

# Package ‘FCtools’

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**Title** Functional Connectivity Tools

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**Description** Analyzing and visualizing brain connectivity data, including network-based statistics (NBS) for linear and linear mixed models, both at edge level and functional network level (Yeo's 7-networks (Schaefer et al. (2017) <[doi:10.1093/cercor/bhx179](https://doi.org/10.1093/cercor/bhx179)>)). Plots include edge-wise connectograms, chord diagrams, network connectograms, heatmaps, and 3D glass brain connectivity plots. 'FCtools' works with vectors of edges (derived from connectivity/adjacency matrices) from the 'Brain-netome' (Fan et al. (2016) <[doi:10.1093/cercor/bhw157](https://doi.org/10.1093/cercor/bhw157)>), 'Schaefer' (100 or 200, each with 19 'ASeg' subcortices) (Schaefer et al. (2017) <[doi:10.1093/cercor/bhx179](https://doi.org/10.1093/cercor/bhx179)>, Fischl et al. (2002) <[doi:10.1016/S0896-6273\(02\)00569-X](https://doi.org/10.1016/S0896-6273(02)00569-X)>), and 'Automated Anatomical Labeling' (AAL) atlases (Tzourio-Mazoyer et al. (2002) <[doi:10.1006/nimg.2001.0978](https://doi.org/10.1006/nimg.2001.0978)>).

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**URL** <https://cogbrainhealthlab.github.io/FCtools/>

**RoxygenNote** 7.3.3

**Depends** R (>= 4.1.0)

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**NeedsCompilation** no

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|          |                 |
|----------|-----------------|
| edgelist | <i>edgelist</i> |
|----------|-----------------|

---

Description

Listing the edges in a connectogram.

Usage

edgelist(data)

Arguments

data                    a vector of edge values with a length of 4005, 7021, 23871 or 30135.

Details

This function takes a vector of edge-to-edge connections, and returns a data.frame object containing the edges (defined by their pair of connecting nodes) and their edge values

Value

a data.frame() object with the columns of node\_1, node\_2 and weight columns

Examples

```
results=sample(c(1,0, -1), 7021, replace = TRUE, prob = c(0.01, 0.98,0.01))
edgelist(data=results)
```

---

|                   |                          |
|-------------------|--------------------------|
| edges_to_networks | <i>edges_to_networks</i> |
|-------------------|--------------------------|

---

**Description**

convert an edge level FC matrix into a network level FC matrix

**Usage**

```
edges_to_networks(FCmat)
```

**Arguments**

|       |                        |
|-------|------------------------|
| FCmat | an FC matrix or vector |
|-------|------------------------|

**Details**

This function first identifies the unique network pairs in the appropriate FC atlas and then averages the edges within each of the network pairs

**Value**

A network level FC matrix

**Examples**

```
edges_to_networks(runif(23871))
```

---

|               |                      |
|---------------|----------------------|
| extract.edges | <i>extract.edges</i> |
|---------------|----------------------|

---

**Description**

Generates edge-wise masks for calculating subject-level network strengths

**Usage**

```
extract.edges(NBS.obj, network = 1)
```

**Arguments**

|         |                                                                                                           |
|---------|-----------------------------------------------------------------------------------------------------------|
| NBS.obj | A list object generated from an earlier NBS() analysis                                                    |
| network | the network number (reported in the earlier NBS results) of the network to be masked. Set to 1 by default |

## Details

This function generates positive and negative masks (vectors of 1s and 0s), where 1s indicate a significant network-thresholded edge. These masks can then be used to perform a matrix multiplication with the vectorized FC matrices to object subject-level network strengths

## Value

Returns a list object containing

- `clust.tstat` thresholded edge-wise t-statistics. Edges not belonging to this cluster will be zeroed.
- `pos.edges` A vector of 1s and 0s indicating the significant network-thresholded positive edges.
- `neg.edges` A vector of -1s and 0s indicating the significant network-thresholded negative edges.
- `pos.mask` A vector of 1s and 0s indicating the significant network-thresholded positive edges.
- `neg.mask` A vector of 1s and 0s indicating the significant network-thresholded negative edges.

## Examples

```
demomat=get('demomat')
contrast=c(1,1,2,2)
random=c('sub1','sub2','sub3','sub4')
model1=NBS(model=contrast, contrast=contrast, FC_data=demomat, nperm=2, nthread=1, p=0.001)

edges=extract.edges(model1,network=1)
```

---

```
intersubject_similarity
      intersubject_similarity
```

---

## Description

This function runs an intersubject similarity analysis to determine if there is a relationship between similarity in FC and similarity in one or multiple outcomes.

## Usage

```
intersubject_similarity(FC_data, outcome, mode = "diff", nperm = 1000)
```

## Arguments

|                      |                                                                                                                       |
|----------------------|-----------------------------------------------------------------------------------------------------------------------|
| <code>FC_data</code> | An N x E matrix containing the vectorized edges; where N = number of subjects, E=number of edges                      |
| <code>outcome</code> | A numerical vector (single outcome) or matrix (multiple outcomes) containing the values of the outcome(s) of interest |

|       |                                                                                                                                                                                                                                                                                         |
|-------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| mode  | When set to "diff", FC similarity is calculated as absolute difference between the FC vectors of a pair of subjects. When set to "corr", FC similarity is calculated as 1 - (pearson's correlation coefficient between the FC vectors of a pair of subjects). Set to "diff" by default. |
| nperm | number of permutations for the correlation test between FC similarity and outcome similarity                                                                                                                                                                                            |

### Details

This function runs an intersubject similarity analysis to determine if there is a relationship between similarity in FC and similarity in one or multiple outcomes. The outcome(s) will be z-standardized prior to calculating the intersubject similarity in the outcome(s).

### Value

A list object containing

- FC\_difference\_matrix The FC difference matrix
- Outcome\_difference\_matrix The outcome difference matrix
- permutation\_data The permuted correlation values

### Examples

```
demomat=get('demomat')
results=intersubject_similarity(FC_data = demomat, outcome=c(1,1,2,2),mode="diff")
```

---

|     |     |
|-----|-----|
| NBS | NBS |
|-----|-----|

---

### Description

Network-based statistics analysis

### Usage

```
NBS(model, contrast, FC_data, nperm = 100, nthread = 1, p = 0.001)
```

### Arguments

|          |                                                                                                            |
|----------|------------------------------------------------------------------------------------------------------------|
| model    | A data.frame or matrix containing all the predictors in the model                                          |
| contrast | The predictor of interest. The edge- and network-wise statistics will only be estimated for this predictor |
| FC_data  | An N x E matrix containing the vectorized edges; where N = number of subjects, E=number of edges           |
| nperm    | The number of permutations to generate the null distribution of network strengths. Set to 100 by default   |
| nthread  | The number of CPU threads to use. Set to 1 by default                                                      |
| p        | the edge-wise threshold. Set to 0.001 by default                                                           |

**Details**

This function implements the NBS analysis described in Zalesky et al. (2010) [doi:10.1016/j.neuroimage.2010.06.041](https://doi.org/10.1016/j.neuroimage.2010.06.041)

**Value**

A list object containing

- results Edge- and network-wise results in a data.frame object
- t.orig Edge-wise t-stats
- tcrit The critical t-value
- max.netstr A vector containing the null distribution of the permuted network strengths

**Examples**

```
demomat=get('demomat')[,1:7021]
contrast=c(1,1,2,2)
random=c('sub1','sub2','sub3','sub4')
model1=NBS(model=contrast,
            contrast=contrast,
            FC_data=demomat,
            nperm=2,
            nthread=2,
            p=0.001)
```

---

NBS\_lme

---

*NBS*


---

**Description**

Network-based statistics analysis

**Usage**

```
NBS_lme(
  model,
  contrast,
  random,
  FC_data,
  nperm = 100,
  nthread = 1,
  p = 0.001,
  perm_type = "row"
)
```

**Arguments**

|                        |                                                                                                                                                                                                                          |
|------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>model</code>     | A data.frame or matrix containing all the predictors in the model                                                                                                                                                        |
| <code>contrast</code>  | The predictor of interest. The edge- and network-wise statistics will only be estimated for this predictor                                                                                                               |
| <code>random</code>    | A N x 1 numeric vector or object containing the values of the random variable (optional). Its length should be equal to the number of subjects in model (it should NOT be inside the model data.frame).                  |
| <code>FC_data</code>   | An N x E matrix containing the vectorized edges; where N = number of subjects, E=number of edges                                                                                                                         |
| <code>nperm</code>     | The number of permutations to generate the null distribution of network strengths. Set to 100 by default                                                                                                                 |
| <code>nthread</code>   | The number of CPU threads to use. Set to 1 by default                                                                                                                                                                    |
| <code>p</code>         | the edge-wise threshold. Set to 0.001 by default                                                                                                                                                                         |
| <code>perm_type</code> | A string object specifying whether to permute the rows ("row"), between subjects ("between"), within subjects ("within") or between and within subjects ("within_between") for random subject effects. Default is "row". |

**Details**

This function implements the NBS analysis described in Zalesky et al. (2010) [doi:10.1016/j.neuroimage.2010.06.041](https://doi.org/10.1016/j.neuroimage.2010.06.041)

**Value**

A list object containing

- `results` Edge- and network-wise results in a data.frame object
- `t.orig` Edge-wise t-stats
- `tcrit` The critical t-value
- `max.netstr` A vector containing the null distribution of the permuted network strengths

**Examples**

```
demomat=get('demomat')[,1:4005]
contrast=c(1,1,2,2)
random=c('sub1','sub2','sub3','sub4')
model1=NBS_lme(model=contrast,
               contrast=contrast,
               random=random,
               FC_data=demomat,
               nperm=1,
               nthread=1,
               p=0.001)
```

network\_lm

*network\_lm***Description**

mass univariate linear regression at the network level

**Usage**

```
network_lm(
  model,
  contrast,
  FC_data,
  threshold.method = "fdr",
  perm = TRUE,
  nperm = 1000
)
```

**Arguments**

|                  |                                                                                                                                                           |
|------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|
| model            | A data.frame or matrix containing all the predictors in the model                                                                                         |
| contrast         | The predictor of interest. The edge- and network-wise statistics will only be estimated for this predictor                                                |
| FC_data          | An N x E matrix containing the vectorized edges; where N = number of subjects, E=number of edges                                                          |
| threshold.method | method for correcting for multiple tests. set to fdr by default                                                                                           |
| perm             | If set to TRUE, p values will be calculated using a permutation approach by shuffling subjects' labels, before correcting for FDR. Set to TRUE by default |
| nperm            | number of permutations to use if perm=TRUE.                                                                                                               |

**Details**

This function first summarizes the FC edges into their respective networks and then carry out mass univariate linear regression analyses on each of the network to network connection

**Value**

A data.frame object with coef and corrected p values

**Examples**

```
demomat=get('demomat')
contrast=c(1,1,2,2)
random=c('sub1','sub2','sub3','sub4')
model1=network_lm(model=contrast,
                  contrast=contrast,
```

```
FC_data=demomat,
nperm=1)
```

---

network\_lme

network\_lme

---

## Description

mass univariate linear mixed effects analysis at the network level

## Usage

```
network_lme(
  model,
  contrast,
  random,
  FC_data,
  threshold.method = "fdr",
  perm = TRUE,
  nperm = 1000,
  perm_type = "within_between",
  nthread = 4
)
```

## Arguments

|                  |                                                                                                                                                                                                                          |
|------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| model            | A data.frame or matrix containing all the predictors in the model                                                                                                                                                        |
| contrast         | The predictor of interest. The edge- and network-wise statistics will only be estimated for this predictor                                                                                                               |
| random           | A N x 1 numeric vector or object containing the values of the random variable (optional). Its length should be equal to the number of subjects in model (it should NOT be inside the model data.frame).                  |
| FC_data          | An N x E matrix containing the vectorized edges; where N = number of subjects, E=number of edges                                                                                                                         |
| threshold.method | method for correcting for multiple tests. set to fdr by default                                                                                                                                                          |
| perm             | If set to TRUE, p values will be calculated using a permutation approach by shuffling subjects' labels, before correcting for FDR. Set to TRUE by default                                                                |
| nperm            | number of permutations to use if perm=TRUE.                                                                                                                                                                              |
| perm_type        | A string object specifying whether to permute the rows ("row"), between subjects ("between"), within subjects ("within") or between and within subjects ("within_between") for random subject effects. Default is "row". |
| nthread          | The number of CPU threads to use. Default is 4.                                                                                                                                                                          |

**Details**

This function first summarizes the FC edges into their respective networks and then carry out mass univariate linear mixed effect analyses on each of the network to network connection

**Value**

A data.frame object with coef and corrected p values

**Examples**

```
demomat=get('demomat')[,1:7021]
contrast=c(1,1,2,2)
random=c('sub1','sub2','sub3','sub4')
model1=network_lme(model=contrast,
                    contrast=contrast,
                    random=random,
                    FC_data=demomat,
                    nperm=1,
                    nthread=2)
```

---

vizChord

*vizChord*


---

**Description**

Visualizing brain connectivity profiles with a chord diagram

**Usage**

```
vizChord(
  data,
  hot = "#F8766D",
  cold = "#00BFC4",
  width = 1200,
  height = 1200,
  filename = paste0(tempdir(), "/conn.png"),
  colorscheme,
  title,
  leg.height = 100,
  ncol = 1,
  nrow = 1,
  colorbar_title = "Connectivity Strength"
)
```

**Arguments**

|                |                                                                                                                           |
|----------------|---------------------------------------------------------------------------------------------------------------------------|
| data           | a vector of edge values with a length of 78, 4005, 7021, 23871 or 30135.                                                  |
| hot            | color for the positive connections. Set to #F8766D by default.                                                            |
| cold           | color for the negative connections. Set to #00BFC4 by default.                                                            |
| width          | width (in pixels) of each connectogram. Set to 1200 by default.                                                           |
| height         | height (in pixels) of each connectogram . Set to 1200 by default.                                                         |
| filename       | output path and file name with a *.png file extension. Set to conn.png by default in the temporary directory (tempdir()). |
| colorscheme    | an optional vector of color names or color codes to color code the networks.                                              |
| title          | a vector of strings to be used as title                                                                                   |
| leg.height     | height (in pixels) of legend, in pixels. Set to 100 by default. Not used for single row data                              |
| ncol           | number of columns in the plot. Not used for single row data                                                               |
| nrow           | number of rows in the plot. Not used for single row data                                                                  |
| colorbar_title | title for the colorbar legend                                                                                             |

**Details**

This function takes a matrix (NROW=number of edges in the connectome; NCOL=number of edges in the connectome) of edge values and visualizes the average network-to-network connectivity in a chord diagram.

**Value**

A .png image

**Examples**

```
results=runif(7021, min = -1, max = 1)
vizChord(data=results, filename=paste0(tempdir(),"/FC_chord119.png"))
```

---

vizConnectogram

---

*vizConnectogram*


---

**Description**

Visualizing brain connectivity profiles with multiple connectogram

**Usage**

```

vizConnectogram(
  data,
  hot = "#F8766D",
  cold = "#00BFC4",
  ncol = 1,
  nrow = 1,
  edgethickness = 0.8,
  filename = paste0(tempdir(), "/conn.png"),
  colorscheme,
  title,
  width = 1000,
  height = 1050,
  leg.height = 200,
  margins = c(1.2, 1.2, 1, 1.5),
  node.size,
  node.text.size = 1,
  legend.text.size = 7,
  legend.title.size = 8,
  limits,
  title.size = 11,
  title.alignment = "center",
  colorbar_title = "Edge Strength",
  edge_labels = c("Positive", "Negative"),
  row_title
)

```

**Arguments**

|                            |                                                                                                                           |
|----------------------------|---------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>          | a matrix of edge values with 4005, 7021, 23871 or 30135 columns                                                           |
| <code>hot</code>           | color for the positive connections. Set to #F8766D by default.                                                            |
| <code>cold</code>          | color for the negative connections. Set to #00BFC4 by default.                                                            |
| <code>ncol</code>          | number of columns in the plot. Not used for single row data                                                               |
| <code>nrow</code>          | number of rows in the plot. Not used for single row data                                                                  |
| <code>edgethickness</code> | a value to adjust the thickness of the edges. Set to 0.8 by default.                                                      |
| <code>filename</code>      | output path and file name with a *.png file extension. Set to conn.png by default in the temporary directory (tempdir()). |
| <code>colorscheme</code>   | an optional vector of color names or color codes to color code the networks.                                              |
| <code>title</code>         | a vector of strings to be used as title                                                                                   |
| <code>width</code>         | width (in pixels) of each connectogram. Set to 1000 by default. Not used for single row data                              |
| <code>height</code>        | height (in pixels) of each connectogram . Set to 1050 by default. Not used for single row data                            |
| <code>leg.height</code>    | height (in pixels) of legend, in pixels. Set to 100 by default. Not used for single row data                              |

|                                |                                                                                                                                                                                                                                                                                                                       |
|--------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>margins</code>           | vector of 4 values specifying the amount of empty space on the left, right, top and bottom for each connectogram. Set to <code>c(1.2, 1.2, 1, 1.5)</code> by default. You might want to adjust these values if the text labels get cut off by a neighbouring connectogram or the legend. Not used for single row data |
| <code>node.size</code>         | size parameter for the dots representing the nodes. If not specified, an appropriate size will be set.                                                                                                                                                                                                                |
| <code>node.text.size</code>    | size parameter for the text labels on the nodes. Set to 1 by default.                                                                                                                                                                                                                                                 |
| <code>legend.text.size</code>  | size parameter for the legend text. Set to 6 by default.                                                                                                                                                                                                                                                              |
| <code>legend.title.size</code> | size parameter for the legend title. Set to 8 by default.                                                                                                                                                                                                                                                             |
| <code>limits</code>            | a pair of values that governs the limits of the edge strengths displayed. If missing <code>limits=range(abs(data), na.rm=TRUE)</code>                                                                                                                                                                                 |
| <code>title.size</code>        | size parameter for the title. Set to 11 by default.                                                                                                                                                                                                                                                                   |
| <code>title.alignment</code>   | string object specifying title's alignment relatively to its plot options are 'left', 'center' (default), 'right'.                                                                                                                                                                                                    |
| <code>colorbar_title</code>    | title for the colorbar legend                                                                                                                                                                                                                                                                                         |
| <code>edge_labels</code>       | Vector of two strings defining the labels for the edge legends. Default is <code>c("Positive", "Negative")</code> .                                                                                                                                                                                                   |
| <code>row_title</code>         | a vector of strings to be used as left vertical titles for each row of plots when there are many                                                                                                                                                                                                                      |

## Details

This function takes a matrix (NROW=number of edges in the connectome; NCOL=number of edges in the connectome) of edge values and visualizes the edge-to-edge connectivity with multiple connectograms

## Value

A .png image

## Examples

```
data=matrix(sample(c(1,0, -1), 23871*1, replace = TRUE, prob = c(0.001, 0.998,0.001)),nrow=1)
vizConnectogram(data=data)
```

---

vizGlassbrain

*vizGlassbrain*

---

## Description

Visualizing brain connectivity with a glass brain plot

**Usage**

```

vizGlassbrain(
  data,
  surf_color = "grey",
  node_color = "#00BA38",
  surf_alpha = 0.2,
  cmap,
  node_size = 8,
  node_label = TRUE,
  node_label_size = 10,
  node_label_color = "black",
  edgethickness = 8,
  limits,
  colorbar_title = "Connectivity strength",
  orientation_labels = TRUE,
  remove_brain = FALSE
)

```

**Arguments**

|                                 |                                                                                                                                                                                                                                                                                                             |
|---------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>               | a vector of edge values with a length of 4005, 7021, 23871 or 30135                                                                                                                                                                                                                                         |
| <code>surf_color</code>         | color of the cortical surface. Set to 'grey' by default                                                                                                                                                                                                                                                     |
| <code>node_color</code>         | color of the nodes. Set to '#00BA38' by default                                                                                                                                                                                                                                                             |
| <code>surf_alpha</code>         | alpha value of the cortical surface, where 0 will cause the cortical surface to disappear and 1 will cause the cortical surface to be completely opaque. Set to 0.2 by default                                                                                                                              |
| <code>cmap</code>               | A string vector containing 2 to 3 color names/codes specifying the colors to be used for the color scale. See <code>RColorBrewer::display.brewer.all()</code> for all possible cmap options. If none are specified, appropriate colors will be automatically selected according to <code>range(data)</code> |
| <code>node_size</code>          | size parameter for the dots representing the nodes. Set to 8 by default.                                                                                                                                                                                                                                    |
| <code>node_label</code>         | option to show node labels. Set to TRUE by default.                                                                                                                                                                                                                                                         |
| <code>node_label_size</code>    | font size of the node labels. Set to 10 by default.                                                                                                                                                                                                                                                         |
| <code>node_label_color</code>   | font color of the node labels. Set to black by default.                                                                                                                                                                                                                                                     |
| <code>edgethickness</code>      | a value to adjust the thickness of the edges. Set to 8 by default.                                                                                                                                                                                                                                          |
| <code>limits</code>             | Numeric vector of length 2, composed of the lower and upper color scale limits of the plot. When left unspecified, the symmetrical limits <code>c(-max(abs(data)), max(abs(data)))</code> will be used.                                                                                                     |
| <code>colorbar_title</code>     | title for the colorbar legend. Set to 'Connectivity strength' by default                                                                                                                                                                                                                                    |
| <code>orientation_labels</code> | A boolean object specifying if orientation labels are to be displayed. Set to TRUE by default                                                                                                                                                                                                               |
| <code>remove_brain</code>       | A boolean object specifying cortical surface should be removed. Set to FALSE by default                                                                                                                                                                                                                     |

**Details**

This function takes a vector of edge values and visualizes the edge-to-edge connectivity with a glass brain plot

**Value**

A plot\_ly object

**Examples**

```
mask=sample(c(1,0), 7021, replace = TRUE, prob = c(0.001, 0.999))
data=runif(7021,min = -1,max=1)*mask
vizGlassbrain(data,orientation_labels = TRUE)
```

---

vizHeatmap

*vizHeatmap*


---

**Description**

Visualizing brain connectivity matrices with heatmaps

**Usage**

```
vizHeatmap(
  data,
  hot = "#F8766D",
  cold = "#00BFC4",
  mid = "white",
  ncol,
  nrow,
  filename = paste0(tempdir(), "/heatmap.png"),
  colorscheme,
  line.color = "black",
  title,
  limits,
  title.size = 12,
  legend.title.size = 8,
  legend.text.size = 7,
  line.width = 0.3,
  width = 1000,
  height = 1000,
  leg.size = 200,
  colorbar_title = "Edge Strengt"
)
```

**Arguments**

|                                |                                                                                                                                                                                                                     |
|--------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>              | a matrix of edge values with 4005, 7021, 23871 or 30135 columns                                                                                                                                                     |
| <code>hot</code>               | color for the positive connections. Set to #F8766D by default.                                                                                                                                                      |
| <code>cold</code>              | color for the negative connections. Set to #00BFC4 by default.                                                                                                                                                      |
| <code>mid</code>               | color for the mid point of the color scale. Set to white by default.                                                                                                                                                |
| <code>ncol</code>              | number of columns in the plot. Not used for single row data                                                                                                                                                         |
| <code>nrow</code>              | number of rows in the plot. Not used for single row data                                                                                                                                                            |
| <code>filename</code>          | output filename with a *.png file extension. Set to heatmap.png by default in the temporary directory (tempdir()).                                                                                                  |
| <code>colorscheme</code>       | an optional vector of color names or color codes to color code the networks.                                                                                                                                        |
| <code>line.color</code>        | color parameter for grid lines dividing the connectome in to networks. Set to "black" by default.                                                                                                                   |
| <code>title</code>             | a vector of strings to be used as title                                                                                                                                                                             |
| <code>limits</code>            | Numeric vector of length 2, composed of the lower and upper scale limits of the plot. When left unspecified, the symmetrical limits $c(-\max(\text{abs}(\text{data}), \max(\text{abs}(\text{data})))$ will be used. |
| <code>title.size</code>        | size parameter for the title. Set to 12 by default.                                                                                                                                                                 |
| <code>legend.title.size</code> | size parameter for the legend title. Set to 8 by default.                                                                                                                                                           |
| <code>legend.text.size</code>  | size parameter for the legend text. Set to 8 by default.                                                                                                                                                            |
| <code>line.width</code>        | line thickness parameter for grid lines dividing the connectome in to networks. Set to 0.3 by default.                                                                                                              |
| <code>width</code>             | width (in pixels) of each heatmap. Set to 1000 by default. Not used for single row data                                                                                                                             |
| <code>height</code>            | height (in pixels) of each heatmap . Set to 1000 by default. Not used for single row data                                                                                                                           |
| <code>leg.size</code>          | height/width (in pixels) of legend, in pixels. Set to 200 by default.                                                                                                                                               |
| <code>colorbar_title</code>    | title for the colorbar legend                                                                                                                                                                                       |

**Details**

This function takes a matrix (NROW=number of edges in the connectome; NCOL=number of edges in the connectome) of edge values and visualizes the edge-to-edge connectivity with multiple connectograms

**Value**

A .png image

**Examples**

```
data=data=runif(7021,min = -1,max=1)
vizHeatmap(data=data)
```

---

|                    |                           |
|--------------------|---------------------------|
| vizNetConnectogram | <i>vizNetConnectogram</i> |
|--------------------|---------------------------|

---

## Description

Generate a Network Connectogram from a Vector of FC network or edge data

## Usage

```
vizNetConnectogram(
  FC_dat,
  show.sig = TRUE,
  title = NULL,
  title.size = 10,
  hot = "#F8766D",
  cold = "#00BFC4",
  node.text.size = 2,
  node.size = 2,
  node.color = "black",
  edge.thickness = 1.5,
  sig.color = "darkgrey",
  legend = TRUE,
  legend.title = "Standardized Coefficient",
  legend.title.size = 6,
  legend.text.size = 5,
  expand = 1.1,
  limits,
  filename,
  width = 1000,
  height = 700
)
```

## Arguments

|                |                                                                                            |
|----------------|--------------------------------------------------------------------------------------------|
| FC_dat         | a matrix of edge values with 4005, 7021, 23871 or 30135 columns                            |
| show.sig       | Logical. If TRUE, significant edges will be outlined with sig.color. Default is FALSE.     |
| title          | Character string for the plot title. Default is NULL (no title).                           |
| title.size     | Numeric. Font size of the plot title. Default is 10.                                       |
| hot            | Character. Color used for positive edges and node highlights. Default is "#F8766D" (red).  |
| cold           | Character. Color used for negative edges and node highlights. Default is "#00BFC4" (teal). |
| node.text.size | Numeric. Size of the node label text. Default is 2.                                        |
| node.size      | Numeric. Size of the node points. Default is 2.                                            |

|                                |                                                                                                                                                                                                          |
|--------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>node.color</code>        | Character. Fill color of the node points. Default is "black".                                                                                                                                            |
| <code>edge.thickness</code>    | Numeric. Width of the edges (and node border stroke). Default is 2.                                                                                                                                      |
| <code>sig.color</code>         | Character. Color for the significant edges. Default is "darkgrey"                                                                                                                                        |
| <code>legend</code>            | Logical. If TRUE, a continuous color bar legend is added to the plot. Default is TRUE.                                                                                                                   |
| <code>legend.title</code>      | Character string for the legend title. Default is "Standardized Coefficient".                                                                                                                            |
| <code>legend.title.size</code> | Numeric. Font size of the legend title. Default is 8.                                                                                                                                                    |
| <code>legend.text.size</code>  | Numeric. Font size of the legend tick labels. Default is 5.                                                                                                                                              |
| <code>expand</code>            | Numeric. Multiplicative expansion factor applied to the x and y axis limits to prevent node labels from being clipped. Default is 1.1.                                                                   |
| <code>limits</code>            | Numeric vector of length 2. Color scale limits for the edge alpha and node alpha mappings. If not supplied, limits are set automatically to $c(0, \max(\text{abs}(\text{weight})))$ inside the function. |
| <code>filename</code>          | Character. Path/filename for the output PNG. If the argument is omitted entirely, no file is written.                                                                                                    |
| <code>width</code>             | Integer. Width of the saved PNG in pixels. Default is 1000.                                                                                                                                              |
| <code>height</code>            | Integer. Height of the saved PNG in pixels. Default is 1000.                                                                                                                                             |

## Details

Creates a circular network connectogram (chord diagram) from a data frame of connectivity results, visualizing edge weights and their signs using color and transparency. Node self-connections (diagonal elements) are highlighted on the node border. Optionally saves the plot to a PNG file.

Row names of `results` must follow the pattern "nodeA to nodeB". Self-connections (from == to) are extracted to colour and shade node borders: if all diagonal values are  $> 1$  the border is drawn in hot; if all are  $< 1$  it is drawn in cold. The diagonal entries are removed before the `igraph` graph object is constructed.

Edge colour encodes sign (hot = positive, cold = negative) and edge transparency encodes absolute magnitude.

The function relies on `igraph`, `ggraph`, and `ggplot2`.

## Value

A `ggraph/ggplot2` plot object (invisibly returned via `print` and `return`). As a side effect the plot is printed to the active graphics device, and — if `filename` is provided — written to a 300 dpi PNG file.

## Examples

```
demomat=get('demomat')
vizNetConnectogram(colMeans(demomat))
```

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