

Package ‘pandaR’

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Title PANDA algorithm

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Description Runs PANDA, an algorithm for discovering novel network structure by combining information from multiple complimentary data sources.

Depends R (>= 3.0.0), methods

Imports matrixStats, igraph

Suggests knitr

biocViews StatisticalMethod, GraphAndNetwork, Microarray, GeneRegulation, NetworkInference, GeneExpression, Transcription, Network

VignetteBuilder knitr

License GPL-2

LazyData true

NeedsCompilation no

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panda *Passing Messages between Biological Networks to Refine Predicted Interactions*

Description

This function runs the PANDA algorithm

Usage

```
panda(motif, expr = NULL, ppi = NULL, alpha = 0.1, hamming = 1e-05,
      k = NA, output = c("regulatory", "coexpression", "cooperative"),
      zScale = TRUE, progress = FALSE, randomize = "None",
      cor.method = "pearson", scale.by.present = FALSE)
```

Arguments

motif	A motif dataset, a data.frame, matrix or exprSet containing 3 columns. Each row describes an motif associated with a transcription factor (column 1) a gene (column 2) and a score (column 3) for the motif.
expr	An expression dataset, as a genes (rows) by samples (columns) data.frame
ppi	A Protein-Protein interaction dataset, a data.frame containing 3 columns. Each row describes a protein-protein interaction between transcription factor 1 (column 1), transcription factor 2 (column 2) and a score (column 3) for the interaction.
alpha	value to be used for update variable, alpha (default=0.1)
hamming	value at which to terminate the process based on hamming distance (default 10 ⁻⁵)
k	sets the maximum number of iterations PANDA can run before exiting.
output	a vector containing which networks to return. Options include "regulatory", "coregulatory", "cooperative".
zScale	Boolean to indicate use of z-scores in output. False will use [0,1] scale.
progress	Boolean to indicate printing of output for algorithm progress.
randomize	method by which to randomize gene expression matrix. Default "None". Must be one of "None", "within.gene", "by.genes". "within.gene" randomization scrambles each row of the gene expression matrix, "by.gene" scrambles gene labels.
cor.method	Correlation method, default is "pearson".
scale.by.present	Boolean to indicate scaling of correlations by percentage of positive samples.

Value

An object of class "panda" containing matrices describing networks achieved by convergence with PANDA algorithm.

"regNet" is the regulatory network

"coregNet" is the coregulatory network

"coopNet" is the cooperative network

References

Glass K, Huttenhower C, Quackenbush J, Yuan GC. Passing Messages Between Biological Networks to Refine Predicted Interactions. PLoS One. 2013 May 31;8(5):e64832.

Examples

```
data(pandaToyData)
pandaRes <- panda(pandaToyData$motif,
                 pandaToyData$expression,pandaToyData$ppi,hamming=.1,progress=TRUE)
```

pandaResult

Analysis result from PANDA algorithm on toy data

Description

This data panda object resulting from running the PANDA algorithm on the supplied toy dataset.

```
data(pandaToyData) pandaResult <- panda(pandaToyData$motif, pandaToyData$expression,pandaToyData$ppi,hamming=.
```

Usage

```
pandaResult
```

Format

A panda object

Value

A panda object

References

Glass K, Huttenhower C, Quackenbush J, Yuan GC. Passing Messages Between Biological Networks to Refine Predicted Interactions. PLoS One. 2013 May 31;8(5):e64832.

pandaToyData

Toy gene expression, motif, and ppi data

Description

This data is a list containing three data.frames. The motif data.frame describes a set of pairwise connections where a specific known sequence motif of a transcription factor was found upstream of the corresponding gene. The expression data.frame is a set of 1000 gene expression levels measured across 50 samples. Finally, the ppi data.frame describes a set of known pairwise protein interactions.

Usage

```
pandaToyData
```

Format

A list containing 3 data.frames

Value

A list of length 3

References

Glass K, Huttenhower C, Quackenbush J, Yuan GC. Passing Messages Between Biological Networks to Refine Predicted Interactions. PLoS One. 2013 May 31;8(5):e64832.

plot.panda

Plot.panda

Description

summarizes the results of a PANDA analysis

Usage

```
## S3 method for class 'panda'
plot(x, ...)
```

Arguments

x an object of class "panda"
 ... further arguments passed to or from other methods.

Value

Plot of the distribution of edge weights in the regulatory network.

Examples

```
data(pandaToyData)
panda.res <- panda(pandaToyData$motif,
                  pandaToyData$expression,pandaToyData$ppi,hamming=.001,progress=TRUE)
plot(panda.res)

data(pandaResult)
plot(pandaResult)
```

plotGraph

Plot graph

Description

plotGraph plots a bipartite graph

Usage

```
plotGraph(x)
```

Arguments

x an object of class "panda"

Value

An matrix describing the subsetted bipartite network.

Examples

```
data(pandaToyData)
pandaRes <- panda(pandaToyData$motif,
                  pandaToyData$expression,pandaToyData$ppi,hamming=.001,progress=TRUE)
topPandaRes <- topedges(pandaRes,1000)
subnet.pandaRes <- subnetwork(topPandaRes,c("AR","ARID3A","ELK1"))
plotGraph(subnet.pandaRes)

data(pandaResult)
topPandaRes <- topedges(pandaResult, 1000)
subnet.pandaRes <- subnetwork(topPandaRes,c("AR","ARID3A","ELK1"))
plotGraph(subnet.pandaRes)
```

 print.panda

print.panda

Description

summarizes the results of a PANDA analysis

Usage

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

Arguments

x an object of class "panda"
 ... further arguments passed to or from other methods.

Value

Summary description of panda S4 object

Examples

```
data(pandaToyData)
panda.res <- panda(pandaToyData$motif,
  pandaToyData$expression, pandaToyData$ppi, hamming=.001, progress=TRUE)
print(panda.res)

data(pandaResult)
print(pandaResult)
```

 subnetwork

Subnetwork

Description

subnetwork gets a bipartite network containing only the transcription factors or genes and their respective connections

Usage

```
subnetwork(x, nodes, subTf = TRUE)
```

Arguments

x	an object of class "panda"
nodes	character vector containing the transcription factor or gene labels to subset
subTf	an optional logical indicating whether to subset by transcription factor. Default is TRUE.

Value

An matrix describing the subsetted bipartite network.

Examples

```
data(pandaToyData)
pandaRes <- panda(pandaToyData$motif,
                 pandaToyData$expression, pandaToyData$ppi, hamming=.001, progress=TRUE)
topPandaRes <- topedges(pandaRes, 1000)
subnet.pandaRes <- subnetwork(topPandaRes, c("AR", "ARID3A", "ELK1"))

data(pandaResult)
topPandaRes <- topedges(pandaResult, 1000)
subnetwork(topPandaRes, c("AR", "ARID3A", "ELK1"))
```

summary.panda

Summary.panda

Description

summarizes the results of a PANDA analysis

Usage

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

Arguments

object	an object of class "panda"
...	further arguments passed to or from other methods.

Value

Summary description of panda S4 object

Examples

```
data(pandaToyData)
panda.res <- panda(pandaToyData$motif,
                  pandaToyData$expression,pandaToyData$ppi,hamming=.001,progress=TRUE)
summary(panda.res)

data(pandaResult)
summary(pandaResult)
```

targetedGenes	<i>targetedGenes</i>
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Description

Gets a set of genes targeted by a specified transcription factor. This function can be applied to a graph that is not complete, subsetting the edges which have non-zero edge weight. See function topEdges for dichotomizing edgeweights.

Usage

```
targetedGenes(x, tfs)
```

Arguments

x	an object of class "panda"
tfs	transcription factors to query

Value

A vector of targeted genes

Examples

```
data(pandaToyData)
pandaRes <- panda(pandaToyData$motif,
                 pandaToyData$expression,pandaToyData$ppi,hamming=.001)
topPandaRes <- topedges(pandaRes,1000)
targetedGenes(topPandaRes,c("AR","ELK1"))

data(pandaResult)
topPandaRes <- topedges(pandaResult,1000)
```

topedges	<i>Top edges</i>
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Description

topedges gets a network from a panda obj with a specified cutoff based on magnitude of edgeweight.

Usage

```
topedges(x, count = NA, cutoff = 2, networks = c("coregulation",  
"cooperation", "regulatory"))
```

Arguments

x	an object of class "panda"
count	an optional integer indicating number of top edges to be included in regulatory network.
cutoff	an optional numeric indicating the z-score edge weight cutoff to be used to identify edges. Default is 3.0. Not used if count is not NA.
networks	an optional vector specifying which networks to be included in output. May be any combination of c("coregulation", "cooperation", "regulatory").

Value

An object of class "panda" containing binary matrices indicating the existence of an edge between two nodes. For regulatory network the matrix indicates an edge between a transcription factor (row) and a gene (column)

Examples

```
data(pandaToyData)  
pandaRes <- panda(pandaToyData$motif,  
                 pandaToyData$expression, pandaToyData$ppi, hamming=.001, progress=TRUE)  
topPandaRes <- topedges(pandaRes, 1000)  
  
data(pandaResult)  
topPandaRes <- topedges(pandaResult, 1000)
```

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