Package ‘omicsViewer’

May 8, 2024

Title Interactive and explorative visualization of SummarizedExpressionSet or ExpressionSet using omicsViewer

Version 1.8.0

Description omicsViewer visualizes ExpressionSet (or SummarizedExperiment) in an interactive way. The omicsViewer has a separate back- and front-end. In the back-end, users need to prepare an ExpressionSet that contains all the necessary information for the downstream data interpretation. Some extra requirements on the headers of phenotype data or feature data are imposed so that the provided information can be clearly recognized by the front-end, at the same time, keep a minimum modification on the existing ExpressionSet object. The pure dependency on R/Bioconductor guarantees maximum flexibility in the statistical analysis in the back-end. Once the ExpressionSet is prepared, it can be visualized using the front-end, implemented by shiny and plotly. Both features and samples could be selected from (data) tables or graphs (scatter plot/heatmap). Different types of analyses, such as enrichment analysis (using Bioconductor package fgsea or fisher’s exact test) and STRING network analysis, will be performed on the fly and the results are visualized simultaneously. When a subset of samples and a phenotype variable is selected, a significance test on means (t-test or ranked based test; when phenotype variable is quantitative) or test of independence (chi-square or fisher’s exact test; when phenotype data is categorical) will be performed to test the association between the phenotype of interest with the selected samples. Additionally, other analyses can be easily added as extra shiny modules. Therefore, omicsViewer will greatly facilitate data exploration, many different hypotheses can be explored in a short time without the need for knowledge of R. In addition, the resulting data could be easily shared using a shiny server. Otherwise, a standalone version of omicsViewer together with designated omics data could be easily created by integrating it with portable R, which can be shared with collaborators or submitted as supplementary data together with a manuscript.

Depends R (>= 4.2)

License GPL-2

Imports survminer, survival, fastmatch, reshape2, stringr, beeswarm, grDevices, DT, shiny, shinythemes, shinyWidgets, plotly, networkD3, htr, matrixStats, RColorBrewer, Biobase, fgsea, openxlsx, psych, shinybusy, ggseqlogo, htmlwidgets, graphics, grid, stats, utils, methods, shinyjs, curl, flatxml, ggplot2, S4Vectors, SummarizedExperiment, RSQLite, Matrix, shinyCSSloaders, ROCR, drc
Contents

Suggests  BiocStyle, knitr, rmarkdown, unittest
VignetteBuilder  knitr
LazyData  false
Encoding  UTF-8
biocViews  Software, Visualization, GeneSetEnrichment,
DifferentialExpression, MotifDiscovery, Network,
NetworkEnrichment

BugReports  https://github.com/mengchen18/omicsViewer
URL  https://github.com/mengchen18/omicsViewer
Video  https://www.youtube.com/watch?v=0nirB-exquY&list=PLo2m88lJf-RRoLKMY8UEGqCpraKYrX5lk
RoxygenNote  7.2.3
git_url  https://git.bioconductor.org/packages/omicsViewer
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convert e (inflection point) to EC50

Usage

`e2EC50(b, d, e, f)`
Arguments

- **b**: Hill’s slope. The Hill’s slope refers to the steepness of the curve. It could either be positive or negative.
- **d**: Highest response value.
- **e**: Inflection point. The inflection point is defined as the point on the curve where the curvature changes direction or signs. In models where \( f = 1 \) (2-4 parameter models), \( e \) is EC50.
- **f**: Asymmetry factor. When \( f = 1 \) we have a symmetrical curve around inflection point and so we have a four-parameters logistic equation.

Note

Only has an effect when using LL.5 and LL2.5 model

Description

*model fitted by drc*

Usage

```
.modelFormula(x, b, c = 0, d = 1, e, f = 1)
```

Arguments

- **x**: numerical vector of doses/time points/concentrations
- **b**: Hill’s slope. The Hill’s slope refers to the steepness of the curve. It could either be positive or negative.
- **c**: Lowest response value.
- **d**: Highest response value.
- **e**: Inflection point. The inflection point is defined as the point on the curve where the curvature changes direction or signs. In models where \( f = 1 \) (2-4 parameter models), \( e \) is EC50.
- **f**: Asymmetry factor. When \( f = 1 \) we have a symmetrical curve around inflection point and so we have a four-parameters logistic equation.

Details

\[ \text{func}(x) = c + (d - c) / (1 + (x/e)^b)^f \]
**app_module**  

Application level 0 module

---

**Description**

Function should only be used for the developers

**Usage**

```r
app_module(
  input,  
  output,  
  session,  
  .dir,  
  filePattern = ".(RDS|db|sqlite|sqlite3)$",  
  additionalTabs = NULL,  
  ESVObj = reactive(NULL),  
  esetLoader = readESVObj,  
  exprsGetter = getExprs,  
  pDataGetter = getpData,  
  fDataGetter = getFData,  
  imputeGetter = getExprsImpute,  
  defaultAxisGetter = getAx,  
  appName = "omicsViewer",  
  appVersion = packageVersion("omicsViewer")
)
```

**Arguments**

- **input**: input
- **output**: output
- **session**: session
- **.dir**: reactive; directory containing the .RDS file of ExpressionSet or SummarizedExperiment
- **filePattern**: file pattern to be displayed.
- **additionalTabs**: additional tabs added to "Analyst" panel
- **ESVObj**: the ESV object given, the drop down list should be disable in the "ui" component.
- **esetLoader**: function to load the eset object, if an RDS file, should be "readRDS"
- **exprsGetter**: function to get the expression matrix from eset
- **pDataGetter**: function to get the phenotype data from eset
- **fDataGetter**: function to get the feature data from eset
- **imputeGetter**: function to get the imputed expression matrix from eset, only used when exporting imputed data to excel
defaultAxisGetter

function to get the default axes to be visualized. It should be a function with two arguments: x - the object loaded to the viewer; what - one of "sx", "sy", "fx" and "fy", representing the sample space x-axis, sample space y-axis, feature space x-axis and feature space y-axis respectively.

appName - name of the application
appVersion - version of the application

Value

do not return any values

Examples

if (interactive()) {
  dir <- system.file("extdata", package = "omicsViewer")
  server <- function(input, output, session) {
    callModule(app_module, id = "app", dir = reactive(dir))
  }
  ui <- fluidPage(
    app_ui("app")
  )
  shinyApp(ui = ui, server = server)
}

---

app_ui  

Application level 0 UI

Description

Function should only be used for the developers

Usage

app_ui(id, showDropList = TRUE, activeTab = "Feature")

Arguments

id - id

showDropList - logical; whether to show the dropdown list to select RDS file, if the ESVObj is given, this should be set to "FALSE"

activeTab - one of "Feature", "Feature table", "Sample", "Sample table", "Heatmap"

Value

a list of UI components
Examples

```r
if (interactive()) {
  dir <- system.file("extdata", package = "omicsViewer")
  server <- function(input, output, session) {
    callModule(app_module, id = "app", dir = reactive(dir))
  }
  ui <- fluidPage(
    app_ui("app")
  )
  shinyApp(ui = ui, server = server)
}
```

---

**asEsetWithAttr** *

Convert SummarizedExperiment to ExpressionSet retaining all attributes

---

**Description**

Convert SummarizedExperiment to ExpressionSet retaining all attributes

**Usage**

```r
asEsetWithAttr(x)
```

**Arguments**

- `x` an object of class SummarizedExperiment

**Value**

an object of class ExpressionSet

---

**correlationAnalysis** *

Correlating a expression matrix with phenotypical variables

---

**Description**

This is a convenience function to perform correlation analysis, the output is in a format ready to be incorporated into object to be visualized by omicsViewer.

**Usage**

```r
correlationAnalysis(x, pheno, min.value = 12, prefix = "Cor")
```
Arguments

x  an expression matrix, rows are the features (e.g. proteins), columns are the samples
pheno  a data.frame storing the numerical phenotypical variable to be correlated with the rows (features) in expression matrix.
min.value  the minimum number of samples required in the correlation analysis, if lower than this number, NA will be returned.
prefix  prefix of the names. Usually don’t need to be changed by the user. When changes are needed, the prefix should be in a format like [analysis name][subset] so the "analysis name" and "subset" can be selected in the omicsViewer.

Value

Every correlation analysis returns a data.frame with five columns: R - pearson correlation coefficient N - number of values used in the analysis P - p-values returned by pearson correlation analysis logP - log transformed p-values range - the range of values in expression matrix used in the analysis

Examples

e1 <- matrix(rnorm(500), 50, 10)
rownames(e1) <- paste0("FT", 1:50)
p1 <- matrix(rnorm(50), 10, 5)
colnames(p1) <- paste0("PH", 1:5)
colnames(e1) <- rownames(p1) <- paste0("S", 1:10)
correlationAnalysis(x = e1, pheno = p1, min.value = 8)

csc2list  convert a column compressed sparse matrix to a list

Description

convert a column compressed sparse matrix to a list

Usage

csc2list(x)

Arguments

x  a matrix or CsparseMatrix object

Value

a sparse frame in data.frame
**draw_roc_pr**  

*Drawing ROC and PR curve*

**Description**

Drawing ROC and PR curve

**Usage**

```r
draw_roc_pr(value, label)
```

**Arguments**

- **value**: a numerical vector indicates the predictions
- **label**: true class labels, could be two or more unique values

**Examples**

```r
v <- sort(rnorm(100))
l <- sample(1:2, size = 100, replace = TRUE)
draw_roc_pr(v, l)
l <- rep(c("b", "c", "a", "d"), each = 25)
draw_roc_pr(v, l)
draw_roc_pr(v, sample(l))
```

---

**drmMat**  

*Fitting dose-response models for omics data matrix*

**Description**

A convenient function to fit dose response models for every row in an omics matrix using `drm` function in the `drc` package.

**Usage**

```r
drmMat(
x,   
fitvar,   
fitvar.name = c("Dose", "Time", "Concentration")[1],   
curveid = NA,   
fct.name = c("LL.4()", "LL.3()", "LL.2()", "LL.5()")[1]
)
```
exprspca

Arguments

x  
a numerical matrix where the rows are features and columns are samples.

fitvar  
a numerical variable has the same length as ncol(x) to indicate the dose/time/concentration conditions.

fitvar.name  
the name of the fitvar, a length one character. Will be used as the label for x-axis when drawing the dose curve.

curveid  
a numeric vector or factor containing the grouping of the columns in x.

fct.name  
the function name, e.g. "LL.4()", "LL.3()", "LL.2()" and "LL.5()", which are defined in the drc package.

Value

a list of drc object

exprspca  
Perform PCA and prepare results for omicsViewer

Description

This is a convenience function to perform PCA on expression matrix, the output of PCA will be in a format ready to be incorporated into object to be visualized by omicsViewer.

Usage

exprspca(x, n = min(8, ncol(x) - 1), prefix = "PCA|All", fillNA = FALSE, ...)

Arguments

x  
an expression matrix, where rows are features and samples are on columns.

n  
number of components to keep

prefix  
prefix of the names. Usually don’t need to be changed by the user. When changes are needed, the prefix should be in a format like [analysis name][subset] so the "analysis name" and "subset" can be selected in the omicsViewer.

fillNA  
logical; whether NA should be filled? If FALSE (default), na.omit will be called before PCA. If TRUE, the missing value will be replaced using fillNA.

...  
other parameters passed to prcomp

Value

a data.frame storing the PCA results
Examples

```r
# reading expression
packdir <- system.file("extdata", package = "omicsViewer")
expr <- read.delim(file.path(packdir, "expressionMatrix.tsv"), stringsAsFactors = FALSE)
# call PCA
pc <- exprspca(expr)
head(pc$samples)
head(pc$features)
```

### extendMetaData

**Description**

Add extra columns to the phenoData/colData or featureData/rowData in ExpressionSet/SummarizedExperiment

**Usage**

```r
extendMetaData(object, newData, where)
```

```r
# S4 method for signature 'ExpressionSet, data.frame'
extendMetaData(
  object,
  newData,
  where = c("pData", "fData", "colData", "rowData")[1]
)
```

```r
# S4 method for signature 'SummarizedExperiment, data.frame'
extendMetaData(
  object,
  newData,
  where = c("pData", "fData", "colData", "rowData")[1]
)
```

```r
# S4 method for signature 'SummarizedExperiment, DFrame'
extendMetaData(
  object,
  newData,
  where = c("pData", "fData", "colData", "rowData")[1]
)
```
extractParamDC

Extracting parameters from drc models

Description

Extracting parameters from drc models

Usage

extractParamDC(mod, prefix = "ResponseCurve")

Arguments

mod 
a drc object
prefix 
for column header, the column will be named as prefix|curveid|curveparameter

Note

when LL2.X is used, e is estimated as log(e), this function will return e in linear scale instead.
extractParamDCList

**Extracting parameter from a list of drc object**

**Description**

Extracting parameter from a list of drc object and return a data.frame, which can be incorporated into the object visualized by omicsViewer.

**Usage**

```r
extractParamDCList(x, prefix = "ResponseCurve")
```

**Arguments**

- `x`: a list of drc object
- `prefix`: for column header

**Value**

a data.frame

---

fgsea1

**Wrapper of fgseaMultilevel function to take binary gene set matrix as input**

**Description**

Wrapper of fgseaMultilevel function to take binary gene set matrix as input.

**Usage**

```r
fgsea1(gs, stats, gs_desc = NULL, ...)
```

**Arguments**

- `gs`: either a data.frame or a (sparse) matrix input. If a data.frame object is given, it should have at least three columns named as "featureId", "gsId" and "weight". If a matrix is given, the matrix is binary matrix where rows are features and columns are gene sets. The values in the matrix should be either 1 or 0 representing the presence and absence of a feature in the genesets, respectively.
- `stats`: ranking stats
- `gs_desc`: description of gene sets, it should be a named vector and the names should be the same as colnames(gs)
- `...`: other parameters passed to fgseaMultilevel
Value

A data.frame of fgsea results.

Examples

```r
## not for users
# library(fgsea)
# library(Biobase)
# dat <- readRDS(system.file(package = "omicsViewer", "extdata/demo.RDS"))
# fd <- pData(dat)
# fdgs <- fd[, grep("^GS\|", colnames(fd))]
# res <- fgsea(fdgs, stats = fd$t-test\|OV\_BR\|md\-
# res <- fgsea(fdgs, stats = fd$t-test\|OV\_BR\|md\-
# minSize = 5, maxSize = 500, gs_desc = colnames(fdgs))
```

fillNA

Filling NAs in a matrix using constants calculated from user defined function.

Description

This function is usually use to impute missing values in expression matrix, where the rows are feature and columns are samples. This function impute the missing values on the row-wise, that is, every row will be imputed using different constant.

Usage

```r
fillNA(
  x,
  maxfill = quantile(x, probs = 0.15, na.rm = TRUE),
  fillingFun = function(x) min(x, na.rm = TRUE) - log10(2)
)
```

Arguments

- `x` a matrix with NA values
- `maxfill` the maximum filled value, if the value calculated by `fillingFun` is greater than `maxfill`, then `maxfill` will the used to replace NAs.
- `fillingFun` function to calculate the filling values. It should be a function accept at least one argument "x", which is a row of input expression matrix. The default is `function(x) min(x, na.rm = TRUE) - log10(2)` corresponds to the "half of lowest detected values" if the expression matrix is log10 transformed. More examples:#' function(x) min(x, na.rm = TRUE) - 1 # half of lowest detected value when expression matrix is in log2 scale
`0` # replace NA by 0.
filterRow

Value

a matrix without NAs

Note

The returned matrix may have -Inf, which may need to be filtered/replaced additionally

Examples

```r
m <- matrix(rnorm(200), 20, 10)
m[sample(1:200, size = 20)] <- NA
mf <- fillNA(m)
```

filterRow

Filter out rows of expression matrix

Description

The function is used to filter rows with values of low intensities or do not reproducible presented in replicates.

Usage

```r
filterRow(x, max.quantile = NULL, max.value = NULL, var = NULL, min.rep = 2)
```

Arguments

- `x`: an expression matrix
- `max.quantile`: a single numerical value between (0, 1), if the row maximum is smaller than this quantile (calculated from the whole matrix), the row will be removed.
- `max.value`: a single numerical value, if the the maximum value of a row is smaller than this value, the row will be removed. Only used if `max.quantile` is set to "NULL.
- `var`: variables has the same length as the column number in `x` to indicate which sample is from which group
- `min.rep`: the minimum number of replicate in at least one of the groups, if less than this value, the row will be removed.

Value

a logical vector where the TRUE means row to keep

Examples

```r
e1 <- matrix(rnorm(5000, sd = 0.3), 500, 10) + rnorm(500)
f <- filterRow(x = e1, max.quantile = 0.25)
table(f)
```
getAutoRIF

Description

Get genes associated with search terms and AutoRIF annotations

Usage

getAutoRIF(term, rif = c("generif", "autorif")[1], filter = TRUE)

Arguments

term a character vector of terms want to search
rif either autorif or generif, see "https://maayanlab.cloud/geneshot/"
filter whether the result should be filtered. The least frequently mentioned genes
(most like 1 or 2 times) will be removed.

Value

a data.frame of 4 columns: gene, n, perc, rank.

Note

https://amp.pharm.mssm.edu/geneshot/

References

Alexander Lachmann, Brian M Schilder, Megan L Wojciechowicz, Denis Torre, Maxim V Kuleshov,
Alexandra B Keenan, Avi Ma’ayan, Geneshot: search engine for ranking genes from arbitrary
text queries, Nucleic Acids Research, Volume 47, Issue W1, 02 July 2019, Pages W571–W577,
https://doi.org/10.1093/nar/gkz393

Alexander Lachmann, Brian M Schilder, Megan L Wojciechowicz, Denis Torre, Maxim V Kuleshov,
Alexandra B Keenan, Avi Ma’ayan, Geneshot: search engine for ranking genes from arbitrary
text queries, Nucleic Acids Research, Volume 47, Issue W1, 02 July 2019, Pages W571–W577,
https://doi.org/10.1093/nar/gkz393

Examples

a <- getAutoRIF("mtor signaling")
**getMQParams**

*Parse mqpar.xml file*

**Description**

Getting the experimental information (TMT or label free) from mqpar.xml file.

**Usage**

```r
getMQParams(x)
```

**Arguments**

- `x`: the path to mqpar.xml file

**Value**

- a list of MQ parameters

---

**getUPRefProteomeID**

*get uniprot reference proteome IDs*

**Description**

- get uniprot reference proteome IDs
- get uniprot reference proteome IDs

**Usage**

```r
getUPRefProteomeID(
  domain = c("Eukaryota", "Archaea", "Bacteria", "Viruses")[[1]]
)
downloadUPRefProteome(
  id,
  domain = c("Eukaryota", "Archaea", "Bacteria", "Viruses")[[1]],
  destdir = "./"
)
```

**Arguments**

- `domain`: the domain, one of "Eukaryota", "Archaea", "Bacteria" or "Viruses"
- `id`: the UP id to download
- `destdir`: destination directory
gsAnnotIdList

Annotation of gene/protein function using multiple IDs.

Description
Annotation of gene/protein function using multiple IDs.

Usage

```r
gsAnnotIdList(
  idList,
  gsIdMap,
  minSize = 5,
  maxSize = 500,
  data.frame = FALSE,
  sparse = TRUE
)
```

Arguments

- **idList**
  list of protein IDs, e.g. list(c("ID1", "ID2"), c("ID13"), c("ID4", "ID8", "ID10"))
- **gsIdMap**
  a data frame for geneset to id map, it has two columns - id: the ID column - term: annotation terms e.g. gsIdMap <- data.frame(id = c("ID1", "ID2", "ID1", "ID2", "ID8", "ID10"), term = c("T1", "T1", "T2", "T2", "T2", "T2"), stringsAsFactors = FALSE)
- **minSize**
  minimum size of gene sets
- **maxSize**
  maximum size of gene sets
- **data.frame**
  logical; whether to organize the result into data.frame format, see "Value" section.
- **sparse**
  logical; whether to return a sparse matrix, only used when data.frame=FALSE

Value

A binary matrix (if data.frame = FALSE), the number of rows is the same with length of idList, the columns are the annotated gene set; or a data.frame (if data.frame = TRUE) with three columns: featureId, gsld, weight.
Examples

terms <- data.frame(
  id = c("ID1", "ID2", "ID1", "ID2", "ID8", "ID10"),
  term = c("T1", "T1", "T2", "T2", "T2", "T2"),
  stringsAsFactors = FALSE
)
features <- list(c("ID1", "ID2"), c("ID13"), c("ID4", "ID8", "ID10"))
gsAnnotIdList(idList = features, gsIdMap = terms, minSize = 1, maxSize = 500)

terms <- data.frame(
  id = c("ID1", "ID2", "ID1", "ID2", "ID8", "ID10", "ID4", "ID4"),
  term = c("T1", "T1", "T2", "T2", "T2", "T2", "T1", "T2"),
  stringsAsFactors = FALSE
)
features <- list(F1 = c("ID1", "ID2", "ID4"), F2 = c("ID13"), F3 = c("ID4", "ID8", "ID10"))
gsAnnotIdList(features, gsIdMap = terms, data.frame = TRUE, minSize = 1)
gsAnnotIdList(features, gsIdMap = terms, data.frame = FALSE, minSize = 1)

hasAttr

Check whether an object has an attribute

Description

Check whether an object has an attribute

Usage

hasAttr(x, attr.name)

Arguments

x
  the object

attr.name
  a character vector containing the name of attributes to be checked

Value

a logical value/vector has the same length as attr.name
hclust2str

Convert hclust object to/from single character

Description
Convert hclust object to/from single character

Usage
hclust2str(x)
str2hclust(x)

Arguments
x
a character of length one or an hclust object

Value
a character stores the hclust object
a hclust object

Note
The $call element in hclust will not retained in the conversion. The conversion decrease the precision in $height element.

Examples
# not for end users
# m <- matrix(rnorm(50), 25)
# hc <- hclust(dist(m))
# plot(hc)
# te <- hclust2str(hc)
# hc2 <- str2hclust(te)
# plot(hc2)
**jaccardList**

*Calculate Jaccard distance from a list*

---

**Description**

Calculate Jaccard distance from a list

**Usage**

```r
jaccardList(x)
```

**Arguments**

- `x` a list

**Value**

an `dist` object

---

**list2csc**

*convert a list to column compressed sparse matrix*

---

**Description**

convert a list to column compressed sparse matrix

**Usage**

```r
list2csc(l, dimnames)
```

**Arguments**

- `l` a data.frame with at least two columns - `featureId`, `gSId`; optionally a "weight" column.
- `dimnames` a list of dimnames, should contain at least one element for the row names.

**Value**

a sparse matrix, CsparseMatrix, column compressed
multi.t.test

Function to perform multiple t-tests on an expression matrix

Description

This is a convenience function to perform multiple student’s t-test. The output is in a format ready to be incorporated into object to be visualized by omicsViewer. This function uses t.test.

Usage

multi.t.test(x, pheno, compare = NULL, fillNA = FALSE, ...)

Arguments

x
an expression matrix, usually log10 transformed.

pheno
phenotype data of x, the number of rows in pheno must equal the number of columns of x. Please refer to examples for more details.

compare
NULL or a matrix with three columns to define the comparisons to do. When a matrix is given, the first column should be one of the column headers in pheno; then the second and third columns should be two values presented (more than once) in the columns of pheno selected by the values in the first column. The samples mapped to the two values are compared. If paired comparisons to be done, the orders of samples should be mapped.

fillNA
logical; whether NA should be filled? If FALSE (default), t test will be performed whenever possible. If not possible, then NA will be returned. If TRUE, the missing value will be replaced using fillNA.

...
other parameters passed to t.test

Value

A data.frame stores the t-test results with the following columns:

- The mean value of group 1: mean[[selected header in pheno]][[group 1 in test]]
- The number of value used in the test for group 1: n value[[selected header in pheno]][[group 1 in test]]
- The quantile of means values in group 1: quantile[[selected header in pheno]][[group 1 in test]]
- The mean value of group 2: mean[[selected header in pheno]][[group 2 in test]]
- The number of value used in the test for group 2: n value[[selected header in pheno]][[group 2 in test]]
- The quantile of means values in group 2: quantile[[selected header in pheno]][[group 2 in test]]
- The p-value returned by t.test: pvalue[[ttest[[group 1 in test]]_vs_[group 2 in test]]
- The -log10 transformed p-value: log.pvalue[[ttest[[group 1 in test]]_vs_[group 2 in test]]
- The BH method corrected p-values, e.g. FDR: fdr[[ttest[[group 1 in test]]_vs_[group 2 in test]]
- The -log10 transformed FDR: log.fdr[[ttest[[group 1 in test]]_vs_[group 2 in test]]
- The difference between the means of the two groups, e.g. fold change: mean.diff[[ttest[[group 1 in test]]_vs_[group 2 in test]]]
Examples

```r
# reading expression
packdir <- system.file("extdata", package = "omicsViewer")
expr <- read.delim(file.path(packdir, "expressionMatrix.tsv"), stringsAsFactors = FALSE)
# reading phenotype data
pd <- read.delim(file.path(packdir, "sampleGeneral.tsv"), stringsAsFactors = FALSE)

## Single t-test
head(pd)
# define comparisons
tests <- c("Origin", "RE", "ME")
tres <- multi.t.test(x = expr, pheno = pd, compare = tests)

## multiple t-test
head(pd)
# define comparisons
tests <- rbind(
c("Origin", "RE", "ME"),
c("Origin", "RE", "LE"),
c("TP53.Status", "MT", "WT")
)
tres <- multi.t.test(x = expr, pheno = pd, compare = tests)
```

nColors

*Generating k distinct colors*

**Description**

Mainly used in the shiny app to generate reproducible k distinct colors.

**Usage**

```
nColors(k, stop = FALSE)
```

**Arguments**

- **k**: a number between 1 to 60 tells how many distinct colors to use
- **stop**: logical; whether the function should return an error message if k is not in the range of 2 to 60. Default FALSE, the function will return NULL.

**Value**

- a vector of hex code for k colors or NULL

**Examples**

```
nColors(5)
nColors(1, stop = FALSE)
```
normalize.nQuantiles  

Normalization using n quantiles

Description

Normalization using n quantiles

Usage

normalize.nQuantiles(x, probs = 0.5, shareFeature = FALSE, ref = 1)

Arguments

x  an expression matrix, usually log transformed
probs  the quantiles to be aligned across samples. If probs is a length 1 numerical vector, the quantiles will aligned. As a special case, probs = 0.5 equals the median centering. If probs' length is > 1, a shift and scaling factor of samples will be calculating by fitting linear models using quantiles of samples, the median and variance of samples will be corrected using the intersect and slope of the fitted model.
shareFeature  logocal; if TRUE, the normalization will be based on the shared features between samples
ref  the columns name or index to specify the reference sample, only used when shareFeature = TRUE

Value

a normalized matrix

Examples

```
e1 <- matrix(rnorm(5000), 500, 10)
e1[, 6:10] <- 0.3 * e1[, 6:10] + 3
boxplot(e1)
# median centering, no variance correction
e2 <- normalize.nQuantiles(x = e1, probs = 0.5)
boxplot(e2)
# median centering + variance stablization
e3 <- normalize.nQuantiles(x = e1, probs = seq(0.25, 0.75, by = 0.1))
boxplot(e3)
```
**normalize.totsum**  
*Normalize total sum*

**Description**

Normalize total sum

**Usage**

```
normalize.totsum(x)
```

**Arguments**

- `x`: a log10 transformed expression matrix

**Value**

a normalized matrix

**Examples**

```r
e1 <- matrix(rnorm(5000), 500, 10)
e1[, 6:10] <- e1[, 6:10]+3
boxplot(e1)
e2 <- normalize.totsum(x = e1)
boxplot(e2)
```

---

**normalizeColWise**  
*Column-wise normalization of expression matrix*

**Description**

A wrapper function of all column-wise normalization methods

**Usage**

```
normalizeColWise(
x,
method = c("Median centering", "Median centering (shared ID)", "Total sum",
    "median centering + variance stabilization")[1]
)
```
normalizeData

Arguments

x
an expression matrix where rows are features and columns are samples, usually log transformed.

method
normalization method to use "Median centering" - median centering, see normalize.nQuantiles
"Median centering (shared ID)" - median centering using shared features, see normalize.nQuantiles
"Total sum" - total sum normalization "median centering + variance stabilization" - 10 quantile normalization using 0.25, 0.3, ..., 0.75, see normalize.nQuantiles

Value

a normalized matrix

Examples

e1 <- matrix(rnorm(5000), 100, 50)+10
boxplot(e1)
e2 <- normalizeColWise(x = e1, method = "Median centering")
boxplot(e2)

desc normalizationData
Normalized expression matrix

Description

A wrapper function of all normalization methods, including row-wise or column-wise normalization.

Usage

normalizeData(
  x,
  colWise = c("None", "Median centering", "Median centering (shared ID)", "Total sum",
              "median centering + variance stabilization")[1],
  rowWise = c("None", "Reference", "Batch mean", "Batch reference")[1],
  ref = NULL,
  batch = NULL
)

Arguments

x
an expression matrix where rows are features and columns are samples, usually log transformed.

colWise
column-wise normalization method to use, see normalizeColWise
rowWise row-wise normalization method to use Reference - using removeVarQC method
Batch mean - using rowshift method without reference samples Batch reference
- using rowshift method with reference samples

ref index of reference samples
batch batch factor

Value
a normalized matrix

Examples

e1 <- matrix(rnorm(5000), 100, 50)+10
boxplot(e1)
e2 <- normalizeData(x = e1, ref = seq(5, 45, by = 10), rowWise = "Reference")
boxplot(e2)

omicsViewer

Description
Start omicsViewer

Usage

omicsViewer(
  dir,
  additionalTabs = NULL,
  filePattern = ".(RDS|DB|SQLITE|SQLITE3)$",
  ESVObj = NULL,
  esetLoader = readESVObj,
  exprsGetter = getExprs,
  pDataGetter = getPData,
  fDataGetter = getFData,
  defaultAxisGetter = getAx,
  appName = "omicsViewer",
  appVersion = packageVersion("omicsViewer")
)

Arguments

dir directory to the ExpressionSet or SummarizedExperiment object. Only give
the directory in this argument, not the .rds file.
additionalTabs additional tabs added to "Analyst" panel
filePattern file pattern to be displayed.
ESVObj the ESV object
esetLoader function to load the eset object, if an RDS file, should be "readRDS"
exprsGetter function to get the expression matrix from eset
pDataGetter function to get the phenotype data from eset
fDataGetter function to get the feature data from eset
defaultAxisGetter function to get the default axes to be visualized. It should be a function with two arguments: x - the object loaded to the viewer; what - one of "sx", "sy", "fx" and "fy", representing the sample space x-axis, sample space y-axis, feature space x-axis and feature space y-axis respectively.
appName name of the application
appVersion version of the application

Value
do not return values

Examples

1
## To start the shiny app:
# omicsViewer(
#   system.file("extdata", package = "omicsViewer")
# )

description

Extract function annotation from uniprot .dat file

Usage

parseDatTerm(file, outputDir = NULL, ...)

Arguments

file the .dat or .dat.gz file
outputDir dir of output file
... other parameters passed to readLines

Value

a data.frame parse from .dat file
**plotDC**

*Draw dose-response curves*

---

**Description**

Draw dose-response curves

**Usage**

```
plotDC(mod, ylab = "Abundance", lty = 2, pch = 19, cex = 1, logx = FALSE)
```

**Arguments**

- `mod`: an drc object
- `ylab`: ylab in plot function
- `lty`: lty in plot function
- `pch`: pch in plot function
- `cex`: cex in plot function
- `logx`: whether the x-axis should be in log scale

---

**plotDCMat**

*Draw dose response curve given parameters in the omicsViewer object*

---

**Description**

Draw dose response curve given the feature Data/rowData, phenotype data/colData and expression matrix. The function is usually used in shinyApp.

**Usage**

```
plotDCMat(
  expr,
  pd,
  fd,
  featid,
  dose.var,
  curve.var = NULL,
  only.par = FALSE,
  ...
)
```
plotly_boxplot_module

Arguments

expr: expression matrix
pd: phenotype data or colData
fd: feature data or rowData
featid: feature id to be visualized
dose.var: the column header indicating the dose/time/concentration
curve.var: the column header indicating the curve ids
only.par: logical value. If true, no plot generated, the function only returns the parameters of models.
...
other parameters passed to plot function, except col, pch, xlab, ylab

plotly_boxplot_module

Shiny module for boxplot using plotly - Module

Description

Shiny module for boxplot using plotly - Module

Usage

plotly_boxplot_module(
  input,
  output,
  session,
  reactive_param_plotly_boxplot,
  reactive_checkpoint = reactive(TRUE)
)

Arguments

input: input
output: output
session: session
reactive_param_plotly_boxplot: reactive value; argument passed to plotly_boxplot
reactive_checkpoint: reactive_value; check this value before render any plot/executing any calculation

Value

do not return any values
Examples

```r
if (interactive()) {

library(shiny)

ui <- fluidPage(
  plotly_boxplot_ui("testplotly")
)

server <- function(input, output, session) {

  x <- cbind(matrix(rnorm(10000, mean = 3), 1000, 10), matrix(rnorm(20000), 1000, 20))
  x[sample(1:length(x), size = 0.3*length(x))] <- NA
  rownames(x) <- paste("R", 1:nrow(x), sep = "")
  colnames(x) <- paste("C", 1:ncol(x), sep = "")
  callModule(plotly_boxplot_module, id = "testplotly",
             reactive_param_plotly_boxplot = reactive(list(
               x = x, i = c(4, 20, 80), highlight = c(1, 4, 5, 20), extvar = 1:30)
             ))

}

shinyApp(ui, server)

```
Examples

```r
if (interactive()) {
  library(shiny)

  ui <- fluidPage(
    plotly_boxplot_ui("testplotly")
  )

  server <- function(input, output, session) {
    x <- cbind(matrix(rnorm(10000, mean = 3), 1000, 10), matrix(rnorm(20000), 1000, 20))
    x[sample(1:length(x), size = 0.3*length(x))] <- NA
    rownames(x) <- paste("R", 1:nrow(x), sep = "")
    colnames(x) <- paste("C", 1:ncol(x), sep = "")
    callModule(plotly_boxplot_module, id = "testplotly",
      reactive_param_plotly_boxplot = reactive(list(
        x = x, i = c(4, 20, 80), highlight = c(1, 4, 5, 20), extvar = 1:30
      )))
  }

  shinyApp(ui, server)
}
```

---

**plotly_scatter_module**

*Shiny module for scatter plot using plotly - Module*

**Description**

Function should only be used for the developers

**Usage**

```r
plotly_scatter_module(
  input, output, session,
  reactive_param_plotly_scatter, reactive_regLine = reactive(FALSE),
  reactive_checkpoint = reactive(TRUE),
  htest_var1 = reactive(NULL),
  htest_var2 = reactive(NULL)
)
```

**Arguments**

- **input**
plotly_scatter_module

output output
session sesion
reactive_param_plotly_scatter reactive parameters for plotly_scatter
reactive_regLine logical show or hide the regression line
reactive_checkpoint checkpoint
htest_var1 when the plot is a beeswarmplot, two groups could be selected for two group comparison, this argument gives the default value. Mainly used for restoring the saved session.
htest_var2 see above

Value

a list containing the information about the selected data points
an reactive object containing the information of selected, brushed points.

Examples

if (interactive()) {
  library(shiny)

  # two random variables
  x <- rnorm(30)
  y <- x + rnorm(30, sd = 0.5)

  # variables mapped to color, shape and size
  cc <- sample(letters[1:4], replace = TRUE, size = 30)
  shape <- sample(c("S1", "S2", "S3"), replace = TRUE, size = 30)
  sz <- sample(c(10, 20, 30, replace = TRUE, size = 30))

  ui <- fluidPage(
    plotly_scatter_ui("test_scatter")
  )

  server <- function(input, output, session) {
    v <- callModule(plotly_scatter_module, id = "test_scatter",
      # reactive_checkpoint = reactive(FALSE),
      reactive_param_plotly_scatter = reactive(list(
        x = x, y = y,
        color = cc,
        shape = shape,
        size = sz,
        tooltips = paste("A", 1:30)
      )))
    observe(print(v()))
  }
  shinyApp(ui, server)
# example beeswarm horizontal
x <- rnorm(30)
y <- sample(c("x", "y", "z"), size = 30, replace = TRUE)
shinyApp(ui, server)

# example beeswarm vertical
x <- sample(c("x", "y", "z"), size = 30, replace = TRUE)
y <- rnorm(30)
shinyApp(ui, server)

# return values
x <- c(5, 6, 3, 4, 1, 2)
y <- c(5, 6, 3, 4, 1, 2)
ui <- fluidPage(
  plotly_scatter_ui("test_scatter")
)
server <- function(input, output, session) {
  v <- callModule(plotly_scatter_module, id = "test_scatter",
                  reactive_param_plotly_scatter = reactive(list(
                    x = x, y = y, tooltips = paste("A", 1:6), highlight = 2:4
                  )))

  observe(print(v()))
}
shinyApp(ui, server)

---

**plotly_scatter_ui**

Shiny module for scatter plot using plotly - UI

**Description**

Function should only be used for the developers

**Usage**

```
plotly_scatter_ui(id, height = "400px")
```

**Arguments**

- `id`  
  - id
- `height`  
  - figure height

**Value**

- a tagList of UI components
Examples

```r
if (interactive()) {
  library(shiny)

  # two random variables
  x <- rnorm(30)
  y <- x + rnorm(30, sd = 0.5)

  # variables mapped to color, shape and size
  cc <- sample(letters[1:4], replace = TRUE, size = 30)
  shape <- sample(c("S1", "S2", "S3"), replace = TRUE, size = 30)
  sz <- sample(c(10, 20, 30, replace = TRUE, size = 30))

  ui <- fluidPage(
    plotly_scatter_ui("test_scatter")
  )

  server <- function(input, output, session) {
    v <- callModule(plotly_scatter_module, id = "test_scatter",
                    reactive_checkpoint = reactive(FALSE),
                    reactive_param_plotly_scatter = reactive(list(
                      x = x, y = y,
                      color = cc,
                      shape = shape,
                      size = sz,
                      tooltips = paste("A", 1:30)
                    )))
    observe(print(v()))
  }

  shinyApp(ui, server)

  # example beeswarm horizontal
  x <- rnorm(30)
  y <- sample(c("x", "y", "z"), size = 30, replace = TRUE)
  shinyApp(ui, server)

  # example beeswarm vertical
  x <- sample(c("x", "y", "z"), size = 30, replace = TRUE)
  y <- rnorm(30)
  shinyApp(ui, server)

  # return values
  x <- c(5, 6, 3, 4, 1, 2)
  y <- c(5, 6, 3, 4, 1, 2)
  ui <- fluidPage(
    plotly_scatter_ui("test_scatter")
  )

  server <- function(input, output, session) {
    v <- callModule(plotly_scatter_module, id = "test_scatter",
                    reactive_param_plotly_scatter = reactive(list(
                      x = x, y = y,
                      color = cc,
                      shape = shape,
                      size = sz,
                      tooltips = paste("A", 1:30)
                    )))
    observe(print(v()))
  }

  shinyApp(ui, server)
```
plot_roc_pr_module

\[
x = x, \ y = y, \ \text{tooltips} = \text{paste("A", 1:6), \ highlight = 2:4}
\]

observe(print(v()))
}
shinyApp(ui, server)
}

---

plot_roc_pr_module  Shiny module for boxplot using plotly - Module

Description

Shiny module for boxplot using plotly - Module

Usage

plot_roc_pr_module(
  input,
  output,
  session,
  reactive_param,
  reactive_checkpoint = reactive(TRUE)
)

Arguments

input  input
output output
session session
reactive_param  reactive value; argument pass to draw_roc_pr
reactive_checkpoint
  reactive_value; check this value before render any plot/executing any calculation

Value

do not return any values

Examples

if (interactive()) {
  library(shiny)

  ui <- fluidPage(
    sliderInput("ngrp", \label = "Number of groups", \min = 2, \max = 5, \value = 2),
    plot_roc_pr_ui("testplot")
  )
server <- function(input, output, session) {
  ng <- reactive(
    sample(letters[1:input$ngrp], size = 100, replace = TRUE)
  )
  callModule(
    plot_roc_pr_module, id = "testplot",
    reactive_param = reactive(list(
      x = ng(),
      y = rnorm(100)
    ))
  )
  shinyApp(ui, server)
}

prepOmicsViewer

Prepare object to be viewed by omicsViewer

Description

This is a convenience function to prepare the data to be visualized using omicsViewer. The result of PCA and t-test could be included directly.

Usage

prepOmicsViewer(
  expr,
  pData,
  fData,
  PCA = TRUE,
  ncomp = min(8, ncol(expr)),
  pca.fillNA = TRUE,
  t.test = NULL,
  ttest.fillNA = FALSE,
  ...
  gs = NULL,
  stringDB = NULL,
  surv = NULL,
  SummarizedExperiment = TRUE
)

Arguments

expr: expression matrix where the rows are feature and columns are samples, matrix should be log10 transformed and have unique row and column names

pData: phenotype data

fData: feature data
PCA    pca
ncomp number of components to keep
pca.fillNA logical, whether the NA should be filled with a constant in PCA.
t.test will be passed to the compare argument in multi.t.test
ttest.fillNA logical, whether the NA should be filled with a constant in t-test.
... arguments passed to t.test, such as paired.
gs gene-set data, please refer to examples for more details about the format
stringDB the IDs that can be used in the STRING database (https://string-db.org/) query.
surv survival data, please refer to examples for more details about the format
SummarizedExperiment logical; whether to return an object of class SummarizedExperiment. If set to FALSE, the function will return an ExpressionSet object.

Value
an object of ExpressionSet or SummarizedExperiment that can be visualized using omicsViewer

Examples
packdir <- system.file("extdata", package = "omicsViewer")
# reading expression
expr <- read.delim(file.path(packdir, "expressionMatrix.tsv"), stringsAsFactors = FALSE)
colnames(expr) <- make.names(colnames(expr))
rownames(expr) <- make.names(rownames(expr))
# reading feature data
fd <- read.delim(file.path(packdir, "featureGeneral.tsv"), stringsAsFactors = FALSE)
# reading phenotype data
pd <- read.delim(file.path(packdir, "sampleGeneral.tsv"), stringsAsFactors = FALSE)
# reading other datasets
drugData <- read.delim(file.path(packdir, "sampleDrug.tsv"))
# survival data
# this data is from cell line, the survival data are fake data to
# show how to use the survival data in #' omicsViewer
surv <- read.delim(file.path(packdir, "sampleSurv.tsv"))
# gene set information
genesets <- read_gmt(file.path(packdir, "geneset.gmt"), data.frame = TRUE)
gsannot <- gsAnnotIdList(idList = rownames(fd), gsIdMap = genesets, data.frame = TRUE)

# Define t-test to be done, a matrix nx3
# every row define a t-test, the format
# [column header] [group 1 in the test] [group 2 in the test]
tests <- rbind(
c("Origin", "RE", "ME"),
c("Origin", "RE", "LE"),
c("TP53.Status", "MT", "WT")
)
# prepare column for stringDB query
strid <- sapply(strsplit(fd$Protein.ID, ";\-"), "[", 1)
### read.proteinGroups

```r
###
d <- prepOmicsViewer(
  expr = expr, pData = pd, fData = fd,
  PCA = TRUE, pca.fillNA = TRUE,
  t.test = tests, ttest.fillNA = FALSE,
  gs = gsannot, stringDB = strid, surv = surv)
# feature space - default x axis
attr(d, "fx") <- "ttest|RE_vs_ME|mean.diff"
# feature space - default y axis
attr(d, "fy") <- "ttest|RE_vs_ME|log.fdr"
# sample space - default x axis
attr(d, "sx") <- "PCA|All|PC1"
# sample space - default y axis
attr(d, "sy") <- "PCA|All|PC2"
# Save object and view
# saveRDS(d, file = "dtest.RDS")
## to open the viewer
# omicsViewer(".~/")
```

---

### Description

A convenience function to read the proteinGroups table of MaxQuant output. The function organize the result into different tables, e.g. iBAQ.

### Usage

```r
read.proteinGroups(x, quant = c("LF", "TMT"))[1])
```

### Arguments

- **x**: the proteinGroup.txt file returned by MaxQuant search
- **quant**: the quantification method, LF or TMT

### Value

A list of tables extracted from proteinGroups.txt file.
read.proteinGroups.lf

*Read protein groups output of maxquant output and split it to columns*

**Description**
Read protein groups output of maxquant output and split it to columns

**Usage**
read.proteinGroups.lf(file)

**Arguments**
- **file**: Maxquant proteinGroup.txt file path

**Value**
a list of tables extracted from proteinGroups.txt file

readESVObj

*Read the object of SummarizedExperiment or ExpressionSet to be visualized using omicsViewer*

**Description**
This function accept a path to a sqlite database or RDS object. If an RDS file to be read, The function is similar to readRDS. It reads the object to R working environment and perform extra two things. 1. If the loaded data an class of SummarizedExperiment, it will be converted to ExpressionSet. 2. If the gene set annotatio is in matrix format, the gene set annotation is converted to data.frame format.

**Usage**
readESVObj(x)

**Arguments**
- **x**: the path of an object of SummarizedExperiment or ExpressionSet, passed to readRDS

**Value**
an object of class ExpressionSet or SummarizedExperiment to be visualized.
Examples

```r
file <- system.file("extdata/demo.RDS", package = "omicsViewer")
obj <- readESVObj(file)
```

---

**read_gmt**  
*Reading gene set .gmt file*

### Description

Frequently the .gmt files are downloaded from MSigDB database

### Usage

```r
read_gmt(x, id = NA, data.frame = FALSE)
```

#### Arguments

- `x`  
  the name/path of the gmt file to be read

- `id`  
  the id used in gene sets, if is not NA, it should be either "SYMBOL" or "ENTREZ". Usually only used when reading the .gmt file downloaded from MSigDB.

- `data.frame`  
  logical; whether to organize the data in `data.frame` format. Default is `FALSE`, a list will be returned.

### Value

a list or data frame of gene set. When `data.frame = TRUE`, the returned object is a `data.frame` with two columns: id and term.

### Examples

```r
file <- system.file("extdata", package = "omicsViewer")
file <- file.path(file, "geneset.gmt")
gs <- read_gmt(file)
```
**removeVarQC**  
*Removing variance of reference samples*

**Description**

This normalization removes the variance in reference samples. The method do not need to specific the batch assignment but cannot work with data contains less than five common reference samples. A typical use of this normalization is to correct some drifting effect in mass spec based label free proteomics or untargeted metabolomics experiment. Usually, this is a very strong normalization should only be used with good reasons.

**Usage**

```r
removeVarQC(x, ref, positive = TRUE, ...)
```

**Arguments**

- `x`: an expression matrix
- `ref`: the index of reference samples
- `positive`: logical; force only positive values in the resulted matrix
- `...`: if given, `normalize.nQuantiles` will be called first, the arguments here will be passed to `normalize.nQuantiles`

**Value**

a normalized matrix

**Examples**

```r
e1 <- matrix(rnorm(5000), 100, 50)+10
e2 <- removeVarQC(x = e1, ref = seq(5, 45, by = 10))
boxplot(e2)
```

**rowshift**  
*Row-wise normalization of expression matrix with or without reference sample*

**Description**

Row-wise normalization of expression matrix with or without reference sample

**Usage**

```r
rowshift(x, batch, ref = NULL, useMean = FALSE)
```
Arguments

- **x**: an expression matrix where rows are features, e.g. genes, proteins and columns are samples. The values in the matrix are usually log transformed.
- **batch**: a factor or vector has the same length as `ncol(x)` to indicate the batch assignment of samples.
- **ref**: a logical vector has the same length as `ncol(x)` to indicated which columns are the common references among batches. If it is NULL (by default), the mean of all channels will be used as batch reference. When NA present in the reference channels, the mean values will be used in correction.
- **useMean**: logical; whether to use means of batches, usually set to TRUE when no reference available.

Value

- a matrix (hopefully without/with less batch effect)

Examples

```r
e1 <- matrix(rnorm(5000), 500, 10)
e1[, 6:10] <- e1[, 6:10] + 3
boxplot(e1)
f <- rep(c("a", "b"), each = 5)
e2 <- rowshift(x = e1, batch = f)
boxplot(e2)
```

Description

Save the xcmsViewer result object as sqlite database

Usage

```r
saveOmicsViewerDb(obj, db.file, overwrite = TRUE)
```

## S4 method for signature 'SummarizedExperiment,character'
```r
saveOmicsViewerDb(obj, db.file, overwrite = TRUE)
```

## S4 method for signature 'ExpressionSet,character'
```r
saveOmicsViewerDb(obj, db.file, overwrite = TRUE)
```

Arguments

- **obj**: an object of class ExpressionSet or SummarizedExperiment
- **db.file**: a character indicate file name of the database file
- **overwrite**: logical. whether the database should be overwritten if exist already.
Value

the directory where the database saved

Examples

```r
f <- system.file("extdata", "demo.RDS", package = "omicsViewer")
es <- readRDS(f)
# The following line will write a database file on your disk
# saveOmicsViewerDb(es, db.file = "./omicsViewerData.db")
```

---

**triselector_module**  
*The three-step selector - the module function*

---

Description

The selector is used to select columns of phenotype and feature data. Function should only be used for the developers.

Usage

```r
triselector_module(
  input, output, session, reactive_x, reactive_selector1 = reactive(NULL),
  reactive_selector2 = reactive(NULL), reactive_selector3 = reactive(NULL),
  label = "Group Label:"
)
```

Arguments

- **input**: input
- **output**: output
- **session**: session
- **reactive_x**: an nx3 matrix
- **reactive_selector1**: default value for selector 1
- **reactive_selector2**: default value for selector 2
- **reactive_selector3**: default value for selector 3
- **label**: of the triselector
triselector_ui

**Value**

an reactive object containing the selected values

**Examples**

```r
if (interactive()) {
  library(shiny)
  library(Biobase)

  file <- system.file("extdata/demo.RDS", package = "omicsViewer")
  dat <- readRDS(file)
  fData <- fData(dat)
  triset <- stringr::str_split_fixed(colnames(fData), '\|', n= 3)

  ui <- fluidPage(
    triselector_ui("tres"),
    triselector_ui("tres2")
  )

  server <- function(input, output, session) {
    v1 <- callModule(triselector_module, id = "tres",
                     reactive_x = reactive(triset),
                     reactive_selector1 = reactive("ttest"),
                     reactive_selector2 = reactive("RE_vs_ME"),
                     reactive_selector3 = reactive("mean.diff")
    )

    v2 <- callModule(triselector_module, id = "tres2",
                     reactive_x = reactive(triset),
                     reactive_selector1 = reactive("ttest"),
                     reactive_selector2 = reactive("RE_vs_ME"),
                     reactive_selector3 = reactive("log.fdr"))

    observe({
      print("/\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\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```}

shinyApp(ui, server)

---

**triselector_ui**

The three-step selector - the ui function

**Description**

Function should only be used for the developers

**Usage**

```
triselector_ui(id, right_margin = "20")
```
Arguments

- **id**: id
- **right_margin**: margin on the right side, in px. For example, "20" translates to "20px".

Value

- a tagList of UI components

Examples

```r
if (interactive()) {
  library(shiny)
  library(Biobase)

  file <- system.file("extdata/demo.RDS", package = "omicsViewer")
  dat <- readRDS(file)
  fData <- fData(dat)
  triset <- stringr::str_split_fixed(colnames(fData), '\|', n = 3)

  ui <- fluidPage(
    triselector_ui("tres"),
    triselector_ui("tres2")
  )
  server <- function(input, output, session) {
    v1 <- callModule(triselector_module, id = "tres",
                     reactive_x = reactive(triset),
                     reactive_selector1 = reactive("ttest"),
                     reactive_selector2 = reactive("RE_vs_ME"),
                     reactive_selector3 = reactive("mean.diff")
    )
    v2 <- callModule(triselector_module, id = "tres2",
                     reactive_x = reactive(triset),
                     reactive_selector1 = reactive("ttest"),
                     reactive_selector2 = reactive("RE_vs_ME"),
                     reactive_selector3 = reactive("log.fdr")
    )

    observe({
      print("////////////////////")
      print(v1())
    })
  }

  shinyApp(ui, server)
}
```

---

**trisetter**  
Create a nx3 matrix that can be use for triselector given a meta and expression table

---

**Description**

- only used inside reactive
validMQFolder

**Usage**

```r
trisetter(meta, expr = NULL, combine)
```

**Arguments**

- `meta`: a meta data, usually either phenotype data or feature data
- `expr`: expression matrix, optional.
- `combine`: how the meta and expression to be combined. Should be either "pheno" or "feature" or "none".

**Value**

- a nx3 matrix
- a `data.frame` with 3 columns

---

**validMQFolder**  
*MQ folder validator Validate whether a folder is a MQ output folder*

**Description**

MQ folder validator Validate whether a folder is a MQ output folder

**Usage**

```r
validMQFolder(dir)
```

**Arguments**

- `dir`: the directory to check

**Details**

from the root level, these files exist: mqpar.xml [[combined/]/txt/][proteinGroups.txt

**Value**

- a list containing the info about MQ folder check
**Description**

variable selector

**Usage**

`varSelector(x, expr, meta, alternative = NULL)`

**Arguments**

- `x`: variable return by triselector, a list of length three named as "analysis", "subset" and "variable"
- `expr`: the expression matrix
- `meta`: a meta matrix
- `alternative`: alternative value to be returned when nothing to select

**Value**

the selected values in input argument `x`
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