

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.

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URL <https://www.r-project.org>,
https://www.researchgate.net/publication/305355965_Detection_of_statistically_significant_network_changes_in_complex_biological_networks

Imports Rcpp (>= 0.12.7), Matrix, qlcMatrix, data.table, Hmisc, gplots, igraph, lsa, 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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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

https://www.researchgate.net/publication/305355965_Detection_of_statistically_significant_network_changes_in_complex_biological_networks

See Also

[differential_subnetwork_analysis_original](#), [differential_subnetwork_analysis_fastapprox](#)

differential_subnetwork_analysis_fastapprox

Fast-Approximation Approach for Identifying Differential Sub-networks 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>

References

https://www.researchgate.net/publication/305355965_Detection_of_statistically_significant_network_changes_in_complex_biological_networks

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

Ruan, D., Young, A. and Montana, G., 2015. Differential analysis of biological networks. *BMC bioinformatics*, **16**(1), 327-334.

See Also

[differential_subnetwork_analysis_closedform](#), [differential_subnetwork_analysis_fastapprox](#)

diffnet	<i>Detection of Statistically Significant Changes in Paired Biological Networks</i>
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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

```
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.

Author(s)

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References

https://www.researchgate.net/publication/305355965_Detection_of_statistically_significant_network_changes_in_complex_biological_networks

Examples

```
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 tehcnique on sample data
p <- diffnet()
```

DiffNet_GHD_Fast

Fast Implementation for Generalized Hamming Distance Statistic

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> ..- attr(*, "class")= chr "DLLInfo" \$ numParameters: int 2 - attr(*, "class")= chr [1:2] "CallRoutine" "NativeSymbol-Info"

Author(s)

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See Also

[DiffNet_MU_Fast](#), [DiffNet_STD_Fast](#)

DiffNet_MU_Fast	<i>Fast Implementation of First Order Moment of Generalized Hamming Distance Statistic</i>
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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](#)

DiffNet_STD_Fast	<i>Fast Implementation of Second Order Moment of Generalized Hamming Distance Statistic</i>
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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>

See Also

[GHD_Fast](#), [MU_Fast](#)

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

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

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](#)

STD_Fast

Fast Implementation of Second Order Moment of Generalized Hamming Distance Statistic

Description

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

Usage

```
STD_Fast(A, B)
```

Arguments

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

Value

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

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See Also

[GHD_Fast](#), [MU_Fast](#)

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