

# Package ‘dmGWAS’

February 19, 2015

**Type** Package

**Title** dmGWAS package

**Version** 3.0

**Date** 2015-02-16

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**Depends** R (>= 2.9.0), igraph

**Description**

dmGWAS\_3.0 implement our upgraded algorithm EW\_dmGWAS, which searches for dense modules in a node- and edge-weighted PPI network.

**License** GPL (>= 2)

**URL** <http://bioinfo.mc.vanderbilt.edu/dmGWAS>

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chooseModule	<i>Choosing dense modules</i>
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## Description

This function will choose the top modules specified by users for downstream analyses. Sub-network can also be plotted if plot=TRUE.

## Usage

```
chooseModule(res.list, top = 0.01, plot = FALSE)
```

## Arguments

<code>res.list</code>	The results from function <i>dms</i>
<code>top</code>	Either a percentage (<1) or an integer (>=1)
<code>plot</code>	To plot the sub-network or not

## Details

The parameter *top* could be either a percentage (<1) or an integer (>=1). For example, if *top* is 0.01, the top 1% modules will be chosen; if *top* is 50, the top 50 modules will be chosen.

## Value

A list contains both the chosen modules and the sub-network constructed from the chosen modules.

## References

Jia P, Zheng S, Long J, Zheng W, and Zhao Z (2011) dmGWAS: dense module searching for genome-wide association studies in protein-protein interaction networks. *Bioinformatics* 27(1):95-102

Wang Q, Yu H, Zhao Z, and Jia P. EW\_dmGWAS: Edge-weighted dense module search for genome-wide association studies and gene expression profiles. Manuscript in preparation

## See Also

[dms](#)

## Examples

```
# res.list <- dms(network, geneweight, expr1, expr2)
# chooseModule(res.list, top = 0.01, plot = FALSE)
```

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dmGWAS\_3.0

*dmGWAS\_3.0 searches for dense modules in a node- and edge-weighted PPI network.*

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## Description

dmGWAS\_3.0 is an upgraded version of dmGWAS. It constructs a node- and edge-weighted PPI network, performs dense module searching, generates simulation data from random networks, normalizes module scores using simulation data, removes unqualified modules, and orders resultant modules according to their significance.

## Details

Package:	dmGWAS
Type:	Package
Version:	3.0
Date:	2015-02-16
License:	GPL (>= 2)

This package takes three types of data as input: a list of genes with association p-values, gene expression profiling in both case and control samples, and a human PPI network. `generate_graph` constructs a node- and edge-weighted PPI network. `dms` performs dense module search upon the node- and edge-weighted PPI network.

### Author(s)

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### References

Jia P, Zheng S, Long J, Zheng W, and Zhao Z (2011) dmGWAS: dense module searching for genome-wide association studies in protein-protein interaction networks. *Bioinformatics* 27(1):95-102

Wang Q, Yu H, Zhao Z, and Jia P. EW\_dmGWAS: Edge-weighted dense module search for genome-wide association studies and gene expression profiles. Manuscript in preparation

### Examples

```
#res.list <- dms(network, geneweight, expr1, expr2, r=0.1)
#chooseModule(res.list, top=0.01, plot=T)
```

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dms	<i>Dense module search function</i>
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### Description

`dms` constructs a node- and edge-weighted PPI network, performs dense module searching, generates simulation data from random networks, normalizes module scores using simulation data, removes un-qualified modules, and orders resultant modules according to their significance.

### Usage

```
dms(network, geneweight, expr1, expr2 = NULL, d=1, r = 0.1, lambda = "default")
```

### Arguments

network	A data frame containing a symbolic edge list of the PPI network.
geneweight	A data frame containing two columns: the first is unique gene identifier (should be coordinate with the node symbol used in PPI); the second is gene-based p-value derived from GWAS.
expr1	A data frame containing gene expression data from case samples. The first column is gene identifier (should be coordinate with the node symbol used in PPI).
expr2	A data frame containing gene expression data from control samples. The first column should be the same as expr1.
d	An integer used to define the order of neighbour genes to be searched. This parameter is always set up as 1 in dmGWAS_3.0, but could be 1 or 2 in dmGWAS_1.0 and dmGWAS_2.X.
r	A float indicating the cut-off for increment during module expanding process. Greater r will generate smaller module. Default is 0.1.
lambda	A float between 0 and 1 to balance node and edge weights. dmGWAS_NEW will estimate it by default.

### Value

A list containing all important data including the node- and edge-weighted network used for searching, resultant dense module list, module score matrix containing  $S_m$  and  $S_n$ , and randomization data for normalization. A resultant file '\*.RData' is also automatically saved in the working folder for future record.

### References

Jia P, Zheng S, Long J, Zheng W, and Zhao Z (2011) dmGWAS: dense module searching for genome-wide association studies in protein-protein interaction networks. *Bioinformatics* 27(1):95-102

Wang Q, Yu H, Zhao Z, and Jia P. EW\_dmGWAS: Edge-weighted dense module search for genome-wide association studies and gene expression profiles. Manuscript in preparation

### Examples

```
#res.list <- dms(network, geneweight, expr1, expr2, r=0.1)
```

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estimate\_lambda      *Estimate the parameter lambda*

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### Description

Lambda is a parameter to balance node and edge weight when expanding modules. This function will estimate it when it is not specified. This function is generally called by function `dms`. Typically users do not need to call it.

### Usage

```
estimate_lambda(G)
```

### Arguments

G                      G is a node- and edge-weighted PPI network, which can be generated from function `generate_graph`.

### Value

A float between 0 and 1.

### See Also

`generate_graph`

### Examples

```
# G <- generate_graph(expr1, expr2, network, geneweight)
# lambda <- estimate_lambda(G)
```

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generate\_edge\_weight  
*Compute edge weight*

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### Description

[generate\\_edge\\_weight](#) computes differential gene co-expression (i.e., the change of gene co-expression between case and control samples) to infer the edge weight of PPI network. [generate\\_edge\\_weight](#) is generally called by function [generate\\_graph](#). Typically users do not need to call it.

### Usage

```
generate_edge_weight(expr1, expr2, network, geneweight)
```

### Arguments

expr1	A data frame containing gene expression data from case samples. The first column is gene identifier (should be coordinate with the node symbol used in PPI).
expr2	A data frame containing gene expression data from control samples. The first column should be the same as expr1.
network	A data frame containing a symbolic edge list of the PPI network.
geneweight	A data frame containing two columns: the first is unique gene identifier (should be coordinate with the node symbol used in PPI); the second is gene-based p-value derived from GWAS.

### Value

A co-expression matrix is returned.

### Examples

```
# edgeweight <- generate_edge_weight(expr1, expr2, network, geneweight)
```

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generate\_graph      *Build background PPI Network*

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### Description

[generate\\_graph](#) constructs a node- and edge-weighted PPI network for function [dms](#). This function is generally called by function [dms](#). Typically users do not need to call it.

### Usage

```
generate_graph(expr1, expr2 , network, geneweight)
```

**Arguments**

<code>expr1</code>	A data frame containing gene expression data from case samples. The first column is gene identifier (should be coordinate with the node symbol used in PPI).
<code>expr2</code>	A data frame containing gene expression data from control samples. The first column should be the same as <code>expr1</code> .
<code>network</code>	A data frame containing a symbolic edge list of the PPI network.
<code>geneweight</code>	A data frame containing two columns: the first is unique gene identifier (should be coordinate with the node symbol used in PPI); the second is gene-based p-value derived from GWAS.

**Value**

A node- and edge-weighted PPI network.

**Examples**

```
# G<- generate_graph (expr1, expr2, network, geneweight)
```

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