

# Package ‘CliquePercolation’

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**Description** Clique percolation community detection for weighted and unweighted networks as well as threshold and plotting functions.  
For more information see Farkas et al. (2007) <doi:10.1088/1367-2630/9/6/180> and Palla et al. (2005) <doi:10.1038/nature03607>.

**Maintainer** Jens Lange <lange.jens@outlook.com>

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**Author** Jens Lange [aut, cre],  
Janis Zickfeld [ctb],  
Alexander P. Christensen [ctb]

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cpAlgorithm	<i>Clique Percolation Community Detection</i>
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## Description

Function for clique percolation community detection algorithms for weighted and unweighted networks.

## Usage

```
cpAlgorithm(W, k, method = c("unweighted", "weighted", "weighted.CFinder"), I)
```

## Arguments

W	A qgraph object or a symmetric matrix; see also <a href="#">qgraph</a>
k	Clique size (number of nodes that should form a clique)
method	A string indicating the method to use ("unweighted", "weighted", or "weighted.CFinder"); see Details
I	Intensity threshold for weighted networks

## Details

method = "unweighted" conducts clique percolation for unweighted networks as described in Palla et al. (2005). method = "weighted" conducts clique percolation for weighted graphs with inclusion of cliques if their Intensity is higher than the specified Intensity (I), which is the method described in Farkas et al. (2007). method = "weighted.CFinder" conducts clique percolation as in the CFinder program. The Intensity (I) threshold is applied twice, namely first to the Intensity of the cliques (as before) and then also to their k-1 overlap with other cliques (e.g., in the case of k = 3, it is applied to the edge that two cliques share).

For weighted networks, the absolute value of the edge weights is taken. Therefore, negative edges are treated like positive edges just like in the CFinder program. Thus, the Intensity threshold I can only be positive.

cpAlgorithm produces a solution for all networks, even if there are no communities or communities have no overlap. The respective output is empty in such cases.

**Value**

A list object with the following elements:

**list.of.communities.numbers** list of communities with numbers as identifiers of nodes

**list.of.communities.labels** list of communities with labels from qgraph object or row or column names of matrix as identifiers of nodes

**shared.nodes.numbers** vector with all nodes that belong to multiple communities with numbers as identifiers of nodes

**shared.nodes.labels** vector with all nodes that belong to multiple communities with labels from qgraph object or row or column names of matrix as identifiers of nodes

**isolated.nodes.numbers** vector with all nodes that belong to no community with numbers as identifiers of nodes

**isolated.nodes.labels** vector with all nodes that belong to no community with labels from qgraph object or row or column names of matrix as identifiers of nodes

**k** user-specified k

**method** user-specified method

**I** user-specified I (if method was "weighted" or "weighted.CFinder")

**Author(s)**

Jens Lange, <lange.jens@outlook.com>

**References**

Farkas, I., Abel, D., Palla, G., & Vicsek, T. (2007). Weighted network modules. *New Journal of Physics*, 9, 180-180. <http://doi.org/10.1088/1367-2630/9/6/180>

Palla, G., Derenyi, I., Farkas, I., & Vicsek, T. (2005). Uncovering the overlapping community structure of complex networks in nature and society. *Nature*, 435, 814-818. <http://doi.org/10.1038/nature03607>

**Examples**

```
## Example for unweighted networks

# create qgraph object
W <- matrix(c(0,1,1,1,0,0,0,0,
             0,0,1,1,0,0,0,0,
             0,0,0,0,0,0,0,0,
             0,0,0,0,1,1,1,0,
             0,0,0,0,0,1,1,0,
             0,0,0,0,0,0,1,0,
             0,0,0,0,0,0,0,1,
             0,0,0,0,0,0,0,0), nrow = 8, ncol = 8, byrow = TRUE)
W <- Matrix::forceSymmetric(W)
W <- qgraph::qgraph(W)

# run clique percolation for unweighted networks
results <- cpAlgorithm(W = W, k = 3, method = "unweighted")
```

```

# print results overview
results

# extract more information about communities
summary(results)

## Example for weighted networks

# create qgraph object
W <- matrix(c(0,1,1,1,0,0,0,0,
              0,0,1,1,0,0,0,0,
              0,0,0,0,0,0,0,0,
              0,0,0,0,1,1,1,0,
              0,0,0,0,0,1,1,0,
              0,0,0,0,0,0,1,0,
              0,0,0,0,0,0,0,1,
              0,0,0,0,0,0,0,0), nrow = 8, ncol = 8, byrow = TRUE)
set.seed(4186)
rand_w <- stats::rnorm(length(which(W == 1)), mean = 0.3, sd = 0.1)
W[which(W == 1)] <- rand_w
W <- Matrix::forceSymmetric(W)
W <- qgraph::qgraph(W)

# run clique percolation for weighted networks
results <- cpAlgorithm(W = W, k = 3, method = "weighted", I = 0.1)

# print results overview
results

# extract more information about communities
summary(results)

## Example with Obama data set (see ?Obama)

# get data
data(Obama)

# estimate network
net <- qgraph::EBICglasso(qgraph::cor_auto(Obama), n = nrow(Obama))

# run clique percolation algorithm with specific k and I
cpk3I.16 <- cpAlgorithm(net, k = 3, I = 0.16, method = "weighted")

# print results overview
cpk3I.16

# extract more information about communities
summary(cpk3I.16)

```

cpColoredGraph

*Colored Network According To Clique Percolation Communities***Description**

Function for plotting the original network with nodes colored according to the community partition identified via the clique percolation community detection algorithm, taking predefined sets of nodes into account.

**Usage**

```
cpColoredGraph(
  W,
  list.of.communities,
  list.of.sets = NULL,
  larger.six = FALSE,
  h.cp = c(0, 360 * (length(cplist) - 1)/length(cplist)),
  c.cp = 80,
  l.cp = 60,
  set.palettes.size = NULL,
  own.colors = NULL,
  avoid.repeated.mixed.colors = FALSE,
  ...
)
```

**Arguments**

<code>W</code>	A <code>qgraph</code> object or a symmetric matrix; see also <a href="#">qgraph</a>
<code>list.of.communities</code>	List object taken from results of <code>cpAlgorithm</code> function; see also <a href="#">cpAlgorithm</a>
<code>list.of.sets</code>	List object specifying predefined groups of nodes in original network; default is <code>NULL</code> ; see Details
<code>larger.six</code>	Integer indicating whether <code>length(list.of.communities)</code> is larger six (if <code>list.of.sets = NULL</code> ) or <code>length(list.of.sets)</code> is larger six (if <code>list.of.sets</code> is not <code>NULL</code> ); default is <code>FALSE</code> ; see Details
<code>h.cp</code>	Vector of integers indicating the range of hue from which colors should be drawn for elements in <code>list.of.communities</code> (if <code>list.of.sets = NULL</code> ) or for elements in <code>list.of.sets</code> (if <code>list.of.sets</code> is not <code>NULL</code> ); default is the value specified in <code>colorspace::qualitative_hcl()</code> ; see Details
<code>c.cp</code>	Integer indicating the chroma from which colors should be drawn for elements in <code>list.of.communities</code> (if <code>list.of.sets = NULL</code> ) or for elements in <code>list.of.sets</code> (if <code>list.of.sets</code> is not <code>NULL</code> ); default is 80 as specified in <code>colorspace::qualitative_hcl()</code> ; see Details
<code>l.cp</code>	Integer indicating the luminance from which colors should be drawn for elements in <code>list.of.communities</code> (if <code>list.of.sets = NULL</code> ) or for elements in

	<code>list.of.sets</code> (if <code>list.of.sets</code> is not NULL); default is 60 as specified in <a href="#">colorspace::qualitative_hcl()</a> ; see Details
<code>set.palettes.size</code>	Integer indicating the number of sets for which smooth gradients of a set color should be generated using <a href="#">colorspace::sequential_hcl()</a> ; default is the number of pure communities of a set plus one; see Details
<code>own.colors</code>	Vector of hex code colors of length of <code>list.of.communities</code> (if <code>list.of.sets</code> = NULL) or <code>list.of.sets</code> (if <code>list.of.sets</code> is not NULL); if specified, colors are used for coloring the communities and no other colors are generated; if NULL (default), reasonable colors are generated; see Details
<code>avoid.repeated.mixed.colors</code>	Logical indicating whether it should be avoided that multiple mixed communities are assigned the same color; default is FALSE; see Details
<code>...</code>	any additional argument from <code>qgraph</code> ; see also <a href="#">qgraph</a>

### Details

The function takes the results of `cpAlgorithm` (see also [cpAlgorithm](#)), that is, either the `list.of.communities.numbers` or the `list.of.communities.labels` and plots the original network, coloring the nodes according to the community partition. If there are no predefined sets of nodes (`list.of.sets` = NULL; the default), each community is assigned a color by using a palette generation algorithm from the package `colorspace`, which relies on HCL color space. Specifically, the function `qualitative_hcl` (see also [colorspace::qualitative\\_hcl\(\)](#)) is used, which generates a balanced set of colors over a range of hue values, holding chroma and luminance constant. This method is preferred over other palette generating algorithms in other color spaces (Zeileis et al., *subm.*). The default values recommended in `qualitative_hcl` are used, adapted to the current context in the case of hue. Yet, `h.cp`, `c.cp`, and `l.cp` can be used to overwrite the default values. Each node gets the color of the community it belongs to. Shared nodes are split equally in multiple colors, one for each community they belong to. Isolated nodes are colored white.

If there are predefined sets of nodes, the qualitatively different colors are assigned to the sets specified in `list.of.sets`. Then, it is checked whether communities are pure (they contain nodes from only one set) or they are mixed (they contain nodes from multiple sets). For pure communities of each set, the assigned color is taken and faded towards white with another function from `colorspace`, namely `sequential_hcl` (see also [colorspace::sequential\\_hcl\(\)](#)). For instance, if there are three pure communities with nodes that are only from Set 1, then the basic color assigned to Set 1 is taken, and faded toward white in  $3 + 1$  steps. There is one color generated more than needed (here four colors for three communities), because the last color in the fading is always white, which is reserved for isolated nodes. The three non-white colors are then assigned to each community, with stronger colors being assigned to larger communities. In that sense, all communities that entail nodes from only one specific set, will have rather similar colors (only faded towards white). All communities that entail nodes from only one specific other set, will also have similar colors, yet they will differ qualitatively from the colors of the communities that entail items from other sets. For communities that entail items from multiple sets, the basic colors assigned to these sets are mixed in proportion to the number of nodes from each set. For instance, if a community entails two nodes from Set 1 and one node from Set 2, then the colors of Sets 1 and 2 are mixed 2:1.

The mixing of colors is subtractive (how paint mixes). Subtractive color mixing is difficult to implement. An algorithm proposed by Scott Burns is used (see <http://scottburns.us/subtractive-color-mixture/> and <http://scottburns.us/fast-rgb-to-spectrum-conversion-for-reflectances/>). Each color is

transformed into a corresponding reflectance curve via the RGBC algorithm. That is, optimized reflectance curves of red, green, and blue are adapted according to the RGB values of the respective color. The reflectance curves of the colors that need to be mixed are averaged via the weighted geometric mean. The resulting mixed reflectance curve is transformed back to RGB values by multiplying the curve with a derived matrix. The algorithm produces rather good color mixing and is computationally efficient. Yet, results may not always be absolutely precise.

The mixing of colors for mixed communities can lead to multiple communities being assigned the same color. For instance, two communities with two nodes each from Sets 1 and 2 would have the same color, namely the colors assigned to the sets mixed in the same proportion. This is reasonable, because these communities are structurally similar. However, it can be confusing to have two actually different communities with the same color. To avoid this, set `avoid_repeated_mixed_colors = TRUE`. Doing so slightly alters the ratio with which the color of a mixed community is determined, if the community would have been assigned a color that was already assigned. This slight variation of the ratio is random. To reproduce results from a previous run, set a seed.

The fading of pure communities via `sequential_hcl` is a function of the number of sets. If there are more pure communities from a specific set, more faded colors will be generated. This makes coloring results hard to compare across different networks, if such a comparison is desired. For instance, if one network has 12 nodes that belong to three communities sized 6, 3, and 3, all of them pure (having nodes from only one set), then their colors will be strong, average, and almost white respectively. If the same 12 nodes belong to two communities size 6 and 6, both of them pure, then their colors will be strong and average to almost white. Different numbers of pure communities therefore change the color range. To circumvent that, one can specify `set_palettes_size` to any number larger than the number of pure communities of a set plus one. For all sets, `sequential_hcl` then generates as many shades towards white of a respective color as specified in `set_palettes_size`. Colors for each community are then picked from the strongest towards whiter colors, with larger communities being assigned stronger colors. Note that in this situation, the range of colors is always the same for all sets in a network, making them comparable across different sets. When there are more pure communities of one set than from another their luminance will be lower. Moreover, also across networks, the luminance of different sets of nodes or of the same set can be compared.

In all cases, qualitatively different colors are assigned to either the elements in `list.of.communities` (when `list.of.sets = NULL`) or the elements in `list.of.sets` (when `list.of.sets` is not `NULL`) with `qualitative_hcl`. Zeileis et al. (subm.) argue that this function can generate up to six different colors that people can still distinguish. For a larger number of qualitative colors, other packages can be used. Specifically, if the argument `larger_six = TRUE` (default is `FALSE`), the qualitatively different colors are generated via the package Polychrome (Coombes et al., 2019) with the function `createPalette` (see also `createPalette`). This function generates maximally different colors in HCL space and can generate a higher number of distinct colors. With these colors, the rest of the procedure is identical. The seedcolors specified in Polychrome are general red, green, and blue. As the procedure relies on randomness, you have to set a seed to reproduce the results of a previous run. Note that the Polychrome palettes are maximally distinct, thus they are most likely not as balanced as the palettes generated with `colorspace`. In general, the function `cpColoredGraph` is recommended only for very small networks anyways, for which `larger_six = FALSE` makes sense. For larger networks, consider plotting the community network instead (see `cpCommunityGraph`).

When `own.colors` are specified, these colors are assigned to the elements in `list.of.communities` (if `list.of.sets = NULL`) or to the elements in `list.of.sets` (if `list.of.sets` is not `NULL`). The rest of the procedure is identical.



```

W <- Matrix::forceSymmetric(W)
rownames(W) <- letters[seq(from = 1, to = nrow(W))]
colnames(W) <- letters[seq(from = 1, to = ncol(W))]

W <- qgraph::qgraph(W, layout = "spring", edge.labels = TRUE)

# run clique percolation algorithm; three communities; two shared nodes, one isolated node
cp <- cpAlgorithm(W, k = 3, method = "weighted", I = 0.09)

# color original graph according to community partition
# all other arguments are defaults; qgraph arguments used to return same layout

results <- cpColoredGraph(W, list.of.communities = cp$list.of.communities.labels,
                          layout = "spring", edge.labels = TRUE)

# own colors (red, green, and blue) assigned to the communities

results <- cpColoredGraph(W, list.of.communities = cp$list.of.communities.labels,
                          own.colors = c("#FF0000", "#00FF00", "#0000FF"),
                          layout = "spring", edge.labels = TRUE)

# define sets of nodes; nodes a to o are in Set 1 and letters p to u in Set 2
list.of.sets <- list(letters[seq(from = 1, to = 15)],
                    letters[seq(from = 16, to = 21)])

# color original graph according to community partition, taking sets of nodes into account
# two communities are pure and therefore get shades of set color; smaller community is more white
# one community is mixed, so both set colors get mixed

results <- cpColoredGraph(W, list.of.communities = cp$list.of.communities.labels,
                          list.of.sets = list.of.sets,
                          layout = "spring", edge.labels = TRUE)

# graph as before, but specifying the set palette size to 6
# from a range of 6 colors, the pure communities get the darker ones
# in a different network with also two pure communities, luminance would therefore be equal

results <- cpColoredGraph(W, list.of.communities = cp$list.of.communities.labels,
                          list.of.sets = list.of.sets, set.palettes.size = 6,
                          layout = "spring", edge.labels = TRUE)

# graph as before, but colors sampled only form yellow to blue range, less chroma, more luminance

results <- cpColoredGraph(W, list.of.communities = cp$list.of.communities.labels,
                          list.of.sets = list.of.sets, set.palettes.size = 6,
                          h.cp = c(50, 210), c.cp = 70, l.cp = 70,
                          layout = "spring", edge.labels = TRUE)

```

```

# own colors (red and green) assigned to the sets
# two communities in shades of red and one community is mix of green and red (brown)

results <- cpColoredGraph(W, list.of.communities = cp$list.of.communities.labels,
                          list.of.sets = list.of.sets,
                          own.colors = c("#FF0000", "#00FF00"),
                          layout = "spring", edge.labels = TRUE)

## Example with Obama data set (see ?Obama)

# get data
data(Obama)

# estimate network
net <- qgraph::EBICglasso(qgraph::cor_auto(Obama), n = nrow(Obama))

# run clique percolation algorithm with specific k and I
cpk3I.16 <- cpAlgorithm(net, k = 3, I = 0.16, method = "weighted")

# color original graph according to community partition
# all other arguments are defaults

results <- cpColoredGraph(net, list.of.communities = cpk3I.16$list.of.communities.labels,
                          layout = "spring", theme = "colorblind")

```

---

cpCommunityGraph

*Plotting Clique Percolation Community Network*


---

## Description

Function for plotting a network with nodes representing communities from clique percolation community detection and edges representing the number of shared nodes of the communities.

## Usage

```

cpCommunityGraph(
  list.of.communities,
  node.size.method = c("proportional", "normal"),
  max.node.size = 10,
  ...
)

```

## Arguments

`list.of.communities`

List object taken from results of `cpAlgorithm` function; see also [cpAlgorithm](#)



```

max.node.size = 7)

# plot community network; proportional; maximum size is 7
# change shape of nodes to triangle via qgraph argument
cp.network2 <- cpCommunityGraph(cp.results$list.of.communities.numbers,
                                node.size.method = "proportional",
                                max.node.size = 7,
                                shape = "triangle")

## Example with Obama data set (see ?Obama)

# get data
data(Obama)

# estimate network
net <- qgraph::EBICglasso(qgraph::cor_auto(Obama), n = nrow(Obama))

# run clique percolation algorithm with specific k and I
cpk3I.16 <- cpAlgorithm(net, k = 3, I = 0.16, method = "weighted")

# plot community network; normal
Obama.network <- cpCommunityGraph(cpk3I.16$list.of.communities.numbers,
                                   node.size.method = "proportional",
                                   theme = "colorblind")

```

---

cpCommunitySizeDistribution

*Plotting Clique Percolation Community Size Distribution*

---

## Description

Function for plotting the frequency distribution of community sizes from clique percolation community detection and testing for power-law.

## Usage

```

cpCommunitySizeDistribution(
  list.of.communities,
  color.line = "#bc0031",
  test.power.law = FALSE
)

```

## Arguments

`list.of.communities` List object taken from results of `cpAlgorithm` function; see also [cpAlgorithm](#)

`color.line` string indicating the color of the line in the plot as described in [par](#); default is "#bc0031"

`test.power.law` Logical indicating whether fit of power-law should be tested; default is FALSE; see Details

### Details

The function takes the results of `cpAlgorithm` (see also [cpAlgorithm](#)), that is, either the `list.of.communities.numbers` or the `list.of.communities.labels` and plots the community size distribution. If there are no communities, no plot can be generated. An error is printed indicating this.

If `test.power.law = TRUE`, test of a fit of a power-law is performed with the function `fit_power_law` (see also [fit\\_power\\_law](#)). Fit is tested for the entire distribution from the smallest community size onward (i.e., typically `k` as specified in `cpAlgorithm`). Moreover, `test` uses the `plfit` implementation of `fit_power_law`. For other arguments, default values are used.

### Value

The function primarily plots the community size distribution. Additionally, it returns a list with a data frame containing all community sizes and their frequencies (`size.distribution`). If `test.power.law = TRUE`, a test of fit of a power-law distribution is also returned as a list object with results from `fit_power_law` (see also [fit\\_power\\_law](#)).

### Author(s)

Jens Lange, <lange.jens@outlook.com>

### Examples

```
## Example with fictitious data

# create qgraph object; 150 nodes; 1/7 of all edges are different from zero
W <- matrix(c(0), nrow = 150, ncol = 150, byrow = TRUE)
set.seed(4186)
W[upper.tri(W)] <- sample(c(rep(0,6),1), length(W[upper.tri(W)]), replace = TRUE)
rand_w <- stats::rnorm(length(which(W == 1)), mean = 0.3, sd = 0.1)
W[which(W == 1)] <- rand_w
W <- Matrix::forceSymmetric(W)
W <- qgraph::qgraph(W, DoNotPlot = TRUE)

# run clique percolation for weighted networks
cp.results <- cpAlgorithm(W, k = 3, method = "weighted", I = 0.38)

# plot community size distribution with blue line
cp.size.dist <- cpCommunitySizeDistribution(cp.results$list.of.communities.numbers,
                                          color.line = "#0000ff")

# test for power-law distribution
cp.size.dist <- cpCommunitySizeDistribution(cp.results$list.of.communities.numbers,
                                          color.line = "#0000ff",
                                          test.power.law = TRUE)

cp.size.dist$fit.power.law

## Example with Obama data set (see ?Obama)
```

```

# get data
data(Obama)

# estimate network
net <- qgraph::EBICglasso(qgraph::cor_auto(Obama), n = nrow(Obama))

# run clique percolation algorithm with specific k and I
cpk3I.16 <- cpAlgorithm(net, k = 3, I = 0.16, method = "weighted")

# plot community size distribution
#the distribution is not very informative with four equally-sized communities
Obama.size.dist <- cpCommunitySizeDistribution(cpk3I.16$list.of.communities.numbers)

```

---

cpPermuteEntropy      *Confidence Intervals Of Entropy Based On Random Permutations Of Network*

---

### Description

Function for determining confidence intervals of entropy values calculated for community partition from clique percolation based on randomly permuted networks of original network.

### Usage

```

cpPermuteEntropy(
  W,
  cpThreshold.object,
  n = 100,
  interval = 0.95,
  CFinder = FALSE,
  ncores,
  seed = NULL
)

```

### Arguments

W	A qgraph object or a symmetric matrix; see also <a href="#">qgraph</a>
cpThreshold.object	A cpThreshold object; see also <a href="#">cpThreshold</a>
n	number of permutations (default is 100)
interval	requested confidence interval (larger than zero and smaller 1; default is 0.95)
CFinder	logical indicating whether clique percolation for weighted networks should be performed as in CFinder ; see also <a href="#">cpAlgorithm</a>
ncores	Numeric. Number of cores to use in computing results. Defaults to <code>parallel::detectCores() / 2</code> or half of your computer's processing power. Set to 1 to not use parallel computing
seed	Numeric. Set seed for reproducible results. Defaults to NULL

## Details

The function generates  $n$  random permutations of the network specified in  $W$ . For each randomly permuted network, it runs `cpThreshold` (see [cpThreshold](#) for more information) with  $k$  and  $I$  values extracted from the `cpThreshold` object specified in `cpThreshold.object`. Across permutations, the confidence intervals of the entropy values are determined for each  $k$  separately.

The confidence interval of the entropy values is determined separately for each  $k$ . This is because larger  $k$  have to produce less communities on average, which will decrease entropy. Comparing confidence intervals of smaller  $k$  to those of larger  $k$  would therefore be disadvantageous for larger  $k$ .

In the output, one can check the confidence intervals of each  $k$ . Moreover, a data frame is produced that takes the `cpThreshold` object that was specified in `cpThreshold.object` and removes all rows that do not exceed the upper bound of the confidence interval of the respective  $k$ .

## Value

A list object with the following elements:

**Confidence.Interval** a data frame with lower and upper bound of confidence interval for each  $k$

**Extracted.Rows** rows extracted from `cpThreshold.object` that are larger than the upper bound of the specified confidence interval for each  $k$

**Settings** user-specified settings

## Author(s)

Jens Lange, <lange.jens@outlook.com>

## Examples

```
## Example with fictitious data

# create qgraph object
W <- matrix(c(0,1,1,1,0,0,0,0,
             0,0,1,1,0,0,0,0,
             0,0,0,0,0,0,0,0,
             0,0,0,0,1,1,1,0,
             0,0,0,0,0,1,1,0,
             0,0,0,0,0,0,1,0,
             0,0,0,0,0,0,0,1,
             0,0,0,0,0,0,0,0), nrow = 8, ncol = 8, byrow = TRUE)
W <- Matrix::forceSymmetric(W)
W <- qgraph::qgraph(W)

# create cpThreshold object
cpThreshold.object <- cpThreshold(W = W, method = "unweighted", k.range = c(3,4),
                                threshold = "entropy")

# run cpPermuteEntropy with 100 permutations and 95% confidence interval

results <- cpPermuteEntropy(W = W, cpThreshold.object = cpThreshold.object,
```

```

n = 100, interval = 0.95, ncores = 1, seed = 4186)

# check results
results

## Example with Obama data set (see ?Obama)

# get data
data(Obama)

# estimate network
net <- qgraph::EBICglasso(qgraph::cor_auto(Obama), n = nrow(Obama))

# create cpThreshold object

threshold <- cpThreshold(net, method = "weighted",
                        k.range = 3:4,
                        I.range = seq(0.1, 0.5, 0.01),
                        threshold = "entropy")

# run cpPermuteEntropy with 50 permutations and 99% confidence interval

permute <- cpPermuteEntropy(net, cpThreshold.object = threshold,
                           interval = 0.99, n = 50, ncores = 1, seed = 4186)

# check results
permute

```

---

cpThreshold

*Optimizing k And I For Clique Percolation Community Detection*


---

### Description

Function for determining threshold value(s) (ratio of largest to second largest community sizes, chi, entropy) of ranges of k and I values to help deciding for optimal k and I values.

### Usage

```

cpThreshold(
  W,
  method = c("unweighted", "weighted", "weighted.CFinder"),
  k.range,
  I.range,
  threshold = c("largest.components.ratio", "chi", "entropy")
)

```







**Format**

An object of class "qgraph" with 1,316 nodes and 6,300 edges.

**Source**

<https://CRAN.R-project.org/package=igraphdata>

**References**

Gfeller, D. (2007). *Simplifying complex networks: From a clustering to a coarse graining strategy*. EPFL. <http://library.epfl.ch/theses/?nr=3888>

**Examples**

```
data(immuno)
```

---

Obama

*Data: Evaluative Reactions Toward Barack Obama (2012)*

---

**Description**

A data set containing evaluative reactions toward Barack Obama from the American National Election Studies in 2012. The study included 5,914 participants, representative of the adult U.S. American population (note missing values). The participants rated Obama on 10 evaluative reactions.

**Usage**

```
data(Obama)
```

**Format**

An object of class "data.frame" with 5,914 observations and 10 variables.

**Mor** "Is moral"

**Led** "Would provide strong leadership"

**Car** "Really cares about people like you"

**Kno** "Is knowledgeable"

**Int** "Is intelligent"

**Hns** "Is honest"

**Ang** "Angry"

**Hop** "Hopeful"

**Afr** "Afraid of him"

**Prd** "Proud"

### Source

<https://electionstudies.org/>

### References

Dalege, J., Borsboom, D., Van Harreveld, F., Van der Maas, H. L. J. (2017). Network analysis on attitudes: A brief tutorial. *Social Psychological and Personality Science*, 8, 528-537. <https://doi.org/10.1177/1948550617709827>

### Examples

```
data(Obama)
```

---

```
print.cpAlgorithm      print.cpAlgorithm
```

---

### Description

Print method for objects of class `cpAlgorithm`.

### Usage

```
## S3 method for class 'cpAlgorithm'  
print(x, ...)
```

### Arguments

<code>x</code>	An object of class <code>cpAlgorithm</code> ; see also <a href="#">cpAlgorithm</a>
<code>...</code>	currently ignored

### Author(s)

Jens Lange, <[lange.jens@outlook.com](mailto:lange.jens@outlook.com)>

---

```
print.cpPermuteEntropy
      print.cpPermuteEntropy
```

---

**Description**

Print method for objects of class cpPermuteEntropy.

**Usage**

```
## S3 method for class 'cpPermuteEntropy'
print(x, ...)
```

**Arguments**

x	An object of class cpPermuteEntropy; see also <a href="#">cpPermuteEntropy</a>
...	currently ignored

**Author(s)**

Jens Lange, <lange.jens@outlook.com>

---

```
summary.cpAlgorithm  summary.cpAlgorithm
```

---

**Description**

Summary method for objects of class cpAlgorithm.

**Usage**

```
## S3 method for class 'cpAlgorithm'
summary(
  object,
  details = c("communities.labels", "shared.nodes.labels", "isolated.nodes.labels"),
  ...
)
```

**Arguments**

object	An object of class cpAlgorithm; see also <a href="#">cpAlgorithm</a>
details	A string or vector indicating about which part of the results more information is requested; default is c("communities.labels", "shared.nodes.labels", "isolated.nodes.labels"); see Details
...	currently ignored

**Details**

The function extracts information from an object produced by `cpAlgorithm`. To do so, the user has to specify in `details` which information is requested. It is possible to extract information about the communities with either numbers (`communities.numbers`) or labels (`communities.labels`) as identifiers of the nodes. Moreover, it is possible to extract information about shared nodes with either numbers (`shared.nodes.numbers`) or labels (`shared.nodes.labels`) as identifiers of the nodes. Finally, it is possible to extract information about isolated nodes with either numbers (`isolated.nodes.numbers`) or labels (`isolated.nodes.labels`) as identifiers of the nodes. Any combination of these options can be specified in `details`.

**Value**

Prints information depending on `details`.

**Author(s)**

Jens Lange, <lange.jens@outlook.com>

**Examples**

```
## Example for unweighted networks

# create qgraph object
W <- matrix(c(0,1,1,1,0,0,0,0,
             0,0,1,1,0,0,0,0,
             0,0,0,0,0,0,0,0,
             0,0,0,0,1,1,1,0,
             0,0,0,0,0,1,1,0,
             0,0,0,0,0,0,1,0,
             0,0,0,0,0,0,0,1,
             0,0,0,0,0,0,0,0,1,
             0,0,0,0,0,0,0,0), nrow = 8, ncol = 8, byrow = TRUE)
colnames(W) <- letters[1:8]
rownames(W) <- letters[1:8]
W <- Matrix::forceSymmetric(W)
W <- qgraph::qgraph(W)

# run clique percolation for unweighted networks
results <- cpAlgorithm(W = W, k = 3, method = "unweighted")

# print results overview
results

# extract details about the communities
summary(results, details = "communities.labels")

# extract information about shared and isolated nodes
summary(results, details = c("shared.nodes.numbers", "isolated.nodes.labels"))
```

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