

# Package: NetSci (via r-universe)

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**Type** Package

**Title** Calculates Basic Network Measures Commonly Used in Network Medicine

**Version** 1.0.1

**Description** Calculates network measures commonly used in Network Medicine. Measures such as the Largest Connected Component, the Relative Largest Connected Component, Proximity and Separation are calculated along with their statistical significance. Significance can be computed both using a degree-preserving randomization and non-degree preserving.

**Imports** igraph, magrittr, wTO, dplyr, Rfast, utils, binr, cubature

**Suggests** CoDiNA

**License** GPL-2

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avr\_proximity\_multiple\_target\_sets

*avr\_proximity\_multiple\_target\_sets*

---

### Description

Calculates the average proximity from a set of targets to a set of source nodes. It is calculate using a degree preserving randomization. It is calculated as described in Guney, E. et al (2016) <doi.org:10.1038/ncomms10331>

### Usage

```
avr_proximity_multiple_target_sets(
  set,
  G,
  ST,
  source,
  N = 1000,
  bins = 100,
  min_per_bin = 20,
  weighted = FALSE
)
```

### Arguments

set	Name of the sets you have targets for. (In a drug-target setup, those would be the drugs of interest).
G	The original graph (often an interactome).
ST	Set-Target data. It is a data.frame with two columns. ID and Target.
source	The source nodes (disease genes).
N	Number of randomizations.
bins	the number os bins for the degree preserving randomization.
min_per_bin	the minimum size of each bin.
weighted	consider a weighted graph? TRUE/FALSE

**Value**

proximity and its significance based on the degree preserving randomization.

**Examples**

```
set.seed(666)
net = data.frame(
  Node.1 = sample(LETTERS[1:15], 15, replace = TRUE),
  Node.2 = sample(LETTERS[1:10], 15, replace = TRUE))
net$value = 1
net = CoDiNA::OrderNames(net)
net = unique(net)
net$weight = runif(nrow(net))

g <- igraph::graph_from_data_frame(net, directed = FALSE )
S = c("N", "A", "F", "I")
T1 = data.frame(ID = "T1", Target = c("H", "M"))
T2 = data.frame(ID = "T2", Target = c("G", "O"))

avr_proximity_multiple_target_sets(set = c('T1', 'T2'),
  G = g,
  source = S,
  ST = rbind(T1,T2),
  bins = 1,
  min_per_bin = 2)

# In a weighted graph
# avr_proximity_multiple_target_sets(set = c('T1', 'T2'),
# G = g,
# source = S,
# ST = rbind(T1,T2),
# bins = 1,
# min_per_bin = 2,
# weighted = TRUE)
```

---

 extract\_LCC

*Extract LCC from a graph*


---

**Description**

Extract LCC from a graph

**Usage**

```
extract_LCC(g)
```

**Arguments**

`g` is the graph you want to extract the largest connected component

**Value**

a graph (from igraph) with only the largest connected component

**Examples**

```
set.seed(12)
x = data.frame(n1 = sample(LETTERS[1:5]),
              n2 = sample(LETTERS[1:20]))

g = igraph::graph_from_data_frame(x, directed = FALSE)
g = igraph::simplify(g)
LCC = extract_LCC(g)
```

---

Histogram\_LCC

*Histogram\_LCC*


---

**Description**

Plots the histogram to evaluate the significance of the Largest Connected Component (LCC).

**Usage**

```
Histogram_LCC(LCC_L, Name = NULL)
```

**Arguments**

LCC_L	an output from the function LCC_Significance or LCC_Bipartide
Name	title of the plot

**Value**

An Histogram of the simulated LCC, and a red line of the actual LCC.

**Examples**

```
set.seed(666)
net = data.frame(
  Node.1 = sample(LETTERS[1:15], 15, replace = TRUE),
  Node.2 = sample(LETTERS[1:10], 15, replace = TRUE))
net$value = 1
net = CoDiNA::OrderNames(net)
net = unique(net)

g <- igraph::graph_from_data_frame(net, directed = FALSE )
targets = c("N", "A", "I", "F")
LCC_Out = LCC_Significance(N = 1000,
                          Targets = targets,
```

```
G = g,  
bins = 5,  
min_per_bin = 2)  
# in a real interactome, please use the default  
  
Histogram_LCC(LCC_Out, "Example")
```

---

Hypergeometric.test    *Hypergeometric.test*

---

### Description

Calculates the significance of an overlap of two sets using an hypergeometric test. It is a wrapper of the 'phyper' function.

### Usage

```
Hypergeometric.test(  
  success,  
  universe_success,  
  universe_failure,  
  size_collected,  
  lower.tail = FALSE  
)
```

### Arguments

success	Is the number of elements in the overlap of the sets.
universe_success	Is the number of elements of the set of interest.
universe_failure	Is the number of elements of the set of the other set.
size_collected	The total of elements in the universe
lower.tail	Should the test be calculated on the lower tail? (Hypothesis test is lower than)

### Value

the p-value for the hypergeometric test.

### Examples

```
require(magrittr)  
s = 10; S = 15; f = 10; T = 30  
Hypergeometric.test(success = s,  
  universe_success = S,  
  universe_failure = f,  
  size_collected = T  
)
```

---

Jaccard	<i>Jaccard</i>
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---

**Description**

Calculates the Jaccard index between different sets.

**Usage**

```
Jaccard(Data)
```

**Arguments**

Data	A data.frame with 2 columns. The first refers to the set and the second the elements
------	--

**Value**

a data.frame with the set names and their Jaccard index

**Examples**

```
set.seed(123)
Data = data.frame(Class = sample(c("X", "Y", "Z"), replace = TRUE, size = 50),
                  Element = sample(LETTERS[1:15], replace = TRUE, size = 50))
Data = unique(Data)
Jaccard(Data)
```

---

LCC_Significance	<i>LCC Significance</i>
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---

**Description**

Calculates the Largest Connected Component (LCC) from a given graph, and calculates its significance using a degree preserving approach. Menche, J., et al (2015) <doi.org:10.1126/science.1065103>

**Usage**

```
LCC_Significance(
  N = N,
  Targets = Targets,
  G,
  bins = 100,
  hypothesis = "greater",
  min_per_bin = 20
)
```

**Arguments**

N	Number of randomizations.
Targets	Name of the nodes that the subgraph will focus on - Those are the nodes you want to know whether it forms an LCC.
G	The graph of interest (often, in NetMed it is an interactome - PPI).
bins	the number of bins for the degree preserving randomization. When bins = 1, assumes a uniform distribution for nodes.
hypothesis	are you expecting an LCC greater or smaller than the average?
min_per_bin	the minimum size of each bin.

**Value**

a list with the LCC - \$LCCZ all values from the randomizations - \$mean the average LCC of the randomizations - \$sd the sd LCC of the randomizations - \$Z The score - \$LCC the LCC of the given targets - \$semp\_p the empirical p-value for the LCC - \$rLCC the relative LCC

**Examples**

```
set.seed(666)
net = data.frame(
  Node.1 = sample(LETTERS[1:15], 15, replace = TRUE),
  Node.2 = sample(LETTERS[1:10], 15, replace = TRUE))
net$value = 1
net = CoDiNA::OrderNames(net)
net = unique(net)

g <- igraph::graph_from_data_frame(net, directed = FALSE )
plot(g)
targets = c("I", "H", "F", "E")
LCC_Significance(N = 100,
  Targets = targets,
  G = g,
  bins = 1,
  min_per_bin = 2)
```

**Description**

Basic global variables to make sure the package runs.

---

proximity\_average      *Proximity from target to source*

---

**Description**

Calculates the proximity (average or closest) from source to targets.

**Usage**

```
proximity_average(G, source, targets)
```

**Arguments**

G	The original graph (often an interactome).
source	nodes from the network (in a drug repurposing set-up those are the disease genes)
targets	targets in the network (in a drug repurposing set-up those are the drug-targets)

**Value**

the proximity value for the source-targets

**Examples**

```
#' set.seed(666)
net = data.frame(
  Node.1 = sample(LETTERS[1:15], 15, replace = TRUE),
  Node.2 = sample(LETTERS[1:10], 15, replace = TRUE))
net$value = 1
net = CoDiNA::OrderNames(net)
net = unique(net)

g <- igraph::graph_from_data_frame(net, directed = FALSE )
T = c("G", "A", "D")
S = c("C", "M")
proximity_average(g, source = S, targets = T)
```

---

proximity\_average\_weighted  
*Proximity from target to source*

---

**Description**

Calculates the weighted average proximity from source to targets.



**Usage**

```
proximity_average_weighted(G, source, targets)
```

**Arguments**

G	The original graph (often a weighted interactome).
source	nodes from the network (in a drug repurposing set-up those are the disease genes)
targets	targets in the network (in a drug repurposing set-up those are the drug-targets)

**Value**

the proximity value for the source-targets

**Examples**

```
set.seed(666)
net = data.frame(
  Node.1 = sample(LETTERS[1:15], 15, replace = TRUE),
  Node.2 = sample(LETTERS[1:10], 15, replace = TRUE))
net$value = 1
net = CoDiNA::OrderNames(net)
net = unique(net)
net$weight = runif(nrow(net))
g <- igraph::graph_from_data_frame(net, directed = FALSE )
T = c("G", "A", "D")
S = c("C", "M")
proximity_average_weighted(g, source = S, targets = T)
```

---

proximity_close	<i>Proximity from target to source</i>
-----------------	--

---

**Description**

Calculates the proximity (average or closest) from source to targets.

**Usage**

```
proximity_close(G, source, targets)
```

**Arguments**

G	The original graph (often an interactome).
source	nodes from the network (in a drug repurposing set-up those are the disease genes)
targets	targets in the network (in a drug repurposing set-up those are the drug-targets)

**Value**

the proximity value for the source-targets

**Examples**

```
set.seed(666)
net = data.frame(
  Node.1 = sample(LETTERS[1:15], 15, replace = TRUE),
  Node.2 = sample(LETTERS[1:10], 15, replace = TRUE))
net$value = 1
net = CoDiNA::OrderNames(net)
net = unique(net)

g <- igraph::graph_from_data_frame(net, directed = FALSE )
T = c("G", "A", "D")
S = c("C", "M")
proximity_close(g, source = S, targets = T)
```

---

separation

*Separation*

---

**Description**

Calculates the separation of two set of targets on a network. Often used to measure separation of disease modules in a interactome. Separation is calculated as in Menche, J. et al (2015) <doi:10.1126/science.1257601>.

**Usage**

```
separation(G, ST)
```

**Arguments**

G	The original graph (often an interactome).
ST	Set-Target data. It is a data.frame with two columns. ID and Target.

**Value**

the separation and distance of modules.

**Examples**

```
require(magrittr)
set.seed(12)
x = data.frame(n1 = sample(LETTERS[1:5]),
               n2 = sample(LETTERS[1:20]))

D1 = data.frame(gene = c("H", "I", "S", "N", "A"), disease = "D1")
D2 = data.frame(gene = c("E", "C", "R", "J", "Q", "O"), disease = "D2")
D3 = data.frame(gene = c("E", "G", "T", "P"), disease = "D3")
```

```
D4 = data.frame(gene = c("A", "B", "E"), disease = "D4")

Diseases = rbind(D1, D2, D3, D4)
Diseases %<>% dplyr::select(disease, gene)
g = igraph::graph_from_data_frame(x, directed = FALSE)
g = igraph::simplify(g)

separation(G = g, ST = Diseases)
```

---

```
separation_Significance
```

*Separation Significance*

---

## Description

Calculates the separation of two set of targets on a network and assigns a p-value to it. Often used to measure separation of disease modules in a interactome. Separation is calculated as in Menche, J. et al (2015) <doi:10.1126/science.1257601>. p-values are calculates based on the permutation of nodes, you can set the full network to be in the set for permutation or can select the ones you include as input.

## Usage

```
separation_Significance(G, ST, Threads = 2, N = 1000, correct_by_target = TRUE)
```

## Arguments

G	The original graph (often an interactome / PPI).
ST	Set-Target data. It is a data.frame with two columns. ID and Target.
Threads	How many threads you'd like to use (for parallel computation).
N	default to 1000. The number of permutations
correct_by_target	TRUE by default. If you want to use the set of targets for the permutation or the full network.

## Value

the separation and distance of modules and its p-value.

## Examples

```
set.seed(12)
require(magrittr)
x = data.frame(n1 = sample(LETTERS[1:5]),
              n2 = sample(LETTERS[1:20]))

D1 = data.frame(gene = c("H", "I", "S", "N", "A"), disease = "D1")
D2 = data.frame(gene = c("E", "C", "R", "J", "Q", "O"), disease = "D2")
```

```
D3 = data.frame(gene = c("E", "G", "T", "P"), disease = "D3")
D4 = data.frame(gene = c("A", "B", "E"), disease = "D4")
D5 = data.frame(gene = c("D", "F", "L"), disease = "D5")
D6 = data.frame(gene = c("D", "F", "K"), disease = "D6")
D7 = data.frame(gene = c("A", "B", "F", "K"), disease = "D7")

Diseases = rbind(D1, D2, D3, D4, D5, D6, D7)
Diseases %<>% dplyr::select(disease, gene)
g = igraph::graph_from_data_frame(x, directed = FALSE)
g = igraph::simplify(g)

separation_Significance(G = g,
ST = Diseases,
correct_by_target = FALSE,
Threads = 2)
```

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