

Package ‘walktrap.gm’

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Type Package

Title Walktrap-GM (Walktrap for genomic modules)

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Description

The following functions run weights for Walktrap-BM, find the optimal step size, and score communities. Included in sample data are an interactome built from KEGG and HPRD pairwise interactions and gene symbols and fold change values for GSE14520.

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Collate ‘calc.weights.R’ ‘opt.step.size.R’ ‘score.communities.R’

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walktrap.gm-package	<i>What the package does (short line) walktrap.gm</i>
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Description

The following functions find vector and edge weights for Walktrap-GM based on expression values, find the optimal step size, and score communities. Included in sample data are an interactome built from KEGG and HPRD pairwise interactions and gene symbols and fold change values for GSE14520.

Requires igraph package

Details

Package:	walktrap.gm
Type:	Package
Version:	1.0
Date:	2013-07-28
License:	GNU GPL

Sample data:

GSE14520.FC is a list of fold change values for GSE14520. GSE14520.GS is a list of HGNC gene symbols for GSE14520. interactome.net is an igraph network with integrated KEGG and HPRD pairwise interactions.

Functions: calc.weights(network, geneSymbols, foldChange)

opt.step.size <- function(network, wtc\$merges, wlk.weights\$vweights, wlk.weights\$dist, 200, modularity)

score.communities(opt.step.size, network, wtcMerges, vweights, dist)

Author(s)

Deanna Petrochilos

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References

Pons P, Latapy M. Computing communities in large networks using random walks. JGAA. 2006;10(2):191-218.

Examples

```
#Example:
#wlk.weights <- calc.weights(interactome.net, GSE14520.GS, GSE14520.FC)
#wtc <- walktrap.community(network, steps, merges, modularity, labels, membership, weights)
#opt.step.size <- function(interactome.net, wtc$merges, wlk.weights$vweights, wlk.weights$dist, 200, wlk.weigh
```

```
#score.communities(opt.step.size, interactome.net, wtc$merges, wlk.weights$vweights, wlk.weights$dist)
```

calc.weights

Calculate Weights

Description

Calculate Vertex and Edge Weights and Weight Distribution for Walktrap-GM

Usage

```
calc.weights(network, geneSymbols, foldChange)
```

Arguments

network	igraph generated interactome
geneSymbols	list of HGNC gene approved gene symbols
foldChange	list of normalized fold change values corresponding to vGS

Details

Vertex and edge weights are calculated from fold change values. Fold change is the mean of the sum of the adjacent vertex weights. The bootstrap distribution is 5000 permutations of of mean weights for a module with n nodes.

Value

A vector of vertex weights, a vector of edge weights and 200 x 50 matrix with mean weight permutations.

`\vweightscomp1`vector weight `\weightscomp2`edge weight `\distcomp3`5000weight permutation

Author(s)

Deanna Petrochilos

References

Pons P, Latapy M. Computing communities in large networks using random walks. JGAA. 2006;10(2):191-218.

Examples

```
#wlk.weights <- calc.weights(interactome.net, GSE14520.GS, GSE7390.FC)
```

GSE14520.FC

GSE14520 fold change values.

Description

List of fold change values for GSE14520, corresponds to HGNC gene symbols in GSE14520.GS

Usage

```
data(GSE14520.FC)
```

Format

The format is: num [1:16360] -5.37 -5.18 4.88 4.21 -4.09 ...

Details

Normalized, log-transformed fold change for GSE14520.

Source

GEO data: GSE14520.

References

Roessler S, Jia HL, Budhu A, et al. A unique metastasis gene signature enables prediction of tumor relapse in early-stage hepatocellular carcinoma patients. *Cancer Res.* 2010;70(24):10202-10212. doi: 10.1158/0008-5472.CAN-10-2607.

Examples

```
data(GSE14520.FC)
```

GSE14520.GS

HGNC gene symbols for GSE14520.

Description

Sample data for calc.weights. HGNC gene symbols for GSE14520, correspond to fold change weights in GSE14520.FC.

Usage

```
data(GSE14520.GS)
```

Format

The format is: chr [1:16360] "HAMP" "CYP1A2" "GPC3" "SPINK1" "CYP2A6" "MT1M" "CYP1A2" "MT1F" ...

Details

Sample data for calc.weights.

Source

GEO data: GSE14520.

References

Roessler S, Jia HL, Budhu A, et al. A unique metastasis gene signature enables prediction of tumor relapse in early-stage hepatocellular carcinoma patients. *Cancer Res.* 2010;70(24):10202-10212. doi: 10.1158/0008-5472.CAN-10-2607.

Examples

```
data(GSE14520.GS)
```

interactome.net

KEGG-HPRD Interaction Network

Description

Interactome containing pairwise interactions parsed from KEGG and HPRD.

Usage

```
data(interactome.net)
```

Format

The format is: List of 9 \$: num 10642 \$: logi FALSE \$: num [1:62407] 15 16 17 18 2 3 4 5 6 7 ... \$: num [1:62407] 0 0 0 0 1 1 1 1 1 1 ... \$: num [1:62407] 4 5 6 7 8 ... \$: num [1:62407] 41255 0 1 2 3 ... \$: num [1:10643] 0 0 0 1 2 3 4 6 11 13 ... \$: num [1:10643] 0 152 240 380 527 ... \$:List of 4 ..\$: num [1:2] 1 0 ..\$: Named list() ..\$:List of 1\$ name: chr [1:10642] "CTNNB1" "KRAS" "PIK3R5" "PIK3CA"\$:List of 1\$ source: chr [1:62407] "KEGG" "KEGG" "KEGG" "KEGG" ... - attr(*, "class")= chr "igraph"

Details

Sample interactome for calc.weights, opt.step.size and score.communities functions. Connected interactome containing pairwise interactions parsed from KEGG and HPRD. Consists of 10,882 nodes and 62,407 interactions. Edge provenance is stored as an edge attribute.

Source

author: Deanna Petrochilos

References

Peri S, Navarro JD, Amanchy R, et al. Development of human protein reference database as an initial platform for approaching systems biology in humans. *Genome Res.* 2003;13(10):2363-2371. doi: 10.1101/gr.1680803.

Ogata H, Goto S, Sato K, Fujibuchi W, Bono H, Kanehisa M. KEGG: Kyoto encyclopedia of genes and genomes. *Nucleic Acids Res.* 1999;27(1):29-34.

Examples

```
data(interactome.net)
```

opt.step.size	<i>Optimal step size for walktrap to communities.</i>
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Description

Function to find optimal step size for walktrap community.to.membership based on genomic module score, module size and maximum modularity.

Usage

```
opt.step.size(network, wtcMerges, vweights, dist, threshold, modularity)
```

Arguments

network	interactome generated by igraph
wtcMerges	walktrap object merge dendogram generated by walktrap.community
vweights	vector of vertex weights generated by calc.weights
dist	bootstrap distribution matrix generated by calc.weights
threshold	maximum size threshold
modularity	walktrap object modularity generated by walktrap.community

Details

Function to find optimal step size for walktrap community.to.membership based on genomic module score, module size and maximum modularity.

Value

Optimal step size.

Author(s)

Deanna Petrochilos

References

Pons P, Latapy M. Computing communities in large networks using random walks. JGAA. 2006;10(2):191-218.

Examples

```
#wlk.weights <- calc.weights(interactome.net, GSE14520.GS, GSE7390.FC)
#wtc <- walktrap.community(network, steps, merges, modularity, labels, membership, weights)
#opt.step.size <- function(interactome.net, wtc$merges, wlk.weights$vweights, wlk.weights$dist, 200, wlk.weights$modularity) {
  #  walktrap.community(interactome.net, steps, wtc$merges, wlk.weights$modularity, labels, membership, wlk.weights)
  #  return(wtc$merges)
}
```

score.communities	<i>Score communities generated by walktrap-gm.</i>
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Description

Function to score communities generated by walktrap-gm using optimal score (opt.step.size), walktrap object and weights and weight distribution (calc.weights).

Usage

```
score.communities(optSize, network, wtcMerges, vweights, dist)
```

Arguments

optSize	optimal step size define generated by opt.step.size
network	interactome generated by igraph
wtcMerges	walktrap object merge dendrogram generated by walktrap.community
vweights	vector of vertex weights generated by calc.weights
dist	bootstrap distribution matrix generated by calc.weights

Details

Function to score communities generated by walktrap-gm using optimal score (opt.step.size), walktrap object and weights and weight distribution (calc.weights).

Value

matrix with with community id, community score and community size

Author(s)

Deanna Petrochilos

References

Pons P, Latapy M. Computing communities in large networks using random walks. JGAA. 2006;10(2):191-218.

Examples

```
#wlk.weights <- calc.weights(interactome.net, GSE14520.GS, GSE7390.FC)
#wtc <- walktrap.community(network, steps, merges, modularity, labels, membership, weights)
#opt.step.size <- function(interactome.net, wtc$merges, wlk.weights$vweights, wlk.weights$dist, 200, wlk.weights$modularity) {
#score.communities(opt.step.size, interactome.net, wtc$merges, wlk.weights$vweights, wlk.weights$dist)
```


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