

Package ‘GeneNetworkBuilder’

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Title Build Regulatory Network from ChIP-chip/ChIP-seq and Expression Data

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Suggests RUnit, BiocGenerics, RBGL, knitr, simpIntLists, shiny, STRINGdb

LinkingTo Rcpp

Description Appliation for discovering direct or indirect targets of transcription factors using ChIP-chip or ChIP-seq, and microarray or RNA-seq gene expression data. Inputting a list of genes of potential targets of one TF from ChIP-chip or ChIP-seq, and the gene expression results, GeneNetworkBuilder generates a regulatory network of the TF.

License GPL (>= 2)

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biocViews Sequencing, Microarray, GraphAndNetwork

VignetteBuilder knitr

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NeedsCompilation yes

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GeneNetworkBuilder-package

Build Regulatory Network from ChIP-chip/ChIP-seq and Expression Data

Description

Application for discovering direct or indirect targets of transcription factors using ChIP-chip or ChIP-seq, and microarray or RNA-seq gene expression data. Inputting a list of genes of potential targets of one TF from ChIP-chip or ChIP-seq, and the gene expression results, GeneNetworkBuilder generates a regulatory network of the TF.

browseNetwork	<i>browse network</i>
---------------	-----------------------

Description

plot network generated by [polishNetwork](#)

Usage

```
browseNetwork(gR = graphNEL(), layoutType = c("fdp", "dot", "neato",
"twopi", "circo"), width = NULL, height = NULL, maxNodes = 500, ...)
```

Arguments

gR	an object of graphNEL
layoutType	layout type. see GraphvizLayouts
width	width of the figure
height	height of the figure
maxNodes	max nodes number to plot. Because if there are too many nodes, the running time will be too long.
...	parameters used by GraphvizLayouts

Value

An object of class `htmlwidget` that will intelligently print itself into HTML in a variety of contexts including the R console, within R Markdown documents, and within Shiny output bindings.

Examples

```
data("ce.miRNA.map")
data("example.data")
data("ce.interactionmap")
data("ce.IDsMap")
sifNetwork<-buildNetwork(example.data$ce.bind, ce.interactionmap, level=2)
cifNetwork<-filterNetwork(rootgene=ce.IDsMap["DAF-16"], sifNetwork=sifNetwork,
                           exprsData=uniqueExprsData(example.data$ce.exprData, "Max", condenseName='logFC'),
                           mergeBy="symbols",
                           miRNAlist=as.character(ce.miRNA.map[, 1]), tolerance=1)
gR<-polishNetwork(cifNetwork)
browseNetwork(gR)
```

browseNetwork-shiny *Shiny bindings for browseNetwork*

Description

Output and render functions for using `browseNetwork` within Shiny applications and interactive Rmd documents.

Usage

```
browseNetworkOutput(outputId, width = "100%", height = "400px")
renderBrowseNetwork(expr, env = parent.frame(), quoted = FALSE)
```

Arguments

<code>outputId</code>	output variable to read from
<code>width, height</code>	Must be a valid CSS unit (like '100%', '400px', 'auto') or a number, which will be coerced to a string and have 'px' appended.
<code>expr</code>	An expression that generates a <code>browseNetwork</code>
<code>env</code>	The environment in which to evaluate <code>expr</code> .
<code>quoted</code>	Is <code>expr</code> a quoted expression (with <code>quote()</code>)? This is useful if you want to save an expression in a variable.

buildNetwork	<i>construct the regulatory network</i>
--------------	---

Description

Get all the connections of interesting genes from regulatory map.

Usage

```
buildNetwork(TFbindingTable, interactionmap, level = 3)
```

Arguments

TFbindingTable a matrix or data.frame with interesting genes. Column names must be 'from', 'to'

interactionmap Transcription regulatory map. Column names of interactionmap must be 'from','to'

level Depth of node path

Value

a dataframe or matrix of all the connections of interesting genes

Examples

```
data("ce.interactionmap")
data("example.data")
xx<-buildNetwork(example.data$ce.bind, ce.interactionmap, level=2)
```

ce.IDsMap	<i>C.elegns gene name to wormbase identifier map</i>
-----------	--

Description

map file for converting gene name or sequence name of *Caenorhabditis elegans* to wormbase identifier

Usage

```
ce.IDsMap
```

Format

character vector

Details

character vector with gene name or sequence name as names and wormbase identifier as values.

Source

<http://www.wormbase.org/>

Examples

```
data(ce.IDsMap)
head(ce.IDsMap)
```

ce.interactionmap	<i>transcript regulatory map of Caenorhabditis elegans</i>
-------------------	--

Description

transcript regulatory map of *Caenorhabditis elegans*

Usage

```
ce.interactionmap
```

Format

```
datafram
```

Details

transcript regulatory map of *Caenorhabditis elegans* is generated using databases edgedb and microCosm Targets.

Source

<http://edgedb.umassmed.edu>, <http://www.ebi.ac.uk/enright-srv/microcosm/htdocs/targets/v5/>

Examples

```
data(ce.interactionmap)
head(ce.interactionmap)
```

ce.mapIDs	<i>map file for converting from wormbase identifier to Caenorhabditis elegans gene name</i>
-----------	---

Description

map file for converting from wormbase identifier to *Caenorhabditis elegans* gene name

Usage

```
ce.mapIDs
```

Format

```
character vector
```

Details

character vector with wormbase identifier as names and gene name as values.

Source

<http://www.wormbase.org/>

Examples

```
data(ce.mapIDs)
head(ce.mapIDs)
```

ce.miRNA.map	<i>micro RNA of Caenorhabditis elegans</i>
--------------	--

Description

micro RNA of *Caenorhabditis elegans*

Usage

```
ce.miRNA.map
```

Format

```
dataframe
```

Details

The first column is wormbase identifier. And the second column is miRNA names.

Source

<http://www.mirbase.org/>

Examples

```
data(ce.miRNA.map)
head(ce.miRNA.map)
```

convertID	<i>convert gene IDs by id map</i>
-----------	-----------------------------------

Description

For same gene, there are multiple gene alias. In order to eliminate the possibility of missing any connections, convert the gene symbols to unique gene ids is important. This function can convert the gene symbols to unique ids and convert it back according a giving map.

Usage

```
convertID(x, IDsMap, ByName = c("from", "to"))
```

Arguments

x	a matrix or dataframe contain the columns to be converted.
IDsMap	a character vector of the identifier map
ByName	the column names to be converted

Value

a matrix or dataframe with converted gene IDs

Examples

```
data("ce.IDsMap")
bind<-cbind(from="daf-16", to=c("fkh-7", "hlh-13", "mxl-3", "nhr-3", "lfi-1"))
convertID(toupper(bind), ce.IDsMap, ByName=c("from", "to"))
```

example.data	<i>example datasets for documentation</i>
--------------	---

Description

example.data is a data list of example datasets. There is a dataset example.microarrayData, which is the example of gene expression data of a gene-chip result of *C.elegans*. Dataset example.data\$ce.bind is a TF binding matrix of ChIP-chip experiment of *C.elegans*. Dataset example.data\$cd.exprData is expression data of a gene-chip result of *C.elegans*. Dataset example.data\$hs.bind is a TF binding matrix of ChIP-chip experiment of *H.sapiens*. Dataset example.data\$hs.exprData is expression data of a combination of a gene-chip result and a RNA-SEQ result of *H.sapiens*.

Usage

```
example.data
```

Format

dataframe

Details

The dataset `example.microarrayData` contains columns: ID, logFC, AveExpr, t, P.Value, adj.P.Val, B, genes and symbols. The columns of ID, logFC and symbols are required by GeneNetwork-Builder. The dataset `example.data$hs.bind` contains columns: ID, symbols, logFC and P.Value. The dataset `example.data$hs.exprData` contains columns: from and to.

Examples

```
data(example.data)
names(example.data)
head(example.data$example.microarrayData)
head(example.data$ce.bind)
head(example.data$ce.exprData)
head(example.data$hs.bind)
head(example.data$hs.exprData)
```

exportNetwork	<i>Save network in various formats</i>
---------------	--

Description

Save graph into HTML, json or xgmml format.

Usage

```
exportNetwork(network, file, format = c("HTML", "json", "XGMML"), ...)
```

Arguments

network	output of browseNetwork
file	Name of the file to save to.
format	type in which graph shall be saved. Could be one of HTML, json or XGMML.
...	Parameter could be used by saveWidget for HTML or <code>writeLines</code> for json or saveXML for XGMML.

Examples

```
data("ce.miRNA.map")
data("example.data")
data("ce.interactionmap")
data("ce.IDsMap")
sifNetwork<-buildNetwork(example.data$ce.bind, ce.interactionmap, level=2)
cifNetwork<-filterNetwork(rootgene=ce.IDsMap["DAF-16"], sifNetwork=sifNetwork,
  exprsData=uniqueExprsData(example.data$ce.exprData, "Max", condenseName='logFC'),
  mergeBy="symbols",
  miRNAlist=as.character(ce.miRNA.map[ , 1]), tolerance=1)
gR<-polishNetwork(cifNetwork)
network <- browseNetwork(gR)
exportNetwork(network, "sample.html")
```

filterNetwork	<i>filter the regulatory network table by expression profile</i>
---------------	--

Description

verify every nodes in the regulatory network by expression profile

Usage

```
filterNetwork(rootgene, sifNetwork, exprsData, mergeBy = "symbols", miRNAlist,
  remove_miRNA = FALSE, tolerance = 0, cutoffPVal = 0.01,
  cutoffLFC = 0.5, minify = TRUE, miRNAtol = FALSE)
```

Arguments

rootgene	name of root gene. It must be the ID used in xx regulatory network
sifNetwork	Transcription regulatory network table. Column names of xx must be 'from','to'
exprsData	dataset of expression comparison data, which should contain column logFC and column given by exprsDataByName
mergeBy	The column name contains ID information used to merge with 'to' column of sifNetwork in exprsData
miRNAlist	vector of microRNA ids.
remove_miRNA	remove miRNA from the network or not. Bool value, TRUE or FALSE
tolerance	maximum number of unverified nodes in each path
cutoffPVal	cutoff p value of valid differential expressed gene/miRNA
cutoffLFC	cutoff log fold change value of a valid differential expressed gene/miRNA
minify	Only keep the best path if multiple paths exists for single node? Bool value, TRUE or FALSE
miRNAtol	take miRNA expression into account for tolerance calculation. Bool value, TRUE or FALSE

Value

a dataframe of filtered regulatory network by expression profile

Examples

```
data("ce.miRNA.map")
data("example.data")
data("ce.interactionmap")
data("ce.IDsMap")
sifNetwork<-buildNetwork(example.data$ce.bind, ce.interactionmap, level=2)
cifNetwork<-filterNetwork(rootgene=ce.IDsMap["DAF-16"], sifNetwork=sifNetwork,
  exprsData=uniqueExprsData(example.data$ce.exprData, "Max", condenseName='logFC'),
  mergeBy="symbols",
  miRNAlist=as.character(ce.miRNA.map[, 1]), tolerance=1)
```

hs.IDsMap	<i>map file for converting gene name or sequence name of Homo sapiens to Entrez identifier</i>
-----------	--

Description

map file for converting gene name or sequence name of *Homo sapiens* to Entrez identifier

Usage

hs.IDsMap

Format

character vector

Details

character vector with gene name as names and Entrez identifier as values.

Examples

```
data(hs.IDsMap)
head(hs.IDsMap)
```

hs.interactionmap	<i>transcript regulation map of Homo sapiens</i>
-------------------	--

Description

transcript regulation map of *Homo sapiens*

Usage

hs.interactionmap

Format

datafram

Details

transcript regulatory map of *Homo sapiens* is generated using databases FANTOM, mirGen and microCosm Targets.

Source

<http://fantom.gsc.riken.jp/5/>, <http://www.ebi.ac.uk/enright-srv/microcosm/htdocs/targets/v5/>, http://carolina.imis.athena-innovation.gr/diana_tools/web/index.php

Examples

```
data(hs.interactionmap)
head(hs.interactionmap)
```

hs.mapIDs	<i>map file for converting from Entrez identifier to Homo sapiens gene name</i>
-----------	---

Description

map file for converting from Entrez identifier to *Homo sapiens* gene name

Usage

```
hs.mapIDs
```

Format

character vector

Details

character vector with Entrez identifier as names and gene name as values.

Examples

```
data(hs.mapIDs)
head(hs.mapIDs)
```

hs.miRNA.map	<i>micro RNA of Homo sapiens</i>
--------------	----------------------------------

Description

micro RNA of *Homo sapiens*

Usage

```
hs.miRNA.map
```

Format

dataframe

Details

The first column is entrez identifier. And the second column is miRNA names.

Source

<http://www.mirbase.org/>

Examples

```
data(hs.miRNA.map)
head(hs.miRNA.map)
```

polishNetwork	<i>generate an object of graphNEL to represent the regulation network</i>
---------------	---

Description

generate an object of graphNEL to represent the regulation network. Each node will have three attributes: size, borderColor and fill.

Usage

```
polishNetwork(cifNetwork, nodesDefaultSize = 48, useLogFCAsWeight = FALSE,
  nodecolor = colorRampPalette(c("green", "yellow", "red"))(5),
  nodeBg = "white", nodeBorderColor = list(gene = "darkgreen", miRNA =
  "darkblue"), edgelwd = 0.25, ...)
```

Arguments

cifNetwork	dataframe used to draw network graph. column names of cifNetwork must contain 'from', 'to', 'logFC' and 'miRNA'
nodesDefaultSize	nodes default size
useLogFCAsWeight	how to determine the weights for each nodes. If TRUE, use logFC value as weight. If FALSE, use constant 1 as weight.
nodecolor	a character vector of color set. The node color will be mapped to color set by log fold change
nodeBg	background of node
nodeBorderColor	a list of border node color set. nodeBorderColor's element must be gene and miRNA
edgelwd	the width of edge
...	any parameters can be passed to graph.par

Value

An object of graphNEL class of the network

Examples

```

data("ce.miRNA.map")
data("example.data")
data("ce.interactionmap")
data("ce.IDsMap")
sifNetwork<-buildNetwork(example.data$ce.bind, ce.interactionmap, level=2)
cifNetwork<-filterNetwork(rootgene=ce.IDsMap["DAF-16"], sifNetwork=sifNetwork,
                          exprsData=uniqueExprsData(example.data$ce.exprData, "Max", condenseName='logFC'),
                          mergeBy="symbols",
                          miRNAlist=as.character(ce.miRNA.map[, 1]), tolerance=1)
gR<-polishNetwork(cifNetwork)
## browseNetwork(gR)

```

saveXGMML

*Save network as xgmml***Description**

Save graph into xgmml format.

Usage

```
saveXGMML(network, file, ...)
```

Arguments

network	output of browseNetwork
file	Name of the file to save to.
...	Parameter could be used by saveXML

uniqueExprsData

*unique the microarray data***Description**

get unique the microarray data for each gene id.

Usage

```
uniqueExprsData(exprsData, method = "Max", condenseName = "logFC")
```

Arguments

exprsData	dataset of expression comparison data
method	method must be Max, Median or Min
condenseName	column names to be condensed

Value

a dataframe of expression data without duplicates

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