

# Package ‘NetworkToolbox’

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**Title** Methods and Measures for Brain, Cognitive, and Psychometric Network Analysis

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**Description** Implements network analysis and graph theory measures used in neuroscience, cognitive science, and psychology. Methods include various filtering methods and approaches such as threshold, dependency (Kenett, Tumminello, Madi, Gur-Gershgoren, Mantegna, & Ben-Jacob, 2010 <[doi:10.1371/journal.pone.0015032](https://doi.org/10.1371/journal.pone.0015032)>), Information Filtering Networks (Barfuss, Massara, Di Matteo, & Aste, 2016 <[doi:10.1103/PhysRevE.94.062306](https://doi.org/10.1103/PhysRevE.94.062306)>), and Efficiency-Cost Optimization (Falani, Latora, & Chavez, 2017 <[doi:10.1371/journal.pcbi.1005305](https://doi.org/10.1371/journal.pcbi.1005305)>). Brain methods include the recently developed Connectome Predictive Modeling (see references in package). Also implements several network measures including local network characteristics (e.g., centrality), community-level network characteristics (e.g., community centrality), global network characteristics (e.g., clustering coefficient), and various other measures associated with the reliability and reproducibility of network analysis.

**Depends** R (>= 3.6.0)

**License** GPL (>= 3.0)

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**Suggests** googledrive

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**NeedsCompilation** no

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NetworkToolbox-package

*NetworkToolbox-package*

---

## Description

Implements network analysis and graph theory measures used in neuroscience, cognitive science, and psychology. Methods include various filtering methods and approaches such as threshold, dependency, Information Filtering Networks, and Efficiency-Cost Optimization. Brain methods include the recently developed Connectome Predictive Modeling. Also implements several network measures including local network characteristics (e.g., centrality), global network characteristics (e.g., clustering coefficient), and various other measures associated with the reliability and reproducibility of network analysis.

## Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

## References

Christensen, A. P. (in press). NetworkToolbox: Methods and measures for brain, cognitive, and psychometric network analysis in R. *The R Journal*, 10, 422-439.

adapt.a

*Adaptive Alpha***Description**

Compute an alpha value adjusted for sample size. The adjusted value is based on Perez and Pericchi's (2014) formula (equation 11, see below) using a reference sample, which can be defined a priori or estimated using the sample size calculation from power.

$$\frac{\alpha * \sqrt{n_0 \times (\log(n_0) + \chi_{\alpha}^2(1))}}{\sqrt{n^* \times (\log(n^*) + \chi_{\alpha}^2(1))}}$$

**Usage**

```
adapt.a(
  test = c("anova", "chisq", "cor", "one.sample", "two.sample", "paired"),
  ref.n = NULL,
  n = NULL,
  alpha = 0.05,
  power = 0.8,
  efxize = c("small", "medium", "large"),
  groups = NULL,
  df = NULL
)
```

**Arguments**

test	Type of statistical test being used. Can be any of the tests listed
ref.n	$n_0$ in the above equation. Reference sample size. If sample size was determined a priori, then the reference number of participants can be set. This removes the calculation of sample size based on power
n	$n^*$ in the above equation. Number of participants in the experiment sample (or per group)
alpha	$\alpha$ in the above equation. Alpha value to adjust. Defaults to .05
power	Power ( $1 - \beta$ ) value. Used to estimate the reference sample size ( $n_0$ ). Defaults to .80
efxize	Effect size to be used to estimate the reference sample size. Effect sizes are based on Cohen (1992). Numeric values can be used. Defaults to "medium"
groups	Number of groups (only for test = "anova")
df	Number of degrees of freedom (only for test = "chisq")

**Value**

A list containing the following objects:

adapt.a	The adapted alpha value
crit.value	The critical value associated with the adapted alpha value
orig.a	The original alpha value
ref.n	The reference sample size based on alpha, power, effect size, and test
exp.n	The sample size of the experimental sample
power	The power used to determine the reference sample size
test	The type of statistical test used

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Cohen, J. (1992). A power primer. *Psychological Bulletin*, 112, 155-159.

Perez, M. E., & Pericchi, L. R. (2014). Changing statistical significance with the amount of information: The adaptive *a* significance level. *Statistics & Probability Letters*, 85, 20-24.

**Examples**

```
#ANOVA
adapt.anova <- adapt.a(test = "anova", n = 200, alpha = .05, power = .80, groups = 3)

#Chi-square
adapt.chisq <- adapt.a(test = "chisq", n = 200, alpha = .05, power = .80, df = 3)

#Correlation
adapt.cor <- adapt.a(test = "cor", n = 200, alpha = .05, power = .80)

#One-sample t-test
adapt.one <- adapt.a(test = "one.sample", n = 200, alpha = .05, power = .80)

#Two-sample t-test
adapt.two <- adapt.a(test = "two.sample", n = 200, alpha = .05, power = .80)

#Paired sample t-test
adapt.paired <- adapt.a(test = "paired", n = 200, alpha = .05, power = .80, efsize = "medium")
```

---

`behavOpen`*NEO-PI-3 for Resting-state Data*

---

**Description**

NEO-PI-3 Openness to Experience associated with resting-state data ( $n = 144$ ).

**Usage**

```
data(behavOpen)
```

**Format**

behavOpen (vector, length = 144)

**Details**

Behavioral data of NEO-PI-3 associated with each connectivity matrix (open).

To access the resting-state brain data, please go to [https://drive.google.com/file/d/1T7\\_mComB6HPxJxZZwvsLLSYHXs0uv0Bt/view?usp=sharing](https://drive.google.com/file/d/1T7_mComB6HPxJxZZwvsLLSYHXs0uv0Bt/view?usp=sharing)

**References**

Beaty, R. E., Chen, Q., Christensen, A. P., Qiu, J., Silvia, P. J., & Schacter, D. L. (2018). Brain networks of the imaginative mind: Dynamic functional connectivity of default and cognitive control networks relates to Openness to Experience. *Human Brain Mapping*, 39, 811-821.

Beaty, R. E., Kenett, Y. N., Christensen, A. P., Rosenberg, M. D., Benedek, M., Chen, Q., ... & Silvia, P. J. (2018). Robust prediction of individual creative ability from brain functional connectivity. *Proceedings of the National Academy of Sciences*, 201713532.

**Examples**

```
data("behavOpen")
```

---

`betweenness`*Betweenness Centrality*

---

**Description**

Computes betweenness centrality of each node in a network

**Usage**

```
betweenness(A, weighted = TRUE)
```

**Arguments**

A An adjacency matrix of network data

weighted Is the network weighted? Defaults to TRUE. Set to FALSE for unweighted measure of betweenness centrality

**Value**

A vector of betweenness centrality values for each node in the network

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

#Weighted BC
BCw <- betweenness(A)

#Unweighted BC
BC <- betweenness(A, weighted = FALSE)
```

---

binarize

*Binarize Network*

---

**Description**

Converts weighted adjacency matrix to a binarized adjacency matrix

**Usage**

```
binarize(A)
```

**Arguments**

A An adjacency matrix of network data (or an array of matrices)

**Value**

Returns an adjacency matrix of 1's and 0's

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

neoB <- binarize(A)
```

---

closeness

*Closeness Centrality*

---

**Description**

Computes closeness centrality of each node in a network

**Usage**

```
closeness(A, weighted = TRUE)
```

**Arguments**

A	An adjacency matrix of network data
weighted	Is the network weighted? Defaults to TRUE. Set to FALSE for unweighted measure of closeness centrality

**Value**

A vector of closeness centrality values for each node in the network

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.



**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

#Weighted LC
LC <- closeness(A)

#Unweighted LC
LC <- closeness(A, weighted = FALSE)
```

---

clustcoeff	<i>Clustering Coefficient</i>
------------	-------------------------------

---

**Description**

Computes global clustering coefficient (CC) and local clustering coefficient (CCi)

**Usage**

```
clustcoeff(A, weighted = FALSE)
```

**Arguments**

A	An adjacency matrix of network data
weighted	Is the network weighted? Defaults to FALSE. Set to TRUE for weighted measures of CC and CCi

**Value**

Returns a list containing:

CC	Global clustering coefficient. The average clustering coefficient for each node in the network
CCi	Local clustering coefficient. The clustering coefficient for each node in the network

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

## Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

#Unweighted CC
CCu <- clustcoeff(A)

#Weighted CC
CCw <- clustcoeff(A, weighted=TRUE)
```

---

 comcat

*Communicating Nodes*


---

## Description

Computes the between-community strength for each node in the network

## Usage

```
comcat(
  A,
  comm = c("walktrap", "louvain"),
  cent = c("strength", "degree"),
  absolute = TRUE,
  metric = c("across", "each"),
  diagonal = 0,
  ...
)
```

## Arguments

A	An adjacency matrix of network data
comm	Can be a vector of community assignments or community detection algorithms ("walktrap" or "louvain") can be used to determine the number of factors. Defaults to "walktrap". Set to "louvain" for <b>louvain</b> community detection
cent	Centrality measure to be used. Defaults to "strength".
absolute	Should network use absolute weights? Defaults to TRUE. Set to FALSE for signed weights
metric	Whether the metric should be compute for across all of the communities (a single value) or for each community (a value for each community). Defaults to "across". Set to "each" for values for each community
diagonal	Sets the diagonal values of the A input. Defaults to 0
...	Additional arguments for <a href="#">cluster_walktrap</a> and <a href="#">louvain</a> community detection algorithms

**Value**

A vector containing the between-community strength value for each node

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Blanken, T. F., Deserno, M. K., Dalege, J., Borsboom, D., Blanken, P., Kerkhof, G. A., & Cramer, A. O. (2018). The role of stabilizing and communicating symptoms given overlapping communities in psychopathology networks. *Scientific Reports*, 8, 5854.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

communicating <- comcat(A, comm = "walktrap", cent = "strength", metric = "across")
```

---

comm.close

*Community Closeness Centrality*

---

**Description**

Computes the community closeness centrality measure of each community in a network

**Usage**

```
comm.close(A, comm, weighted = FALSE)
```

**Arguments**

A	An adjacency matrix of network data
comm	A vector or matrix corresponding to the community each node belongs to
weighted	Is the network weighted? Defaults to FALSE. Set to TRUE for weighted measures

**Value**

A vector of community closeness centrality values for each specified community in the network (larger values suggest more central positioning)

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

## References

Christensen, A. P. (in press). NetworkToolbox: Methods and measures for brain, cognitive, and psychometric network analysis in R. *The R Journal*, 10, 422-439.

## Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

comm <- igraph::walktrap.community(convert2igraph(abs(A)))$membership

#Weighted
result <- comm.close(A, comm)

#Unweighted
result <- comm.close(A, comm, weighted = FALSE)
```

---

comm.eigen

*Community Eigenvector Centrality*

---

## Description

Computes the [flow.frac](#) for each community in the network. The values are equivalent to the community's eigenvector centrality

## Usage

```
comm.eigen(A, comm, weighted = TRUE)
```

## Arguments

A	An adjacency matrix
comm	A vector or matrix corresponding to the community each node belongs to
weighted	Is the network weighted? Defaults to TRUE. Set to FALSE for weighted measures

## Value

A vector of community eigenvector centrality values for each specified community in the network (larger values suggest more central positioning)

## Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

## References

Giscard, P. L., & Wilson, R. C. (2018). A centrality measure for cycles and subgraphs II. *Applied Network Science*, 3, 9.

## Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

comm <- igraph::walktrap.community(convert2igraph(abs(A)))$membership

result <- comm.eigen(A, comm)
```

---

comm.str

*Community Strength/Degree Centrality*

---

## Description

Computes the community [strength/degree](#) centrality measure of each community in a network or computes the [strength/degree](#) centrality measure of each community's connections to the other communities

## Usage

```
comm.str(A, comm, weighted = TRUE, measure = c("within", "between"))
```

## Arguments

A	An adjacency matrix of network data
comm	A vector corresponding to the community each node belongs to
weighted	Is the network weighted? Defaults to TRUE. Set to FALSE for weighted measures
measure	Type of measure to compute: <ul style="list-style-type: none"><li>• "within" — Computes the community strength or degree of nodes within its own community</li><li>• "between" — Computes the community strength or degree of nodes outside of its own community</li></ul>

## Value

A vector of community strength/degree centrality values for each specified community in the network (larger values suggest more central positioning)

## Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

## Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

comm <- igraph::walktrap.community(convert2igraph(abs(A)))$membership

#Strength
within.ns <- comm.str(A, comm, measure = "within")
between.ns <- comm.str(A, comm, measure = "between")

#Degree
within.deg <- comm.str(A, comm, weighted = FALSE, measure = "within")
between.deg <- comm.str(A, comm, weighted = FALSE, measure = "between")
```

---

conn

*Network Connectivity*

---

## Description

Computes the average and standard deviation of the weights in the network

## Usage

```
conn(A)
```

## Arguments

A                    An adjacency matrix of a network

## Value

Returns a list containing:

weights	Each edge weight in the network
mean	The mean of the edge weights in the network
sd	The standard deviation of the edge weights in the network
total	The sum total of the edge weights in the network

## Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

## Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

connectivity <- conn(A)
```

---

convert2igraph	<i>Convert Network(s) to igraph's Format</i>
----------------	--

---

### Description

Converts single or multiple networks into igraph's format for network analysis

### Usage

```
convert2igraph(A, neural = FALSE)
```

### Arguments

A	Adjacency matrix (network matrix) or brain connectivity array (from <a href="#">convertConnBrainMat</a> )
neural	Is input a brain connectivity array (i.e., m x m x n)? Defaults to FALSE. Set to TRUE to convert each brain connectivity matrix

### Value

Returns a network matrix in igraph's format or returns a list of brain connectivity matrices each of which have been convert to igraph's format

### Author(s)

Alexander Christensen <[alexpaulchristensen@gmail.com](mailto:alexpaulchristensen@gmail.com)>

### Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

igraphNetwork <- convert2igraph(A)

## Not run:
neuralarray <- convertConnBrainMat()

igraphNeuralList <- convert2igraph(neuralarray, neural = TRUE)

## End(Not run)
```

---

convertConnBrainMat     *Import CONN Toolbox Brain Matrices to R format*

---

### Description

Converts a Matlab brain z-score connectivity array ( $n \times n \times m$ ) where  $n$  is the  $n \times n$  connectivity matrices and  $m$  is the participant. If you would like to simply import a connectivity array from Matlab, then see the examples

### Usage

```
convertConnBrainMat(MatlabData, progBar = TRUE)
```

### Arguments

MatlabData	Input for Matlab data file. Defaults to interactive file choice
progBar	Should progress bar be displayed? Defaults to TRUE. Set FALSE for no progress bar

### Value

Returns a list containing:

rmat	Correlation matrices for each participant ( $m$ ) in an array ( $n \times n \times m$ )
zmat	Z-score matrices for each participant ( $m$ ) in an array ( $n \times n \times m$ )

### Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

### Examples

```
## Not run:
neuralarray <- convertConnBrainMat()

#Import correlation connectivity array from Matlab
library(R.matlab)
neuralarray<-readMat(file.choose())

## End(Not run)
```



---

cor2cov	<i>Convert Correlation Matrix to Covariance Matrix</i>
---------	--

---

**Description**

Converts a correlation matrix to a covariance matrix

**Usage**

```
cor2cov(cormat, data)
```

**Arguments**

cormat	A correlation matrix
data	The dataset the correlation matrix is from

**Value**

Returns a covariance matrix

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
cormat <- cor(neoOpen)
covmat <- cor2cov(cormat, neoOpen)
```

---

core.items	<i>Core Items</i>
------------	-------------------

---

**Description**

Automatically determines core, intermediary, and peripheral items in the network. The entire network or within-community gradations can be determined. Based on the [hybrid](#) centrality

**Usage**

```
core.items(A, comm, by = c("network", "communities"))
```

**Arguments**

A	An adjacency matrix of network data
comm	A vector or matrix corresponding to the community each node belongs to
by	Should the core items be defined by network or communities? Defaults to "network". Set to "communities" to define core items within communities

**Value**

Returns a list containing:

core	Core items for each community
inter	Intermediate items for each community
peri	Peripheral items for each community

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
#network
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

#core items by network
coreBYnetwork <- core.items(A, by = "network")

#theoretical factors
comm <- c(rep(1,8),rep(2,8),rep(3,8),rep(4,8),rep(5,8),rep(6,8))

#core items by communities
coreBYcomm <- core.items(A, comm, by = "communities")
```

---

cpm

---

*Connectome-based Predictive Modeling*


---

**Description**

Suite of functions for Connectome-based Predictive Modeling (CPM). **See and cite Finn et al., 2015; Rosenberg et al., 2016; Shen et al., 2017**

- cpmIV — Internal Validation method (Rosenberg et al., 2016; Shen et al., 2017). Using a leave-one-out approach, this method correlates a behavioral statistic *bstat* with each edge of a whole-brain network across participants. Using the significant edges in the network *thresh*, a connectome model is built (without the participant's network). A linear regression model is fit, with the behavioral statistic being regressed on the connectome model. The left out

participants connectome model is then used with the linear regression weights to compute their predicted behavioral score. This is repeated for every participant. The predicted scores are correlated with their observed score. Significant values suggest that the connectome is related to the behavioral statistic

- `cpmIVperm` — Performs a permutation test of the results obtained by `cpmIV`. The permutation test quantifies whether the results obtained by the original `cpmIV` are significantly different than a random model (see Shen et al., 2017)
- `cpmEV` — UNDER DEVELOPMENT. External Validation method (Beaty et al., 2018). Performs similar function as `cpmIV` but uses data to train `train_na` the connectome model using a behavioral statistic `train_b`. This training connectome model is then used to predict another dataset `valid_na`, using the same behavioral statistic `valid_b`. The full training dataset `FALSE` or the leave-one-out `overlap = TRUE` approach can be used
- `cpmFP` — Fingerprinting method (Finn et al., 2015). Uses CPM approach to identify participants across two sessions
- `cpmFPperm` — Fingerprinting method (Finn et al., 2015). Uses permutation method to estimate the significance of the `cpmFP` results
- `cpmPlot` — Plots the CPM results

## Usage

```
cpmIV(neuralarray, bstat, kfolds, covar, thresh = .01,
      connections = c("separate", "overall"), groups = NULL,
      method = c("mean", "sum"), model = c("linear", "quadratic", "cubic"),
      corr = c("pearson", "spearman"), nEdges,
      standardize = FALSE, cores, progBar = TRUE, plots = TRUE)
```

```
cpmIVperm(iter = 1000, ...)
```

```
cpmEV(train_na, train_b, valid_na, valid_b, thresh = .01,
      overlap = FALSE, progBar = TRUE)
```

```
cpmFP(session1, session2, progBar = TRUE)
```

```
cpmFPperm(session1, session2, iter = 1000, progBar = TRUE)
```

```
cpmPlot(cpm.obj, visual.nets = FALSE)
```

## Arguments

<code>neuralarray</code>	Array from <code>convertConnBrainMat</code> function
<code>bstat</code>	Behavioral statistic for each participant with neural data (a vector)
<code>kfolds</code>	Numeric. Number of $k$ -fold validation samples. Defaults to the number of participants in the sample (i.e., $n$ ), which is also known as leave-one-out validation. Recommended folds are 5 and 10
<code>covar</code>	Covariates to be included in predicting relevant edges ( <b>time consuming</b> ). <b>Must</b> be input as a <code>list()</code> (see examples)

thresh	Sets an $\alpha$ threshold for edge weights to be retained. Defaults to .01
connections	Character. Should positive and negative correlations be separated or used together? Defaults to "separate"
groups	Allows grouping variables to be used for plotting points. <b>Must</b> be a vector. Defaults to NULL
method	Use "mean" or "sum" of edge strengths in the positive and negative connectomes. Defaults to "mean"
model	Regression model to use for fitting the data. Defaults to "linear"
corr	Correlation method for assessing the relationship between the behavioral measure and edges between ROIs. Defaults to "pearson". Set to "spearman" for non-linear or monotonic associations
nEdges	Number of participants that are required to have an edge to appear in the plots. Defaults to 10 percent of edges in participants
standardize	Should the behavioral statistic (bstat) be standardized? Defaults to FALSE
cores	Number of computer processing cores to use when performing covariate analyses. Defaults to $n - 1$ total number of cores. Set to any number between 1 and maximum amount of cores on your computer
progBar	Should progress bar be displayed? Defaults to TRUE. Set to FALSE for no progress bar
plots	Should plots be plotted? Defaults to TRUE. Set to FALSE to hide plots
train_na	Training dataset (an array from <a href="#">convertConnBrainMat</a> function)
train_b	Behavioral statistic for each participant for the <b>training</b> neural data (a vector)
valid_na	Validation dataset (an array from <a href="#">convertConnBrainMat</a> function)
valid_b	Behavioral statistic for each participant for the <b>validation</b> neural data (a vector)
overlap	Should leave-one-out cross-validation be used? Defaults to FALSE (use full dataset, no leave-one-out). Set to TRUE to select edges that appear in every leave-one-out cross-validation network ( <i>time consuming</i> )
session1	Array from <a href="#">convertConnBrainMat</a> function (first session)
session2	Array from <a href="#">convertConnBrainMat</a> function (second session)
iter	Number of iterations to perform. Defaults to 1000
cpm.obj	<a href="#">cpm</a> object
visual.nets	Boolean. Uses <a href="#">qgraph</a> to plot connectivity between the networks as a network. Defaults to FALSE. Set to TRUE to visualize the networks
...	Additional arguments to be passed from a cpm function

### Value

cpmIV and cpmEV:

Returns a list containing:

results	A matrix containing: r coefficient (r), p-value (p-value), mean absolute error (mae), root mean square error (rmse)
---------	---

posMask            Positive connectivity for input in [BioImage Suite Connectivity Viewer](#)  
 negMask            Negative connectivity for input in [BioImage Suite Connectivity Viewer](#)

cpmIVperm:

Returns a matrix containing  $p$ -values for positive and negative prediction models

cpmFP:

Returns a matrix containing the percentage and number of correctly identified subjects for sessions 1 and 2

cpmPlot:

Returns plot of connectivity differences between the positive and negative masks

### Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

### References

Beaty, R. E., Kenett, Y. N., Christensen, A. P., Rosenberg, M. D., Benedek, M., Chen, Q., Fink, A., Qiu, J., Kwapil, T. R., Kane, M. J., & Silvia, P. J. (2018). Robust prediction of individual creative ability from brain functional connectivity. *Proceedings of the National Academy of Sciences*, *115*, 1087-1092.

Finn, E. S., Shen, X., Scheinost, D., Rosenberg, M. D., Huang, J., Chun, M. M., Papademetris, X., Constable, R. T. (2015). Functional connectome fingerprinting: Identifying individuals using patterns of brain connectivity. *Nature Neuroscience*, *18*, 1664-1671.

Rosenberg, M. D., Finn, E. S., Scheinost, D., Papademetris, X., Shen, X., Constable, R. T., Chun, M. M. (2016). A neuromarker of sustained attention from whole-brain functional connectivity. *Nature Neuroscience*, *19*, 165-171.

Shen, X. Finn, E. S., Scheinost, D., Rosenberg, M. D., Chun, M. M., Papademetris, X., Constable, R. T. (2017). Using connectome-based predictive modeling to predict individual behavior from brain connectivity. *Nature Protocols*, *12*, 506-518.

Wei, T. & Simko, V.(2017). R package "corrplot": Visualization of a correlation matrix (Version 0.84).

### Examples

```
# Load data
behav <- behavOpen

## Not run:

# Create path to temporary file
temp <- tempfile()

# Download to temporary file
googledrive::drive_download(
  paste("https://drive.google.com/file/d/",
    "1T7_mComB6HPxJxZZwvsLLSYHXsOuvOBt",
```

```

"/view?usp=sharing", sep = ""),
path = temp
)

# Load resting state brain data
load(temp)

# Run cpmIV
res <- cpmIV(neuralarray = restOpen, bstat = behav, cores = 4)

# Plot cpmIV results
cpmPlot(res)

## End(Not run)

```

---

dCor

*Distance Correlation for ROI Time Series*


---

### Description

Computes the distance correlation (Yoo et al., 2019) for ROI time series data. This function is mainly a subroutine for the `dCor.parallel` function

### Usage

```
dCor(neurallist, centering = c("U", "double"))
```

### Arguments

neurallist	List. A time series list from <code>convertConnBrainMat</code> function
centering	Character. Options for centering the Euclidean distances. <ul style="list-style-type: none"> <li>"U" — Uses number of time points minus 2 in the computation of the mean</li> <li>"double" — Uses the mean</li> </ul>

### Value

Returns a  $m \times m$  matrix corresponding to distance correlations between ROIs

### Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

### References

Yoo, K., Rosenberg, M. D., Noble, S., Scheinost, D., Constable, R. T., & Chun, M. M. (2019). Multivariate approaches improve the reliability and validity of functional connectivity and prediction of individual behaviors. *NeuroImage*, *197*, 212-223.

**Examples**

```
## Not run:  
# Import time series data  
neurallist <- convertConnBrainMat()  
  
# Run distance correlation  
dCor(neurallist)  
  
## End(Not run)
```

---

`dCor.parallel`*Parallelization of Distance Correlation for ROI Time Series*

---

**Description**

Parallelizes the `dCor` function for faster computation times

**Usage**

```
dCor.parallel(neurallist, cores)
```

**Arguments**

<code>neurallist</code>	List of lists. A list containing the time series list from all participants imported from the <code>convertConnBrainMat</code> function
<code>cores</code>	Number of computer processing cores to use when performing covariate analyses. Defaults to $n - 1$ total number of cores. Set to any number between 1 and maximum amount of cores on your computer

**Value**

Returns a  $m \times m \times n$  array corresponding to distance correlations between ROIs ( $m \times m$  matrix) for  $n$  participants

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Yoo, K., Rosenberg, M. D., Noble, S., Scheinost, D., Constable, R. T., & Chun, M. M. (2019). Multivariate approaches improve the reliability and validity of functional connectivity and prediction of individual behaviors. *NeuroImage*, *197*, 212-223.

**Examples**

```
## Not run:
# Import time series data
for(i in 1:5)

# Run distance correlation
dCor.parallel(mat.list, cores = 2)

## End(Not run)
```

---

degree	<i>Degree</i>
--------	---------------

---

**Description**

Computes degree of each node in a network

**Usage**

```
degree(A)
```

**Arguments**

A                    An adjacency matrix of network data

**Value**

A vector of degree values for each node in the network.

If directed network, returns a list containing:

inDegree	Degree of incoming edges (pointing to the node)
outDegree	Degree of outgoing edges (pointing away from the node)
relInf	Relative degree of incoming and outgoing edges. Positive values indicate more outgoing degree relative to incoming degree. Negative values indicate more incoming degree relative to outgoing degree

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.



**Examples**

```

#Undirected network
## Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

deg <- degree(A)

#Directed network
## Not run:
dep <- depend(neoOpen)

Adep <- TMFG(dep, depend = TRUE)$A

deg <- degree(Adep)

## End(Not run)

```

---

depend

*Dependency Network Approach*


---

**Description**

Generates a dependency matrix of the data (index argument is still in testing phase)

**Usage**

```

depend(
  data,
  normal = FALSE,
  na.data = c("pairwise", "listwise", "fiml", "none"),
  index = FALSE,
  fisher = FALSE,
  progBar = TRUE
)

```

**Arguments**

data	A set of data
normal	Should data be transformed to a normal distribution? Defaults to FALSE. Data is not transformed to be normal. Set to TRUE if data should be transformed to be normal (computes correlations using the <a href="#">cor_auto</a> function)
na.data	How should missing data be handled? For "listwise" deletion the <a href="#">na.omit</a> function is applied. Set to "fiml" for Full Information Maximum Likelihood ( <a href="#">corFiml</a> ). Full Information Maximum Likelihood is <b>recommended</b> but time consuming

index	Should correlation with the latent variable (i.e., weighted average of all variables) be removed? Defaults to FALSE. Set to TRUE to remove common latent factor
fisher	Should Fisher's Z-test be used to keep significantly higher influences (index only)? Defaults to FALSE. Set to TRUE to remove non-significant influences
progBar	Should progress bar be displayed? Defaults to TRUE. Set to FALSE for no progress bar

**Value**

Returns an adjacency matrix of dependencies

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Kenett, D. Y., Tumminello, M., Madi, A., Gur-Gershgoren, G., Mantegna, R. N., & Ben-Jacob, E. (2010). Dominating clasp of the financial sector revealed by partial correlation analysis of the stock market. *PLoS one*, *5*, e15032.

Kenett, D. Y., Huang, X., Vodenska, I., Havlin, S., & Stanley, H. E. (2015). Partial correlation analysis: Applications for financial markets. *Quantitative Finance*, *15*, 569-578.

**Examples**

```
## Not run:
D <- depend(neoOpen)

Dindex <- depend(neoOpen, index = TRUE)

## End(Not run)
```

---

 depna

*Dependency Neural Networks*


---

**Description**

Applies the dependency network approach to neural network array

**Usage**

```
depna(neuralarray, cores, ...)
```

**Arguments**

neuralarray     Array from [convertConnBrainMat](#) function  
cores            Numeric. Number of cores to use in computing results. Set to 1 to not use parallel computing. Recommended to use maximum number of cores minus one  
...                Additional arguments from [depend](#) function

**Value**

Returns an array of  $n \times n \times m$  dependency matrices

**Author(s)**

Alexander Christensen <[alexpaulchristensen@gmail.com](mailto:alexpaulchristensen@gmail.com)>

**References**

Jacob, Y., Winetraub, Y., Raz, G., Ben-Simon, E., Okon-Singer, H., Rosenberg-Katz, K., ... & Ben-Jacob, E. (2016). Dependency Network Analysis (DEPNA) reveals context related influence of brain network nodes. *Scientific Reports*, 6, 27444.

Kenett, D. Y., Tumminello, M., Madi, A., Gur-Gershgoren, G., Mantegna, R. N., & Ben-Jacob, E. (2010). Dominating clasp of the financial sector revealed by partial correlation analysis of the stock market. *PLoS one*, 5, e15032.

**Examples**

```
## Not run:  
neuralarray <- convertConnBrainMat()  
  
dependencyneuralarray <- depna(neuralarray)  
  
## End(Not run)
```

---

desc

*Variable Descriptive Statistics*

---

**Description**

Computes mean, standard deviation (sd), minimum value (min), maximum value (max), and univariate normal statistics (normal?) for a variable

**Usage**

```
desc(data, column, histplot = TRUE)
```

**Arguments**

data	A matrix or data frame
column	Column name or number in data
histplot	A histogram plot of the variable

**Value**

A data frame containing values for `n` (number of cases), `missing` (number of missing cases), `mean`, `sd`, `min`, and `max`. `normal?` will contain yes/no for whether the variable is normally distributed based on the [shapiro.test](#) for a variable

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
desc(neoOpen, 1)
```

---

desc.all

*Dataset Descriptive Statistics*

---

**Description**

Computes mean, standard deviation (`sd`), minimum value (`min`), maximum value (`max`), and univariate normal statistics (`normal?`) for the entire dataset

**Usage**

```
desc.all(data)
```

**Arguments**

data	A matrix or data frame
------	------------------------

**Value**

A data frame containing values for `n` (number of cases), `missing` (number of missing cases), `mean`, `sd`, `min`, and `max`. `normal?` will contain yes/no for whether the variable is normally distributed based on the [shapiro.test](#) for the entire dataset

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
desc.all(neoOpen)
```

---

distance	<i>Distance</i>
----------	-----------------

---

**Description**

Computes distance matrix of the network

**Usage**

```
distance(A, weighted = FALSE)
```

**Arguments**

A	An adjacency matrix of network data
weighted	Is the network weighted? Defaults to FALSE. Set to TRUE for weighted measure of distance

**Value**

A distance matrix of the network

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

#Unweighted
Du <- distance(A)

#Weighted
Dw <- distance(A, weighted = TRUE)
```

diversity

*Diversity Coefficient***Description**

Computes the diversity coefficient for each node. The diversity coefficient measures a node's connections to communities outside of its own community. Nodes that have many connections to other communities will have higher diversity coefficient values. Positive and negative signed weights for diversity coefficients are computed separately.

**Usage**

```
diversity(A, comm = c("walktrap", "louvain"))
```

**Arguments**

A	Network adjacency matrix
comm	A vector of corresponding to each item's community. Defaults to "walktrap" for the <code>cluster_walktrap</code> community detection algorithm. Set to "louvain" for the <code>louvain</code> community detection algorithm. Can also be set to user-specified communities (see examples)

**Details**

Values closer to 1 suggest greater between-community connectivity and values closer to 0 suggest greater within-community connectivity

**Value**

Returns a list containing:

overall	Diversity coefficient without signs considered
positive	Diversity coefficient with only positive sign
negative	Diversity coefficient with only negative sign

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

#theoretical communities
comm <- rep(1:8, each = 6)

gdiv <- diversity(A, comm = comm)

#walktrap communities
wdiv <- diversity(A, comm = "walktrap")
```

---

ECO

*ECO Neural Network Filter*

---

**Description**

Applies the ECO neural network filtering method

**Usage**

```
ECO(data, directed = FALSE)
```

**Arguments**

data	Can be a dataset or a correlation matrix
directed	Is the network directed? Defaults to FALSE. Set TRUE if the network is directed

**Value**

A sparse association matrix

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Fallani, F. D. V., Latora, V., & Chavez, M. (2017). A topological criterion for filtering information in complex brain networks. *PLoS Computational Biology*, *13*, e1005305.

**Examples**

```
eco.net <- ECO(neoOpen)
```

---

ECOplusMaST

*ECO+MaST Network Filter*

---

**Description**

Applies the [ECO](#) neural network filtering method combined with the [MaST](#) filtering method

**Usage**

```
ECOplusMaST(data)
```

**Arguments**

data                    Can be a dataset or a correlation matrix

**Value**

A sparse association matrix

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Fallani, F. D. V., Latora, V., & Chavez, M. (2017). A topological criterion for filtering information in complex brain networks. *PLoS Computational Biology*, *13*, e1005305.

**Examples**

```
# half the variables for CRAN checks
ECOplusMaST.net <- ECOplusMaST(neoOpen[,c(1:24)])
```

---

edgerep

*Edge Replication*

---

**Description**

Computes the number of edges that replicate between two cross-sectional networks

**Usage**

```
edgerep(A, B, corr = c("pearson", "spearman", "kendall"))
```



**Arguments**

A	An adjacency matrix of network A
B	An adjacency matrix of network B
corr	Correlation method for assessing the relationship between the replicated edge weights. Defaults to "pearson". Set to "spearman" for non-linear or monotonic associations. Set to "kendall" for rank-order correlations

**Value**

Returns a list containing:

replicatedEdges	The edges that replicated and their weights
replicated	Number of edges that replicated
meanDiff	The average edge weight difference between the edges that replicated
sdDiff	The standard deviation edge weight difference between the edges that replicated
cor	The correlation between the edges that replicated

Lists for each network contain:

totalEdges	Total possible number of edges to be replicated
percentage	Percentage of edges that replicated relative to total possible
density	The density of the network

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
# normal set to FALSE for CRAN tests
tmfg <- TMFG(neoOpen, normal = FALSE)$A

# normal set to FALSE for CRAN tests
mast <- MaST(neoOpen, normal = FALSE)

edges <- edgerep(tmfg, mast)
```

---

eigenvector

*Eigenvector Centrality*

---

### Description

Computes eigenvector centrality of each node in a network

### Usage

```
eigenvector(A, weighted = TRUE)
```

### Arguments

A	An adjacency matrix of network data
weighted	Is the network weighted? Defaults to TRUE. Set to FALSE for unweighted measure of eigenvector centrality

### Value

A vector of eigenvector centrality values for each node in the network

### Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

### References

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

### Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

#Weighted
EC <- eigenvector(A)

#Unweighted
EC <- eigenvector(A, weighted = FALSE)
```

---

flow.frac	<i>Flow Fraction</i>
-----------	----------------------

---

### Description

Computes [eigenvector](#) centrality over nodes in a subset of nodes in the network. This measure generalizes across any subset of nodes and is not specific to communities

### Usage

```
flow.frac(A, nodes)
```

### Arguments

A	An adjacency matrix
nodes	A subset of nodes in the network

### Value

Returns a flow fraction value

### Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

### References

Giscard, P. L., & Wilson, R. C. (2018). A centrality measure for cycles and subgraphs II. *Applied Network Science*, 3, 9.

### Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

nodes <- seq(1,48,2)

result <- flow.frac(A, nodes)
```

gain.functions

*MFCF Gain Functions***Description**

These functions maximize a gain criterion for adding a node to a clique (and the larger network). The flexibility of **MFCF** allows for any multivariate function to be used as a scoring function.

- "logLik" — The log determinant of the matrix restricted to the separator minus the log determinant of the matrix restricted to the clique.
- "logLik.val" — "logLik" with a further validation based on the likelihood ratio. If the increase in gain is not significant the routine stops adding nodes to the separator.
- "rSquared.val" — The R squared from the regression of the node against the clique. Only the clique nodes with a regression coefficient significantly different from zero are added to the separator / new clique. The gain is different from zero only if the F-values is significant, It assumed that the data matrix is a dataset of realizations (i.e., p variables and n observations).

**Usage**

```
"logLik"
gfcnv_logdet(data, clique_id, cl, excl_nodes, ctreeControl)

"logLik.val"
gfcnv_logdet_val(data, clique_id, cl, excl_nodes, ctreeControl)

"rSquared.val"
gdcnv_lmfit(data, clique_id, cl, excl_nodes, ctreeControl)
```

**Arguments**

data	Matrix or data frame. Can be a dataset or a correlation matrix
clique_id	Numeric. Number corresponding to clique to add another node to
cl	List. List of cliques already assembled in the network
excl_nodes	Numeric vector. A vector of numbers corresponding to nodes not already included in the network
ctreeControl	List (length = 5). A list containing several parameters for controlling the clique tree sizes: <ul style="list-style-type: none"> <li>• min_size — Numeric. Minimum number of nodes allowed per clique. Defaults to 1</li> <li>• max_size — Numeric. Maximum number of nodes allowed per clique. Defaults to 8</li> <li>• pval — Numeric. <i>p</i>-value used to determine cut-offs for nodes to include in a clique. Defaults to .05</li> <li>• pen — Numeric. Multiplies the number of edges added to penalize complex models. Similar to the penalty term in AIC</li> </ul>

- `drop_sep` — Boolean. This parameter influences the MFCF only. If TRUE any separator can be used only once, as in the TMFG.
- `use_returns` — Boolean. Only used in `rSquared.val`. If set to TRUE the regression is performed on log-returns. Defaults to FALSE

### Value

Returns the value with the maximum gain

### Author(s)

Guido Previde Massara <gprevide@gmail.com> and Alexander Christensen <alexpaulchristensen@gmail.com>

### References

Massara, G. P. & Aste, T. (2019). Learning clique forests. *ArXiv*.

---

gateway	<i>Gateway Coefficient</i>
---------	----------------------------

---

### Description

Computes the gateway coefficient for each node. The gateway coefficient measures a node's connections between its community and other communities. Nodes that are solely responsible for inter-community connectivity will have higher gateway coefficient values. Positive and negative signed weights for gateway coefficients are computed separately.

### Usage

```
gateway(
  A,
  comm = c("walktrap", "louvain"),
  cent = c("strength", "betweenness")
)
```

### Arguments

A	Network adjacency matrix
comm	A vector of corresponding to each item's community. Defaults to "walktrap" for the <a href="#">cluster_walktrap</a> community detection algorithm. Set to "louvain" for the <a href="#">louvain</a> community detection algorithm. Can also be set to user-specified communities (see examples)
cent	Centrality to community gateway coefficient. Defaults to "strength". Set to "betweenness" to use the <a href="#">betweenness</a> centrality

**Value**

Returns a list containing:

overall	Gateway coefficient without signs considered
positive	Gateway coefficient with only positive sign
negative	Gateway coefficient with only negative sign

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

Vargas, E. R., & Wahl, L. M. (2014). The gateway coefficient: A novel metric for identifying critical connections in modular networks. *The European Physical Journal B*, 87, 1-10.

**Examples**

```
#theoretical communities
comm <- rep(1:8, each = 6)

# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

gw <- gateway(A, comm = comm)

#walktrap communities
w gw <- gateway(A, comm = "walktrap")
```

---

hybrid	<i>Hybrid Centrality</i>
--------	--------------------------

---

**Description**

Computes hybrid centrality of each node in a network

**Usage**

```
hybrid(A, BC = c("standard", "random"), beta)
```

**Arguments**

A	An adjacency matrix of network data
BC	How should the betweenness centrality be computed? Defaults to "random". Set to "standard" for standard <a href="#">betweenness</a> .
beta	Beta parameter to be passed to the <a href="#">rspbc</a> function Defaults to .01

**Value**

A vector of hybrid centrality values for each node in the network (higher values are more central, lower values are more peripheral)

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Christensen, A. P., Kenett, Y. N., Aste, T., Silvia, P. J., & Kwapił, T. R. (2018). Network structure of the Wisconsin Schizotypy Scales-Short Forms: Examining psychometric network filtering approaches. *Behavior Research Methods*, *50*, 2531-2550.

Pozzi, F., Di Matteo, T., & Aste, T. (2013). Spread of risk across financial markets: Better to invest in the peripheries. *Scientific Reports*, *3*, 1655.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

HC <- hybrid(A)
```

---

impact

*Node Impact*

---

**Description**

Computes impact measure or how much the average distance in the network changes with that node removed of each node in a network (**Please see and cite Kenett et al., 2011**)

**Usage**

```
impact(A)
```

**Arguments**

A                      An adjacency matrix of network data

**Value**

A vector of node impact values for each node in the network (impact > 0, greater ASPL when node is removed; impact < 0, lower ASPL when node is removed)

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

## References

- Cotter, K. N., Christensen, A. P., & Silvia, P. J. (in press). Understanding inner music: A dimensional approach to musical imagery. *Psychology of Aesthetics, Creativity, and the Arts*.
- Kenett, Y. N., Kenett, D. Y., Ben-Jacob, E., & Faust, M. (2011). Global and local features of semantic networks: Evidence from the Hebrew mental lexicon. *PLoS one*, 6, e23912.

## Examples

```
# normal set to FALSE for CRAN tests
A <- TMFG(neoOpen, normal = FALSE)$A

nodeimpact <- impact(A)
```

---

is.graphical

*Determines if Network is Graphical*

---

## Description

Tests for whether the network is graphical. Input must be a partial correlation network. Function assumes that partial correlations were computed from a multivariate normal distribution

## Usage

```
is.graphical(A)
```

## Arguments

A                    A partial correlation network (adjacency matrix)

## Value

Returns a TRUE/FALSE for whether network is graphical

## Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

## Examples

```
## Not run:
A <- LoGo(neoOpen, normal = TRUE, partial = TRUE)

is.graphical(A)

## End(Not run)
```



---

kld *Kullback-Leibler Divergence*

---

### Description

Estimates the Kullback-Leibler Divergence which measures how one probability distribution diverges from the original distribution (equivalent means are assumed) Matrices **must** be positive definite inverse covariance matrix for accurate measurement. This is a **relative** metric

### Usage

```
kld(base, test)
```

### Arguments

base	Full or base model
test	Reduced or testing model

### Value

A value greater than 0. Smaller values suggest the probability distribution of the reduced model is near the full model

### Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

### References

Kullback, S., & Leibler, R. A. (1951). On information and sufficiency. *The Annals of Mathematical Statistics*, 22, 79-86.

### Examples

```
A1 <- solve(cov(neoOpen))  
  
## Not run:  
A2 <- LoGo(neoOpen)  
  
kld_value <- kld(A1, A2)  
  
## End(Not run)
```

---

lattnet	<i>Generates a Lattice Network</i>
---------	------------------------------------

---

**Description**

Generates a lattice network

**Usage**

```
lattnet(nodes, edges)
```

**Arguments**

nodes	Number of nodes in lattice network
edges	Number of edges in lattice network

**Value**

Returns an adjacency matrix of a lattice network

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

**Examples**

```
latt <- lattnet(10, 27)
```

---

leverage	<i>Leverage Centrality</i>
----------	----------------------------

---

**Description**

Computes leverage centrality of each node in a network (the degree of connected neighbors; **Please see and cite Joyce et al., 2010**)

**Usage**

```
leverage(A, weighted = TRUE)
```

**Arguments**

A	An adjacency matrix of network data
weighted	Is the network weighted? Defaults to TRUE. Set to FALSE for unweighted measure of leverage centrality

**Value**

A vector of leverage centrality values for each node in the network

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Joyce, K. E., Laurienti, P. J., Burdette, J. H., & Hayasaka, S. (2010). A new measure of centrality for brain networks. *PLoS One*, 5 e12200.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

#Weighted
levW <- leverage(A)

#Unweighted
levU <- leverage(A, weighted = FALSE)
```

---

LoGo

*Local/Global Inversion Method*

---

**Description**

Applies the Local/Global method to estimate a Gaussian Graphical Model (GGM) using a [TMFG](#)-filtered network (**see and cite Barfuss et al., 2016**). Also used to convert clique and separator structure from [MFCF](#) into partial correlation and precision matrices

**Usage**

```
LoGo(
  data,
  cliques,
  separators,
  normal = TRUE,
  na.data = c("pairwise", "listwise", "fiml", "none"),
  partial = TRUE,
  ...
)
```

**Arguments**

<code>data</code>	Must be a dataset
<code>cliques</code>	Cliques defined in the network. Input can be a list or matrix
<code>separators</code>	Separators defined in the network. Input can be a list or matrix
<code>normal</code>	Should data be transformed to a normal distribution? Defaults to TRUE (computes correlations using the <code>cor_auto</code> function). Set to FALSE for Pearson's correlations
<code>na.data</code>	How should missing data be handled? For "listwise" deletion the <code>na.omit</code> function is applied. Set to "fiml" for Full Information Maximum Likelihood ( <code>corFiml</code> ). Full Information Maximum Likelihood is <b>recommended</b> but time consuming
<code>partial</code>	Should the output network's connections be the partial correlation between two nodes given all other nodes? Defaults to TRUE, which returns a partial correlation matrix. Set to FALSE for a sparse inverse covariance matrix
<code>...</code>	Additional arguments (deprecated arguments)

**Value**

Returns the sparse LoGo-filtered inverse covariance matrix (`partial = FALSE`) or LoGo-filtered partial correlation matrix (`partial = TRUE`)

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Barfuss, W., Massara, G. P., Di Matteo, T., & Aste, T. (2016). Parsimonious modeling with information filtering networks. *Physical Review E*, *94*, 062306.

**Examples**

```
# normal set to FALSE for CRAN tests
LoGonet <- LoGo(neoOpen, normal = FALSE, partial = TRUE)
```

---

louvain

*Louvain Community Detection Algorithm*

---

**Description**

Computes a vector of communities (community) and a global modularity measure (Q)

**Usage**

```
louvain(A, gamma, M0)
```

**Arguments**

A	An adjacency matrix of network data
gamma	Defaults to 1. Set to $\gamma > 1$ to detect smaller modules and $\gamma < 1$ for larger modules
M0	Input can be an initial community vector. Defaults to NULL

**Value**

Returns a list containing:

community	A community vector corresponding to each node's community
Q	Modularity statistic. A measure of how well the communities are compartmentalized

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

- Blondel, V. D., Guillaume, J. L., Lambiotte, R., & Lefebvre, E. (2008). Fast unfolding of communities in large networks. *Journal of Statistical Mechanics: Theory and Experiment*, 2008, P10008.
- Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

modularity <- louvain(A)
```

---

MaST

*Maximum Spanning Tree*

---

**Description**

Applies the Maximum Spanning Tree (MaST) filtering method

**Usage**

```
MaST(
  data,
  normal = TRUE,
  na.data = c("pairwise", "listwise", "fiml", "none"),
  depend = FALSE
)
```

**Arguments**

data	Can be a dataset or a correlation matrix
normal	Should data be transformed to a normal distribution? Input must be a dataset. Defaults to TRUE. Computes correlations using the <code>cor_auto</code> function. Set to FALSE for Pearson's correlation
na.data	How should missing data be handled? For "listwise" deletion the <code>na.omit</code> function is applied. Set to "fiml" for Full Information Maximum Likelihood ( <code>corFiml</code> ). Full Information Maximum Likelihood is <b>recommended</b> but time consuming
depend	Is network a dependency (or directed) network? Defaults to FALSE. Set TRUE to generate a MaST-filtered dependency network (output obtained from the <code>depend</code> function)

**Value**

A sparse association matrix

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
# Pearson's correlation only for CRAN checks
MaST.net <- MaST(neoOpen, normal = FALSE)
```

---

MFCF

*Maximally Filtered Clique Forest*


---

**Description**

Applies the Maximally Filtered Clique Forest (MFCF) filtering method (**Please see and cite Mas-sara & Aste**).

**Usage**

```
MFCF(
  data,
  cases = NULL,
  na.data = c("pairwise", "listwise", "fiml", "none"),
  time.series = FALSE,
  gain.fxn = c("logLik", "logLik.val", "rSquared.val"),
  min_size = 0,
  max_size = 8,
  pval = 0.05,
```

```

    pen = 0,
    drop_sep = FALSE,
    use_returns = FALSE
  )

```

### Arguments

<code>data</code>	Matrix (n x n or p x n) or data frame. Can be a dataset or a correlation matrix
<code>cases</code>	Numeric. If data is a (partial) correlation matrix, then number of cases must be input. Defaults to NULL
<code>na.data</code>	Character. How should missing data be handled? <ul style="list-style-type: none"> <li>• "listwise" — Removes case if <b>any</b> missing data exists. Applies <code>na.omit</code></li> <li>• "pairwise" — Estimates correlations using the available data for each variable</li> <li>• "fiml" — Estimates correlations using the Full Information Maximum Likelihood. Recommended and most robust but time consuming</li> <li>• "none" — Default. No missing data or missing data has been handled by the user</li> </ul>
<code>time.series</code>	Boolean. Is data a time-series dataset? Defaults to FALSE. Set to TRUE to handle time-series data (n x p)
<code>gain.fxn</code>	Character. Gain function to be used for inclusion of nodes in cliques. There are several options available (see <a href="#">gain.functions</a> for more details): "logLik", "logLik.val", "rSquared.val". Defaults to "rSquared.val"
<code>min_size</code>	Numeric. Minimum number of nodes allowed per clique. Defaults to 0
<code>max_size</code>	Numeric. Maximum number of nodes allowed per clique. Defaults to 8
<code>pval</code>	Numeric. <i>p</i> -value used to determine cut-offs for nodes to include in a clique
<code>pen</code>	Numeric. Multiplies the number of edges added to penalise complex models. Similar to the penalty term in AIC
<code>drop_sep</code>	Boolean. This parameter influences the MFCF only. Defaults to FALSE. If TRUE, then any separator can be used only once (similar to the <a href="#">TMFG</a> )
<code>use_returns</code>	Boolean. Only used in "gain.fxn = rSquared.val". If set to TRUE the regression is performed on log-returns. Defaults to FALSE

### Value

Returns a list containing:

<code>A</code>	MFCF filtered partial correlation network (adjacency matrix)
<code>J</code>	MFCF filtered inverse covariance matrix (precision matrix)
<code>cliques</code>	Cliques in the network (output for <a href="#">LoGo</a> )
<code>separators</code>	Separators in the network (output for <a href="#">LoGo</a> )

### Author(s)

Guido Previde Massara <gprevide@gmail.com> and Alexander Christensen <alexpaulchristensen@gmail.com>

## References

Massara, G. P. & Aste, T. (2019). Learning clique forests. *ArXiv*.

## Examples

```
# Load data
data <- neoOpen

## Not run:
# Use polychoric correlations and R-squared method
MFCF.net <- MFCF(qgraph::cor_auto(data), cases = nrow(neoOpen))$A

## End(Not run)
```

---

neoOpen

*NEO-PI-3 Openness to Experience Data*

---

## Description

A response matrix ( $n = 802$ ) of NEO-PI-3's Openness to Experience from Christensen, Cotter, & Silvia (2019).

## Usage

```
data(neoOpen)
```

## Format

A 802x48 response matrix

## References

Christensen, A. P., Cotter, K. N., & Silvia, P. J. (2019). Reopening openness to experience: A network analysis of four openness to experience inventories. *Journal of Personality Assessment*, *101*, 574-588.

## Examples

```
data("neoOpen")
```



---

net.coverage	<i>Network Coverage</i>
--------------	-------------------------

---

### Description

Computes the mean distance across a subset of nodes in a network. This measure can be used to identify the effectiveness of a subset of nodes' coverage of the network space

### Usage

```
net.coverage(A, nodes, weighted = FALSE)
```

### Arguments

A	An adjacency matrix
nodes	Subset of nodes to examine the coverage of the network
weighted	Is the network weighted? Defaults to FALSE. Set to TRUE for weighted measures

### Value

Returns a list containing:

mean	The average distance from the subset of nodes to all other nodes in the network
sd	The standard deviation of distance from the subset of nodes to all other nodes in the network
range	The range of distance from the subset of nodes to all other nodes in the network

### Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com> and Mathias Benedek <mathias.benedek@uni-graz.at>

### References

Christensen, A. P., Cotter, K. N., Silvia, P. J., & Benedek, M. (2018) Scale development via network analysis: A comprehensive and concise measure of Openness to Experience *PsyArXiv*, 1-40.

### Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

nodes <- seq(1,48,2)

result <- net.coverage(A, nodes)
```

---

network.coverage	<i>Network Coverage</i>
------------------	-------------------------

---

### Description

Computes the mean distance across a subset of nodes in a network. This measure can be used to identify the effectiveness of a subset of nodes' coverage of the network space

### Usage

```
network.coverage(A, nodes, weighted = FALSE)
```

### Arguments

A	An adjacency matrix
nodes	Subset of nodes to examine the coverage of the network
weighted	Is the network weighted? Defaults to FALSE. Set to TRUE for weighted measures

### Value

Returns a list containing:

mean	The average distance from the subset of nodes to all other nodes in the network
sd	The standard deviation of distance from the subset of nodes to all other nodes in the network
range	The range of distance from the subset of nodes to all other nodes in the network

### Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com> and Mathias Benedek <mathias.benedek@uni-graz.at>

### References

Christensen, A. P., Cotter, K. N., Silvia, P. J., & Benedek, M. (2018) Scale development via network analysis: A comprehensive and concise measure of Openness to Experience *PsyArXiv*, 1-40.

### Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

nodes <- seq(1,48,2)

result <- network.coverage(A, nodes)
```

---

network.permutation    *Permutation Test for Network Measures*

---

## Description

Computes a permutation test to determine whether there are difference in centrality and global network measures

## Usage

```
network.permutation(
  sample1 = NULL,
  sample2 = NULL,
  iter,
  network = c("glasso", "ising", "TMFG", "LoGo"),
  measure = c("betweenness", "closeness", "strength", "eigenvector", "rspbc", "hybrid",
    "ASPL", "CC", "S", "Q"),
  alternative = c("less", "greater", "two.tailed"),
  ncores,
  prev.perm = NULL,
  ...
)
```

## Arguments

sample1	Matrix or data frame. Sample to be compared with sample2
sample2	Matrix or data frame. Sample to be compared with sample1
iter	Numeric. Number of iterations to perform. Defaults to 1000
network	Character. Network estimation method to apply to the datasets. Defaults to "glasso"
measure	Character. Network measure to be compared in the permutation test
alternative	Character. Alternative hypothesis test to perform. Defaults to "two.tailed"
ncores	Numeric. Number of computer processing cores to use for bootstrapping samples. Defaults to $n - 1$ total number of cores. Set to any number between 1 and maximum amount of cores on your computer (see <code>parallel::detectCores()</code> )
prev.perm	network.permutation class object. An object of previously performed permutation test. The networks generated in the previous permutation will be used to compute other network measures. This saves time when computing multiple permutation tests
...	Additional arguments for <a href="#">EBICglasso</a>

**Value**

Returns a list containing two objects:

result	The results of the permutation test. For centrality measures, this is a matrix where the rows represent each node and the columns are the observed values of the centrality measure for sample1, sample2, and the $p$ -value from the permutation test. For global network measures, this is a vector with the observed values of the global network measure for sample1, sample2, and the $p$ -value from the permutation test.
networks	A list containing two lists: network1 and network2. The network lists correspond to the networks generated in the permutation test for sample1 and sample2, respectively. This output is used primarily for the computation of other network measures using the same datasets (see <code>prev.perm</code> explanation)

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
# Split data (only for example)
split1 <- neoOpen[c(1:401),]
split2 <- neoOpen[c(402:802),]

# Perform permutation test
perm.str <- network.permutation(split1, split2, iter = 1000, network = "glasso",
measure = "strength", alternative = "two.tailed", ncores = 2)

# Check results
perm.str$result

# Permutation to check other measures (using networks from previous result)
perm.aspl <- network.permutation(prev.perm = perm.str, measure = "ASPL", ncores = 2)

# Check results
perm.aspl$result
```

**Description**

Applies a network filtering methodology to neural network array. Removes edges from the neural network output from [convertConnBrainMat](#) using a network filtering approach

**Usage**

```
neuralnetfilter(
  neuralarray,
  method = c("TMFG", "MaST", "ECOplusMaST", "ECO", "threshold"),
  progBar = TRUE,
  ...
)
```

**Arguments**

neuralarray	Array from <a href="#">convertConnBrainMat</a> function
method	Filtering method to be applied
progBar	Should progress bar be displayed? Defaults to TRUE. Set FALSE for no progress bar
...	Additional arguments from network filtering methods

**Value**

Returns an array of  $n \times n \times m$  filtered matrices

**Author(s)**

Alexander Christensen <[alexpaulchristensen@gmail.com](mailto:alexpaulchristensen@gmail.com)>

**Examples**

```
## Not run: neuralarray <- convertConnBrainMat()

filteredneuralarray <- neuralnetfilter(neuralarray, method = "threshold", thresh = .50)

dependencyarray <- depna(neuralarray)

filtereddependencyarray <- neuralnetfilter(dependencyarray, method = "TMFG", depend = TRUE)

## End(Not run)
```

---

openness

*Four Inventories of Openness to Experience*

---

**Description**

A response matrix ( $n = 794$ ) of all four Openness to Experience inventories from Christensen, Cotter, & Silvia (2019). The key provides inventory, facet, and item description information for the item labels. Note that because of NEO's copyrights the items have been shortened and paraphrased

**Usage**

```
data(openness)
```

```
data(openness.key)
```

**Format**

A 794 x 138 response matrix (openness) and 138 x 7 matrix (openness.key). Here are detailed descriptions of the key:

- Inventory — The personality inventory the item belongs to
- Facet — The personality inventory defined facet
- JPA.Domains — The broad domains identified by Christensen, Cotter, and Silvia (2019)
- JPA.Facets — The facets identified by Christensen, Cotter, and Silvia (2019)
- Item.Label — The labels used in Christensen, Cotter, and Silvia (2019)
- Item.Description — Descriptions of each item. Note that the NEO-PI-3 items are protected by copyright and therefore have been paraphrased. These item descriptions do not represent the item as given to the participant
- Reversed — Whether an item should be reversed or not (openness is already reversed)

**References**

Christensen, A. P., Cotter, K. N., & Silvia, P. J. (2019). Reopening openness to experience: A network analysis of four openness to experience inventories. *Journal of Personality Assessment*, *101*, 574-588.

**Examples**

```
# Loading data
data("openness")
data("openness.key")

# Change item labels
colnames(openness) <- openness.key$Item.Description
```

---

participation

*Participation Coefficient*

---

**Description**

Computes the participation coefficient for each node. The participation coefficient measures the strength of a node's connections within its community. Positive and negative signed weights for participation coefficients are computed separately.

**Usage**

```
participation(A, comm = c("walktrap", "louvain"))
```

**Arguments**

A	Network adjacency matrix
comm	A vector of corresponding to each item's community. Defaults to "walktrap" for the <code>cluster_walktrap</code> community detection algorithm. Set to "louvain" for the <code>louvain</code> community detection algorithm. Can also be set to user-specified communities (see examples)

**Details**

Values closer to 0 suggest greater within-community connectivity and values closer to 1 suggest greater between-community connectivity

**Value**

Returns a list containing:

overall	Participation coefficient without signs considered
positive	Participation coefficient with only positive sign
negative	Participation coefficient with only negative sign

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Guimera, R., & Amaral, L. A. N. (2005). Functional cartography of complex metabolic networks. *Nature*, 433, 895-900.

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

**Examples**

```
#theoretical factors
comm <- rep(1:8, each = 6)

# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

pc <- participation(A, comm = comm)

# Walktrap factors
wpc <- participation(A, comm = "walktrap")
```

---

pathlengths                      *Characteristic Path Lengths*

---

**Description**

Computes global average shortest path length, local average shortest path length, eccentricity, and diameter of a network

**Usage**

```
pathlengths(A, weighted = FALSE)
```

**Arguments**

A	An adjacency matrix of network data
weighted	Is the network weighted? Defaults to FALSE. Set to TRUE for weighted measures

**Value**

Returns a list containing:

ASPL	Global average shortest path length
ASPLi	Local average shortest path length
ecc	Eccentricity (i.e., maximal shortest path length between a node and any other node)
D	Diameter of the network (i.e., the maximum of eccentricity)

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

#Unweighted
PL <- pathlengths(A)

#Weighted
PL <- pathlengths(A, weighted = TRUE)
```



---

plot.cpm	<i>Plots CPM results</i>
----------	--------------------------

---

**Description**

Plots CPM results

**Usage**

```
## S3 method for class 'cpm'  
plot(x, ...)
```

**Arguments**

x	A <a href="#">cpm</a> object
...	Additional arguments for <a href="#">plot</a>

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

---

randnet	<i>Generates a Random Network</i>
---------	-----------------------------------

---

**Description**

Generates a random binary network

**Usage**

```
randnet(nodes = NULL, edges = NULL, A = NULL)
```

**Arguments**

nodes	Numeric. Number of nodes in random network
edges	Numeric. Number of edges in random network
A	Matrix or data frame. An adjacency matrix (i.e., network) to be used to estimate a random network with fixed edges (allows for asymmetric network estimation)

**Value**

Returns an adjacency matrix of a random network

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

## References

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

Csardi, G., & Nepusz, T. (2006). The *igraph* software package for complex network research. *InterJournal, Complex Systems*, 1695.

## Examples

```
rand <- randnet(10, 27)
```

---

reg

*Regression Matrix*

---

## Description

Computes regression such that one variable is regressed over all other variables

## Usage

```
reg(
  data,
  family = c("binomial", "gaussian", "Gamma", "poisson"),
  symmetric = TRUE
)
```

## Arguments

data	A dataset
family	Error distribution to be used in the regression model. Defaults to "logistic". Set to any family used in function <a href="#">family</a>
symmetric	Should matrix be symmetric? Defaults to TRUE, taking the mean of the two edge weights (i.e., [i, j] and [j, i]) Set to FALSE for asymmetric weights (i.e., [i, j] does not equal [j, i])

## Value

A matrix of fully regressed coefficients where one variable is regressed over all others

## Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
#binarize responses
psyb <- ifelse(neo0open>=4, 1, 0)

## Not run:
#perform logistic regression
mat <- reg(psyb)
## End(Not run)
```

---

resp.rep	<i>Repeated Responses Check</i>
----------	---------------------------------

---

**Description**

Screens data to identify potential cases of repeated responding. The function is based on two criteria: no variance (i.e., a standard deviation of zero for given responses) and frequency proportion of the response values (which is set by freq.prop). Note that these criteria are highly related. Additional criteria will be added in the future.

**Usage**

```
resp.rep(data, scale.lens = NULL, max.val, reverse = NULL, freq.prop = 0.8)
```

**Arguments**

data	A dataset
scale.lens	The number of items for each scale in the data. A vector indicating the length for each scale to be checked in the data
max.val	Maximum value for data (or scales). If scales have different maximum values, then a vector must be input with each scale's maximum value (see examples)
reverse	Reverse scored responses. If responses have not yet reversed, then do not reverse them. If responses have been reversed, then a vector indicating which responses have been reverse-scored should be input (see examples). Can be TRUE/FALSE or 1/0 (reversed/not reversed)
freq.prop	Frequency proportion of the response values. Allows the researcher to determine the maximum frequency proportion of a certain response value is suspicious. The default is set to .80 (or 80 percent responses are a single value)

**Details**

If a case is returned, then it does not mean that it is a bad case. Researchers should thoroughly inspect each case that is returned. A general guideline is that if a participant responded with all middle values (e.g., all 3's on a 5-point Likert scale), then they should be dropped. Note that a participant who responds with all maximum or minimum values may be a real case or a bad case. It is up to the researcher to decide and justify why or why not a case is kept.

**Value**

Returns a matrix when `scale.lens = NULL` and a list with elements corresponding to the order of scales. In general, the output contains potential bad cases that should be further inspected by the researcher.

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
#Re-reverse responses
rev.vec <- c(TRUE, FALSE, TRUE, FALSE, TRUE, TRUE, TRUE, FALSE, TRUE, FALSE,
TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, FALSE, TRUE, TRUE, FALSE, TRUE, FALSE, TRUE,
FALSE, FALSE, TRUE, FALSE, TRUE, FALSE, TRUE, TRUE, FALSE, TRUE, FALSE, TRUE,
FALSE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE)

#Maximum value (5-point Likert scale)
mv.vec <- 5

#Repeated responses check
resp.rep(neoOpen, reverse = rev.vec, max.val = mv.vec)

#Example with multiple scales

#Facet scale lengths of NEO-PI-3 Openness to Experience
s.len <- c(8, 8, 8, 8, 8, 8)

#Maximum values
mv.vec <- c(5, 5, 5, 5, 5, 5)

#Re-reverse responses
rev.vec <- c(TRUE, FALSE, TRUE, FALSE, TRUE, TRUE, TRUE, FALSE, TRUE, FALSE,
TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, FALSE, TRUE, TRUE, FALSE, TRUE, FALSE, TRUE,
FALSE, FALSE, TRUE, FALSE, TRUE, FALSE, TRUE, TRUE, FALSE, TRUE, FALSE, TRUE,
FALSE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE)

#Repeated responses check
resp.rep(neoOpen, scale.lens = s.len, max.val = mv.vec, reverse = rev.vec)
```

---

 rmse

*Root Mean Square Error*


---

**Description**

Computes the root mean square error (RMSE) of a sparse model to a full model

**Usage**

```
rmse(base, test)
```

**Arguments**

base	Base (or full) model to be evaluated against
test	Reduced (or testing) model (e.g., a sparse correlation or covariance matrix)

**Value**

RMSE value (lower values suggest more similarity between the full and sparse model)

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
A1 <- solve(cov(neoOpen))

## Not run:
A2 <- LoGo(neoOpen)

root <- rmse(A1, A2)

## End(Not run)
```

---

 rspbc

---

*Randomized Shortest Paths Betweenness Centrality*


---

**Description**

Computes betweenness centrality based on randomized shortest paths of each node in a network  
**(Please see and cite Kivimaki et al., 2016)**

**Usage**

```
rspbc(A, beta = 0.01, comm = NULL)
```

**Arguments**

A	An adjacency matrix of network data
beta	Sets the beta parameter. Defaults to 0.01 (recommended). Beta > 0.01 measure gets closer to weighted betweenness centrality (10) and beta < 0.01 measure gets closer to degree (.0001)
comm	Vector. Community vector containing a value for each node. Computes "bridge" RSPBC, where the number of times a node is used on a random path between to another community

**Value**

A vector of randomized shortest paths betweenness centrality values for each node in the network

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Kivimaki, I., Lebichot, B., Saramaki, J., & Saerens, M. (2016). Two betweenness centrality measures based on Randomized Shortest Paths. *Scientific Reports*, 6, 19668.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

rspbc <- rspbc(A, beta=0.01)
```

---

 sim.chordal

---

*Simulate Chordal Network*


---

**Description**

Simulates a chordal network based on number of nodes. Data will also be simulated based on the true network structure

**Usage**

```
sim.chordal(
  nodes,
  inverse = c("cases", "matrix"),
  n = NULL,
  ordinal = FALSE,
  ordLevels = NULL,
  idio = NULL,
  eps = NULL
)
```

**Arguments**

nodes            Numeric. Number of nodes in the simulated network

inverse          Character. Method to produce inverse covariance matrix.

- "cases" — Estimates inverse covariance matrix based on n number of cases and nodes number of variables, which are drawn from a random normal distribution `rnorm`. Data generated will be continuous unless `ordinal` is set to `TRUE`

- "matrix" — Estimates inverse covariance matrix based on sigma

n	Numeric. Number of cases in the simulated dataset
ordinal	Boolean. Should simulated continuous data be converted to ordinal? Defaults to FALSE. Set to TRUE for simulated ordinal data
ordLevels	Numeric. If ordinal = TRUE, then how many levels should be used? Defaults to 5. Set to desired number of intervals
idio	Numeric. DESCRIPTION. Defaults to 0.10
eps	Numeric. DESCRIPTION. Defaults to 2

**Value**

Returns a list containing:

cliques	The cliques in the network
separators	The separators in the network
inverse	Simulated inverse covariance matrix of the network
data	Simulated data from sim.correlation in the psych package based on the simulated network

**Author(s)**

Guido Previde Massara <gprevide@gmail.com>

**References**

Massara, G. P. & Aste, T. (2019). Learning clique forests. *ArXiv*.

**Examples**

```
#Continuous data
sim.Norm <- sim.chordal(nodes = 20, inverse = "cases", n = 1000)

#Ordinal data
sim.Likert <- sim.chordal(nodes = 20, inverse = "cases", n = 1000, ordinal = TRUE)

#Dichotomous data
sim.Binary <- sim.chordal(nodes = 20, inverse = "cases", n = 1000, ordinal = TRUE, ordLevels = 5)
```

sim.swn

*Simulate Small-world Network***Description**

Simulates a small-world network based on specified topological properties. Data will also be simulated based on the true network structure

**Usage**

```
sim.swn(
  nodes,
  n,
  pos = 0.8,
  ran = c(0.3, 0.7),
  nei = 1,
  p = 0.5,
  corr = FALSE,
  replace = NULL,
  ordinal = FALSE,
  ordLevels = NULL
)
```

**Arguments**

nodes	Number of nodes in the simulated network
n	Number of cases in the simulated dataset
pos	Proportion of positive correlations in the simulated network
ran	Range of correlations in the simulated network
nei	Adjusts the number of connections each node has to neighboring nodes (see <a href="#">sample_smallworld</a> )
p	Adjusts the rewiring probability (default is .5). $p > .5$ rewires the simulated network closer to a random network. $p < .5$ rewires the simulated network closer to a lattice network
corr	Should the simulated network be a correlation network? Defaults to FALSE. Set to TRUE for a simulated correlation network
replace	If noise > 0, then should participants be sampled with replacement? Defaults to TRUE. Set to FALSE to not allow the potential for participants to be consecutively entered into the simulated dataset.
ordinal	Should simulated continuous data be converted to ordinal? Defaults to FALSE. Set to TRUE for simulated ordinal data
ordLevels	If ordinal = TRUE, then how many levels should be used? Defaults to NULL. Set to desired number of intervals (defaults to 5)



**Value**

Returns a list containing:

simNetwork	Adjacency matrix of the simulated network
simData	Simulated data from sim.correlation in the psych package based on the simulated network
simRho	Simulated correlation from sim.correlation in the psych package

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Csardi, G., & Nepusz, T. (2006). The *igraph* software package for complex network research. *InterJournal, Complex Systems*, 1695, 1-9.

**Examples**

```
#Continuous data
sim.Norm <- sim.swn(25, 500, nei = 3)

#Ordinal data
sim.Likert <- sim.swn(25, 500, nei = 3, replace = TRUE, ordinal = TRUE, ordLevels = 5)

#Dichotomous data
sim.Binary <- sim.swn(25, 500, nei = 3, replace = TRUE, ordinal = TRUE, ordLevels = 2)
```

---

smallworldness	<i>Small-worldness Measure</i>
----------------	--------------------------------

---

**Description**

Computes the small-worldness measure of a network

**Usage**

```
smallworldness(  
  A,  
  iter = 100,  
  progBar = FALSE,  
  method = c("HG", "rand", "TJHBL")  
)
```

**Arguments**

A	An adjacency matrix of network data
iter	Number of random (or lattice) networks to generate, which are used to calculate the mean random ASPL and CC (or lattice)
progBar	Defaults to FALSE. Set to TRUE to see progress bar
method	Defaults to "HG" (Humphries & Gurney, 2008). Set to "rand" for the CC to be calculated using a random network or set to "TJHBL" for (Telesford et al., 2011) where CC is calculated from a lattice network

**Details**

For "rand", values > 1 indicate a small-world network. For "HG", values > 3 indicate a small-world network. For "TJHBL", values near 0 indicate a small-world network, while < 0 indicates a more regular network and > 0 indicates a more random network

**Value**

Returns a list containing:

swm	Small-worldness value
rASPL	Global average shortest path length from random network
lrCCt	When "rand", clustering coefficient from a random network. When "HG", transitivity from a random network. When "TJHBL", clustering coefficient from a lattice network

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Humphries, M. D., & Gurney, K. (2008). Network 'small-world-ness': A quantitative method for determining canonical network equivalence. *PLoS one*, 3, e0002051.

Telesford, Q. K., Joyce, K. E., Hayasaka, S., Burdette, J. H., & Laurienti, P. J. (2011). The ubiquity of small-world networks. *Brain Connectivity*, 1(5), 367-375.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

swmHG <- smallworldness(A, method="HG")

swmRand <- smallworldness(A, method="rand")

swmTJHBL <- smallworldness(A, method="TJHBL")
```

---

stable	<i>Stabilizing Nodes</i>
--------	--------------------------

---

**Description**

Computes the within-community centrality for each node in the network

**Usage**

```
stable(
  A,
  comm = c("walktrap", "louvain"),
  cent = c("betweenness", "rspbc", "closeness", "strength", "degree", "hybrid"),
  absolute = TRUE,
  diagonal = 0,
  ...
)
```

**Arguments**

A	An adjacency matrix of network data
comm	Can be a vector of community assignments or community detection algorithms ("walktrap" or "louvain") can be used to determine the number of factors. Defaults to "walktrap". Set to "louvain" for <a href="#">louvain</a> community detection
cent	Centrality measure to be used. Defaults to "strength".
absolute	Should network use absolute weights? Defaults to TRUE. Set to FALSE for signed weights
diagonal	Sets the diagonal values of the A input. Defaults to 0
...	Additional arguments for <a href="#">cluster_walktrap</a> and <a href="#">louvain</a> community detection algorithms

**Value**

A matrix containing the within-community centrality value for each node

**Author(s)**

Alexander Christensen <[alexpaulchristensen@gmail.com](mailto:alexpaulchristensen@gmail.com)>

**References**

Blanken, T. F., Deserno, M. K., Dalege, J., Borsboom, D., Blanken, P., Kerkhof, G. A., & Cramer, A. O. (2018). The role of stabilizing and communicating symptoms given overlapping communities in psychopathology networks. *Scientific Reports*, *8*, 5854.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

stabilizing <- stable(A, comm = "walktrap")
```

---

strength	<i>Node Strength</i>
----------	----------------------

---

**Description**

Computes strength of each node in a network

**Usage**

```
strength(A, absolute = TRUE)
```

**Arguments**

A	An adjacency matrix of network data
absolute	Should network use absolute weights? Defaults to TRUE. Set to FALSE for signed weights

**Value**

A vector of strength values for each node in the network.

If directed network, returns a list containing:

inStrength	Strength of incoming edges (pointing to the node)
outStrength	Strength of outgoing edges (pointing away from the node)
relInf	Relative degree of incoming and outgoing edges. Positive values indicate more outgoing strength relative to incoming strength. Negative values indicate more incoming strength relative to outgoing strength

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52 1059-1069.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

str <- strength(A)

#Directed network
## Not run:
dep <- depend(neoOpen)

Adep <- TMFG(dep, depend = TRUE)$A

str <- strength(Adep)

## End(Not run)
```

---

threshold

*Threshold Network Estimation Methods*


---

**Description**

Filters the network based on an r-value, alpha, adaptive alpha, bonferroni, false-discovery rate (FDR), or proportional density (fixed number of edges) value

**Usage**

```
threshold(
  data,
  a,
  thresh = c("alpha", "adaptive", "bonferroni", "FDR", "proportional"),
  normal = FALSE,
  na.data = c("pairwise", "listwise", "fiml", "none"),
  ...
)
```

**Arguments**

data	Can be a dataset or a correlation matrix
a	When thresh = "alpha", "adaptive", and "bonferroni" an $\alpha$ threshold is applied (defaults to .05). For "adaptive", beta (Type II error) is set to $\alpha * 5$ for a medium effect size ( $r = .3$ ). When thresh = "FDR", a q-value threshold is applied (defaults to .10). When thresh = "proportional", a density threshold is applied (defaults to .15)
thresh	Sets threshold. Defaults to "alpha". Set to any value $0 > r > 1$ to retain values greater than set value, "adaptive" for an <a href="#">adapt.a</a> based on sample size (Perez & Pericchi, 2014), "bonferroni" for the bonferroni correction on alpha, "FDR" for local false discovery rate, and "proportional" for a fixed density of edges (keeps strongest correlations within density)

normal	Should data be transformed to a normal distribution? Defaults to FALSE. Data is not transformed to be normal. Set to TRUE if data should be transformed to be normal (computes correlations using the <code>cor_auto</code> function)
na.data	How should missing data be handled? For "listwise" deletion the <code>na.omit</code> function is applied. Set to "fiml" for Full Information Maximum Likelihood ( <code>corFiml</code> ). Full Information Maximum Likelihood is <b>recommended</b> but time consuming
...	Additional arguments for <code>fdrtool</code> and <code>adapt.a</code>

### Value

Returns a list containing:

A	The filtered adjacency matrix
r.cv	The critical correlation value used to filter the network

### Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

### References

Strimmer, K. (2008). fdrtool: A versatile R package for estimating local and tail area-based false discovery rates. *Bioinformatics*, 24, 1461-1462.

### Examples

```
threshnet<-threshold(neoOpen)

alphanet<-threshold(neoOpen, thresh = "alpha", a = .05)

bonnet<-threshold(neoOpen, thresh = "bonferroni", a = .05)

FDRnet<-threshold(neoOpen, thresh = "FDR", a = .10)

propnet<-threshold(neoOpen, thresh = "proportional", a = .15)
```

---

TMFG

*Triangulated Maximally Filtered Graph*

---

### Description

Applies the Triangulated Maximally Filtered Graph (TMFG) filtering method (**Please see and cite Massara et al., 2016**). The TMFG method uses a structural constraint that limits the number of zero-order correlations included in the network ( $3n - 6$ ; where  $n$  is the number of variables). The TMFG algorithm begins by identifying four variables which have the largest sum of correlations to all other variables. Then, it iteratively adds each variable with the largest sum of three correlations to nodes already in the network until all variables have been added to the network. This structure

can be associated with the inverse correlation matrix (i.e., precision matrix) to be turned into a GGM (i.e., partial correlation network) by using [LoGo](#). See Details for more information on this network estimation method.

### Usage

```
TMFG(
  data,
  normal = TRUE,
  na.data = c("pairwise", "listwise", "fiml", "none"),
  depend = FALSE
)
```

### Arguments

data	Can be a dataset or a correlation matrix
normal	Should data be transformed to a normal distribution? Input must be a dataset. Defaults to TRUE. Computes correlations using the <a href="#">cor_auto</a> function. Set to FALSE for Pearson's correlation
na.data	How should missing data be handled? For "listwise" deletion the <a href="#">na.omit</a> function is applied. Set to "fiml" for Full Information Maximum Likelihood ( <a href="#">corFiml</a> ). Full Information Maximum Likelihood is <b>recommended</b> but time consuming
depend	Is network a dependency (or directed) network? Defaults to FALSE. Set to TRUE to generate a TMFG-filtered dependency network (output obtained from the <a href="#">depend</a> function)

### Details

The TMFG method applies a structural constraint on the network, which restrains the network to retain a certain number of edges ( $3n-6$ , where  $n$  is the number of nodes; Massara et al., 2016). The network is also composed of 3- and 4-node cliques (i.e., sets of connected nodes; a triangle and tetrahedron, respectively). The TMFG method constructs a network using zero-order correlations and the resulting network can be associated with the inverse covariance matrix (yielding a GGM; Barfuss, Massara, Di Matteo, & Aste, 2016). Notably, the TMFG can use any association measure and thus does not assume the data is multivariate normal.

Construction begins by forming a tetrahedron of the four nodes that have the highest sum of correlations that are greater than the average correlation in the correlation matrix. Next, the algorithm iteratively identifies the node that maximizes its sum of correlations to a connected set of three nodes (triangles) already included in the network and then adds that node to the network. The process is completed once every node is connected in the network. In this process, the network automatically generates what's called a planar network. A planar network is a network that could be drawn on a sphere with no edges crossing (often, however, the networks are depicted with edges crossing; Tumminello, Aste, Di Matteo, & Mantegna, 2005).

### Value

Returns a list containing:

A	The filtered adjacency matrix
separators	The separators (3-cliques) in the network (wrapper output for <a href="#">LoGo</a> )
cliques	The cliques (4-cliques) in the network (wrapper output for <a href="#">LoGo</a> )

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Christensen, A. P., Kenett, Y. N., Aste, T., Silvia, P. J., & Kwapil, T. R. (2018). Network structure of the Wisconsin Schizotypy Scales-Short Forms: Examining psychometric network filtering approaches. *Behavior Research Methods*, *50*, 2531-2550.

Massara, G. P., Di Matteo, T., & Aste, T. (2016). Network filtering for big data: Triangulated maximally filtered graph. *Journal of Complex Networks*, *5*, 161-178.

**Examples**

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A
```

---

transitivity	<i>Transitivity</i>
--------------	---------------------

---

**Description**

Computes transitivity of a network

**Usage**

```
transitivity(A, weighted = FALSE)
```

**Arguments**

A	An adjacency matrix of network data
weighted	Is the network weighted? Defaults to FALSE. Set to TRUE for a weighted measure of transitivity

**Value**

Returns a value of transitivity

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>



## References

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *NeuroImage*, 52, 1059-1069.

## Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

trans <- transitivity(A, weighted=TRUE)
```

---

un.direct	<i>Convert Directed Network to Undirected Network</i>
-----------	---

---

## Description

Converts a directed network to an undirected network

## Usage

```
un.direct(A, diagonal = 0)
```

## Arguments

A	Matrix or data frame. Adjacency matrix (network matrix)
diagonal	Numeric. Number to be placed on the diagonal. Defaults to 0

## Value

Returns a symmetric adjacency matrix

## Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

## Examples

```
# Pearson's correlation only for CRAN checks
A <- TMFG(neoOpen, normal = FALSE)$A

# create a directed network
dir <- A * sample(c(0,1), size = length(A), replace = TRUE)

# undirect the directed network
undir <- un.direct(dir)
```

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