Package ‘DCD’

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calculate_jaccard

Calculate jaccard coefficient w.r.t. to a hub differential node

Description

Calculate jaccard coefficients of all nodes w.r.t. a hub differential node which help in formation of approximate block diagonals

Usage

calculate_jaccard(nodeid, matrix_A, mink)

Arguments

- nodeid: Id of the hub differential node
- matrix_A: Noisy differential topological adjacency matrix
- mink: Minimum number of neighbours that each node should have in common with hub node to have a non-zero Jaccard co-efficient.

Value

Returns a data-frame with fields: jaccard_coefficient, intersection_length and degree. Here jaccard_coefficient between hub node and every node, intersection_length is number of common nodes and degree represents degree of each node in differential topological matrix.

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References


Examples

```r
library(igraph)
mink<-7;
g_A <- sample_grg(200, 0.15, torus=FALSE, coords = FALSE)
A <- get.adjacency(g_A)
nodeid <- 1;

#Calculate Jaccard coefficient of all nodes w.r.t. nodeid 1 given the adjacency matrix A
output <- calculate_jaccard(nodeid,A,mink)
```
**Description**

The task of identifying differential sub-networks in paired biological networks (A:control,B:case) can be re-phrased as one of finding dense communities in a single noisy differential topological (DT) graph constructed by taking absolute difference between the topological graphs of A and B. In this software, we propose a fast three-stage approach, namely Differential Community Detection (DCD), to identify differential sub-networks as differential communities in a de-noised version of the DT graph. In the first stage, we iteratively re-order the nodes of the DT graph to determine approximate block diagonals present in the DT adjacency matrix using neighbourhood information of the nodes and Jaccard similarity. In the second stage, the ordered DT adjacency matrix is traversed along the diagonal to remove all the edges associated with a node, if that node has no immediate edges within a window. Finally, we apply community detection methods on this de-noised DT graph to discover differential sub-networks as communities.

**Usage**

```r
DCD(g_A = sample_grg(200, 0.15, torus = FALSE, coords = FALSE),
   g_B = permute(g_A, c(sample(20), 21:200)), method = "Louvain",
   mink = 7, ground_truth = c(rep(1, 20), rep(0, 180)),
   plot_flag = 1, color = "blue", iter = 1, cores = 1)
```

**Arguments**

- `g_A`: Igraph object representing graph A
- `g_B`: Igraph object representing graph B
- `method`: Community detection method can be either: "Louvain", "Infomap" or "Spectral", default "Louvain".
- `mink`: Minimum number of nodes for a community to be considered differential community, default 7.
- `ground_truth`: In case ground truth community information is available i.e. which nodes are part of differential communities and which are not. For example in 2 networks comprising 1000 nodes, if first 100 nodes are differential then `ground_truth = c(rep(1,100),rep(0,900))`.
- `plot_flag`: Makes a precision recall plot if `plot_flag=1` when `ground_truth` is available, else set `plot_flag` to 0.
- `color`: Colour for the area under precision recall curve. Can be "blue", "black", "red" etc.
- `iter`: No of iterations of experiment to run, default `iter = 1`.
- `cores`: No of cores to use to calculate the Jaccard co-efficient in parallel for the hub node during each iteration of the greedy block diagonal identification approach.
get_ordered_community_output

Value

Returns a data frame with NodeIds and Predicted_Label columns. The Predicted_Label corresponds to the Differential ClusterId a node belongs to. All nodes with Predicted_Label = 0 are non-differential nodes or are nodes which are not part of any differential community.

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References


See Also

get_ordered_community_output, calculate_jaccard, order_topological_matrix, prune_edges

Examples

```r
DCD_output <- DCD()
## Not run:
library(igraph)
g_A <- sample_grg(200, 0.15, torus=FALSE, coords = FALSE)
g_B <- permute(g_A,c(sample(20),21:200))
ground_truth <- c(rep(1,20),rep(0,180))
DCD_output2 <- DCD(g_A = g_A, g_B = g_B, method = "Spectral", mink = 7,
                   ground_truth = ground_truth, plot_flag = 1, color = "red",
                   iter = 1, cores = 1)
## End(Not run)
```

get_ordered_community_output

Get differential communities and nodes belonging to each such community

Description

Third step of DCD: Performs community detection on de-noised ordered differential topological graph.

Usage

```
get_ordered_community_output(g_output, method, output_adjacency, plot_flags = 0,
                           ground_truth = NULL, color = NULL, iter = 0)
```
get_ordered_community_output

Arguments

- **g_output**: De-noised ordered differential topological graph.
- **method**: Method can be either "Louvain", "Infomap" or "Spectral", by default "Louvain".
- **output_adjacency**: De-noised ordered differential topological adjacency matrix.
- **plot_flags**: Makes a precision recall plot if plot_flag=1 when ground_truth is available, else set plot_flag to 0.
- **ground_truth**: In case ground truth community information is available i.e. which nodes are part of differential communities and which are not. For example in 2 networks comprising 1000 nodes, if first 100 nodes are differential then ground_truth = c(rep(1,100),rep(0,900)).
- **color**: Colour for the area under precision recall curve. Can be "blue", "black", "red" etc.
- **iter**: No of iterations of experiment to run, default iter = 1.

Value

Returns a data frame with NodeIds and Predicted_Label columns. The Predicted_Label corresponds to the Differential ClusterId a node belongs to. All nodes with Predicted_Label = 0 are non-differential nodes or are nodes which are not part of any differential community.

Author(s)

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References


Examples

```r
library(igraph)
library(WGCNA)
g_A <- sample_grg(200, 0.15, torus=FALSE, coords = FALSE)
A <- get.adjacency(g_A)
g_B = permute(g_A,c(sample(20),21:200))
B <- get.adjacency(g_B)

cosine_sim_A <- TOMsimilarity(as.matrix(A),TOMType = "unsigned",TOMDenom = "min");
cosine_sim_B <- TOMsimilarity(as.matrix(B),TOMType = "unsigned",TOMDenom = "min")
edgelist_A <- get.edgelist(g_A);
edgelist_B <- get.edgelist(g_B);
if (is.null(E(g_A)$weight))
{
   edgelist_A <- cbind(edgelist_A,rep(1,nrow(edgelist_A)));
}else
```
```r
edgelist_A <- cbind(edgelist_A,E(g_A)$weight);
}
if (is.null(E(g_B)$weight))
{
edgelist_B <- cbind(edgelist_B,rep(1,nrow(edgelist_B)));
}
else
{
edgelist_B <- cbind(edgelist_B,E(g_B)$weight);
}
edgelist_A <- as.data.frame(edgelist_A);
edgelist_B <- as.data.frame(edgelist_B);
mink <- 7
#Noisy Difference in topological matrices
diff_topological_matrix <- abs(cosine_sim_A-cosine_sim_B);
#Order the nodes in topological graph using greedy approach
ordered_list <- order_topological_matrix(diff_topological_matrix,mink);
temp_output_adjacency <- diff_topological_matrix[ordered_list,ordered_list];
output_adjacency <- prune_edges(temp_output_adjacency,mink);
g_output <- graph_from_adjacency_matrix(output_adjacency,mode=c("undirected"),weighted=TRUE);
#Community detection using Louvain method
louvain_cluster_node_rank <- get_ordered_community_output(g_output,"Louvain",
output_adjacency);
output <- cbind(as.numeric(louvain_cluster_node_rank$NodeIds),
louvain_cluster_node_rank$Predicted_Label)
```

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**order_topological_matrix**

Order the noisy differential topological adjacency matrix

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**Description**

First step of DCD approach. Orders the noisy differential topological adjacency matrix to generate approximate block diagonals.

**Usage**

```r
order_topological_matrix(A, mink)
```

**Arguments**

- **A**: Noisy differential topological adjacency matrix
- **mink**: Minimum size of a community for it to be considered differential, default value is 7.
Value

Returns an ordered list for nodeids, by using which the noisy differential matrix is ordered such that it consists of approximate block diagonals.

Author(s)

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References

Francois R (2014). _bibtex: bibtex parser_. R package version 0.4.0, [https://CRAN.R-project.org/package=bibtex](https://CRAN.R-project.org/package=bibtex).

See Also

calculate_jaccard

Examples

```r
# Get ordered list for approximate block diagonals
library(igraph)
library(WGCNA)
g_A <- sample_grg(200, 0.15, torus=FALSE, coords = FALSE)
A <- get.adjacency(g_A)
g_B = permute(g_A,c(sample(20),21:200))
B <- get.adjacency(g_B)

cosine_sim_A <- TOMsimilarity(as.matrix(A),TOMType = "unsigned",TOMDenom = "min");
cosine_sim_B <- TOMsimilarity(as.matrix(B),TOMType = "unsigned",TOMDenom = "min")
edgelist_A <- get.edgelist(g_A);
edgelist_B <- get.edgelist(g_B);
if (is.null(E(g_A)$weight))
{
edgelist_A <- cbind(edgelist_A,rep(1,nrow(edgelist_A)));
}else
{
edgelist_A <- cbind(edgelist_A,E(g_A)$weight);
}
if (is.null(E(g_B)$weight))
{
edgelist_B <- cbind(edgelist_B,rep(1,nrow(edgelist_B)));
}else
{
edgelist_B <- cbind(edgelist_B,E(g_B)$weight);
}
edgelist_A <- as.data.frame(edgelist_A);
edgelist_B <- as.data.frame(edgelist_B);
mink <- 7

# Noisy Difference in topological matrices
diff_topological_matrix <- abs(cosine_sim_A-cosine_sim_B);
```
Order the nodes in topological graph using greedy approach
ordered_list <- order_topological_matrix(diff_topological_matrix,mink);

---

**prune_edges**

*De-noises ordered differential topological matrix*

**Description**

Second step of DCD: De-noises the ordered differential topological matrix to generate BDs.

**Usage**

```r
prune_edges(A, min_size_cluster)
```

**Arguments**

- **A**
  - Ordered noisy differential topological adjacency matrix
- **min_size_cluster**
  - Minimum size of a community for it to be considered differential, default value is 7.

**Value**

De-noised ordered topological adjacency matrix

**Author(s)**

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**References**


**Examples**

```r
# Denoise the noisy ordered adjacency matrix
library(igraph)
library(WGCNA)
g_A <- sample_grg(200, 0.15, torus=FALSE, coords = FALSE)
A <- get.adjacency(g_A)
g_B = permute(g_A,c(sample(20),21:200))
B <- get.adjacency(g_B)

cosine_sim_A <- TOMsimilarity(as.matrix(A),TOMType = "unsigned",TOMDenom = "min")
cosine_sim_B <- TOMsimilarity(as.matrix(B),TOMType = "unsigned",TOMDenom = "min")
```
edgelist_A <- get.edgelist(g_A);
edgelist_B <- get.edgelist(g_B);
if (is.null(E(g_A)$weight))
{
  edgelist_A <- cbind(edgelist_A, rep(1, nrow(edgelist_A)));
} else
{
  edgelist_A <- cbind(edgelist_A, E(g_A)$weight);
}
if (is.null(E(g_B)$weight))
{
  edgelist_B <- cbind(edgelist_B, rep(1, nrow(edgelist_B)));
} else
{
  edgelist_B <- cbind(edgelist_B, E(g_B)$weight);
}
edgelist_A <- as.data.frame(edgelist_A);
edgelist_B <- as.data.frame(edgelist_B);

mink <- 7
#Noisy Difference in topological matrices
diff_topological_matrix <- abs(cosine_sim_A-cosine_sim_B);

#Order the nodes in topological graph to create block diagonals
ordered_list <- order_topological_matrix(diff_topological_matrix, mink);
temp_output_adjacency <- diff_topological_matrix[ordered_list, ordered_list];

#Perform the greedy deterministic approach to remove spurious edges and keep significant ones
output_adjacency <- prune_edges(temp_output_adjacency, mink);
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