

# Package ‘walktrap.gm’

July 28, 2013

**Type** Package

**Title** Walktrap-GM (Walktrap for genomic modules)

**Version** 1.0

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**Description** walktrap.gm customizes the Walktrap random walk algorithm to discover communities associated with specific phenotypes in a genomic interactome. Functions in this package include: calc.weights, opt.step.size, score.communities. calc.weights calculates edge and vertex weights in the network and a random distribution of weights to be used in significance scoring. opt.step.size searches for an optimal number of merge steps in community finding. score.communities determines scores for genomic modules. Included in sample data are an interactome built from KEGG and HPRD pairwise interactions and gene symbols and fold change values for GSE14520.

**License** GNU GPL

**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

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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

Maintainer: dpetroch@uw.edu Deanna Petrochilos

## 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$dists)
```

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calc.weights

*Calculate Weights*

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## 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` 5000 weight 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)
```

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GSE14520.FC

*GSE14520 fold change values.*


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**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)
```

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GSE14520.GS

*HGNC gene symbols for GSE14520.*


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**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)
```

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interactome.net

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*KEGG-HPRD Interaction Network*


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**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)
```

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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.weigh
```

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score.communities	<i>Score communités 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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