

# 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 (>= 3.1.3)

**Suggests** knitr, igraph

**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*

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## 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")
```

## 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 <sup>-5</sup> )  |
| 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.              |

## 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.

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pandaToyData

*Toy gene expression, motif, and ppi data*

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### 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.

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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)
```

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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"))
```

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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)
```

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|               |                      |
|---------------|----------------------|
| 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)
```



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|          |                  |
|----------|------------------|
| 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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