

Package ‘HiCociety’

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Type Package

Title Inferring Chromatin Interaction Modules from 3C-Based Data

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Description Identifies chromatin interaction modules by constructing a Hi-C contact network based on statistically significant interactions, followed by network clustering. The method enables comparison of module connectivity across two Hi-C datasets and is capable of detecting cell-type-specific regulatory modules. By integrating network analysis with chromatin conformation data, this approach provides insights into the spatial organization of the genome and its functional implications in gene regulation. Author: Sora Yoon (2025) <<https://github.com/ysora/HiCociety>>.

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add_Genes	<i>Add gene information</i>
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Description

This function adds a column with a list of genes included in each locus to the ModuleSummary data frame of the hic2community function.

Usage

```
add_Genes(df, speciesObj)
```

Arguments

- df The ModuleSummary data frame obtained by running hic2community function
- speciesObj Any Txdb package name corresponding

Details

Adding gene list to ModuleSummary data frame obtained from hic2community function.

Value

A data.frame identical to the input, with an additional "Genes" column. Each entry in this column lists the gene(s) that overlap with the corresponding genomic region. If multiple genes are present, they are concatenated with commas.

Author(s)

Sora Yoon, PhD

Examples

```
modulefile = system.file('extdata', 'mouse_naiveCD4T_Vahedi_short.rds',  
  package = 'HiCocietyExample')  
mycom = readRDS(modulefile)  
mycom$ModuleSummary = add_Genes(mycom$ModuleSummary,  
  'TxDb.Mmusculus.UCSC.mm10.knownGene')
```

calculate_avg_count	<i>Calculate Average Count within 5-pixel Padding</i>
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Description

This function calculates the average count within a 25kb padding around each (x, y) coordinate pair.

Usage

```
calculate_avg_count(x, y, counts, resol)
```

Arguments

x	Numeric vector of x-coordinates of contact frequency data frame.
y	Numeric vector of y-coordinates of contact frequency data frame.
counts	Numeric vector of contact frequency counts.
resol	Integer specifying the HiC resolution.

Value

A numeric vector of average counts.

Examples

```
x <- c(1, 2, 3, 4, 5)  
y <- c(1, 2, 3, 4, 5)  
counts <- c(10, 20, 30, 40, 50)  
resol <- 10000  
calculate_avg_count(x, y, counts, resol)
```

check_package	<i>Check if a package is installed</i>
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Description

This function checks whether a package is installed. If the package is not installed, it informs the user that the package is missing.

Usage

```
check_package(package)
```

Arguments

package	The name of the package to check.
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Details

This function checks whether a package is installed. If the package is not installed, it informs the user that the package is missing.

Value

A logical value: TRUE if the package is installed, FALSE otherwise.

Author(s)

Sora Yoon, PhD

Examples

```
check_package('dplyr')
```

ConnectivityDiff	<i>Connectivity difference between two conditions</i>
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Description

output table of connectivity difference of modules between cell types is generated.

Usage

```
ConnectivityDiff(wt, ko, prefix.wt, prefix.ko, resolution = 5000)
```

Arguments

wt	hic2community result from condition 1
ko	hic2community result from condition 2
prefix.wt	Prefix for wt to be presented in the column names
prefix.ko	Prefix for ko to be presented in the column names
resolution	Resolution of Hi-C dataset

Details

Connectivity difference between two conditions

Value

A list of two data.frame objects, each representing the network connectivity differences of modules in condition 1 or condition 2 when compared to the counterpart cell type. Each data.frame contains the following columns: "chr", "module_start", "module_end", "connectivity", "transitivity", "centrality_node", "idx" (the row index of the module in the input module object), "connectivity_in_(counterpart_c", "connectivity_difference", and "connectivity_foldchange".

Author(s)

Sora Yoon, PhD

Examples

```
modulefile1 = system.file('extdata', 'mouse_naiveCD4T_Vahedi_short.rds',  
  package = 'HiCocietyExample')  
modulefile2 = system.file('extdata', 'mouse_Th1_Vahedi_short.rds',  
  package = 'HiCocietyExample')  
mycom1 = readRDS(modulefile1)  
mycom2 = readRDS(modulefile2)  
result = ConnectivityDiff(mycom1, mycom2, 'NaiveCD4T', 'Th1',  
  resolution = 5000)  
head(print(result))
```

getContactFrequency	<i>Get contact Frequency</i>
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Description

Retrieve contact frequency from .hic file using strawR package.

Usage

```
getContactFrequency(fname, chr, resol)
```

Arguments

fname	.hic data for any types of genome conformation capture data
chr	Chromosome number of network extraction
resol	DNA basepair Resolution. Default=10000

Details

Get Contact Frequency from .hic file

Value

A data.frame containing three columns: x and y (genomic coordinate pairs), and counts (the contact frequency between them).

Author(s)

Sora Yoon, PhD

Examples

```
myhic=system.file('extdata', 'example.hic', package = 'HiCocietyExample')
A = getContactFrequency(myhic,19,5000)
head(print(A))
```

getContactProbability *Contact probability*

Description

It estimates contact probability based on the distance of a pair of a loci.

Usage

```
getContactProbability(
  tab,
  farthest = 2000000,
  resol = 10000,
  prob,
  n_cores = NULL
)
```

Arguments

tab	Output from getContactFrequency function.
farthest	Maximum 1-D distance to search. Default=2Mb
resol	Hi-C resolution for test. Default = 10000
prob	Significance cutoff for negative binomial distribution. Default =0.975
n_cores	The number of cores used for parallel computing. If set as NULL, n_cores is automatically set to the number of cores in the computer if it is not exceed 30. If it is more than 30, it is set as 30. Default = NULL

Details

Get Contact probability

Value

A list containing three objects: AREA, original, and len1, representing the statistical significance of each chromatin interaction pair.

Author(s)

Sora Yoon, PhD

Examples

```
# This example might take a long time to run, so we wrap it in donttest{}

myhic = system.file('extdata','example.hic',package = 'HiCocietyExample')
mydf=getContactFrequency(myhic, 19, 5000);
myprob=getContactProbability(mydf, farthest=2000000, resol=5000, prob=0.975,
n_cores=2);
```

getElbowPoint

Estimation of elbow point from J-shaped-curve

Description

It provides a point of the highest curvature from a J-shaped-plot

Usage

```
getElbowPoint(numbers)
```

Arguments

numbers	Numeric vector
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Details

Estimation of elbow point from J-shaped curve

Value

A list containing two elements: `index`, the index of a point in a sorted vector of numbers in descending order, representing the point where the tangent is closest to one, and `ConnectivityCutoff`, the corresponding value at that point.

Author(s)

Sora Yoon, PhD

Examples

```
modulefile = system.file('extdata', 'mouse_naiveCD4T_Vahedi_short.rds',
package = 'HiCocietyExample')
mycom = readRDS(modulefile)
connec = mycom$ModuleSummary$connectivity
getElbowPoint(connec)
```

get_all_chr_names	<i>Retrieve chromosome names from .hic file</i>
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Description

It retrieves all chromosome names having longer than 2.5Mbp.

Usage

```
get_all_chr_names(fname)
```

Arguments

fname	Path to .hic file
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Details

To extract all chromosome names from .hic file

Value

A character vector containing the names of chromosomes whose genomic lengths exceed 2.5 Mbp.

Author(s)

Sora Yoon, PhD

Examples

```
myhic=system.file('extdata', 'example.hic', package = 'HiCocietyExample')
get_all_chr_names(myhic)
```

get_txdb

All available Txdb

Description

It finds all available Txdb packages used in add_Genes function.

Usage

```
get_txdb()
```

Details

Check all available Txdb package

Value

A character vector containing the names of all available TxDb packages.

Author(s)

Sora Yoon, PhD

Examples

```
get_txdb()
```

hic2community

Create module objects from the Hi-C data

Description

It generates a list of graph of significant interactions, module table and module elements.

Usage

```

hic2community(
  fname,
  chr,
  resol,
  nbprob,
  farthest,
  par.noise = 1,
  network.cluster.method = "louvain",
  n_cores = NULL
)

```

Arguments

fname	Path to .hic file
chr	chromosome numbers to run.
resol	Resolution of Hi-C data
nbprob	Negative binomial probability. Higher value gives smaller number of stronger interaction.
farthest	The maximum searching distance between two nodes
par.noise	Parameter for noise removal. Default is 1, higher value gives more filtered interactions.
network.cluster.method	Can select between 'louvain' as default and 'label_prop' which means the label propagation method.
n_cores	The number of cores used for parallel computing. If set as NULL, n_cores is automatically set to the number of cores in the computer if it is not exceed 30. If it is more than 30, it is set as 30. Default = NULL

Details

It generates a list of graph of significant interactions, module table and module elements.

Value

A list containing three elements: Graphs (an igraph object representing significant chromatin interactions for each chromosome), ModuleSummary (a data.frame containing information about chromatin interaction modules), and ModuleElements (a list of nodes forming significant chromatin interactions within each module).

Author(s)

Sora Yoon, PhD

Examples

```
# This example might take a long time to run, so we wrap it in donttest{}

myhic=system.file('extdata', 'example.hic', package='HiCocietyExample')
mycom = hic2community(myhic, "19", 5000, 0.975, 2000000,
  par.noise=1, 'louvain', n_cores=2)
```

hic2network	<i>HiC to network data format</i>
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Description

It converts Hi-C dataframe to network object.

Usage

```
hic2network(ftab)
```

Arguments

ftab three-column data composed of locus1, locus2 and value

Details

Convert HiC to network data format

Value

An igraph object representing statistically significant chromatin interactions.

Author(s)

Sora Yoon, PhD

Examples

```
# This example might take a long time to run, so we wrap it in donttest{}

myhic=system.file('extdata', 'example.hic', package='HiCocietyExample')
ftab=getContactFrequency(myhic,19,5000);
net = hic2network(ftab[1:100,]);
plot(net)
```

visualizeModule	<i>Visualization of module</i>
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Description

It draws a triangle heatmap and arcplot of a module

Usage

```
visualizeModule(
  hicpath,
  HC.object,
  moduleNum,
  resolution,
  hic.norm,
  heatmap.color.range = NULL,
  heatmap.color = colorRampPalette(c("white", "red")),
  arc.depth = 10,
  arc.color = "gray80",
  nbnom.param = 0.99,
  txdb = "TxDb.Mmusculus.UCSC.mm10.knownGene",
  gene.strand.arrow.lwd = 3,
  gene.strand.lwd = 6,
  col.forward.gene = "purple",
  col.reverse.gene = "pink",
  highlight.centrality = FALSE,
  highlight.cent.col = FALSE,
  highlight.node = NULL,
  highlight.node.col = NULL,
  show.sig.int = TRUE,
  netinfo
)
```

Arguments

hicpath	Path to the .hic file
HC.object	The object name from hic2community result
moduleNum	The row index of module to draw
resolution	Resolution of HiC data
hic.norm	Normalization method. If not, set 'NONE'
heatmap.color.range	Min and max value of contact frequency, e.g., c(0,10)
heatmap.color	Color for heatmap. For example, colorRampPalette(c("white","red"))
arc.depth	Height of arc plot
arc.color	Arc color

<code>nbnom.param</code>	Negative binomial probability cutoff. Higher cutoff gives less number of arcs.
<code>txdb</code>	Character. One of Txdb list obtained from <code>get_txdb()</code> .
<code>gene.strand.arrow.lwd</code>	Numeric. Line width of arrowhead indicating the strands of genes. Same as <code>arr.lwd</code> option in <code>Arrows</code> function in <code>shape</code> package.
<code>gene.strand.lwd</code>	Numeric. Line width of arrow body indicating the strands of genes. Same as <code>lwd</code> option in <code>Arrows</code> function in <code>shape</code> package.
<code>col.forward.gene</code>	Character. Color of arrows within gene track for forward genes.
<code>col.reverse.gene</code>	Character. Color of arrows within gene track for reverse genes
<code>highlight.centraliity</code>	Boolean input to set if highlight eigenvector centrality node.
<code>highlight.cent.col</code>	The color of arcs stemming from the centrality node.
<code>highlight.node</code>	The coordiante of a node of which the user will highlight the arcs stemming from this node. Default=NULL
<code>highlight.node.col</code>	The color of arcs stemming from the node which the user highlight.
<code>show.sig.int</code>	Boolean. If TRUE, it marks significant contact on the triangle heatmap.
<code>netinfo</code>	Boolean. If TRUE, it shows network information of the module as text in the plot.

Details

Visualization of module

Value

No return value; the function generates a plot.

Author(s)

Sora Yoon, PhD

Examples

```
# A slow example that takes too long to run, wrapped in donttest{}

myhic = system.file('extdata','example.hic',package = 'HiCocietyExample')
HC.object = hic2community(myhic, "19", 5000, 0.975, 2000000, par.noise=1,
'louvain', n_cores=2)
mNum = 1
visualizeModule(hicpath = myhic, HC.object = HC.object, moduleNum = mNum,
resolution = 5000,
hic.norm = 'NONE', heatmap.color.range=c(0,10),
heatmap.color = colorRampPalette(c('white','red'))),
```

```
arc.depth=10, arc.color = "gray80", nbnom.param=0.99,  
txdb = 'TxDb.Mmusculus.UCSC.mm10.knownGene',  
gene.strand.arrow.lwd = 3, gene.strand.lwd = 3,  
col.forward.gene = 'purple', col.reverse.gene = 'pink',  
highlight.centraliity=FALSE, highlight.cent.col=FALSE,  
highlight.node=NULL, highlight.node.col=NULL,  
show.sig.int=FALSE, netinfo=FALSE)
```

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