

# Package ‘omicsViewer’

June 5, 2026

**Title** Interactive and explorative visualization of SummarizedExpressionSet or ExpressionSet using omicsViewer

**Version** 1.17.0

**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** htmltools, shinydashboard, survminer, survival, fastmatch, reshape2, stringr, beeswarm, grDevices, DT, shiny, shinythemes, shinyWidgets, plotly, networkD3, httr, 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

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**BugReports** <https://github.com/mengchen18/omicsViewer>

**URL** <https://github.com/mengchen18/omicsViewer>

**Video** <https://www.youtube.com/watch?v=0nirB-exquY&list=PLo2m88lJf-RRoLKMY8UEGqCpraKYrX5lk>

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---

.e2EC50	<i>convert e (inflection point) to EC50</i>
---------	---

---

### Description

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

---

.modelFormula	<i>model fitted by drc</i>
---------------	----------------------------

---

### 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

*omicsViewer Application Server Logic (Level 0)*


---

**Description**

Implements the main server-side logic for the omicsViewer Shiny application. Handles data loading, validation, state management, snapshot functionality, and orchestrates communication between sub-modules. Uses modern Shiny module pattern with `moduleServer`. Primarily intended for developers extending the application.

**Usage**

```
app_module(
  id,
  .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**

id	Character. Namespace ID for the Shiny module. Must match the ID used in <code>app_ui</code> .
.dir	Reactive expression. Returns the directory path containing data files (ExpressionSet or SummarizedExperiment .RDS files).
filePattern	Character. Regular expression to filter displayed files. Default: <code>".(RDS db sqlite sqlite3)\$"</code> (case-insensitive).
additionalTabs	List or NULL. Custom analysis modules to add to the application. Each element should contain: <code>tabName</code> , <code>moduleName</code> , <code>moduleUi</code> , and <code>moduleServer</code> . Default: NULL (no additional tabs).
ESVObj	Reactive expression. Returns a pre-loaded ExpressionSet or SummarizedExperiment object, bypassing file loading. Default: <code>reactive(NULL)</code> .
esetLoader	Function. Loads data objects from disk. Takes file path as input, returns ExpressionSet or SummarizedExperiment. Default: <code>readESVObj</code> .
exprsGetter	Function. Extracts expression matrix from loaded object. Default: <code>getExprs</code> .
pDataGetter	Function. Extracts sample/phenotype metadata. Default: <code>getPData</code> .
fDataGetter	Function. Extracts feature metadata. Default: <code>getFData</code> .
imputeGetter	Function. Extracts imputed expression matrix (if available) for Excel export. Should return NULL if no imputed data. Default: <code>getExprsImpute</code> .
defaultAxisGetter	Function. Determines default plot axes. Takes object and what ("sx", "sy", "fx", "fy") as arguments. Default: <code>getAx</code> .
appName	Character. Application name displayed in UI. Default: "omicsViewer".
appVersion	Character or <code>package_version</code> . Version shown in UI. Default: current package version.

**Details**

The module coordinates several key functionalities:

- **Data Loading:** Validates file paths, checks file sizes, loads with error handling
- **Data Validation:** Ensures rownames/colnames consistency across expression and metadata
- **State Management:** Tracks selected features/samples across sub-modules
- **Snapshots:** Save and restore analysis states to disk (.ESS files)
- **Data Export:** Generate Excel files with expression data, metadata, and gene sets
- **Module Coordination:** Manages data space (`L1_data_space_module`) and result space (`L1_result_space_module`) interactions

Security features include path traversal prevention, file type validation, and size limits (2GB maximum).

**Value**

NULL (invisibly). The module manages reactive state internally and communicates with child modules. No explicit return value.

**See Also**

[app\\_ui](#) for the corresponding UI function. [L1\\_data\\_space\\_module](#), [L1\\_result\\_space\\_module](#) for sub-modules. [omicsViewer](#) for the high-level launcher.

**Examples**

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

---

app_ui	<i>omicsViewer Application UI (Level 0)</i>
--------	---

---

**Description**

Generates the user interface for the main omicsViewer application. This function creates a responsive layout with data exploration panels, snapshot functionality, and data export capabilities. Primarily intended for developers extending the application.

**Usage**

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

**Arguments**

id	Character. Namespace ID for the Shiny module. Must match the ID used in <a href="#">app_module</a> .
showDropList	Logical. Whether to display the file selection dropdown menu. Set to FALSE when providing data directly via <code>ESVObj</code> parameter in <a href="#">app_module</a> . Default: TRUE.
activeTab	Character. Initial tab to display when data is loaded. Options: <ul style="list-style-type: none"> <li>• "Feature" - Feature space scatter plot</li> <li>• "Feature table" - Feature metadata table</li> <li>• "Sample" - Sample space scatter plot</li> <li>• "Sample table" - Sample metadata table</li> <li>• "Cor" - Correlation heatmap</li> <li>• "Heatmap" - Expression heatmap</li> <li>• "Dynamic heatmap" - Interactive heatmap with selection</li> <li>• "Expression" - Expression matrix table</li> <li>• "GSList" - Gene set membership table</li> </ul> Default: "Feature".

**Value**

A `fluidRow` containing the complete UI structure, including:

- File selection dropdown (if `showDropList = TRUE`)
- Data summary display
- Export and snapshot buttons
- Two-column layout with data space (left) and analysis space (right)

**See Also**

[app\\_module](#) for the corresponding server logic. [omicsViewer](#) for the high-level application launcher.

**Examples**

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

---

asEsetWithAttr

*Convert SummarizedExperiment to ExpressionSet retaining all attributes*

---

**Description**

Convert `SummarizedExperiment` to `ExpressionSet` retaining all attributes

**Usage**

```
asEsetWithAttr(x)
```

**Arguments**

`x` an object of class `SummarizedExperiment`

**Value**

an object of class `ExpressionSet`

---

`batch_comparison_module`*Batch Comparison Server Function*

---

## Description

Server logic for the batch comparison module. Automatically tests all phenotype variables or all features for differences between selected and unselected samples with appropriate statistical tests and FDR correction.

## Usage

```
batch_comparison_module(  
  id,  
  reactive_expr,  
  reactive_phenoData,  
  reactive_featureData,  
  reactive_i_samples  
)
```

## Arguments

<code>id</code>	Character. Namespace ID for the Shiny module.
<code>reactive_expr</code>	Reactive expression. Returns numeric matrix with features as rows and samples as columns.
<code>reactive_phenoData</code>	Reactive expression. Returns data.frame of sample metadata.
<code>reactive_featureData</code>	Reactive expression. Returns data.frame of feature metadata.
<code>reactive_i_samples</code>	Reactive expression. Returns integer vector of selected sample indices.

## Value

Reactive value containing information about the selected row from the results table.

## See Also

[batch\\_comparison\\_ui](#) for the corresponding UI function.

Other analysis modules: [batch\\_comparison\\_ui\(\)](#), [dose\\_response\\_module\(\)](#), [dose\\_response\\_ui\(\)](#)

---

batch\_comparison\_ui     *Batch Comparison UI Function*

---

### Description

Creates the user interface for the batch comparison module that automatically compares either all phenotype variables or all features between selected and unselected sample groups.

### Usage

```
batch_comparison_ui(id)
```

### Arguments

id                     Character. Namespace ID for the Shiny module. Must match the ID used in [batch\\_comparison\\_module](#).

### Value

A tagList containing:

- Toggle buttons to select comparison mode (phenotype vs features)
- Results table with p-values and FDR correction
- Download functionality for results
- Selected row information panel

### See Also

[batch\\_comparison\\_module](#) for the corresponding server logic.

Other analysis modules: [batch\\_comparison\\_module\(\)](#), [dose\\_response\\_module\(\)](#), [dose\\_response\\_ui\(\)](#)

---

constants                     *Application Constants*

---

### Description

This file contains named constants used throughout the omicsViewer application. Using named constants instead of "magic numbers" improves code readability, maintainability, and makes it easier to update values in a single location.

---

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

```
correlationAnalysis(  
  x,  
  pheno,  
  min.value = MIN_SAMPLES_CORRELATION,  
  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	<i>convert a column compressed sparse matrix to a list</i>
----------	--

---

**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

---

documentation_template	<i>Documentation Template for omicsViewer Modules</i>
------------------------	---

---

**Description**

This file provides the standard documentation template for all Shiny modules in the omicsViewer package. All module functions should follow this structure to ensure consistency and completeness.

---

dose_response_module	<i>Dose Response Curve Server Function</i>
----------------------	--

---

**Description**

Server logic for the dose response curve visualization module. Fits dose-response curves using the drc package and displays fitted parameters and plots for selected features.

**Usage**

```
dose_response_module(  
  id,  
  reactive_expr,  
  reactive_phenoData,  
  reactive_featureData,  
  reactive_i,  
  reactive_attr_drc  
)
```

**Arguments**

id	Character. Namespace ID for the Shiny module. Must match the ID used in <a href="#">dose_response_ui</a> .
reactive_expr	Reactive expression. Returns a numeric matrix with features as rows and samples as columns containing expression/response values.
reactive_phenoData	Reactive expression. Returns a data.frame of sample metadata including dose and curve ID columns.
reactive_featureData	Reactive expression. Returns a data.frame of feature metadata with features as rows.
reactive_i	Reactive expression. Returns a single integer index indicating which feature row to display. Must have length 1.
reactive_attr_drc	Reactive expression. Returns a named character vector with elements "dose_col" and "curveid_col" specifying the column names in phenoData for dose values and curve identifiers.

**Details**

The module fits 4-parameter or 5-parameter log-logistic curves to the dose-response data and extracts parameters including EC50, hill slope, minimum and maximum responses. Only single feature selection is supported.

**Value**

NULL (invisibly). The module displays plots and tables but does not return a reactive value.

**See Also**

[dose\\_response\\_ui](#) for the corresponding UI function. [plotDCMat](#) for the plotting function. [drmMat](#) for curve fitting.

Other analysis modules: [batch\\_comparison\\_module\(\)](#), [batch\\_comparison\\_ui\(\)](#), [dose\\_response\\_ui\(\)](#)

---

dose\_response\_ui      *Dose Response Curve UI Function*

---

**Description**

Creates the user interface for the dose response curve visualization module. Displays dose-response curves with fitted parameters and feature information in a multi-panel layout.

**Usage**

```
dose_response_ui(id)
```

**Arguments**

id	Character. Namespace ID for the Shiny module. Must match the ID used in <a href="#">dose_response_module</a> .
----	--

**Value**

A fluidRow containing:

- Plot panel: Dose-response curve visualization
- Parameter table: Fitted curve parameters (hill slope, EC50, etc.)
- Feature table: Selected feature information

**See Also**

[dose\\_response\\_module](#) for the corresponding server logic. [plotDCMat](#) for the underlying plotting function.

Other analysis modules: [batch\\_comparison\\_module\(\)](#), [batch\\_comparison\\_ui\(\)](#), [dose\\_response\\_module\(\)](#)

---

draw\_roc\_pr

*Drawing ROC and PR curve*

---

**Description**

Drawing ROC and PR curve

**Usage**

```
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**

```
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(1))
```

---

 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

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

### Arguments

<code>x</code>	a numerical matrix where the rows are features and columns are samples.
<code>fitvar</code>	a numerical variable has the same length as <code>ncol(x)</code> to indicate the dose/time/concentration conditions.
<code>fitvar.name</code>	the name of the <code>fitvar</code> , a length one character. Will be used as the label for x-axis when drawing the dose curve.
<code>curveid</code>	a numeric vector or factor containing the grouping of the columns in <code>x</code> .
<code>fct.name</code>	the function name, e.g. "LL.4()", "LL.3()", "LL.2()" and "LL.5()", which are defined in the <code>drc</code> package.

### Value

a list of `drc` object

---

 error\_handling

*Error Handling Utilities for API Calls*


---

### Description

Utility functions for robust error handling of external API calls. Provides consistent error messages and graceful degradation when network requests fail.

---

exprspca	<i>Perform PCA and prepare results for omicsViewer</i>
----------	--

---

### 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 <a href="#">fillNA</a> .
...	other parameters passed to <a href="#">prcomp</a>

### Value

a data.frame storing the PCA results

### Examples

```
# 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	<i>Add extra columns to the phenoData/colData or featureData/rowData in ExpressionSet/SummarizedExperiment</i>
----------------	--

---

### Description

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

**Usage**

```

extendMetaData(object, newData, where)

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

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

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

```

**Arguments**

object	an object of ExpressionSet-class
newData	a data.frame containing the data to be added
where	where to add the extra columns, should be one of "pData", "fData", "rowData" and "colData".

**Value**

an object of ExpressionSet-class

**Note**

The attributes in the pheno data and feature data will be preserved

**Examples**

```

est <- Biobase::ExpressionSet(assayData=matrix(runif(1000), nrow=100, ncol=10))
Biobase::pData(est)
est <- extendMetaData(est, data.frame(letter = letters[1:10]), where = "pData")
Biobase::pData(est)

```

---

extractParamDC	<i>Extracting parameters from drc models</i>
----------------	--

---

**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 prefixlcurveidlcurveparameter

**Note**

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

---

extractParamDCList	<i>Extracting parameter from a list of drc object</i>
--------------------	---

---

**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**

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

**Arguments**

x	a list of drc object
prefix	for column header

**Value**

a data.frame

---

fgsea1	<i>Wrapper of fgseaMultilevel function to take binary gene set matrix as input</i>
--------	--

---

### Description

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

### Usage

```
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

```
## not for users
# library(fgsea)
# library(Biobase)
# dat <- readRDS(system.file(package = "omicsViewer", "extdata/demo.RDS"))
# fd <- fData(dat)
# fdgs <- fd[, grep("^GS\\|", colnames(fd))]
# res <- fgsea1(fdgs, stats = fd$t-test|OV_BR|md`, minSize = 5, maxSize = 500)
# res <- fgsea1(
#   fdgs, stats = fd$t-test|OV_BR|md`,
#   minSize = 5, maxSize = 500, gs_desc = colnames(fdgs))
```

---

fillNA	<i>Filling NAs in a matrix using constants calculated from user the defined function</i>
--------	--

---

### 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**

```
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 be 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 function(x) 0 # replace NA by 0

**Value**

a matrix without NAs

**Note**

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

**Examples**

```
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**

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

**Arguments**

<code>x</code>	an expression matrix
<code>max.quantile</code>	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.
<code>max.value</code>	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 <code>max.quantile</code> is set to "NULL".
<code>var</code>	variables has the same length as the column number in <code>x</code> to indicate which sample is from which group
<code>min.rep</code>	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**

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

---

geneshot\_module

*Geneshot Search Server Function*


---

**Description**

Server logic for the Geneshot gene search module. Queries the Geneshot API to find genes associated with user-provided text terms, ranks results by publication metrics, and highlights overlap with selected features.

**Usage**

```
geneshot_module(
  id,
  pdata,
  fdata,
  expr,
  feature_selected,
  sample_selected,
  object,
  reactive_status = reactive(NULL)
)
```

**Arguments**

<code>id</code>	Character. Namespace ID for the Shiny module. Must match the ID used in <a href="#">geneshot_ui</a> .
<code>pdata</code>	Reactive expression. Returns a data.frame of sample metadata (phenotype data). Currently unused but required for module consistency.

<code>fdata</code>	Reactive expression. Returns a data.frame of feature metadata with features as rows. Used for ID mapping and overlap detection.
<code>expr</code>	Reactive expression. Returns a numeric matrix with features as rows and samples as columns. Currently unused but required for module consistency.
<code>feature_selected</code>	Reactive expression. Returns a character vector or integer vector of currently selected feature IDs/indices. Used to highlight overlap with search results.
<code>sample_selected</code>	Reactive expression. Returns selected sample IDs. Currently unused but required for module consistency.
<code>object</code>	Reactive expression. Returns the full ExpressionSet or SummarizedExperiment object. Currently unused but required for module consistency.
<code>reactive_status</code>	Reactive expression. Returns a list containing saved state for session restoration. Optional. Default: <code>reactive(NULL)</code> .

### Details

The module performs the following steps:

1. Accepts semicolon-separated search terms from user
2. Queries Geneshot API via `getAutoRIF`
3. Filters results to top 20 genes (`GENESHOT_TOP_RESULTS`)
4. Highlights genes that overlap with currently selected features
5. Displays results in interactive scatter plot and table

Handles API errors gracefully with user notifications.

### Value

A reactive expression returning a list with module state for session saving.

### See Also

`geneshot_ui` for the corresponding UI function. `getAutoRIF` for the API call function.

Other search modules: `geneshot_ui()`

---

`geneshot_ui`

*Geneshot Search UI Function*

---

### Description

Creates the user interface for the Geneshot gene search module. Allows users to search for genes associated with arbitrary text queries using the Geneshot API and visualize results by publication metrics.

### Usage

```
geneshot_ui(id)
```

**Arguments**

`id` Character. Namespace ID for the Shiny module. Must match the ID used in [geneshot\\_module](#).

**Value**

A `tagList` containing:

- Text input for search terms (semicolon-separated)
- Submit button to trigger search
- Gene ID mapper selector
- Interactive scatter plot of search results
- Results table with download functionality

**References**

Lachmann et al. (2019) Geneshot: search engine for ranking genes from arbitrary text queries. *Nucleic Acids Research* 47(W1):W571-W577.

**See Also**

[geneshot\\_module](#) for the corresponding server logic. [getAutoRIF](#) for the underlying API function. Other search modules: [geneshot\\_module\(\)](#)

---

getAutoRIF	<i>Get genes associated with search terms and AutoRIF annotations</i>
------------	---

---

**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	<i>Parse mqpar.xml file</i>
-------------	-----------------------------

---

## Description

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

## Usage

```
getMQParams(x)
```

## Arguments

x                    the path to mqpar.xml file

## Value

a list of MQ paramters

---

getStringId	<i>Mapping ids to string ids</i>
-------------	----------------------------------

---

## Description

the string ids can be used as background in the string enrichment analysis

## Usage

```
getStringId(genes, taxid = 9606, caller = "omicsViewer")
```

## Arguments

genes                a character vector of gene ids  
taxid                taxonomy ids  
caller                your identifier for string-db.org

**Note**

<https://string-db.org/cgi/help.pl?subpage=api>

**Examples**

```
1
# gg = c('P04637', 'P00533', 'P04626', "Q8IYB3", "O75494", "Q9Y696")
# getStringId(gg)
```

---

getUPRefProteomeID	<i>get uniprot reference proteome IDs</i>
--------------------	---

---

**Description**

get uniprot reference proteome IDs

get uniprot reference proteome IDs

**Usage**

```
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

**Value**

a character vector of UP ids

a character vector of UP ids

**Functions**

- `getUPRefProteomeID()`: get uniprot reference protein IDs

---

 gsAnnotIdList

*Annotation of gene/protein function using multiple IDs.*


---

## Description

Annotation of gene/protein function using multiple IDs.

## Usage

```
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, gsId, 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)
```

---

gslist\_module

*Gene Set List Server Function*

---

## Description

Server logic for the gene set membership display module. Retrieves and displays gene set annotations for selected features from the feature data attributes.

## Usage

```
gslist_module(id, reactive_featureData, reactive_i)
```

## Arguments

id	Character. Namespace ID for the Shiny module. Must match the ID used in <a href="#">gslist_ui</a> .
reactive_featureData	Reactive expression. Returns a data.frame of feature metadata with a "GS" attribute containing gene set membership information. The "GS" attribute should be a data.frame with columns: <ul style="list-style-type: none"><li>• featureId: Feature identifiers</li><li>• gsId: Gene set identifiers</li><li>• Additional annotation columns (optional)</li></ul>
reactive_i	Reactive expression. Returns feature IDs or indices to display. Can be: <ul style="list-style-type: none"><li>• Character vector of feature IDs</li><li>• Integer vector of feature indices</li><li>• Logical scalar TRUE (show all features)</li><li>• NULL or NA (show all features)</li></ul>

## Details

The module extracts gene set annotations from the "GS" attribute of feature data and filters to show only selected features. Gene sets are displayed with associated feature annotations from columns starting with "General".

## Value

A reactive expression returning a character vector of feature IDs for the selected table row, or NULL if no row is selected.

## See Also

[gslist\\_ui](#) for the corresponding UI function.

Other enrichment modules: [gslist\\_ui\(\)](#)

---

gslist_ui	<i>Gene Set List UI Function</i>
-----------	----------------------------------

---

**Description**

Creates the user interface for the gene set membership display module. Shows which gene sets contain the selected features with downloadable results.

**Usage**

```
gslist_ui(id)
```

**Arguments**

id	Character. Namespace ID for the Shiny module. Must match the ID used in <a href="#">gslist_module</a> .
----	---

**Value**

A tagList containing a data table with download functionality showing gene set memberships for selected features.

**See Also**

[gslist\\_module](#) for the corresponding server logic.

Other enrichment modules: [gslist\\_module\(\)](#)

---

hasAttr	<i>Check whether an object has an attribute</i>
---------	---

---

**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	<i>Convert hclust object to/from single character</i>
------------	---

---

**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 be retained in the conversion. The conversion decreases the precision in the \$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	<i>Calculate Jaccard distance from a list</i>
-------------	---

---

**Description**

Calculate Jaccard distance from a list

**Usage**

```
jaccardList(x)
```

**Arguments**

x                    a list

**Value**

an dist object

---

L1\_data\_space\_module    *Application level 1 module - data space*

---

**Description**

Application level 1 module - data space

**Usage**

```
L1_data_space_module(
  id,
  expr,
  pdata,
  fdata,
  reactive_x_s = reactive(NULL),
  reactive_y_s = reactive(NULL),
  reactive_x_f = reactive(NULL),
  reactive_y_f = reactive(NULL),
  cormat = reactive(NULL),
  status = reactive(NULL)
)
```

**Arguments**

id	module id
expr	reactive value; expression matrix
pdata	reactive value; phenotype data
fdata	reactive value; feature data
reactive_x_s	pre-selected x axis for sample space
reactive_y_s	pre-selected y axis for sample space
reactive_x_f	pre-selected x axis for feature space
reactive_y_f	pre-selected y axis for feature space
cormat	reactive value; correlation matrix. if not given, calculated on the fly.
status	initial status

---

L1_data_space_ui	<i>Application level 1 ui - data space</i>
------------------	--

---

**Description**

Application level 1 ui - data space

**Usage**

```
L1_data_space_ui(id, activeTab = "Feature")
```

**Arguments**

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

---

L1_result_space_module	<i>Utility L1 result space ui</i>
------------------------	-----------------------------------

---

**Description**

Utility L1 result space ui

**Usage**

```
L1_result_space_module(
  id,
  reactive_expr,
  reactive_phenoData,
  reactive_featureData,
  reactive_i = reactive(NULL),
  reactive_highlight = reactive(NULL),
  additionalTabs = NULL,
  object = NULL,
  status = reactive(NULL)
)
```

**Arguments**

id	module id
reactive_expr	expression matrix
reactive_phenoData	phentype data
reactive_featureData	feature data
reactive_i	row ID/name of rows selected

reactive_highlight	col ID/name of columns selected
additionalTabs	additional tabs added to "Analyst" panel
object	originally loaded object, mostly an ExpressionSet or SummarizedExperiment object
status	initial status

---

L1_result_space_ui	<i>Utility L1 result space ui</i>
--------------------	-----------------------------------

---

**Description**

Utility L1 result space ui

**Usage**

L1\_result\_space\_ui(id)

**Arguments**

id	id
----	----

---

list2csc	<i>convert a list to column compressed sparse matrix</i>
----------	--

---

**Description**

convert a list to column compressed sparse matrix

**Usage**

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

---

meta\_scatter\_module     *Utility - scatter plot for meta shiny module*

---

### Description

Utility - scatter plot for meta shiny module

### Usage

```
meta_scatter_module(
  id,
  reactive_meta = reactive(NULL),
  reactive_expr = reactive(NULL),
  combine = c("pheno", "feature"),
  source = "plotlyscattersource",
  reactive_x = reactive(NULL),
  reactive_y = reactive(NULL),
  reactive_status = reactive(NULL)
)
```

### Arguments

id	Character. Namespace ID for the Shiny module.
reactive_meta	reactive meta data, phenotype data or feature data
reactive_expr	reactive expression data
combine	how to combine the expression and meta data, pheno or feature?
source	source id for plotly object
reactive_x	reactive value for pre-selected x-axes
reactive_y	reactive value for pre-selected y-axes
reactive_status	the status of scatter plot, e.g. x-, y-axis, color variable, shape variable, etc.

---

meta\_scatter\_ui     *Meta Scatter Plot UI Function*

---

### Description

Creates the user interface for the metadata scatter plot visualization module. Provides interactive scatter plots with advanced selection tools including corner selection for volcano plots.

### Usage

```
meta_scatter_ui(id)
```

### Arguments

id	Character. Namespace ID for the Shiny module. Must match the ID used in <a href="#">meta_scatter_module</a> .
----	---

**Value**

A tagList containing:

- Figure attribute selector (color, shape, size controls)
- Clear selection button
- X-axis and Y-axis variable selectors
- Interactive plotly scatter plot with lasso/box selection

**See Also**

[meta\\_scatter\\_module](#) for the corresponding server logic. [plotly\\_scatter\\_module](#) for the scatter plot implementation.

---

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 use [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 <a href="#">fillNA</a> .
...	other parameters passed to <a href="#">t.test</a>

**Value**

a data.frame stores the t-test results with the follow columns: mean|[selected header in pheno]|[group 1 in test] - The mean value of group 1 n value|[selected header in pheno]|[group 1 in test] - The number of value used in the test for group 1 quantile|[selected header in pheno]|[group 1 in test] - The quantile of means values in group 1 mean|[selected header in pheno]|[group 2 in test] - The mean value of group 2 n value|[selected header in pheno]|[group 2 in test] - The number of value used in the test for group 2 quantile|[selected header in pheno]|[group

2 in test] - The quantile of means values in group 2 `ttest|[group 1 in test]_vs_[group 2 in test]|pvalue` - The p-value return by `t.test` `ttest|[group 1 in test]_vs_[group 2 in test]|log.pvalue`  
 - The `-log10` transformed p-value `ttest|[group 1 in test]_vs_[group 2 in test]|fdr` - The BH method corrected p-values, e.g. FDR `ttest|[group 1 in test]_vs_[group 2 in test]|log.fdr`  
 - The `-log10` transformed FDR `ttest|[group 1 in test]_vs_[group 2 in test]|mean.diff` - The difference between the means of the two groups, e.g. fold change

## Examples

```
# 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	logical; 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	<i>Normalize total sum</i>
------------------	----------------------------

---

**Description**

Normalize total sum

**Usage**

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

**Arguments**

x a log10 transformed expression matrix

**Value**

a normalized matrix

**Examples**

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

---

normalizeColWise	<i>Column-wise normalization of expression matrix</i>
------------------	---

---

**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 stablization")[1]
)
```

**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 stablization" - 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)
```

---

normalizeData	<i>Normalized expression matrix</i>
---------------	-------------------------------------

---

**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 stablization")[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 <a href="#">normalizeColWise</a>
rowWise	row-wise normalization method to used Reference - using <a href="#">removeVarQC</a> method Batch mean - using <a href="#">rowshift</a> method without reference samples Batch reference - using <a href="#">rowshift</a> 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

*Launch the omicsViewer Shiny Application***Description**

Starts an interactive Shiny application for exploring omics data, including visualization of expression matrices, feature and sample metadata, statistical analyses, and functional enrichment results. The viewer supports both `ExpressionSet` and `SummarizedExperiment` objects.

**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**

<code>dir</code>	Character. Path to directory containing the <code>ExpressionSet</code> or <code>SummarizedExperiment</code> object saved as <code>.RDS</code> file. Provide only the directory path, not the full file path. The viewer will list all compatible files in this directory.
<code>additionalTabs</code>	List. Optional custom Shiny modules to add as tabs in the "Analyst" panel. Each element should be a list with: <code>tabName</code> (character), <code>moduleName</code> (character), <code>moduleUi</code> (UI function), and <code>moduleServer</code> (server function).
<code>filePattern</code>	Character. Regular expression pattern to filter files displayed in the directory. Default: <code>".(RDS DB SQLITE SQLITE3)\$"</code> (case-insensitive).
<code>ESVObj</code>	<code>ExpressionSet</code> or <code>SummarizedExperiment</code> . Optional pre-loaded object to view directly without file selection. If provided, the file dropdown will show "ESVObj.RDS".
<code>esetLoader</code>	Function. Custom loader for reading saved objects. Default: <code>readESVObj</code> . Should accept a file path and return an <code>ExpressionSet</code> or <code>SummarizedExperiment</code> object.
<code>exprsGetter</code>	Function. Extracts expression matrix from loaded object. Default: <code>getExprs</code> . Should return a numeric matrix.
<code>pDataGetter</code>	Function. Extracts phenotype/sample metadata. Default: <code>getPData</code> . Should return a <code>data.frame</code> with rownames matching sample names.
<code>fDataGetter</code>	Function. Extracts feature metadata. Default: <code>getFData</code> . Should return a <code>data.frame</code> with rownames matching feature names.

defaultAxisGetter	Function. Determines default axes for plots. Takes two arguments: x (the loaded object) and what (one of "sx", "sy", "fx", "fy" for sample/feature space x/y axes). Should return column name from metadata.
appName	Character. Application title displayed in the UI. Default: "omicsViewer".
appVersion	Character or package_version. Version number displayed in UI. Default: current package version.

**Value**

NULL (invisibly). Launches the Shiny application. The app runs until stopped by the user.

**See Also**

[prepOmicsViewer](#) for preparing data objects for visualization. [app\\_module](#) for the main application module (developers only).

**Examples**

```
if (interactive()) {
  # Basic usage with example data
  omicsViewer(system.file("extdata", package = "omicsViewer"))

  # With pre-loaded object
  packdir <- system.file("extdata", package = "omicsViewer")
  eset <- readRDS(file.path(packdir, "exampleEset.RDS"))
  omicsViewer(packdir, ESVObj = eset)
}
```

---

parseDatTerm

*Extract function annotation from uniprot .dat file*

---

**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	<i>Draw dose-response curves</i>
--------	----------------------------------

---

**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	<i>Draw dose response curve given parameters in the omicsViewer object</i>
-----------	--

---

**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,
  ...
)
```

**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(
  id,
  reactive_param_plotly_boxplot,
  reactive_checkpoint = reactive(TRUE)
)
```

**Arguments**

id	module id
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**

```
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 = "")
plotly_boxplot_module("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\_boxplot\_ui      *Shiny module for boxplot using plotly - UI*

---

## Description

Function should only be used for the developers

## Usage

```
plotly_boxplot_ui(id)
```

## Arguments

id                      id

## Value

a tagList of UI components

a tagList of UI components

## Examples

```

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 = "")
    plotly_boxplot_module("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

```

plotly_scatter_module(
  id,
  reactive_param_plotly_scatter,
  reactive_regLine = reactive(FALSE),
  reactive_checkpoint = reactive(TRUE),
  htest_var1 = reactive(NULL),
  htest_var2 = reactive(NULL)
)

```

### Arguments

id	module id
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 <- plotly_scatter_module("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 <- plotly_scatter_module("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

```

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)
}

```

---

plot\_roc\_pr\_module      *Shiny module for ROC/PR plot - Module*

---

## Description

Shiny module for ROC/PR plot - Module

## Usage

```
plot_roc_pr_module(id, reactive_param, reactive_checkpoint = reactive(TRUE))
```

## Arguments

`id`                    module id

`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)
    )
    plot_roc_pr_module("testplot",
      reactive_param = reactive(list(
        x = ng(),
        y = rnorm(100)
      ))
    )
  }
  shinyApp(ui, server)
}

```

---

```
prepOmicsViewer
```

---

```
Prepare Omics Data for Visualization with omicsViewer
```

---

**Description**

A comprehensive data preparation function that processes expression matrices and associated meta-data for interactive visualization with [omicsViewer](#). Automatically performs dimensionality reduction (PCA), statistical testing (t-tests), and integrates gene set annotations, STRING database IDs, and survival data.

**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**

<code>expr</code>	Numeric matrix. Expression data with features in rows and samples in columns. Should be log-transformed (e.g., log2 or log10). Row and column names must be unique. Missing values (NA) are permitted if <code>pca.fillNA</code> or <code>ttest.fillNA</code> are TRUE.
<code>pData</code>	Data.frame. Sample/phenotype metadata with one row per sample. Row names must match column names of <code>expr</code> . Should contain grouping variables for statistical tests.
<code>fData</code>	Data.frame. Feature metadata with one row per feature. Row names must match row names of <code>expr</code> . Can include gene symbols, descriptions, database IDs, etc.
<code>PCA</code>	Logical. Whether to perform Principal Component Analysis. Default: TRUE. Results are added to both sample and feature metadata.
<code>ncomp</code>	Integer. Number of principal components to compute. Default: minimum of 8 or the number of samples. Ignored if <code>PCA = FALSE</code> .
<code>pca.fillNA</code>	Logical. If TRUE, missing values in <code>expr</code> are imputed before PCA by replacing with minimum value * 0.9. Default: TRUE. Two PCAs are performed: one with imputation and one without (if possible).
<code>t.test</code>	Matrix or NULL. Definition of t-tests to perform. Should be an $n \times 3$ matrix where each row specifies: [column_name, group1, group2]. The column should exist in <code>pData</code> . Example: <code>rbind(c("Treatment", "Drug", "Control"), c("Genotype", "WT", "KO"))</code> . Results are added as columns to <code>fData</code> . NULL = no t-tests.
<code>ttest.fillNA</code>	Logical. Whether to impute missing values before t-tests. Default: FALSE (features with NAs are excluded from testing).
<code>...</code>	Additional arguments passed to <code>t.test</code> , such as <code>paired = TRUE</code> for paired t-tests or <code>var.equal = TRUE</code> for equal variance assumption.
<code>gs</code>	Gene set annotations in one of two formats: <ul style="list-style-type: none"> <li>• Data.frame with columns: <code>featureId</code> (indices), <code>gsId</code> (gene set IDs), <code>weight</code> (optional weights). See <a href="#">gsAnnotIdList</a>.</li> <li>• Matrix or sparse matrix (<code>dgCMatrix</code>) with features in rows and gene sets in columns. Values indicate membership (0/1 or weights).</li> </ul> <p>NULL = no gene set annotations. Enables ORA and GSEA analyses in viewer.</p>
<code>stringDB</code>	Character vector of length <code>nrow(expr)</code> . Protein/gene identifiers compatible with STRING database queries (e.g., Ensembl protein IDs, gene names). NULL = STRING network analysis disabled.
<code>surv</code>	Survival data in one of three formats: <ul style="list-style-type: none"> <li>• Vector of length <code>ncol(expr)</code>: single survival time with censoring indicated by "+" suffix (e.g., "120+", "45").</li> <li>• Matrix/data.frame: multiple survival endpoints with samples in rows. Column names will be prefixed with "Surv all ". Values must be numeric with optional "+" suffix.</li> </ul> <p>NULL = no survival analysis.</p>
<code>SummarizedExperiment</code>	Logical. If TRUE, returns a <code>SummarizedExperiment</code> object; if FALSE, returns an <code>ExpressionSet</code> . Default: TRUE.

## Details

The function performs the following processing steps:

1. Validates dimensions and ensures unique row/column names
2. Standardizes column names by prefixing with data type (e.g., "GeneralAll")
3. Performs PCA on expression data (with and without imputation)
4. Conducts statistical tests (t-tests) between specified groups
5. Computes feature rankings across samples
6. Integrates gene set, STRING, and survival annotations
7. Sets sensible default axes for visualization

All metadata columns are prefixed with standardized headers following the pattern "Category/Subcategory/Variable" to organize variables in the viewer interface.

## Value

A SummarizedExperiment or ExpressionSet object ready for visualization with [omicsViewer](#). The object includes:

- Expression matrix (and optionally imputed matrix)
- Enhanced metadata with PCA results, t-test statistics, rankings
- Gene set annotations (as attributes)
- Default axis selections (as attributes: "sx", "sy", "fx", "fy")

an object of ExpressionSet or SummarizedExperiment that can be visualized using [omicsViewer](#)

## See Also

[omicsViewer](#) for launching the viewer. [multi.t.test](#) for details on t-test implementation. [gsAnnotIdList](#) for gene set annotation formatting.

## 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)
###
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("./")

```

---

read.proteinGroups      *Reading proteinGroup table of MaxQuant output*

---

## Description

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

## Usage

```
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**

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

---

read_gmt	<i>Reading gene set .gmt file</i>
----------	-----------------------------------

---

**Description**

Frequently the .gmt files are downloaded from MSigDB database

**Usage**

```
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**

```
file <- system.file("extdata", package = "omicsViewer")
file <- file.path(file, "geneset.gmt")
gs <- read_gmt(file)
```

---

removeVarQC	<i>Removing variance of reference samples</i>
-------------	---

---

**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**

```
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, <a href="#">normalize.nQuantiles</a> will be called first, the arguments here will be passed to <a href="#">normalize.nQuantiles</a>

**Value**

a normalized matrix

**Examples**

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

---

rowshift	<i>Row-wise normalization of expression matrix with or without reference sample</i>
----------	---

---

**Description**

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

**Usage**

```
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 <code>ncol(x)</code> to indicate the batch assignment of samples.
ref	a logical vector has the same length as <code>ncol(x)</code> to indicated which columns are the common references among batches. If it is <code>NULL</code> (by default), the mean of all channels will be used as batch reference. When <code>NA</code> present in the reference channels, the mean values will be used in correction.
useMean	logical; whether to use means of batches, usually set to <code>TRUE</code> when no reference available

**Value**

a matrix (hopefully without/with less batch effect)

**Examples**

```
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)
```

---

safe\_GET

*Safe HTTP GET wrapper with error handling*


---

**Description**

Wraps httr::GET with comprehensive error handling including: - Network connectivity errors - HTTP status code errors (4xx, 5xx) - Timeout handling - SSL/TLS errors

**Usage**

```
safe_GET(url, query = NULL, timeout = 30, api_name = "API", ...)
```

**Arguments**

url	The URL to fetch
query	Query parameters (optional)
timeout	Timeout in seconds (default: 30)
api_name	Name of the API for error messages (default: "API")
...	Additional parameters passed to httr::GET

**Value**

A list with: - success: logical, TRUE if request succeeded - data: response content if successful, NULL otherwise - error: error message if failed, NULL otherwise - status\_code: HTTP status code if available

---

safe\_POST

*Safe HTTP POST wrapper with error handling*


---

**Description**

Wraps httr::POST with comprehensive error handling including: - Network connectivity errors - HTTP status code errors (4xx, 5xx) - Timeout handling - SSL/TLS errors

**Usage**

```
safe_POST(
  url,
  body = NULL,
  encode = "json",
  timeout = 30,
  api_name = "API",
  ...
)
```

**Arguments**

url	The URL to post to
body	Request body
encode	Encoding method (default: "json")
timeout	Timeout in seconds (default: 30)
api_name	Name of the API for error messages (default: "API")
...	Additional parameters passed to httr::POST

**Value**

A list with: - success: logical, TRUE if request succeeded - data: response content if successful, NULL otherwise - error: error message if failed, NULL otherwise - status\_code: HTTP status code if available

---

saveOmicsViewerDb	<i>Save the xcmsViewer result object as sqlite database</i>
-------------------	---

---

**Description**

Save the xcmsViewer result object as sqlite database

**Usage**

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

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

## S4 method for signature 'ExpressionSet,character'
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**

```
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")
```

---

stringD3Net	<i>Drawing network given network and gene set result</i>
-------------	--

---

**Description**

Drawing network given network and gene set result

**Usage**

```
stringD3Net(ntwk, gsa, i, label = FALSE)
```

**Arguments**

ntwk	network result, often returned by "stringNetwork" function.
gsa	gene set result, often returned by "stringGSA" function
i	row index of gsa, which should be highlighted in the network
label	whether the point should be labelled in the network

---

stringGSA	<i>Performing gene set analysis using string-db</i>
-----------	---

---

**Description**

Performing gene set analysis using string-db

**Usage**

```
stringGSA(
  genes,
  taxid = 9606,
  background = NULL,
  backgroundStringId = FALSE,
  caller = "omicsViewer"
)
```

**Arguments**

genes	a character vector of gene ids
taxid	taxonomy ids (species NCBI identifier)
background	the background genes
backgroundStringId	logical value, whether the identifier given in background is already stringid, only used when background != NULL. You can use <a href="#">getStringId</a> to convert your id to string id.
caller	your identifier for string-db.org

**Note**

<https://string-db.org/cgi/help.pl?subpage=api>

**Examples**

```
1
# gg = c('P04637', 'P00533', 'P04626', "Q8IYB3", "O75494", "Q9Y696")
# u <- stringGSA(gg)
```

---

stringNetwork	<i>Retrieve string network</i>
---------------	--------------------------------

---

**Description**

get string network

**Usage**

```
stringNetwork(genes, taxid = 9606, caller = "omicsViewer")
```

**Arguments**

genes	the gene ids
taxid	taxonomy ids
caller	your identifier for string-db.org

---

string_module	<i>STRING Network Analysis Server Function</i>
---------------	--

---

**Description**

Server logic for the STRING protein-protein interaction network analysis module. Queries the STRING database API to retrieve protein interactions and perform functional enrichment analysis on selected features.

**Usage**

```
string_module(
  id,
  reactive_ids,
  reactive_status = reactive(NULL),
  active = reactive(FALSE)
)
```

## Arguments

id	Character. Namespace ID for the Shiny module. Must match the ID used in <a href="#">string_ui</a> .
reactive_ids	Reactive expression. Returns a character vector of protein/gene identifiers to query. Maximum of 300 features allowed (enforced by STRING API limits).
reactive_status	Reactive expression. Returns a list containing saved state for session restoration (tax ID, label settings). Optional. Default: <code>reactive(NULL)</code> .
active	Reactive expression. Returns a logical indicating whether the module should auto-run on initialization. Used for session restoration. Default: <code>reactive(FALSE)</code> .

## Details

## API Interaction The module makes two separate API calls to STRING database:

1. Network query: Retrieves protein-protein interactions
2. Enrichment query: Performs gene set enrichment analysis

Both queries are rate-limited and may fail with network errors. The module handles errors gracefully with user notifications.

## Feature Limits - Maximum 300 genes (STRING\_MAX\_GENES constant) - Maximum 999 network edges displayed (STRING\_MAX\_NETWORK\_EDGES constant)

## Value

A reactive expression returning a list with:

- tax: Taxonomy ID used
- showLabel: Logical, whether labels are shown in network

## See Also

[string\\_ui](#) for the corresponding UI function. [stringNetwork](#) for network retrieval. [stringGSA](#) for enrichment analysis. [stringD3Net](#) for network visualization.

Other network modules: [string\\_ui\(\)](#)

---

string\_ui

*STRING Network Analysis UI Function*

---

## Description

Creates the user interface for the STRING protein-protein interaction network analysis module. Displays network visualization, enrichment results, and taxonomy configuration.

## Usage

```
string_ui(id)
```

## Arguments

`id` Character. Namespace ID for the Shiny module. Must match the ID used in [string\\_module](#).

## Value

A tagList containing:

- Taxonomy code input
- Feature count display with max limit warning
- Action button to trigger analysis
- Enrichment results table with download
- Interactive network visualization with label toggle

## See Also

[string\\_module](#) for the corresponding server logic. [stringNetwork](#) for network API calls. [stringGSA](#) for enrichment analysis.

Other network modules: [string\\_module\(\)](#)

---

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

```
triselector_module(  
  id,  
  reactive_x,  
  reactive_selector1 = reactive(NULL),  
  reactive_selector2 = reactive(NULL),  
  reactive_selector3 = reactive(NULL),  
  label = "Group Label:"  
)
```

## Arguments

<code>id</code>	module id
<code>reactive_x</code>	an nx3 matrix
<code>reactive_selector1</code>	default value for selector 1
<code>reactive_selector2</code>	default value for selector 2
<code>reactive_selector3</code>	default value for selector 3
<code>label</code>	of the triselector

**Value**

an reactive object containing the selected values

**Examples**

```
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 <- triselector_module("tres", reactive_x = reactive(triset),
      reactive_selector1 = reactive("ttest"),
      reactive_selector2 = reactive("RE_vs_ME"),
      reactive_selector3 = reactive("mean.diff"))
    }
    v2 <- triselector_module("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)
}
```

---

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**

```
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 <- triselector_module("tres", reactive_x = reactive(triset),
      reactive_selector1 = reactive("ttest"),
      reactive_selector2 = reactive("RE_vs_ME"),
      reactive_selector3 = reactive("mean.diff")
    )
    v2 <- triselector_module("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

**Usage**

```
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

---

validate\_api\_response    *Validate API response data*

---

### Description

Validates that API response data is in expected format and not empty.

### Usage

```
validate_api_response(data, expected_type = "data.frame", api_name = "API")
```

### Arguments

data                The response data to validate

expected\_type    Expected type ("data.frame", "list", "character", etc.)

api\_name           Name of the API for error messages

### Value

A list with: - valid: logical, TRUE if data is valid - error: error message if invalid, NULL otherwise

---

validate\_character\_vector            *Validate character vector input*

---

### Description

Validate character vector input

### Usage

```
validate_character_vector(
  vec,
  name = "vector",
  required = TRUE,
  min_length = 1,
  max_length = Inf,
  allow_empty = FALSE
)
```

**Arguments**

vec	Reactive expression or vector to validate
name	Character. Name of the vector for error messages
required	Logical. Whether NULL values are allowed. Default: TRUE
min_length	Integer. Minimum length required. Default: 1
max_length	Integer. Maximum length allowed. Default: Inf
allow_empty	Logical. Whether empty strings are allowed. Default: FALSE

**Value**

List with \$valid (logical) and \$message (character) fields

---

validate\_dataframe     *Input Validation Utilities*

---

**Description**

Provides comprehensive validation functions for Shiny module inputs to ensure data integrity and provide user-friendly error messages.

**Usage**

```
validate_dataframe(
  data,
  name = "data",
  required = TRUE,
  min_rows = 1,
  min_cols = 1
)
```

**Arguments**

data	Reactive expression or data.frame to validate
name	Character. Name of the data for error messages
required	Logical. Whether NULL values are allowed. Default: TRUE
min_rows	Integer. Minimum number of rows required. Default: 1
min_cols	Integer. Minimum number of columns required. Default: 1

**Value**

List with \$valid (logical) and \$message (character) fields

**Examples**

```
## Not run:
validation <- validate_dataframe(
  pData(eset),
  name = "phenotype data",
  min_rows = 3,
  min_cols = 2
)
if (!validation$valid) {
  showNotification(validation$message, type = "error")
  return(NULL)
}

## End(Not run)
```

---

```
validate_matching_dimensions
  Validate matching dimensions
```

---

**Description**

Validate matching dimensions

**Usage**

```
validate_matching_dimensions(
  obj1,
  obj2,
  dimension = c("rows", "cols"),
  name1 = "object1",
  name2 = "object2"
)
```

**Arguments**

obj1	First object (matrix or data.frame)
obj2	Second object (matrix or data.frame)
dimension	Character. Either "rows" or "cols" to check
name1	Character. Name of first object for error messages
name2	Character. Name of second object for error messages

**Value**

List with \$valid (logical) and \$message (character) fields

---

```
validate_numeric_matrix
```

*Validate numeric matrix input*

---

### Description

Validate numeric matrix input

### Usage

```
validate_numeric_matrix(  
  mat,  
  name = "matrix",  
  required = TRUE,  
  min_rows = 1,  
  min_cols = 1,  
  allow_na = TRUE  
)
```

### Arguments

mat	Reactive expression or matrix to validate
name	Character. Name of the matrix for error messages
required	Logical. Whether NULL values are allowed. Default: TRUE
min_rows	Integer. Minimum number of rows required. Default: 1
min_cols	Integer. Minimum number of columns required. Default: 1
allow_na	Logical. Whether NA values are allowed. Default: TRUE

### Value

List with \$valid (logical) and \$message (character) fields

---

```
validate_numeric_range
```

*Validate numeric range*

---

### Description

Validate numeric range

### Usage

```
validate_numeric_range(  
  value,  
  name = "value",  
  min = -Inf,  
  max = Inf,  
  allow_na = FALSE  
)
```

**Arguments**

value	Numeric value to validate
name	Character. Name for error messages
min	Numeric. Minimum allowed value (inclusive). Default: -Inf
max	Numeric. Maximum allowed value (inclusive). Default: Inf
allow_na	Logical. Whether NA is allowed. Default: FALSE

**Value**

List with \$valid (logical) and \$message (character) fields

---

validate\_triselector\_input

*Validate triselector input matrix*

---

**Description**

Validate triselector input matrix

**Usage**

```
validate_triselector_input(
  triset,
  name = "triselector data",
  allow_null = FALSE
)
```

**Arguments**

triset	Matrix or reactive expression. Should be nx3 matrix from str_split_fixed
name	Character. Name for error messages
allow_null	Logical. Whether NULL is allowed (e.g., during app startup). Default: FALSE

**Value**

List with \$valid (logical) and \$message (character) fields

---

validMQFolder	<i>MQ folder validator Validate whether a folder is a MQ output folder</i>
---------------	--

---

**Description**

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

**Usage**

```
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

---

varSelector	<i>variable selector</i>
-------------	--------------------------

---

**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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