

# Package ‘multiOmicsViz’

April 12, 2018

**Type** Package

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

**Version** 1.2.0

**Date** 2017-03-03

**Author** Jing Wang <jingwang.uestc@gmail.com>

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

**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

**NeedsCompilation** no

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

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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.

### Details

Package: multiOmicsViz  
Type: Package  
License: LGPL  
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](#)

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calculateCorForTwoMatrices

*Identify the significant correlations between two matrices.*

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### Description

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

### Usage

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

**Arguments**

<code>matrix1</code>	A R matrix, data.frame or SummarizedExperiment object containing the numeric values.
<code>matrix2</code>	A R matrix, data.frame or SummarizedExperiment object containing the numeric values. <code>matrix2</code> should have at least 6 overlapping samples with <code>matrix1</code> .
<code>fdr</code>	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)
```

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exampleData

*Description of the data in the package*

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**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.

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 represent 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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