure acts in the same way of birewire.analysis.bipartite but in the case of dsg. The similarity is measured using birewire.similarity.dsg.

Value

A list containing two lists: data that is a list collecting all the Jaccard index computed (each row is a run of the SA) for the positive and negative part, and a list with the analytically derived lower bounds N for the positive and negative part of g.

Author(s)

Andrea Gobbi
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References


Examples

```r
library(BiRewire)
data(test_dsg)
dsg <- birewire.induced.bipartite(test_dsg,sparse=FALSE)
a=birewire.analysis.dsg(dsg,verbose=FALSE,step=1,exact=TRUE,max.iter.pos=200,max.iter.neg=50)
```

Description

This function performs a sequence of `max.iter` switching steps on the input undirected graph `g` and compute the Jaccard similarity between `g` (the initial network) and its rewired version each `step` switching steps. This procedure is performed `n.networks` times and a simple explorative plot, with mean and CI, is visualized if `display` is set to `TRUE`.

Usage

```r
birewire.analysis.undirected(adjacency, step=10, max.iter="n", accuracy=0.00005, verbose=TRUE, MAXITER_MUL=10, exact=FALSE, n.networks=50, display=TRUE)
```

Arguments

- `adjacency`: Incidence matrix of the initial bipartite graph `g` (can be extracted from an igraph undirected graph using the `get.adjacency` function). Since 3.6.0 this matrix can contain also NAs and the position of such entries will be preserved by the SA;
- `step`: 10 (default): the interval (in terms of switching steps) at which the Jaccard index between `g` and its current rewired version is computed;
- `max.iter`: "n" (default) the number of switching steps to be performed (or if `exact=`TRUE the number of successful switching steps). If equal to "n" then this number is considered equal to the analytically derived lower bound presented in Gobbi et al. (see References): \( N = \frac{e}{(2d^3 - dd^2 + 2d + 2)} \ln \left( \frac{(e - de)}{\delta} \right) \) if exact is FALSE, \( N = \frac{e(1 - d)}{2} \ln \left( \frac{(e - de)}{\delta} \right) \) otherwise , where `e` is the number of edges of `g` and `d` its edge density . This bound is much lower than the empirical one proposed in Milo et al. 2003 (see References);
- `accuracy`: 0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;
birewire.analysis.undirected

verbose  TRUE (default). When TRUE a progression bar is printed during computation;
MAXITER_MUL  10 (default). If exact=TRUE in order to prevent a possible infinite loop the program stops anyway after MAXITER_MUL*max.iter iterations;
exact  FALSE (default). If TRUE the program performs max.iter switching steps, otherwise the program will count also the not-performed switching steps;
n.networks  50 (default), the number of independent rewiring process starting from the same initial graph from which the mean value and the CI is computed.
display  TRUE (default). If TRUE two explorative plots are displayed summarizing the trend of the Jaccard index in terms of mean and confidence interval.

Details

This function performs max.iter switching steps (see references). In particular, at each step two edges are randomly selected from the current version of \( g \). Let these two edges be \((a, b)\) and \((c, d)\), with \( a \neq c, b \neq d, a \neq d, b \neq c \). If the \((a, d)\) and \((c, b)\) (or \((a, d)\) and \((b, d)\)) edges are not already present in the current version of \( g \) then \((a, d)\) and \((c, b)\) replace \((a, b)\) and \((c, d)\) (or \((a, b)\) and \((c, d)\) replace \((a, c)\) and \((b, d)\)). If both of the configurations are allowed, then one of them is randomly selected.

At each step number of switching steps the function computes the Jaccard index between the original graph \( g \) and its current version. This procedure is performed n.networks times and if display is set to TRUE, two explorative plots showing the mean value of the Jaccard Index over the SS and its CI are displayed.

Value

A list containing a data.frame data collecting all the Jaccard index computed (each row is a run of the SA), and the analytically derived lower bound \( N \) of switching steps to be performed by the switching algorithm in order to provide the revived version of \( g \) with the maximal level of achievable randomness (in terms of dissimilarity from the initial \( g \)).

Author(s)

Andrea Gobbi
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Special thanks to:
Davide Albanese

References


**Examples**

```r
library(BiRewire)
g <- erdos.renyi.game(1000, 0.1)
## get the incidence matrix of g
m <- as.matrix(get.adjacency(graph=g, sparse=FALSE))
## set parameters
step = 1000
max = 100 * length(E(g))
## perform two different analysis using two different numbers of switching steps
scores <- birewire.analysis.undirected(m, step, max, n.networks = 10, verbose = FALSE)
scores2 <- birewire.analysis.undirected(m, step, "n", n.networks = 10, verbose = FALSE)
```

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**birewire.bipartite.from.incidence**

Converts an incidence matrix into a bipartite graph.

**Description**

This function creates an igraph bipartite graph from an incidence matrix.

**Usage**

```r
birewire.bipartite.from.incidence(matrix, directed = FALSE)
```

**Arguments**

- **matrix**: incidence matrix: an (n-by-m) binary matrix where rows correspond to vertices in the first class while columns correspond to vertices in the second one;
- **directed**: Logical, if TRUE a directed graph is created.

**Details**

The function calls `graph.incidence` of package igraph. See igraph documentation for more details.

**Value**

Bipartite igraph graph.
birewire.build.dsg

Transform a dsg object in a SIF file.

Description
The routine transforms the initial dsg (two bipartite graphs) into SIF dsg format.

Usage
birewire.build.dsg(dsg, delimitators=list(negative='-', positive='+'))

Arguments

- **dsg**  The dsg to be converted;
- **delimitators**  list(negative='-', positive='+')(default): a list with 'positive' and 'negative' names identifying the character encoding the relation;

Details
This function converts the dsg object into a SIF format that can be saved using birewire.write.dsg, an internal function, using the given delimitators for encoding the relations. It is the inverse function of birewire.induced.bipartite.

Value
A dsg in SIF format.
Examples

data(test_dsg)
dsg=birewire.induced.bipartite(test_dsg)
tmp= birewire.rewire.dsg(dsg,verbose=FALSE)
dsg2=birewire.build.dsg(tmp)

birewire.induced.bipartite

Transform a SIF data frame into a dsg object (a list of positive and negative incidence matrix).

Description

The routine transforms the initial dsg graph in SIF format into a dsg object made of two bipartite graphs: one for positive edges and the other for negative edges.

Usage

birewire.induced.bipartite(g,delimitators=list(negative='-',positive='+'),sparse=FALSE)

Arguments

g A dataframe in SIF format describing a dsg (for example the output of birewire.load.dsg);
delimitators list(negative='-',positive='+') (default): a list with 'positive' and 'negative' names identifying the character encoding the relation;
sparse FALSE (default): if TRUE the two bipartite graphs are saved as igraph bipartite graphs;

Details

This function extract the positive and negative part of \( g \) and create a dsg object that can be used for example in the rewiring algorithm. Is is the inverse function of birewire.build.dsg.

Value

A list of two incidence matrix or bipartite igraph objects.

References


Examples

data(test_dsg)
dsg=birewire.induced.bipartite(test_dsg)
birewire.load.dsg  Read a SIF file from a given path

Description
The routine reads a SIF file and return a R table.

Usage
birewire.load.dsg(path)

Arguments
path  Path to the SIF file.

Value
A R table that can be transformed into a dsg using birewire.induced.bipartite

birewire.rewire.bipartite  Efficient rewiring of bipartite graphs

Description
Optimal implementation of the switching algorithm. It returns the rewired version of the initial bipartite graph or its incidence matrix.

Usage
birewire.rewire.bipartite(incidence, max.iter="n", accuracy=0.00005, verbose=TRUE, MAXITER_MUL=10, exact=FALSE)

Arguments
incidence  Incidence matrix of the initial bipartite graph \( g \) (can be extracted from an igraph bipartite graph using the get.incidence function; or the entire bipartite igraph graph. Since 3.6.0, in the case the matrix is provided, such matrix can contain also NAs and the position of such entries will be preserved by the SA
max.iter  "n" (default) the number of switching steps to be performed (or if exact=TRUE the number of successful switching steps). If equal to "n" then this number is considered equal to the analytically derived lower bound presented in Gobbi et al. (see References): \( N = \frac{e}{2(1 - d)} \ln \left( \frac{(e - de)/\delta}{\left( e - de \right)/\delta} \right) \) if exact is FALSE, \( N = \frac{e(1 - d)}{2 \ln \left( \frac{(e - de)/\delta}{\left( e - de \right)/\delta} \right)} \) otherwise , where \( e \) is the number of edges of \( g \) and \( d \) its edge density . This bound is much lower than the empirical one proposed in Milo et al. 2003 (see References);
accuracy  0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;
verbose

TRUE (default). When TRUE a progression bar is printed during computation.

MAXITER_MUL

10 (default). If exact=TRUE in order to prevent a possible infinite loop the program stops anyway after MAXITER_MUL*max.iter iterations;

exact

FALSE (default). If TRUE the program performs max.iter switching steps, otherwise the program will count also the not-performed switching steps;

Details

Main function of the package. It performs at most max.iter switching steps producing a rewired version of an initial bipartite graph.

Value

Incidence matrix of the rewired graph or the igraph corresponding object depending on the input type.

Author(s)

Andrea Gobbi
Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>

References


Examples

library(igraph)
library(BiRewire)
g <- graph.bipartite( rep(0:1,length=10), c(1:10))
##gets the incidence matrix of g
m<-as.matrix(get.incidence(graph=g))
##rewiring
m2=birewire.rewire.bipartite(m,100*length(E(g)))
##creates the corresponding bipartite graph
g2<birewire.bipartite.from.incidence(m2,directed=TRUE)
birewire.rewire.bipartite.and.projections

Analysis and rewiring function processing a bipartite graphs and its two projections

Description

This function performs the same analysis of birewire.analysis.bipartite but additionally it provides in output a rewired version of the two networks resulting from the natural projections of the initial graph, together with the corresponding Jaccard index trends.

Usage

birewire.rewire.bipartite.and.projections(graph, step=10, max.iter="n", accuracy=0.00005, verbose=TRUE, MAXITER_MUL=10)

Arguments

graph A bipartite graph g;
max.iter "n" (default) the number of successful switching steps to be performed. If equal to "n" then this number is considered equal to the analytically derived lower bound \( N = e(1 - d)/2\ln((e - de)/\delta) \) presented in Gobbi et al. (see References);
step 10 (default): the interval (in terms of switching steps) at which the Jaccard index between g and the its current rewired version is computed;
accuracy 0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;
verbose TRUE (default) boolean value. If TRUE print a processing bar during the rewiring algorithm.
MAXITER_MUL 10 (default).Since \( N \) indicates the number of successful switching steps, in order to prevent a possible infinite loop the program stops anyway after MAX-ITER_MUL*max.iter iterations ;

Details

See birewire.analysis.bipartite for details.

Value

A list containing the three sequences of Jaccard index values (similarity_scores, similarity_scores.proj1, similarity_scores.proj2) for the three resulting graphs respectively (rewired, rewired.proj1, rewired.proj2). The first one is the rewired version of the initial graph g, while the second and the third one are rewired versions of its natural projections.

Author(s)

Andrea Gobbi
Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>
References


Examples

```r
library(igraph)
library(BiRewire)
g <- simplify(graph.bipartite(rep(0:1,length=100),
c(c(1:100), seq(1,100,3), seq(1,100,7), 100, seq(1,100,13),
   seq(1,100,17), seq(1,100,19), seq(1,100,23), 100)))
## gets the incidence matrix of g
m<-as.matrix(get.incidence(graph=g))
## rewires g and its projections
result=birewire.rewire.bipartite.and.projections(g,step=10,max.iter="n",accuracy=0.00005)
```

### birewire.rewire.dsg

**Efficient rewiring of directed signed graphs**

**Description**

Optimal implementation of the switching algorithm. It returns the rewired version of the initial directed signed graph (dsg).

**Usage**

```r
birewire.rewire.dsg(dsg,exact=FALSE,verbose=1,max.iter.pos='n',max.iter.neg='n',
   accuracy=0.00005,MAXITER_MUL=10,path=NULL,delimitators=list(positive='+',negative='-'))
```

**Arguments**

- **dsg**
  A dsg object: is a list of two incidence matrices (see References), "positive" and "negative", encoding the positive edges and negative edges. This list can be obtained reading a SIF file using `birewire.load.dsg` function and converting the resulting dataframe using `birewire.induced.bipartite`;

- **exact**
  FALSE (default). If TRUE the program performs `max.iter` successful switching steps, otherwise the program will count also the not-performed switching steps;

- **verbose**
  TRUE (default). When TRUE a progression bar is printed during computation;
max.iter.pos  "n" (default) the number of switching steps to be performed on the positive part of dsg (or if exact==TRUE the number of successful switching steps). If equal to "n" then this number is considered equal to the analytically derived lower bound presented in Gobbi et al. (see References): $N = e/2(1-d) \ln ((e-de)/\delta) $ if exact is FALSE, $N = e(1-d)/2 \ln ((e-de)/\delta)$ otherwise , where $e$ is the number of edges of g and $d$ its edge density . This bound is much lower than the empirical one proposed in Milo et al. 2003 (see References);

max.iter.neg  "n" (default) the number of switching steps to be performed on the negative part of dsg (or if exact==TRUE the number of successful switching steps). If equal to "n" then this number is considered equal to the analytically derived lower bound presented in Gobbi et al. (see References): $N = e/2(1-d) \ln ((e-de)/\delta) $ if exact is FALSE, $N = e(1-d)/2 \ln ((e-de)/\delta)$ otherwise , where $e$ is the number of edges of g and $d$ its edge density . This bound is much lower than the empirical one proposed in Milo et al. 2003 (see References);

accuracy  0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;

MAXITER_MUL  10 (default). If exact==TRUE in order to prevent a possible infinite loop the program stops anyway after MAXITER_MUL*max.iter iterations;

path  NULL (default). If not NULL, the dsg is saved in path in SIF format;

delimimiters  list(positive='+',negative=' -') (default). If save.file is true, the dsg is saved using delimiters as characters encoding the relations. See birewire.build.dsg for more details.

Details

This function runs birewire.rewire.bipartite on the positive and negative part of dsg. See references for more details.

Value

Rewired dsg.

Author(s)

Andrea Gobbi: <gobbi.andrea@mail.com>

References


birewire.rewire.undirected

Examples

```r
library(BiRewire)
data(test_dsg)
dsg=birewire.induced.bipartite(test_dsg)
tmp= birewire.rewire.dsg(dsg,verbose=FALSE)
```

birewire.rewire.undirected

**Efficient rewiring of undirected graphs**

Description

Optimal implementation of the switching algorithm. It returns the rewired version of the initial undirected graph or its adjacency matrix.

Usage

```r
birewire.rewire.undirected(adjacency, max.iter="n",accuracy=0.00005, verbose=TRUE,MAXITER_MUL=10,exact=FALSE)
```

Arguments

- **adjacency**: An igraph undirected graph `g` or its adjacency matrix (can be extracted from `g` using `get.adjacency`). Since 3.6.0, if the matrix is provided, such matrix can contain also NAs and the position of such entries will be preserved by the SA
- **max.iter**: "n" (default) the number of switching steps to be performed (or if `exact`=`TRUE` the number of successful switching steps). If equal to "n" then this number is considered equal to the analytically derived lower bound presented in Gobbi et al. (see References): $N = \frac{e}{(2d^3 - 6d^2 + 2d + 2)} \ln \left( \frac{e - de}{\delta} \right)$ if exact is FALSE, $N = \frac{e(1 - d)}{2} \ln \left( \frac{(e - de)}{\delta} \right)$ otherwise, where $e$ is the number of edges of `g` and $d$ its edge density. This bound is much lower than the empirical one proposed in Milo et al. 2003 (see References);
- **accuracy**: 0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;
- **verbose**: TRUE (default) boolean value. If TRUE print a processing bar during the rewiring algorithm.
- **MAXITER_MUL**: 10 (default). If `exact`=`TRUE` in order to prevent a possible infinite loop the program stops anyway after `MAXITER_MUL`*`max.iter` iterations;
- **exact**: FALSE (default). If TRUE the program performs `max.iter` switching steps, otherwise the program will count also the not-performed switching steps;

Details

Performs at most `max.iter` number of rewiring steps producing a rewired version of an initial undirected graph.
Value

Adjacency matrix of the rewired graph or the relative igraph object depending on the input type.

Author(s)

Andrea Gobbi

Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>

Special thanks to: Davide Albanese

References


Examples

library(igraph)
library(BiRewire)
g <- erdos.renyi.game(1000,0.1)
## gets the incidence matrix of g
m<-as.matrix(get.adjacency(graph=g,sparse=FALSE))

## sets parameters
step=1000
max=100*length(E(g))

## rewiring
m2=birewire.rewire.undirected(m,100*length(E(g)))
## creates the corresponding bipartite graph
g2<-graph.adjacency(m2,mode="undirected")
birewire.sampler.bipartite

Efficient generation of a null model for a given bipartite graph

Description

The routine samples correctly from the null model of a given bipartite graph creating a set of randomized version of the initial bipartite graph.

Usage

birewire.sampler.bipartite(incidence, K, path, max.iter=“n”, accuracy=0.00005, verbose=TRUE, MAXITER_MUL=10, exact=FALSE, write.sparse=TRUE)

Arguments

incidence
Incidence matrix of the initial bipartite graph. Since 3.6.0 this matrix can contain also NAs and the position of such entries will be preserved by the SA;

K
The number of networks that has to be generated;

path
The directory in which the routine stores the outputs;

max.iter
"n" (default) the number of switching steps to be performed (or if exact==TRUE the number of successful switching steps). If equal to "n" then this number is considered equal to the analytically derived lower bound presented in Gobbi et al. (see References): 
\[ N = \frac{e}{2(1-d)} \ln\left(\frac{e - de}{\delta}\right) \]
if exact is FALSE,
\[ N = \frac{e(1-d)}{2} \ln\left(\frac{e - de}{\delta}\right) \]
otherwise , where \( e \) is the number of edges of \( g \) and \( d \) its edge density . This bound is much lower than the empirical one proposed in Milo et al. 2003 (see References);

accuracy
0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;

verbose
TRUE (default). When TRUE a progression bar is printed during computation.

MAXITER_MUL
10 (default). If exact==TRUE in order to prevent a possible infinite loop the program stops anyway after MAXITER_MUL*max.iter iterations;

exact
FALSE (default). If TRUE the program performs max.iter swithcing steps, otherwise the program will count also the not-performed switching steps;

write.sparse
TRUE (default). If FALSE the table is written as an R data.frame (long time and more space needed)

Details

The routine creates, starting from the given path, different subfolders in order to have maximum 1000 files for folder . Moreover the incidence matrices are saved using write_stm_CLUTO (sparse matrices) that can be loaded using read_stm_CLUTO. The set is generated calling birewire.rewire.bipartite on the last generated graph starting from the input graph.

Author(s)

Andrea Gobbi: <gobbi.andrea@mail.com>
birewire.sampler.dsg

References


birewire.sampler.dsg  Efficient generation of a null model for a given dsg.

Description

Efficient generation of a null model for a given dsg. The routine samples correctly from the null model of a given dsg creating a set of randomized dsgs.

Usage

birewire.sampler.dsg(dsg,K,path,delimitators=list(negative='-',positive='+'),exact=FALSE, verbose=TRUE, max.iter.pos='n',max.iter.neg='n', accuracy=0.00005,MAXITER_MUL=10)

Arguments

dsg  A dsg object: is a list of two incidence matrices (see References), "positive" and "negative", encoding the positive edges and negative edges. This list can be obtained reading a SIF file using birewire.load.dsg function and converting the resulting dataframe using birewire.induced.bipartite.

max.iter.pos  "n" (default) the number of switching steps to be performed on the positive part of dsg (or if exact==TRUE the number of successful switching steps). If equal to "n" then this number is considered equal to the analytically derived lower bound presented in Gobbi et al. (see References): \( N = \frac{e}{2(1-d)} \ln \left( \frac{(e-de)}{\delta} \right) \) if exact is FALSE, \( N = \frac{e}{2(1-d)} \frac{1}{2} \ln \left( \frac{(e-de)}{\delta} \right) \) otherwise , where \( e \) is the number of edges of \( g \) and \( d \) its edge density . This bound is much lower than the empirical one proposed in Milo et al. 2003 (see References);

max.iter.neg  "n" (default) the number of switching steps to be performed on the negative part of dsg (or if exact==TRUE the number of successful switching steps). If equal to "n" then this number is considered equal to the analytically derived lower bound presented in Gobbi et al. (see References): \( N = \frac{e}{2(1-d)} \ln \left( \frac{(e-de)}{\delta} \right) \) if exact is FALSE, \( N = \frac{e}{2(1-d)} \frac{1}{2} \ln \left( \frac{(e-de)}{\delta} \right) \) otherwise , where \( e \) is the number of edges of \( g \) and \( d \) its edge density . This bound is much lower than the empirical one proposed in Milo et al. 2003 (see References);

accuracy  0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;
birewire.sampler.undirected

**Description**

The routine samples correctly from the null model of a given undirected graph creating a set of randomized version of the initial undirected graph.

**Usage**

```r
birewire.sampler.undirected(adjacency,K,path,max.iter="n", accuracy=0.00005, verbose=TRUE,MAXITER_MUL=10,exact=FALSE,write.sparse=TRUE)
```
Arguments

adjacency Adjacency matrix of the initial undirected graph. Since 3.6.0 this matrix can contain also NAs and the position of such entries will be preserved by the SA;

K The number of networks that has to be generated;

path The directory in which the routine stores the outputs;

max.iter "n" (default) see birewire.rewire.undirected for references

accuracy 0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;

verbose TRUE (default). When TRUE a progression bar is printed during computation.

MAXITER_MUL 10 (default). If exact==TRUE in order to prevent a possible infinite loop the program stops anyway after MAXITER_MUL*max.iter iterations;

exact FALSE (default). If TRUE the program performs max.iter switching steps, otherwise the program will count also the not-performed switching steps;

write.sparse TRUE (default). If FALSE the table is written as an R data.frame (long time and more space needed)

Details

The routine creates, starting from the given path, different subfolders in order to have maximum 1000 files for folder . Moreover the incidence matrices are saved using write_stm_CLUTO (sparse matrices) that can be loaded using read_stm_CLUTO. The set is generated calling birewire.rewire.undirected on the last generated graph starting from the input graph.

Author(s)

Andrea Gobbi: <gobbi.andrea@mail.com>

References


Compute the Jaccard similarity index between two binary matrices with the same number of non-null entries and the same row- and column-wise sums.

Usage

\[
\text{birewire.similarity}(\text{m1,m2})
\]

Arguments

- \texttt{m1} First matrix or graph;
- \texttt{m2} Second matrix or graph.

Details

The \textbf{Jaccard} index between two sets \( M \) and \( N \) is defined as:
\[
\frac{|M \cup N|}{|M \cap N|}
\]
With \( M \) and \( N \) binary matrices, the Jaccard index is computed as:
\[
\frac{\sum N_{i,j} \land M_{i,j}}{\sum N_{i,j} \lor M_{i,j}}.
\]

The Jaccard index ranges between 0 and 1 and since 3.6.0 can be computed also among matrix with NAs.

Value

Returns the Jaccard similarity index between the objects.

Author(s)

Andrea Gobbi
Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>

Examples

```r
library(igraph)
library(BiRewire)
g <- graph.bipartite( rep(0:1,length=10), c(1:10))
g2=birewire.rewire.bipartite(g)
birewire.similarity(get.incidence(g,sparse=FALSE),get.incidence(g2,sparse=FALSE))
birewire.similarity(g,g2)
```
birewire.similarity.dsg

Compute the Jaccard similarity index between dsg.

Description

Compute the Jaccard similarity index between dsg objects described in the same way (matrices of graphs).

Usage

birewire.similarity.dsg( m1,m2)

Arguments

m1    First dsg;
m2    Second dsg.

Details

See birewire.similarity for more details.

Value

Returns the Jaccard similarity index between the objects.

Author(s)

Andrea Gobbi
Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>

Examples

library(BiRewire)
data(test_dsg)
dsg <- birewire.induced.bipartite(test_dsg,sparse=FALSE)
birewire.similarity.dsg(dsg,birewire.rewire.dsg(dsg))
dsg <- birewire.induced.bipartite(test_dsg,sparse=TRUE)
birewire.similarity.dsg(dsg,birewire.rewire.dsg(dsg))
birewire.slum.to.sparseMatrix

The function transforms a triplet sparse matrix from slum package to a Matrix sparse matrix.

Description

Transform a triplet sparse matrix from slum package to a Matrix sparse matrix that can be used by igraph for creating a network. This function could be used in order to analyze graphs obtained from samplers routines (birewire.sampler.undirected, birewire.sampler.dsg and birewire.sampler.bipartite.)

Usage

birewire.slum.to.sparseMatrix( simple_triplet_matrix_sparse)

Arguments

simple_triplet_matrix_sparse
A triplet sparse matrix, usually the object coming from read_stm_CLUTO.

Value

Returns an Matrix sparse matrix that could be used for building an igraph graph using graph.adjacency.

Author(s)

Andrea Gobbi
Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>

birewire.visual.monitoring.bipartite

Visual monitoring of the Markov chain underlying the SA for directed graphs.

Description

This function generates a cascade-sampling from the model at different switching steps given in sequence. For each step the routine computes the pairwise Jaccard distance (1-JI) among the samples and perfroms, on the resulting matrix, a dimentional scaling reduction (using tsne). If display is set to TRUE the relative plot is displayed.

Usage

birewire.visual.monitoring.bipartite(data, accuracy=0.00005, verbose=FALSE, MAXITER_MUL=10, exact=FALSE, n.networks=100, perplexity=15, sequence=c(1,5,100,"n"), ncol=2, nrow=length(sequence)/ncol, display=TRUE)
Arguments

- **data**: The initial bipartite graph, either an incidence matrix or an `igraph` bipartite graph object. Since 3.6.0, if the matrix is provided, such matrix can contain also NAs and the position of such entries will be preserved by the SA;
- **accuracy**: 0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;
- **verbose**: TRUE (default). When TRUE a progression bar is printed during computation.
- **MAXITER_MUL**: 10 (default). If `exact==TRUE` in order to prevent a possible infinite loop the program stops anyway after `MAXITER_MUL*max.iter` iterations;
- **exact**: FALSE (default). If TRUE the program performs `max.iter` switching steps, otherwise the program will count also the not-performed switching steps;
- **n.networks**: 100 (default): the number of network generated for each step defined in `sequence`;
- **perplexity**: 15 (default): the value of perplexity passed to the function `tsne`;
- **sequence**: `c(1,5,100,"n")` (default) the sequence of step for which generating a sampler (see `birewire.sampler.bipartite`);
- **ncol**: 2 (default). The number of column in the plot;
- **nrow**: `length(sequence)/ncol` (default). The number of row in the plot;
- **display**: TRUE (default). If TRUE the result is displayed.

Details

For each value `p` in `sequence` (it that can also contain the special character "n", see `birewire.rewire.bipartite`), the routine generates `n.networks` sampled each `p SS` from the SA initialized with the given `data`. Pariwise distance are computed using the Jaccard distance and the resulting matrix is the input for the dimensional scaling performed by the function `tsne`. An explorative plot is displayed if `display` is set to TRUE.

Value

A list containing the list containing the distance matrices `dist` and the list containing the `tsne` results.

Author(s)

Andrea Gobbi
Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>

References


**Examples**

```r
library(BiRewire)
g <- graph.bipartite( rep(0:1,length=100), c(1:100))
birewire.visual.monitoring.bipartite(g,display=FALSE,n.networks=10)
```

**Description**

This function generates a cascade-sampling from the model at different switching steps given in sequence. For each step the routine computes the pairwise Jaccard distance (1-JI) among the samples and performs, on the resulting matrix, a dimensional scaling reduction (using tsne). If display is set to `TRUE` the relative plot is displayed.

**Usage**

```r
birewire.visual.monitoring.dsg(data,accuracy=0.00005,verbose=FALSE,MAXITER_MUL=10,exact=FALSE,n.networks=100,perplexity=15,
sequence.pos=c(1,5,100,"n"),
sequence.neg=c(1,5,100,"n"),ncol=2,nrow=length(sequence.pos)/ncol,display=TRUE)
```

**Arguments**

- **data**: The initial dsg either in matrix or graph formulation (see `birewire.induced.bipartite`).
- **accuracy**: 0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;
- **verbose**: `TRUE` (default). When `TRUE` a progression bar is printed during computation.
- **MAXITER_MUL**: 10 (default). If `exact=TRUE` in order to prevent a possible infinite loop the program stops anyway after MAXITER_MUL*max.iter iterations;
- **exact**: `FALSE` (default). If `TRUE` the program performs max.iter switching steps, otherwise the program will count also the not-performed switching steps;
- **n.networks**: 100 (default): the number of network generated for each step defined in sequence;
- **perplexity**: 15 (default): the value of perplexity passed to the function `tsne`;
sequence.pos  c(1,5,100,"n") (default) the sequence of step for which generating a sampler (see `birewire.sampler.dsg`) for the positive part of `data`

sequence.neg  same as `sequence.pos` but for the negative part

ncol  2 (default). The number of column in the plot;

nrow  length(sequence)/ncol (default). The number of row in the plot;

display  TRUE (default). If TRUE the result of tsne is displayed.

Details

See `birewire.visual.monitoring.bipartite` for more details.

Value

A list containing the list containing the distance matrices `dist` and the list containing the tsne results `tsne`.

Author(s)

Andrea Gobbi
Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>

References


Examples

```r
library(BiRewire)

data(test_dsg)
## bigger dsg
test_dsg_2=test_dsg
test_dsg_2[,1]=paste(test_dsg_2[,1],"_",sep="")
test_dsg_2[,3]=paste(test_dsg_2[,3],"_",sep="")

dsg <- birewire.induced.bipartite(rbind(test_dsg,test_dsg_2),sparse=FALSE)
```
birewire.visual.monitoring.undirected

Visual monitoring of the Markov chain underlying the SA for undirected graphs.

Description

This function generates a cascade-sampling from the model at different switching steps given in sequence. For each step the routine computes the pairwise Jaccard distance (1-JI) among the samples and performs, on the resulting matrix, a dimensional scaling reduction (using tsne). If display is set to TRUE the relative plot is displayed.

Usage

birewire.visual.monitoring.undirected(data, accuracy=0.00005, verbose=FALSE, MAXITER_MUL=10, exact=FALSE, n.networks=100, perplexity=15, sequence=c(1,5,100,"n"), ncol=2, nrow=length(sequence)/ncol, display=TRUE)

Arguments

data The initial undirected graph, either an adjacency matrix or an igraph undirected graph object. Since 3.6.0, if the matrix is provided, such matrix can contain also NAs and the position of such entries will be preserved by the SA;
accuracy 0.00005 (default) is the desired level of accuracy reflecting the average distance between the Jaccard index at the N-th step and its analytically derived fixed point in terms of fraction of common edges;
verbose TRUE (default). When TRUE a progression bar is printed during computation.
MAXITER_MUL 10 (default). If exact==TRUE in order to prevent a possible infinite loop the program stops anyway after MAXITER_MUL*max.iter iterations;
exact FALSE (default). If TRUE the program performs max.iter switching steps, otherwise the program will count also the not-performed switching steps;
n.networks 100 (default): the number of network generated for each step defined in sequence;
perplexity 15 (default): the value of perplexity passed to the function tsne;
sequence c(1,5,100,"n") (default) the sequence of step for which generating a sampler (see birewire.sampler.undirected)
ncol 2 (default). The number of column in the plot;
nrow length(sequence)/ncol (default). The number of row in the plot;
display TRUE (default). If TRUE the result of tsne is displayed.

Details

For each value p in sequence (it that can also contain the special character "n", see birewire.rewire.bipartite), the routine generates n.networks sampled each p SS from the SA initialized with the given data. Pairwise distance are computed using the Jaccard distance and the resulting matrix is the input for the dimensional scaling performed by the function tsne. An explorative plot is displayed if display is set to TRUE.
Value

A list containing the list containing the distance matrices `dist` and the list containing the tsne results `tsne`.

Author(s)

Andrea Gobbi
Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>

References


Examples

```
library(BiRewire)
g <- erdos.renyi.game(1000,0.1)
birewire.visual.monitoring.undirected(g,display=FALSE,n.networks=10)
```

Description

Breast cancer samples and their respective mutations downloaded from the Cancer Cancer Genome Atlas (TCGA), used in Gobbi et al.. Germline mutations were filtered out of the list of reported mutations; synonymous mutations and mutations identified as benign and tolerated were also removed from the dataset. The bipartite graph resulting when considering this matrix as an incidence matrix has \( n_r = 757, n_c = 9757, e = 19758 \) for an edge density equal to 0.27%.

Usage

```
data(BRCA_binary_matrix)
```
**Source**

http://tcga.cancer.gov/dataportal/

**References**


---

**test_dsg**

**Tool example of dsg**

**Description**

A simple dsg for testing routines.

**Usage**

```r
data(test_dsg)
```
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