Package 'BiRewire'

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Version 2.4.0

Date 2015-07-09

Title High-performing routines for the randomization of a bipartite
graph (or a binary event matrix) and directed signed graph
preserving degree distribution (or marginal totals).

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

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 function for the analysis of
the introduced randomness across the switching and several
other routines to analyse the resulting networks and their
natural projections.
Extension to undirected networks and directed signed networks (not
bipartite) 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
useful and a visual montioring of the underlying Markov Chain has been implemented.

License GPL-3

Depends igraph, slam, tsne

Suggests RUnit, BiocGenerics

Author Andrea Gobbi [aut], Davide Albanese [cbt], Francesco Iorio
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URL http://www.ebi.ac.uk/~iorio/BiRewire

biocViews Network

NeedsCompilation yes

R topics documented:

1

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 patways 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 swithicng algorithm has been implemented.

Details

Summary:

Package:	BiRewire
Version:	2.3.5
Date: 2015-07-07	
Require: slam, igraph,tsne, 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].

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

References

Iorio, F. and Gobbi, A. (2015) *In Preparation* In Preparation.

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.
Jaccard, P. (1901), *Étude comparative de la distribution florale dans une portion des Alpes et des Jura*, Bulletin de la Société Vaudoise des Sciences Naturelles 37: 547–579.

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028 Csardi, G. and Nepusz, T (2006)
Van der Maaten, L.J.P. and Hinton, G.E., *Visualizing High-Dimensional Data Using t-SNE*. Journal of Machine Learning Research 9(Nov):2579-2605, 2008 *The igraph software package for complex network research*, InterJournal, Complex Systems http://igraph.sf.net

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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 pefromed *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);
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): $N = e/2(1-d)\ln\left((e-de)/\delta\right)$ if exact is FALSE, $N = e(1-d)/2\ln\left((e-de)/\delta\right)$ 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 fracion 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 swithcing steps;
n.networks	50 (default), the number of independent rewiring process starting from the same inital 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 Jaccad 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)

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Special thanks to:
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References

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

Jaccard, P. (1901), *Étude comparative de la distribution florale dans une portion des Alpes et des Jura*, Bulletin de la Société Vaudoise des Sciences Naturelles 37: 547–579.

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

Examples

```
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.iter.pos* (and *max.iter.pos*) 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 pefromed *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 positve (and negative) part of *g*

Usage

```
birewire.analysis.dsg(dsg, step=10, max.iter.pos='n',max.iter.neg='n',accuracy=0.00005,verbose=TI
```

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.bipartit` 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 fracion 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 swithcing steps;
n.networks	50 (default), the number of independent rewiring process starting from the same inital 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 measurwe using `birewire.similarity.dsg`.

Value

A list containing two lists: *data* that is a list collecting all the Jacard 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)

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References

Iorio, F. and Gobbi, A. (2015) *In Preparation* In Preparation.

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

Jaccard, P. (1901), *Étude comparative de la distribution florale dans une portion des Alpes et des Jura*, Bulletin de la Société Vaudoise des Sciences Naturelles 37: 547–579.

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

Examples

```
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)
```

birewire.analysis.undirected

Analysis of Jaccard similarity trends across switching steps.

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 pefromed *n.networks* times and a simple explorative plot, with mean and CI, is visualized if *display* is set to true.

Usage

```
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);
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): $N = e/(2d^3 - dd^2 + 2d + 2) \ln((e - de)/\delta)$ 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 fracion 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 swithcing steps;
n.networks	50 (default), the number of independent rewiring process starting from the same inital 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 configuarations 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 perfomed *n.networks* times and if *display* is set to TRUE, two explorative plots showing the mean value of the Jaccad 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)

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Special thanks to:
Davide Albanese

References

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

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R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

Examples

```
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)
scores2<-birewire.analysis.undirected(m,step,"n",n.networks=10)
```

---

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

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

Arguments

matrix
: incidence matrix: an (n-by-m) binary matrix where rows correspond to vertices in the frist 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.

Author(s)

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

References

Csardi, G. and Nepusz, T (2006) *The igraph software package for complex network research*, Inter-Journal, Complex Systems url http://igraph.sf.net

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))

##rewire the current graph
m2=birewire.rewire.bipartite(m,100)

#create the rewired bipartite graph
g2<-birewire.bipartite.from.incidence(m2,TRUE)
```

---

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 fuction converts the dsg object into a SIF format that can be saved using `bipartite.write.dsg`
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 fuction 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

Iorio, F. and Gobbi, A. (2015) *In Preparation* In Preparation.

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 transfomred 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
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): $N = e/2(1-d)\ln((e-de)/\delta)$ 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 fracion 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 swithcing 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 graphn or the *igraph* corresponding object depending on the input type.

Author(s)

Andrea Gobbi
Special thanks to:
Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>
Davide Albanese

References

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

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 fracion 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 or-
                der 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)

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References

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov,
L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast
randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014
30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

Examples

```
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

```
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** swithcing steps, otherwise the program will count also the not-performed swithcing 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 fracion 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;
delimitators	list(positive='+',negative= '-') (default). If *save.file* is true, the dsg is saved using *delimitators* as characters encoding the relations. See `birewire.build.dsg` for more details.

Details

This fuction 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>
Special thanks to: Davide Albanese

References

Iorio, F. and Gobbi, A. (2015) *In Preparation* In Preparation.

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

Examples

```
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

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

Arguments

adjacency   An `igraph` undirected graph *g* or its adjacency matrix (can be extracted from *g*
                 using `get.adjacency(g)`);

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): $N = e/(2d^3 - 6d^2 + 2d + 2)\ln(e - de)$ 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 fracion 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* swithcing steps, otherwise the program will count also the not-performed swithcing 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
Special thanks to:
Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>
Davide Albanese

References

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

Gobbi, A. and Jurman, G. (in preparation), *Number of required Switching Steps in the Switching Algorithm for undirected graphs*.

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

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;
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): $N = e/2(1-d)\ln((e-de)/\delta)$ 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 fracion 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 swithcing 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>
Special thanks to: Davide Albanese

References

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

---

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 `getbirewire.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): $N = e/2(1 - d) \ln \left((e - de)/\delta \right)$ if exact is FALSE, $N = e(1 - d)/2 \ln \left((e - de)/\delta \right)$ 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): $N = e/2(1 - d)\ln((e - de)/\delta)$ 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 fracion 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 swithcing steps;
path	The directory in which the routine stores the outputs;
K	The number of network that has to be generated;
delimitators	list(negative='-',positive='+') (default):a list with 'positive' and 'negative' names identifying the character encoding the relation used for writing the ouput with `birewire.build.dsg`;

Details

The routine creates, starting from a given path, different subfolders in order to have maximum 1000 files for folder; the SIF files are saved using `birewire.save.dsg`. The set is generated calling birewire.rewire.dsg on the last generated dsg starting from the input dsg.

Author(s)

Andrea Gobbi: <gobbi.andrea@mail.com>
Special thanks to: Davide Albanese

References

Iorio, F. and Gobbi, A. (2015) *In Preparation* In Preparation.

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

Examples

```
library(BiRewire)
data(test_dsg)
dsg=birewire.induced.bipartite(test_dsg)
```

```
tmp= birewire.rewire.dsg(dsg,verbose=FALSE)
```

---

birewire.sampler.undirected

Efficient generation of a null model for a given undirected graph

---

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

```
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;
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 fracion 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 swithcing 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>
Special thanks to: Davide Albanese

References

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

Gobbi, A. and Jurman, G. (in preparation), *Number of required Switching Steps in the Switching Algorithm for undirected graphs.*

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

---

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

Description

Compute the Jaccard similarity index between two binary matrices with the same number of non-null entries and the sam row- and column-wise sums. The function accept also two *igraph* objects.

Usage

```
birewire.similarity( m1,m2)
```

Arguments

m1	First matrix or graph;
m2	Second matrix or graph.

Details

The **Jaccard** index between two sets *M* and *N* is defined as:

$|M \cup N|/|M \cap N|$

With M and N binary matrices, the Jaccard index is computed as:

$$\frac{\sum N_{i,j} \wedge M_{i,j}}{\sum N_{i,j} \vee M_{i,j}}.$$

The Jaccard index ranges between 0 and 1.

Value

Returns the Jaccard similarity index between the objects.

Author(s)

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

Examples

```
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.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 matix, a dimentional scaling reduction (using tsne). If *display* is 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;
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 fracion 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 swithcing 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 wich generating a sampler (seebirewire.rewire.sam
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 *tsne*.

Author(s)

Andrea Gobbi
Maintainer: Andrea Gobbi <gobbi.andrea@mail.com>
Special thanks to:
Davide Albanese

References

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

Jaccard, P. (1901), *Étude comparative de la distribution florale dans une portion des Alpes et des Jura*, Bulletin de la Société Vaudoise des Sciences Naturelles 37: 547–579.

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

Van der Maaten, L.J.P. and Hinton, G.E. Visualizing High-Dimensional Data Using t-SNE. Journal of Machine Learning Research 9(Nov):2579-2605, 2008

Examples

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

---

birewire.visual.monitoring.dsg
Visual monitoring of the Markov chain underlying the SA for dsgs.

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 matix, a dimentional scaling reduction (using tsne). If *display* is true, the relative plot is displayed.

Usage

```
birewire.visual.monitoring.dsg(data,accuracy=0.00005,verbose=FALSE,MAXITER_MUL=10,exact=FALSE,n.
  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 9see `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 fracion 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 swithcing 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 wich generating a sampler (see`birewire.rewire.san` 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

Iorio, F. and Gobbi, A. (2015) *In Preparation* In Preparation.

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

Jaccard, P. (1901), *Étude comparative de la distribution florale dans une portion des Alpes et des Jura*, Bulletin de la Société Vaudoise des Sciences Naturelles 37: 547–579.

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

Van der Maaten, L.J.P. and Hinton, G.E. Visualizing High-Dimensional Data Using t-SNE. Journal of Machine Learning Research 9(Nov):2579-2605, 2008

Examples

```
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)

 a=birewire.visual.monitoring.dsg(dsg,exact=TRUE,sequence.pos=c(1,2,"n",100),sequence.neg=c(1,2,"n",60),n.r
```

---

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 perfroms, on the resulting matix, a dimentional scaling reduction (using tsne). If *display* is 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;
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 fracion 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 swithcing 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 wich generating a sampler (see`birewire.rewire.sam`)
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*. 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 *tsne*.

Author(s)

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References

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

Jaccard, P. (1901), *Étude comparative de la distribution florale dans une portion des Alpes et des Jura*, Bulletin de la Société Vaudoise des Sciences Naturelles 37: 547–579.

R. Milo, N. Kashtan, S. Itzkovitz, M. E. J. Newman, U. Alon (2003), *On the uniform generation of random graphs with prescribed degree sequences*, eprint arXiv:cond-mat/0312028

Van der Maaten, L.J.P. and Hinton, G.E. Visualizing High-Dimensional Data Using t-SNE. Journal of Machine Learning Research 9(Nov):2579-2605, 2008

Examples

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

BRCA_binary_matrix   *TCGA Brest Cancer data*

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

Gobbi, A. and Iorio, F. and Dawson, K. J. and Wedge, D. C. and Tamborero, D. and Alexandrov, L. B. and Lopez-Bigas, N. and Garnett, M. J. and Jurman, G. and Saez-Rodriguez, J. (2014) *Fast randomization of large genomic datasets while preserving alteration counts* Bioinformatics 2014 30 (17): i617-i623 doi: 10.1093/bioinformatics/btu474.

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test_dsg   *Tool example of dsg*

Description

A simple dsg for testing routines.

Usage

```
data(test_dsg)
```

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