

# Package: DNLC (via r-universe)

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**Type** Package

**Title** Differential Network Local Consistency Analysis

**Version** 1.0.0

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**Description** Using Local Moran's I for detection of differential network local consistency.

**License** GPL (>= 2)

**Imports** igraph, spdep, fdrtool, GOstats, locfdr, mvtnorm, caTools

**LazyData** true

**Depends** R (>= 2.10)

**NeedsCompilation** no

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**Repository** <https://yushengding.r-universe.dev>

**RemoteUrl** <https://github.com/cran/DNLC>

**RemoteRef** HEAD

**RemoteSha** a471544877fe1bdfcba0d42b15598b9c02b44cff

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cal_lmi_data	<i>Calculate local moran's I matrix for a network and a gene expression matrix</i>
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## Description

cal\_lmi\_data() will calculate the local moran's I data for a input igraph object and gene expression data matrix.

## Usage

```
cal_lmi_data(gene_expr, gene_graph)
```

## Arguments

gene_expr	Expression for genes. Each row is a gene, and each column is a sample.
gene_graph	The graph of gene network.

## Details

cal\_lmi\_data() will calculate the local moran's I matrix for a input igraph object and gene expression data matrix. The function will return a matrix in the same dimension of the input gene expression matrix. Every gene x's lmi data takes a row.

## Value

A table of local moran's I data. Row name is gene id. Each row stands for the local moran's I data of gene x. Each column stands for a sample.

## Examples

```
## Not run:  
simulation <- init_simulation_gene_net()  
lmi_data = cal_lmi_data( simulation$gene_expr, simulation$gene_graph)  
t_data = DNLC_statistics(simulation$gene_graph, simulation$gene_expr,  
  simulation$patient_matrix, lmi_data = lmi_data)  
fdr_result <- gene_fdrtest(t_data)  
sig_genes <- significant_genes(fdr_obj = fdr_result, thres = 0.2)  
## End(Not run)
```

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DNLC_statistics	<i>calculate t statistics for gene graph using DNLC method.</i>
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### Description

a function to calculate t statistics for genes in the graph.

### Usage

```
DNLC_statistics(gene_graph, gene_expr = "x", clinic_data = "y",  
               confounder_matrix = NULL, lmi_data = NULL)
```

### Arguments

gene_graph	graph of gene
gene_expr	expr of gene
clinic_data	patient data
confounder_matrix	other message describe clinic message
lmi_data	lmi data for each gene.

### Details

This function first calculates the matrix of local moran's I, and then conducts testing for the association of each gene's local moran's I with the clinical outcome variable. Clinical confounder variables such as age, gender etc can be included.

### Value

all_gene_id	gene ids in graph
t_data	t-data for each gene

### Examples

```
## Not run:  
simulation <- init_simulation_gene_net()  
t_data = DNLC_statistics(simulation$gene_graph, simulation$gene_expr,  
                        simulation$patient_matrix, lmi_data = simulation$lmi_matrix)  
fdr_result <- gene_fdrtest(t_data)  
sig_genes <- significant_genes(fdr_obj = fdr_result, thres = 0.2)  
  
## End(Not run)
```

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gene_fdrtest	<i>Use local false discovery rate for the detection of genes with significant LMI change</i>
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**Description**

This function use locfdr function to calculate fdr\_result

**Usage**

```
gene_fdrtest(gene.data)
```

**Arguments**

gene.data      gene\_id\_all: gene id t\_data: t statistic for each gene

**Value**

return fdr\_result for t\_data

fdr\$name      all gene id

fdr\$fdr      fdr value for gene

**Examples**

```
## Not run:
simulation <- init_simulation_gene_net()
t_data = DNLC_statistics(simulation$gene_graph, simulation$gene_expr,
  simulation$patient_matrix, lmi_data=simulation$lmi_matrix)
fdr_result <- gene_fdrtest(t_data)
sig_genes <- significant_genes(fdr_obj = fdr_result, thres = 0.2)

## End(Not run)
```

---

```
init_simulation_gene_net
```

*Create a random network for simulation*

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**Description**

This function will create a network for DNLC. This function will change correlation of chosen genes and its one hop neighbor between treatment groups to simulate LMI changes.

**Usage**

```
init_simulation_gene_net(base_correlation = 0.4,
  change_correlation = 0.8, sample_size = 100, num_gene = 5000, change_gene_num=5)
```

**Arguments**

base_correlation	base correlation of network
change_correlation	change correlation for selected genes
sample_size	multi size of patient data
num_gene	gene number in the network
change_gene_num	number of genes around which the correlation structure is to be changed

**Value**

lmi_matrix	matrix of local moran's I data
patient_matrix	matrix of patient data
neigh_list	id of changed gene.
gene_graph	igraph object of gene network
gene_expr	gene expression data matrix

**Examples**

```
## Not run:
simulation <- init_simulation_gene_net()
t_data = DNLC_statistics(simulation$gene_graph, simulation$gene_expr,
  simulation$patient_matrix, lmi_data = simulation$lmi_matrix)
fdr_result <- gene_fdrtest(t_data)
sig_genes <- significant_genes(fdr_obj = fdr_result, thres = 0.2)
## End(Not run)
```

---

significant\_genes      *Selecting significant genes according to fdr result*

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**Description**

Choose the significant genes according to fdr result

**Usage**

```
significant_genes(fdr_obj, thres)
```

**Arguments**

fdr_obj	fdr result come from function gene_fdrtest
thres	threshold to identify significant genes

**Value**

ID of significant genes

**Examples**

```
## Not run:  
simulation <- init_simulation_gene_net()  
t_data = DNLC_statistics(simulation$gene_graph, simulation$gene_expr,  
  simulation$patient_matrix, lmi_data = simulation$lmi_matrix)  
fdr_result <- gene_fdrtest(t_data)  
sig_genes <- significant_genes(fdr_obj = fdr_result, thres = 0.2)  
  
## End(Not run)
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