Package ‘GeneNetworkBuilder’

May 29, 2024

Type Package
Version 1.46.0
Title GeneNetworkBuilder: a bioconductor package for building regulatory network using ChIP-chip/ChIP-seq data and Gene Expression Data
Author Jianhong Ou, Haibo Liu, Heidi A Tissenbaum and Lihua Julie Zhu
Maintainer Jianhong Ou <jianhong.ou@duke.edu>
Imports plyr, graph, htmlwidgets, Rgraphviz, rjson, XML, methods, grDevices, stats, graphics
Depends R (>= 2.15.1), Rcpp (>= 0.9.13)
Suggests RUnit, BiocGenerics, RBGL, knitr, simpIntLists, shiny, STRINGdb, BiocStyle, magick, rmarkdown, org.Hs.eg.db
LinkingTo Rcpp
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.
License GPL (>= 2)
Lazyload yes
LazyData true
biocViews Sequencing, Microarray, GraphAndNetwork
VignetteBuilder knitr
RoxygenNote 7.2.1
Encoding UTF-8
git_url https://git.bioconductor.org/packages/GeneNetworkBuilder
git_branch RELEASE_3_19
git_last_commit 13bd7a1
git_last_commit_date 2024-04-30
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.

Author(s)

Maintainer: Jianhong Ou Developer <jianhong.ou@duke.edu>

Authors:

- Lihua Julie Zhu Developer <Julie.Zhu@umassmed.edu>
browseNetwork

---

**Description**

plot network generated by `polishNetwork`

**Usage**

```r
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**

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

buildNetwork  construct the regulatory network

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
ce.IDsMap

Examples

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

ce.IDsMap  C.elegns gene name to wormbase identifier map

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  transcript regulatory map of Caenorhabditis elegans

Description

transcript regulatory map of Caenorhabditis elegans

Usage

ce.interactionmap
### ce.mapIDs

**Format**

dataframe

**Details**

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

**Source**


**Examples**

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

---

| ce.mapIDs | map file for converting from wormbase identifier to Caenorhabditis elegans gene name |

**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**

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

micro RNA of *Caenorhabditis elegans*

**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**


**Examples**

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

---

convertID

convert gene IDs by id map

**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", "mxe-3", "nhr-3", "lfi-1"))
convertID(toupper(bind), ce.IDsMap, ByName=c("from", "to"))


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$ce.bind is a TF binding matrix of ChIP-chip experiment of *C. elegans*. Dataset example.data$ce.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$ce.bind contains columns: ID, symbols, logFC and P.Value. The dataset example.data$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

Save network in various formats

Description

Save graph into HTML, json or xgmml format.

Usage

```r
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 `writeLines` for json or `saveXML` for XGMML.

Examples

```r
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

filter the regulatory network table by expression profile

Description

verify every nodes in the regulatory network by expression profile
Usage

```r
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

```r
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'),
)
hs.IDsMap

```r
mergeBy="symbols",
miRNAlist=as.character(ce.miRNA.map[,1]), tolerance=1)
```

---

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

---

**Description**

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

**Usage**

```r
hs.IDsMap
```

**Format**

character vector

**Details**

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

**Examples**

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

---

**hs.interactionmap**  
transcript regulation map of *Homo sapiens*

---

**Description**

transcript regulation map of *Homo sapiens*

**Usage**

```r
hs.interactionmap
```

**Format**

dataframe

**Details**

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


Examples

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

hs.mapIDs

| hs.mapIDs | map file for converting from Entrez identifier to Homo sapiens gene name |

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

micro RNA of Homo sapiens

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)

networkFromGenes

Build network by a list of given genes

Description
By providing a list of given genes, build a network for input of filterNetwork.

Usage
networkFromGenes(genes, interactionmap, level = 3, unrooted = FALSE)

Arguments
genes A vector of character for interested genes.
interactionmap Transcription regulatory map. Column names of interactionmap must be 'from','to'
level Depth of node path
unrooted Return unrooted regulatory network table or not.
Value

a list with elements: rootgene: The nodes with maximal connections. sifNetwork: Transcription regulatory network table.

Examples

data("ce.interactionmap")
data("example.data")
genes <- as.character(example.data$ce.bind$from)
xx<-networkFromGenes(example.data$ce.bind, ce.interactionmap, level=2)

polishNetwork

generate an object of grahpNEL to represent the regulation network

Description

generate an object of grahpNEL 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 node. 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. Or the column names for the colors.
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
subsetNetwork

**Subset a polished network**

**Description**
Subset the output of polishNetwork by a list of nodes name

**Usage**
subsetNetwork(graph, genes)

**Arguments**
- **graph** A graphNEL object. The output of polishNetwork.
- **genes** A list of nodes names

**Value**
An object of graph.

**Examples**
```
library(graph)
set.seed(123)
g1 <- randomEGraph(LETTERS[seq.int(15)], edges=100)
g1 <- subsetNetwork(g1, LETTERS[seq.int(5)])
plot(g1)
```

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
**uniqueExprsData**

**Value**

a dataframe of expression data without duplicates

**Examples**

```r
data("example.data")
example.microarrayData<-uniqueExprsData(example.data$example.microarrayData,
                                          method="Max", condenseName='logFC')
```
# Index

* **IO**
  - exportNetwork, 9
  - saveXGMML, 15

* **convert**
  - convertID, 7

* **data**
  - ce.IDsMap, 5
  - ce.interactionmap, 5
  - ce.mapIDs, 6
  - ce.miRNA.map, 7
  - example.data, 8
  - hs.IDsMap, 11
  - hs.interactionmap, 11
  - hs.mapIDs, 12
  - hs.miRNA.map, 13

* **network**
  - buildNetwork, 4
  - filterNetwork, 9
  - networkFromGenes, 13
  - polishNetwork, 3, 14
  - uniqueExprsData, 16

* **plot**
  - browseNetwork, 3
  - browseNetwork, 3, 9, 15
  - browseNetwork-shiny, 4
  - browseNetworkOutput
    (browseNetwork-shiny), 4
  - buildNetwork, 4
  - ce.IDsMap, 5
  - ce.interactionmap, 5
  - ce.mapIDs, 6
  - ce.miRNA.map, 7
  - convertID, 7
  - example.data, 8
  - exportNetwork, 9
  - filterNetwork, 9

GeneNetworkBuilder
  (GeneNetworkBuilder-package), 2
GeneNetworkBuilder-package, 2
graph.par, 15
graphNEL, 3
GraphvizLayouts, 3
hs.IDsMap, 11
hs.interactionmap, 11
hs.mapIDs, 12
hs.miRNA.map, 13
networkFromGenes, 13
polishNetwork, 3, 14
renderBrowseNetwork
  (browseNetwork-shiny), 4
saveWidget, 9
saveXGMML, 15
saveXML, 9
subsetNetwork, 16
uniqueExprsData, 16