

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-Gershogoren, Mantegna, & Ben-Jacob, 2010 <doi:10.1371/journal.pone.0015032>), Information Filtering Networks (Barfuss, Massara, Di Matteo, & Aste, 2016 <doi:10.1103/PhysRevE.94.062306>), and Efficiency-Cost Optimization (Falani, Latora, & Chavez, 2017 <doi: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 (>= 3.3.0)

License GPL (>= 3.0)

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qgraph, ppcor, parallel, foreach, doParallel

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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*. doi: [10.31234/osf.io/6kmav](https://doi.org/10.31234/osf.io/6kmav)

 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	α 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. doi:[10.1037/0033-2909.112.1.155](https://doi.org/10.1037/0033-2909.112.1.155)

Perez, M. E., & Pericchi, L. R. (2014). Changing statistical significance with the amount of information: The adaptive α significance level. *Statistics & Probability Letters*, *85*, 20-24. doi:[10.1016/j.spl.2013.10.018](https://doi.org/10.1016/j.spl.2013.10.018)

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/1ugwi7nRr1HQYuGPzEB4wYzsizFr/view>

References

Beatty, 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. doi: [10.1002/hbm.23884](https://doi.org/10.1002/hbm.23884)

Beatty, 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. doi: [10.1073/pnas.1713532115](https://doi.org/10.1073/pnas.1713532115)

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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

```
A <- TMFG(neoOpen)$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

```
A <- TMFG(neoOpen)$A

neoB <- binarize(A)
```

`centlist`*List of Centrality Measures*

Description

Computes centrality measures of the network

Usage

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

Arguments

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

Value

Returns a list containing:

BC	betweenness centrality
LC	closeness centrality
k	degree (weighted = FALSE)
Str	strength (weighted = TRUE)
EC	eigenvector centrality
lev	leverage centrality
HC	hybrid centrality (weighted = TRUE)

Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

References

Pozzi, F., Di Matteo, T., & Aste, T. (2013). Spread of risk across financial markets: Better to invest in the peripheries. *Scientific Reports*, 3(1655), 1-7. doi: [10.1038/srep01665](https://doi.org/10.1038/srep01665)

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *Neuroimage*, 52, 1059-1069. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

```
A <- TMFG(neoOpen)$A

#Weighted
centW <- centlist(A, weighted = TRUE)

#Unweighted
centU <- centlist(A, weighted = FALSE)
```

closeness	<i>Closeness Centrality</i>
-----------	-----------------------------

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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

```
A <- TMFG(neoOpen)$A

#Weighted LC
LC <- closeness(A)

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

clustcoeff *Clustering Coefficient*

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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

```
A <- TMFG(neoOpen)$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"), metric = c("across", "each"), ...)
```

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 louvain community detection
cent	Centrality measure to be used. Defaults to "strength".
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
...	Additional arguments for cluster_walktrap and louvain 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. doi: [10.1038/s41598-018-24224-2](https://doi.org/10.1038/s41598-018-24224-2)

Examples

```
A <- TMFG(neoOpen)$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*. doi: 10.31234/osf.io/6kmav

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. doi: [10.31234/osf.io/3raxt](https://doi.org/10.31234/osf.io/3raxt)

Examples

```
A <- TMFG(neoOpen)$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	<i>Community Eigenvector Centrality</i>
------------	---

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. doi: [10.1007/s41109-018-0064-5](https://doi.org/10.1007/s41109-018-0064-5)

Examples

```
A <- TMFG(neoOpen)$A
comm <- igraph::walktrap.community(convert2igraph(abs(A)))$membership
result <- comm.eigen(A, comm)
```

comm.str	<i>Community Strength/Degree Centrality</i>
----------	---

Description

Computes the community strength/degree centrality measure of each community in a network

Usage

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

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

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

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

#Strength
result <- comm.str(A, comm)

#Degree
result <- comm.str(A, comm, weighted = FALSE)
```

conn	<i>Network Connectivity</i>
------	-----------------------------

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

```
A <- TMFG(neoOpen)$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 convertConnBrainMat)
neural	Is input a brain connectivity array (i.e., $m \times m \times n$)? 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>

Examples

```
A <- TMFG(neoOpen)$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 x n x m)
zmat	Z-score matrices for each participant (m) in an array (n x n x 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

Convert Correlation Matrix to Covariance Matrix

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

Core Items

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
A <- TMFG(neoOpen)$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")
```

cpmEV

Connectome-based Predictive Modeling–External Validation

Description

Applies the Connectome-based Predictive Modeling approach to neural data. This method predicts a behavioral statistic using neural connectivity from the sample. Results **may** differ from *Matlab* results because of robust GLM methodology. This function is still in its **testing phase**. **Please cite Finn et al., 2015; Rosenberg et al., 2016; Shen et al., 2017**

Usage

```
cpmEV(train_na, train_b, valid_na, valid_b, thresh = 0.01,
      overlap = FALSE, progBar = TRUE)
```

Arguments

train_na	Training dataset (an array from convertConnBrainMat function)
train_b	Behavioral statistic for each participant for the training neural data (a vector)
valid_na	Validation dataset (an array from convertConnBrainMat function)
valid_b	Behavioral statistic for each participant for the validation neural data (a vector)
thresh	Sets an α threshold for edge weights to be retained. Defaults to .01
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>)
progBar	Should progress bar be displayed? Defaults to TRUE. Set to FALSE for no progress bar

Value

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

Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

References

- 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. doi: [10.1038/nn.4135](https://doi.org/10.1038/nn.4135)
- 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. doi: [10.1038/nn.4179](https://doi.org/10.1038/nn.4179)
- 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. doi: [10.1038/nprot.2016.178](https://doi.org/10.1038/nprot.2016.178)
- Wei, T. & Simko, V.(2017). R package "corrplot": Visualization of a correlation matrix (Version 0.84). Available from <https://github.com/taiyun/corrplot>

 cpmFP

Connectome-based Predictive Modeling–Fingerprinting

Description

Applies the Connectome-based Predictive Modeling approach to neural data. This method identifies individuals based on their specific connectivity patterns. **Please cite Finn et al., 2015; Rosenberg et al., 2016; Shen et al., 2017**

Usage

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

Arguments

session1	Array from convertConnBrainMat function (first session)
session2	Array from convertConnBrainMat function (second session)
progBar	Should progress bar be displayed? Defaults to TRUE. Set to FALSE for no progress bar

Value

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

Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

References

- 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. doi: [10.1038/nn.4135](https://doi.org/10.1038/nn.4135)
- 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. doi: [10.1038/nn.4179](https://doi.org/10.1038/nn.4179)
- 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. doi: [10.1038/nprot.2016.178](https://doi.org/10.1038/nprot.2016.178)

cpmFPperm

Connectome-based Predictive Modeling–Fingerprinting Permutation

Description

Applies the Connectome-based Predictive Modeling approach to neural data. This method identifies individuals based on their specific connectivity patterns. **Please cite Finn et al., 2015; Rosenberg et al., 2016; Shen et al., 2017**

Usage

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

Arguments

session1	Array from convertConnBrainMat function (first session)
session2	Array from convertConnBrainMat function (second session)
iter	Number of iterations to perform. Defaults to 1000
progBar	Should progress bar be displayed? Defaults to TRUE. Set to FALSE for no progress bar

Value

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

Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

References

- 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. doi: [10.1038/nn.4135](https://doi.org/10.1038/nn.4135)
- 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. doi: [10.1038/nn.4179](https://doi.org/10.1038/nn.4179)
- 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. doi: [10.1038/nprot.2016.178](https://doi.org/10.1038/nprot.2016.178)

cpmIV

Connectome-based Predictive Modeling–Internal Validation

Description

Applies the Connectome-based Predictive Modeling approach to neural data. This method predicts a behavioral statistic using neural connectivity from the sample. **Please cite Finn et al., 2015; Rosenberg et al., 2016; Shen et al., 2017**

Usage

```
cpmIV(neuralarray, bstat, covar, thresh = 0.01, method = c("mean",
  "sum"), model = c("linear", "quadratic", "cubic"),
  corr = c("pearson", "spearman"), shen = FALSE, cores,
  progBar = TRUE)
```

Arguments

neuralarray	Array from convertConnBrainMat function
bstat	Behavioral statistic for each participant with neural data (a vector)
covar	Covariates to be included in predicting relevant edges (time consuming). Must be input as a <code>list()</code> (see examples)
thresh	Sets an α threshold for edge weights to be retained. Defaults to <code>.01</code>
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
shen	Are ROIs from Shen et al. 2013 atlas? Defaults to FALSE. Set to TRUE for canonical networks plot

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

Value

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

Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

References

- 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. doi: [10.1038/nn.4135](https://doi.org/10.1038/nn.4135)
- 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. doi: [10.1038/nn.4179](https://doi.org/10.1038/nn.4179)
- 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. doi: [10.1038/nprot.2016.178](https://doi.org/10.1038/nprot.2016.178)
- Wei, T. & Simko, V.(2017). R package "corrplot": Visualization of a correlation matrix (Version 0.84). Available from <https://github.com/taiyun/corrplot>

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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

```
#Undirected network
A <- TMFG(neoOpen)$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 cor_auto function)
na.data	How should missing data be handled? For "listwise" deletion the na.omit function is applied. Set to "fiml" for Full Information Maximum Likelihood (corFiml). Full Information Maximum Likelihood is recommended 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. doi: [10.1371/journal.pone.0015032](https://doi.org/10.1371/journal.pone.0015032)

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. doi: [10.1080/14697688.2014.946660](https://doi.org/10.1080/14697688.2014.946660)

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, pB = TRUE, ...)
```

Arguments

neuralarray	Array from convertConnBrainMat function
pB	Should progress bar be displayed? Defaults to TRUE. Set FALSE for no progress bar
...	Additional arguments from depend function

Value

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

Author(s)

Alexander Christensen <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. doi: [10.1038/srep27444](https://doi.org/10.1038/srep27444)

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. doi: [10.1371/journal.pone.0015032](https://doi.org/10.1371/journal.pone.0015032)

Examples

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

desc	<i>Variable Descriptive Statistics</i>
------	--

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	<i>Dataset Descriptive Statistics</i>
----------	---------------------------------------

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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

```
A <- TMFG(neoOpen)$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 cluster_walktrap community detection algorithm. Set to "louvain" for the louvain 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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

```
A <- TMFG(neoOpen)$A

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

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. doi: [10.1371/journal.pcbi.1005305](https://doi.org/10.1371/journal.pcbi.1005305)

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. doi: [10.1371/journal.pcbi.1005305](https://doi.org/10.1371/journal.pcbi.1005305)

Examples

```
ECOplusMaST.net <- ECOplusMaST(neoOpen)
```

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

```
tmfg <- TMFG(neoOpen)$A
mast <- MaST(neoOpen)
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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

```
A <- TMFG(neoOpen)$A
#Weighted
EC <- eigenvector(A)

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

`flow.frac`*Flow Fraction*

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. doi: [10.1007/s41109-018-0064-5](https://doi.org/10.1007/s41109-018-0064-5)

Examples

```
A <- TMFG(neoOpen)$A
nodes <- c(1, 3, 5, 7, 11, 13, 17, 19, 23, 29, 31, 37, 41, 43, 47)
result <- flow.frac(A, nodes)
```

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 cluster_walktrap community detection algorithm. Set to "louvain" for the louvain 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 betweenness 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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)
- 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. doi: [10.1140/epjb/e2014-40800-7](https://doi.org/10.1140/epjb/e2014-40800-7)

Examples

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

A <- TMFG(neoOpen)$A

gw <- gateway(A, comm = comm)

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

 hybrid

Hybrid Centrality

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 betweenness .
beta	Beta parameter to be passed to the rspbc 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., & Kwapil, T. R. (2018). Network structure of the Wisconsin Schizotypy Scales-Short Forms: Examining psychometric network filtering approaches. *Behavior Research Methods*, 1-20. doi: [10.3758/s13428-018-1032-9](https://doi.org/10.3758/s13428-018-1032-9)

Pozzi, F., Di Matteo, T., & Aste, T. (2013). Spread of risk across financial markets: Better to invest in the peripheries. *Scientific Reports*, 3, 1655. doi: [10.1038/srep01665](https://doi.org/10.1038/srep01665)

Examples

```
A <- TMFG(neoOpen)$A
HC <- hybrid(A)
```

impact	<i>Node Impact</i>
--------	--------------------

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. doi: [10.1371/journal.pone.0023912](https://doi.org/10.1371/journal.pone.0023912)

Examples

```
A <- TMFG(neoOpen)$A
nodeimpact <- impact(A)
```

is.graphical	<i>Determines if Network is Graphical</i>
--------------	---

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	<i>Kullback-Leibler Divergence</i>
-----	------------------------------------

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. doi: [10.1214/aoms/1177729694](https://doi.org/10.1214/aoms/1177729694)

Examples

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

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

kld_value <- kld(A1, A2)

## End(Not run)
```

lattnet

Generates a Lattice Network

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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

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

leverage

Leverage Centrality

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. doi: [10.1371/journal.pone.0012200](https://doi.org/10.1371/journal.pone.0012200)

Examples

```
A <- TMFG(neoOpen)$A

#Weighted
levW <- leverage(A)

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

 LoGo

Local/Global Inversion Method (GGM of TMFG)

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](#))

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 cor_auto function). Set to FALSE for Pearson's correlations
<code>na.data</code>	How should missing data be handled? For "listwise" deletion the na.omit function is applied. Set to "fiml" for Full Information Maximum Likelihood (corFiml). Full Information Maximum Likelihood is recommended 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. doi: [10.1103/PhysRevE.94.062306](https://doi.org/10.1103/PhysRevE.94.062306)

Examples

```
## Not run:  
LoGonet <- LoGo(neoOpen, partial = TRUE)  
  
## End(Not run)
```

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. doi: [10.1088/1742-5468/2008/10/P10008](https://doi.org/10.1088/1742-5468/2008/10/P10008)

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *Neuroimage*, 52, 1059-1069. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

```
A <- TMFG(neoOpen)$A
modularity <- louvain(A)
```

MaST	<i>Maximum Spanning Tree</i>
------	------------------------------

Description

Applies the Maximum Spanning Tree (MaST) filtering method

Usage

```
MaST(data, normal = FALSE, 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? 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 recommended 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>

References

Adapted from: <https://www.mathworks.com/matlabcentral/fileexchange/23276-maximum-weight-spanning-tree>

Examples

```
MaST.net <- MaST(neoOpen)
```

nams	<i>Network Adjusted Mean/Sum</i>
------	----------------------------------

Description

The [hybrid](#) centrality is used to adjust the mean or sum score of participant's community scores based on each node's centrality. Each participant's response values are multiplied by the corresponding [hybrid](#) centrality value (uses "random" for BC argument). In this way, more central nodes contribute a greater score and less central nodes contribute a lesser score. See Christensen (in press) for more details

Usage

```
nams(data, A, adjusted = c("mean", "sum"), comm = c("walktrap",
  "louvain"), ...)
```

Arguments

data	Must be a dataset
A	Adjacency matrix that has already been filtered
adjusted	Should adjusted values be the mean or sum score? Defaults to "mean". Set to "sum" for sum scores
comm	Can be a vector of community assignments or community detection algorithms ("walktrap" or "louvain") can be used to determine the number of communities. Defaults to 1 community. Set to "walktrap" for the cluster_walktrap algorithm. Set to "louvain" for louvain community detection
...	Additional arguments for cluster_walktrap and louvain community detection algorithms

Value

Returns a list containing:

Standardized	The standardized network adjusted score for each participant
Unstandardized	The unstandardized network adjusted score (mean or sum) for each participant
CommItems	The items associated with the specified or identified communities
CommCor	Correlations between the specified or identified communities

Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

References

Christensen, A. P. (2018). NetworkToolbox: Methods and measures for brain, cognitive, and psychometric network analysis in R. *PsyArXiv*. doi: [10.31234/osf.io/6kmav](https://doi.org/10.31234/osf.io/6kmav)

Examples

```
A <- TMFG(neoOpen)$A

#one community
sumadj <- nams(neoOpen, A, adjusted = "sum")

#theoretical communities
knowncomm <- nams(neoOpen, A,
comm = c(rep(1,8),rep(2,8),rep(3,8),rep(4,8),rep(5,8),rep(6,8)))

#walktrap communities
walkadj <- nams(neoOpen, A, adjusted = "sum", comm = "walktrap")
```

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 (2018).

Usage

```
data(neoOpen)
```

Format

A 802x48 response matrix

References

Christensen, A. P., Cotter, K. N., & Silvia, P. J. (2018). Reopening openness to experience: A network analysis of four openness to experience inventories. *Journal of Personality Assessment*, 1-15. doi: [10.1080/00223891.2018.1467428](https://doi.org/10.1080/00223891.2018.1467428). OSF: osf.io/954a7/

Examples

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

net.coverage *Network Coverage*

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> 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. doi: [10.31234/osf.io/3raxt](https://doi.org/10.31234/osf.io/3raxt)

Examples

```
A <- TMFG(neoOpen)$A
nodes <- c(1,3,5,7,11,13,17,19,23,29,31,37,41,43,47)
result <- net.coverage(A, nodes)
```

`neuralnetfilter`*Neural Network Filter*

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

<code>neuralarray</code>	Array from <code>convertConnBrainMat</code> function
<code>method</code>	Filtering method to be applied
<code>progBar</code>	Should progress bar be displayed? Defaults to TRUE. Set FALSE for no progress bar
<code>...</code>	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>

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)
```

participation	<i>Participation Coefficient</i>
---------------	----------------------------------

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 cluster_walktrap community detection algorithm. Set to "louvain" for the louvain community detection algorithm. Can also be set to user-specified communities (see examples)

Details

Values closer to 1 suggest greater within-community connectivity and values closer to 0 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. doi: [10.1038/nature03288](https://doi.org/10.1038/nature03288)

Rubinov, M., & Sporns, O. (2010). Complex network measures of brain connectivity: Uses and interpretations. *Neuroimage*, 52, 1059-1069. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

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

A <- TMFG(neoOpen)$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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

```
A<-TMFG(neoOpen)$A

#Unweighted
PL <- pathlengths(A)

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

randnet

Generates a Random Network

Description

Generates a random network

Usage

```
randnet(nodes, edges)
```

Arguments

nodes	Number of nodes in random network
edges	Number of edges in random network

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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

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

reg	<i>Regression Matrix</i>
-----	--------------------------

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 family
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(neo0pen>=4, 1, 0)  
  
#perform logistic regression  
mat <- reg(psyb)
```

resp.rep *Repeated Responses Check*

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)
```

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)

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. doi: [10.1038/srep19668](https://doi.org/10.1038/srep19668)

Examples

```
A <- TMFG(neoOpen)$A
rspbc <- rspbc(A, beta=0.01)
```

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 sample_smallworld)
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 based on the simulated network
simRho	Simulated correlation from sim.correlation

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. Retrieved from [here](#)

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.Likert <- sim.swn(25, 500, nei = 3, replace = TRUE, ordinal = TRUE, ordLevels = 2)
```

smallworldness

Small-worldness Measure

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. doi: [10.1371/journal.pone.0002051](https://doi.org/10.1371/journal.pone.0002051)
- 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. doi: [10.1089/brain.2011.0038](https://doi.org/10.1089/brain.2011.0038)

Examples

```
A<-TMFG(neoOpen)$A
swmHG <- smallworldness(A, method="HG")
swmRand <- smallworldness(A, method="rand")
swmTJHBL <- smallworldness(A, method="TJHBL")
```

stable

Stabilizing Nodes

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"), ...)
```

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 louvain community detection
cent	Centrality measure to be used. Defaults to "strength".
...	Additional arguments for cluster_walktrap and louvain community detection algorithms

Value

A matrix containing the within-community centrality 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. doi: [10.1038/s41598-018-24224-2](https://doi.org/10.1038/s41598-018-24224-2)

Examples

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

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

Description

Computes strength of each node in a network

Usage

```
strength(A)
```

Arguments

A	An adjacency matrix of network data
---	-------------------------------------

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. doi: [10.1016/j.neuroimage.2009.10.003](https://doi.org/10.1016/j.neuroimage.2009.10.003)

Examples

```
#Undirected network
A <- TMFG(neoOpen)$A

str <- strength(A)

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

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

str <- strength(Adep)

## End(Not run)
```

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 α 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 adapt.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 cor_auto function)
na.data	How should missing data be handled? For "listwise" deletion the na.omit function is applied. Set to "fiml" for Full Information Maximum Likelihood (corFiml). Full Information Maximum Likelihood is recommended but time consuming
...	Additional arguments for fdrtool and adapt.a

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. doi: [10.1093/bioinformatics/btn209](https://doi.org/10.1093/bioinformatics/btn209)

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](#).

Usage

```

TMFG(data, normal = FALSE, 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 FALSE. Data is not transformed to be normal. Set to TRUE if data should be transformed to be normal (computes correlations using the cor_auto function)
na.data	How should missing data be handled? For "listwise" deletion the na.omit function is applied. Set to "fiml" for Full Information Maximum Likelihood (corFiml). Full Information Maximum Likelihood is recommended 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 depend function)

Value

Returns a list containing:

A	The filtered adjacency matrix
separators	The separators (3-cliques) in the network (wrapper output for LoGo)
cliques	The cliques (4-cliques) in the network (wrapper output for LoGo)

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*, 1-20. doi: [10.3758/s13428-018-1032-9](https://doi.org/10.3758/s13428-018-1032-9)

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. doi: [10.1093/comnet/cnw015](https://doi.org/10.1093/comnet/cnw015)

Examples

```
TMFG.net <- TMFG(neoOpen)
```

transitivity	<i>Transitivity</i>
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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)

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References

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Examples

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

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