Package ‘DiffNet’

February 28, 2017

Type Package
Title Detection of Statistically Significant Changes in Complex Biological Networks
Version 1.0-0
Date 2017-02-27
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Repository CRAN
Description Provides an implementation of statistically significant differential sub-network analysis for paired biological networks.
License GPL (>= 3)
URL https://www.r-project.org,
Imports Rcpp (>= 0.12.7), Matrix, qlecMatrix, data.table, Hmisc, gplots, igraph, IsA, foreach, doParallel
LazyLoad yes
LinkingTo Rcpp, RcppEigen
Depends R (>= 3.3.2)
NeedsCompilation yes
Date/Publication 2017-02-28 11:08:32

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**calculate_p_value**

*Calculate asymptotic p-values*

**Description**

Calculate p-values given first order moment mu and second order moment std

**Usage**

```r
calculate_p_value(mu, std, val)
```

**Arguments**

- **mu**
  - First order moment: mean for the GHD statistic
- **std**
  - Second order moment: std for the GHD statistic
- **val**
  - Value of GHD statistic

**Value**

Returns the p-value for the GHD statistic (whose distribution follows normal distribution).

**Author(s)**

Raghvendra Mall <rmall@hbku.edu.qa>

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**differential_subnetwork_analysis_closedform**

*Closed-Form Approach for Identifying Differential Sub-networks in Paired Graphs*

**Description**

This method identifies the differential sub-network between two graphs using the proposed Closed-Form approach of Mall et al paper.

**Usage**

```r
differential_subnetwork_analysis_closedform(ghd_val, mu_perm, p,
                                           matrixA, matrixB, threshold)
```
**Arguments**

ghd_val  Generalized Hamming Distance value calculated using topological graphs of g_A and g_B.

mu_perm  Asymptotic value of mean permutation for graph g_A.

p  Represents the number of nodes in graph g_A which is the same as number of nodes in graph g_B.

matrixA  Topological matrix obtained from graph g_A.

matrixB  Topological matrix obtained from graph g_B.

threshold  Threshold after which the "closed-form" technique switches to use a model selection criterion similar to the "original" approach to identify statistically significant changes between two networks. By default its value is 1e-250 and a good range for this value is between 1e-50 to 1e-250.

**Value**

A data frame comprising of:

actual_id  Id of a node from the set of nodes in g_A

dim_name  Name associated with a node from the set of nodes in g_A.

p_val  P-value associated with that node.

ghd_val  Generalized Hamming Distance between the topological matrices after removal of that node.

mu_perm  Asymptotic first order moment: mean value.

std_perm  Asymptotic second order moment: standard deviation value.

v7  Adjusted p-value associated with that node.

**Author(s)**

Raghvendra Mall <rmall@hbku.edu.qa>

**References**


**See Also**

differential_subnetwork_analysis_original, differential_subnetwork_analysis_fastapprox
differential_subnetwork_analysis_fastapprox

Fast-Approximation Approach for Identifying Differential Subnetworks in Paired Graphs

Description

This method identifies the differential sub-network between two graphs using the proposed Fast-Approximation approach of Mall et al paper.

Usage

differential_subnetwork_analysis_fastapprox(ghd_val, mu_perm, p,
matrixA, matrixB, threshold)

Arguments

ghd_val Generalized Hamming Distance value calculated using topological graphs of g_A and g_B.
mu_perm Asymptotic value of mean permutation for graph g_A.
p Represents the number of nodes in graph g_A which is the same as number of nodes in graph g_B.
matrixA Topological matrix obtained from graph g_A.
matrixB Topological matrix obtained from graph g_B.
threshold Threshold after which the "fast-approx" technique switches to use a model selection criterion similar to the "original" approach to identify statistically significant changes between two networks. By default its value is 1e-250 and a good range for this value is between 1e-50 to 1e-250.

Value

A data frame comprising of:

actual_id Id of a node from the set of nodes in g_A
dim_name Name associated with a node from the set of nodes in g_A.
p_val P-value associated with that node.
ghd_val Generalized Hamming Distance between the topological matrices after removal of that node.
mu_perm Asymptotic first order moment: mean value.
std_perm Asymptotic second order moment: standard deviation value.
v7 Adjusted p-value associated with that node.

Author(s)

Raghvendra Mall <rmall@hbku.edu.qa>
differential_subnetwork_analysis_original

References


See Also
differential_subnetwork_analysis_original, differential_subnetwork_analysis_closedform

differential_subnetwork_analysis_original

Original dGHD Approach for Identifying Differential Sub-networks in Paired Graphs

Description

This method identifies the differential sub-network between two graphs using the original dGHD approach of Ruan et al paper.

Usage

differential_subnetwork_analysis_original(ghd_val, mu_perm, p, matrixA, matrixB, threshold)

Arguments

ghd_val Generalized Hamming Distance value calculated using topological graphs of g_A and g_B.
mu_perm Asymptotic value of mean permutation for graph g_A.
p Represents the number of nodes in graph g_A which is the same as number of nodes in graph g_B.
matrixA Topological matrix obtained from graph g_A.
matrixB Topological matrix obtained from graph g_B.
threshold Not used in the original approach.

Value

A data frame comprising of:

actual_id Id of a node from the set of nodes in g_A
dim_name Name associated with a node from the set of nodes in g_A.
p_val P-value associated with that node.
ghd_val Generalized Hamming Distance between the topological matrices after removal of that node.
mu_perm Asymptotic first order moment: mean value.
std_perm Asymptotic second order moment: standard deviation value.
v7 Adjusted p-value associated with that node.
**Author(s)**
Raghvendra Mall <rmall@hbku.edu.qa>

**References**

**See Also**
differential_subnetwork_analysis_closedform, differential_subnetwork_analysis_fastapprox

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**diffnet**

*Detection of Statistically Significant Changes in Paired Biological Networks*

**Description**
Performs differential network analysis for paired biological networks to identify statistically significant changes between two graphs. Currently, the approaches available for doing this include the "closed-form", "original" (dGHD) and the "fast-approx" techniques described in the paper of Mall et al. The methods works better for large-scale complex biological networks (in pairs).

**Usage**
```r
diffnet(g_A = sample_grg(6, 0.15, torus = TRUE, coords = TRUE),
g_b = permute(g_A, c(sample(5), 6)), p = 6,
threshold = 1e-50, approach = "closed-form")
```

**Arguments**
- `g_A`: An igraph object representing graph g_A
- `g_B`: An igraph object representing the second graph B with same number of nodes.
- `p`: Represents the number of nodes in graph g_A which is the same as number of nodes in graph g_B
- `threshold`: Threshold after which the "closed-form" and "fast-approx" techniques switch to use a model selection criterion similar to the "original" approach to identify statistically significant changes between two networks. By default its value is 1e-250 and a good range for this value is between 1e-50 to 1e-250.
- `approach`: Either "closed-form"/"original"/"fast-approx". By default its "closed-form"

**Value**
An ordered vector representing the p-value for each node. Nodes whose p-values are less than 0.01 form the differential sub-networks in paired graphs g_A and g_B.
**DiffNet_GHD_Fast**

**Author(s)**

Raghvendra Mall <rmall@hbku.edu.qa>

**References**


**Examples**

```r
library("DiffNet")
# this step is optional, it helps speed up calculations, run in parallel on 2 processors
library(doParallel)
registerDoParallel(2)
# Run the differential network analysis technique on sample data
p <- diffnet()
```

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**Description**

Provides a very fast implementation for generalized hamming distance statistic.

**Format**

The format is: List of 4

- `name`: chr "DiffNet_GHD_Fast"  
- `address`: Class 'RegisteredNativeSymbol' <externalptr>  
- `dll`: List of 5
  - `name`: chr "DiffNet"  
  - `path`: chr "/home/rmall/R/x86_64-pc-linux-gnu-library/3.3/DiffNet/libs/DiffNet.so"  
  - `dynamicLookup`: logi FALSE  
  - `handle`: Class 'DLLHandle' <externalptr>  
  - `info`: Class 'DLLInfoReference' <externalptr>  
  - `numParameters`: int 2 - attr(*, "class")= chr "DLLInfo"  

**Author(s)**

Raghvendra Mall <rmall@hbku.edu.qa>

**See Also**

DiffNet_MU_Fast, DiffNet_STD_Fast
### Description

Provides a very fast implementation for obtaining the asymptotic mean for GHD statistic

### Format

The format is: List of 4 $ name : chr "DiffNet_MU_Fast" $ address :Class 'RegisteredNativeSymbol' <externalptr> $ dll :List of 5 ..$ name : chr "DiffNet" ..$ path : chr "/home/rmall/R/x86_64-pc-linux-gnu-library/3.3/DiffNet/libs/DiffNet.so" ..$ dynamicLookup : logi FALSE ..$ handle :Class 'DLLHandle' <externalptr> ..$ info :Class 'DLLInfoReference' <externalptr> ..- attr(*, "class")= chr "DLLInfo" $ numParameters: int 2 - attr(*, "class")= chr [1:2] "CallRoutine" "NativeSymbol-Info"

### Author(s)

Raghvendra Mall <rmall@hbku.edu.qa>

### See Also

[ghd_fast](#), [std_fast](#)

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### Description

Provides a very fast implementation for obtaining the asymptotic standard deviation for GHD statistic

### Format

The format is: List of 4 $ name : chr "DiffNet_STD_Fast" $ address :Class 'RegisteredNativeSymbol' <externalptr> $ dll :List of 5 ..$ name : chr "DiffNet" ..$ path : chr "/home/rmall/R/x86_64-pc-linux-gnu-library/3.3/DiffNet/libs/DiffNet.so" ..$ dynamicLookup : logi FALSE ..$ handle :Class 'DLLHandle' <externalptr> ..$ info :Class 'DLLInfoReference' <externalptr> ..- attr(*, "class")= chr "DLLInfo" $ numParameters: int 2 - attr(*, "class")= chr [1:2] "CallRoutine" "NativeSymbol-Info"

### Author(s)

Raghvendra Mall <rmall@hbku.edu.qa>
**GHD_Fast**

**Fast Implementation for Generalized Hamming Distance Statistic**

**Description**

Provides a very fast implementation for generalized hamming distance statistic.

**Usage**

GHD_Fast(A, B)

**Arguments**

<table>
<thead>
<tr>
<th>A</th>
<th>Topological matrix obtained from graph g_A.</th>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
<td>Topological matrix obtained from graph g_B.</td>
</tr>
</tbody>
</table>

**Value**

Returns the Generalized Hamming Distance between topological matrices of graphs g_A and g_B.

**Author(s)**

Raghvendra Mall <rmall@hbku.edu.qa>

**See Also**

MU_Fast, STD_Fast

**MU_Fast**

**Fast Implementation of First Order Moment of Generalized Hamming Distance Statistic**

**Description**

Provides a very fast implementation for obtaining the asymptotic mean for GHD statistic

**Usage**

MU_Fast(A, B)
Arguments

A Topological matrix obtained from graph g_A.
B Topological matrix obtained from graph g_B.

Value

Returns the asymptotic mean value for GHD statistic between permutations of topological matrices of graphs g_A and graph g_B.

Author(s)

Raghvendra Mall <rmall@hbku.edu.qa>

See Also

GHD_Fast, STD_Fast
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