

Package ‘multiOmicsViz’

October 17, 2020

Type Package

Title Plot the effect of one omics data on other omics data along the chromosome

Version 1.12.0

Date 2017-03-03

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Description Calculate the spearman correlation between the source omics data and other target omics data, identify the significant correlations and plot the significant correlations on the heat map in which the x-axis and y-axis are ordered by the chromosomal location.

License LGPL

LazyLoad yes

Depends R (>= 3.3.2)

Imports methods, parallel, doParallel, foreach, grDevices, graphics, utils, SummarizedExperiment, stats

Suggests BiocGenerics

Collate multiOmicsViz.R calculateCorForTwoMatrices.R zzz.R

biocViews Software, Visualization, SystemsBiology

git_url <https://git.bioconductor.org/packages/multiOmicsViz>

git_branch RELEASE_3_11

git_last_commit 08a3f2a

git_last_commit_date 2020-04-27

Date/Publication 2020-10-16

R topics documented:

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multiOmicsViz-package *Plot the effect of one omics data on other omics data along the chromosome*

Description

Calculate the spearman correlation between the source omics data and other target omics data, identify the significant correlations and plot the significant correlations on the heat map in which the x-axis and y-axis are ordered by the chromosomal location.

Details

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LazyLoad: yes

Author(s)

Jing Wang Maintainer: Jing Wang <jingwang.uestc@gmail.com>

References

Proteogenomic characterization of human colon and rectal cancer. Nature. 2014 Sep 18;513(7518):382-7. (PMID: 25043054)

See Also

[multiOmicsViz](#)

calculateCorForTwoMatrices

Identify the significant correlations between two matrices.

Description

The calculateCorForTwoMatrices function uses the spearman correlation to identify the significant correlations between two matrices.

Usage

```
calculateCorForTwoMatrices(matrix1,matrix2,fdr)
```

Arguments

| | |
|---------|---|
| matrix1 | A R matrix, data.frame or SummarizedExperiment object containing the numeric values. |
| matrix2 | A R matrix, data.frame or SummarizedExperiment object containing the numeric values. matrix2 should have at least 6 overlapping samples with matrix1. |
| fdr | The FDR threshold for identifying significant correlations. |

Value

This function will return a R matrix object containing significant correlations. "1" represents the significant positive correlation, "-1" represents the significant negative correlation and "0" represents no significant correlation.

Author(s)

Jing Wang

Examples

```
matrix1 <- system.file("extdata", "sourceOmics.txt", package="multiOmicsViz")
matrix1 <- read.table(matrix1, header=TRUE, sep="\t", stringsAsFactors=FALSE,
  check.names=FALSE)

matrix2 <- system.file("extdata", "targetOmics.txt", package="multiOmicsViz")
matrix2 <- read.table(matrix2, header=TRUE, sep="\t", stringsAsFactors=FALSE,
  check.names=FALSE)

sig <- calculateCorForTwoMatrices(matrix1=matrix1,
  matrix2=matrix2, fdr=0.01)
```

exampleData

Description of the data in the package

Description

chromLength is the length of 24 human chromosome. The first column is chromosome name and the second one is the length. genelocate is location of all genes in the human chromosome. The first column is gene symbol, second is the chromosome, third is the start position and fourth is the end position. sourceOmics is the copy number alteration data of human colorectal cancer, which was downloaded from firehose (<http://gdac.broadinstitute.org>) and contains 40 samples and genes from chromosome 20. targetOmics is the RNASeq data of human colorectal cancer, which was downloaded from the Nature paper (Proteogenomic characterization of human colon and rectal cancer. Nature. 2014 Sep 18;513(7518):382-7. (PMID: 25043054)) and contains 3764 genes and 40 samples.

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|---------------|---|
| multiOmicsViz | <i>Plot the effect of one omics data on other omics data along the chromosome</i> |
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Description

Calculate the spearman correlation between the source omics data and other target omics data, identify the significant correlations and plot the significant correlations on the heat map in which the x-axis and y-axis are ordered by the chromosomal location.

Usage

```
multiOmicsViz(sourceOmics, sourceOmicsName, chrome_sourceOmics, targetOmicsList,
targetOmicsName, chrome_targetOmics, fdrThr, outputfile, nThreads=NULL, legend=TRUE)
```

Arguments

| | |
|--------------------|---|
| sourceOmics | A R matrix, data.frame or SummarizedExperiment object containing the omics data. The data should contain the row names representing the genes and column names representing the samples. |
| sourceOmicsName | The name of the source omics data (e.g. CNA). |
| chrome_sourceOmics | The multiOmicsViz function will extract the genes in the selected chromosome(s) from genes in the source omics data and then identify and visualize the significant correlations based on the selected genes. chrome_sourceOmics can be one character containing the chromosome name (e.g. "1"), a R vector object containing multiple chromosomes (e.g. c("1","2","3")) or "All" representing all 24 chromosomes. |
| targetOmicsList | A R list object containing at most 5 target omics data. Each omics data in the list should be a R matrix, data.frame or SummarizedExperiment object and contain the row names representing the genes and column names representing the samples. There should have multiple overlapping genes among all target omics data and at least 6 overlapping sample between source omics data and each target omics data. |
| targetOmicsName | A R vector object containing the name of all target omics data stored in the targetOmicsList. |
| chrome_targetOmics | The multiOmicsViz function will extract the genes in the selected chromosome(s) from the overlapping genes among all target omics data and then identify and visualize the significant correlations based on the selected genes. chrome_sourceOmics can be one character containing the chromosome name (e.g. "1"), a R vector object containing multiple chromosomes (e.g. c("1","2","3")) or "All" representing all 24 chromosomes. |
| fdrThr | The FDR threshold for identifying the significant correlations. |
| outputfile | The output file name. |

| | |
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| nThreads | If targetOmicsList contains 2 or 3 omics data, multiOmicsViz will use the parallel computing method to calculate the significant correlations between the source omics data and each of target omics data. nThreads is the number of cores used for the parallel computing. |
| legend | If legend is TRUE, the output heat map will contain the legend. |

Value

If the targetOmicsList contains one target omics data, the multiOmicsViz function will plot a heat map in which x-axis represents the genes in the source omics data, y-axis represents the genes in the target omics data, x-axis and y-axis are ordered by chromosomal location, each point represents a significant correlation, red color represents the significant positive correlation and blue color represents the significant negative correlation. If the targetOmicsList contains multiple target omics data, the multiOmicsViz function will not only plot multiple heat maps for each target omics data but also plot multiple bar charts in which blue bars represent the number of specific significant correlations for the target omics data and black bars represents the number of common significant correlations among all target omics data.

Author(s)

Jing Wang

Examples

```
sourceOmics <- system.file("extdata", "sourceOmics.txt", package="multiOmicsViz")
sourceOmics <- read.table(sourceOmics, header=TRUE, sep="\t", stringsAsFactors=FALSE,
check.names=FALSE)

targetOmics1 <- system.file("extdata", "targetOmics.txt", package="multiOmicsViz")
targetOmics1 <- read.table(targetOmics1, header=TRUE, sep="\t", stringsAsFactors=FALSE,
check.names=FALSE)

targetOmicsList <- list()
targetOmicsList[[1]] <- targetOmics1

outputfile <- paste(tempdir(), "/heatmap", sep="")
multiOmicsViz(sourceOmics, "CNA", "20", targetOmicsList,
"mRNA", "All", 0.001, outputfile)
```

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