

# Package ‘psychomics’

January 3, 2025

**Title** Graphical Interface for Alternative Splicing Quantification,  
Analysis and Visualisation

**Version** 1.32.0

**Encoding** UTF-8

**Description** Interactive R package with an intuitive Shiny-based graphical interface for alternative splicing quantification and integrative analyses of alternative splicing and gene expression based on The Cancer Genome Atlas (TCGA), the Genotype-Tissue Expression project (GTEx), Sequence Read Archive (SRA) and user-provided data. The tool interactively performs survival, dimensionality reduction and median- and variance-based differential splicing and gene expression analyses that benefit from the incorporation of clinical and molecular sample-associated features (such as tumour stage or survival). Interactive visual access to genomic mapping and functional annotation of selected alternative splicing events is also included.

**Depends** R (>= 4.0), shiny (>= 1.7.0), shinyBS

**License** MIT + file LICENSE

**LazyData** true

**RoxygenNote** 7.3.1

**Imports** AnnotationDbi, AnnotationHub, BiocFileCache, cluster, colourpicker, data.table, digest, dplyr, DT (>= 0.2), edgeR, fastICA, fastmatch, ggplot2, ggrepel, graphics, grDevices, highcharter (>= 0.5.0), htmltools, httr, jsonlite, limma, pairsD3, plyr, purrr, Rcpp (>= 0.12.14), recount, Rfast, R.utils, reshape2, shinyjs, stringr, stats, SummarizedExperiment, survival, tools, utils, XML, xtable, methods

**Suggests** testthat, knitr, parallel, devtools, rmarkdown, gplots, covr, car, rstudioapi, spelling

**LinkingTo** Rcpp

**VignetteBuilder** knitr

**Collate** 'RcppExports.R' 'utils.R' 'globalAccess.R' 'app.R'  
'analysis.R' 'analysis\_correlation.R'  
'analysis\_diffExpression.R' 'analysis\_diffExpression\_event.R'  
'analysis\_diffExpression\_table.R' 'analysis\_diffSplicing.R'  
'analysis\_diffSplicing\_event.R' 'analysis\_diffSplicing\_table.R'  
'analysis\_dimReduction.R' 'analysis\_dimReduction\_ica.R'

'analysis\_dimReduction\_pca.R' 'analysis\_information.R'  
 'analysis\_survival.R' 'analysis\_template.R' 'data.R'  
 'formats.R' 'data\_firebrowse.R'  
 'data\_geNormalisationFiltering.R' 'data\_gtex.R'  
 'data\_inclusionLevels.R' 'data\_inclusionLevelsFilter.R'  
 'data\_local.R' 'data\_recount.R' 'events\_suppa.R'  
 'events\_vastTools.R' 'events\_miso.R' 'events\_mats.R' 'events.R'  
 'formats\_SraRunTableSampleInfo.R'  
 'formats\_firebrowseGeneExpression.R'  
 'formats\_firebrowseJunctionReads.R'  
 'formats\_firebrowseMergeClinical.R'  
 'formats\_firebrowseNormalizedGeneExpression.R'  
 'formats\_genericClinical.R' 'formats\_genericGeneExpression.R'  
 'formats\_genericInclusionLevels.R'  
 'formats\_genericJunctionReads.R' 'formats\_genericSampleInfo.R'  
 'formats\_gtexClinical.R' 'formats\_gtexGeneReadsFormat.R'  
 'formats\_gtexJunctionReads.R' 'formats\_gtexSampleInfo.R'  
 'formats\_gtexV7Clinical.R' 'formats\_gtexV7JunctionReads.R'  
 'formats\_gtexV8JunctionReads.R'  
 'formats\_psichomicsGeneExpression.R'  
 'formats\_psichomicsInclusionLevels.R'  
 'formats\_recountSampleInfo.R'  
 'formats\_vasttoolsGeneExpression.R'  
 'formats\_vasttoolsInclusionLevels.R'  
 'formats\_vasttoolsInclusionLevelsTidy.R' 'groups.R' 'help.R'  
 'utils\_drawSplicingEvent.R' 'utils\_eventParsing.R'  
 'utils\_fileBrowserDialog.R' 'utils\_interactiveGgplot.R'  
 'utils\_interface.R'

**biocViews** Sequencing, RNASeq, AlternativeSplicing,  
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 GeneExpression, DifferentialExpression

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---

.onAttach	<i>Print startup message</i>
-----------	------------------------------

---

## Description

Print startup message

## Usage

```
.onAttach(libname, pkgname)
```

## Arguments

libname	Character: library name
pkgname	Character: package name

## Value

Startup message



---

addObjectAttrs	<i>Set attributes to an object</i>
----------------	------------------------------------

---

**Description**

Set attributes to an object

**Usage**

```
addObjectAttrs(object, ..., replace = TRUE)
```

**Arguments**

object	Object
...	Named parameters to convert to attributes
replace	Boolean: replace an attribute if already set?

**Value**

Object with attributes set

**Examples**

```
ll <- list(a="hey", b="there")
psychomics::addObjectAttrs(ll, "words"=2, "language"="English")
```

---

addTCGAdata	<i>Creates a UI set with options to add data from TCGA/FireBrowse</i>
-------------	---

---

**Description**

Creates a UI set with options to add data from TCGA/FireBrowse

**Usage**

```
addTCGAdata(ns)
```

**Arguments**

ns	Namespace function
----	--------------------

**Value**

A UI set that can be added to a UI definition

---

analysesTableSet      *Set of functions to render differential analyses (plot and table)*

---

### Description

Set of functions to render differential analyses (plot and table)

Set up environment and redirect user to a page based on click information

### Usage

```
analysesTableSet(  
  session,  
  input,  
  output,  
  analysesType,  
  analysesID,  
  getAnalysesData,  
  getAnalysesFiltered,  
  setAnalysesFiltered,  
  getAnalysesSurvival,  
  getAnalysesColumns,  
  setAnalysesColumns,  
  getResetPaging,  
  setResetPaging  
)  
  
processClickRedirection(click, psi = NULL, survival = FALSE)  
  
analysesPlotSet(  
  session,  
  input,  
  output,  
  analysesType,  
  analysesID,  
  getAnalysesData,  
  getAnalysesFiltered,  
  getAnalysesSurvival  
)
```

### Arguments

session	Shiny session
input	Shiny input
output	Shiny output
analysesType	Character: type of analyses (GE or PSI)
analysesID	Character: identifier
getAnalysesData	Function: get analyses data

getAnalysesFiltered	Function: get filtered analyses data
setAnalysesFiltered	Function: set filtered analyses data
getAnalysesSurvival	Function: get survival data
getAnalysesColumns	Function: get columns
setAnalysesColumns	Function: set columns
getResetPaging	Function: get toggle of reset paging
setResetPaging	Function: set toggle of reset paging
click	List: click information
psi	Data frame or matrix: alternative splicing quantification
survival	Boolean: redirect to survival page?

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

appendNewGroups	<i>Append new groups to already existing groups</i>
-----------------	---

---

**Description**

Retrieve previous groups, rename duplicated group names in the new groups and append new groups to the previous ones

**Usage**

```
appendNewGroups(type, new, clearOld = FALSE)
```

**Arguments**

type	Character: type of groups (either Patients, Samples, ASevents or Genes)
new	Rows of groups to be added
clearOld	Boolean: clear old groups?

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

appServer

*Server logic*

---

### **Description**

Instructions to build the Shiny app

### **Usage**

appServer(input, output, session)

analysesServer(input, output, session)

diffEventServer(ns, input, output, session, psi)

correlationServer(input, output, session)

diffExpressionServer(input, output, session)

diffExpressionEventServer(input, output, session)

diffExpressionTableServer(input, output, session)

diffSplicingServer(input, output, session)

diffSplicingEventServer(input, output, session)

diffSplicingTableServer(input, output, session)

dimReductionServer(input, output, session)

icaServer(input, output, session)

pcaServer(input, output, session)

infoServer(input, output, session)

survivalServer(input, output, session)

templateServer(input, output, session)

dataServer(input, output, session)

firebrowseServer(input, output, session)

geNormalisationFilteringServer(input, output, session)

gtexDataServer(input, output, session)

inclusionLevelsServer(input, output, session)

```
inclusionLevelsFilterServer(input, output, session)
```

```
localDataServer(input, output, session)
```

```
recountDataServer(input, output, session)
```

```
groupsServer(input, output, session)
```

```
helpServer(input, output, session)
```

### Arguments

input	Shiny input
output	Shiny output
session	Shiny session

### Value

NULL (function is only used to modify the Shiny session's state or internal variables)

---

appUI

*User interface*

---

### Description

The user interface (UI) controls the layout and appearance of the app. All CSS modifications are in the file shiny/www/styles.css

### Usage

```
appUI()
```

```
analysesUI(id, tab)
```

```
diffEventUI(id, ns, psi = TRUE)
```

```
correlationUI(id)
```

```
diffExpressionUI(id, tab)
```

```
diffExpressionEventUI(id)
```

```
diffExpressionTableUI(id)
```

```
diffSplicingUI(id, tab)
```

```
diffSplicingEventUI(id)
```

```
diffSplicingTableUI(id)
```

```
dimReductionUI(id, tab)
```

icaUI(id)  
pcaUI(id)  
infoUI(id)  
survivalUI(id)  
templateUI(id)  
dataUI(id, tab)  
firebrowseUI(id, panel)  
geNormalisationFilteringUI(id, panel)  
gtexDataUI(id, panel)  
inclusionLevelsUI(id, panel)  
inclusionLevelsFilterUI(id, panel)  
localDataUI(id, panel)  
recountDataUI(id, panel)  
groupsUI(id, tab)  
helpUI(id, tab)

**Arguments**

id	Character: identifier
tab	Function to process HTML elements
panel	Function to enclose interface

**Value**

HTML elements

---

areSplicingEvents	<i>Check if string identifies splicing events</i>
-------------------	---

---

**Description**

Check if string identifies splicing events

**Usage**

```
areSplicingEvents(char, data = NULL, num = 6)
```

**Arguments**

char	Character vector
data	Object containing event data
num	Integer: number of elements to check

**Value**

TRUE if first elements are splicing events; FALSE, otherwise

---

articleUI	<i>Return the interface to display an article</i>
-----------	---

---

**Description**

Return the interface to display an article

**Usage**

```
articleUI(article)
```

**Arguments**

article	PubMed article
---------	----------------

**Value**

HTML to render an article's interface

---

assignColours	<i>Assign colours to groups</i>
---------------	---------------------------------

---

**Description**

Assign colours to groups

**Usage**

```
assignColours(new, groups = NULL)
```

**Arguments**

new	Matrix: groups to which colours will be assigned
groups	Matrix: groups to check which colours are already assigned

**Value**

Groups with an added column to state the colour

---

assignValuePerSubject *Assign average sample values to their corresponding subjects*

---

### Description

Assign average sample values to their corresponding subjects

### Usage

```
assignValuePerSubject(
  data,
  match,
  clinical = NULL,
  patients = NULL,
  samples = NULL
)
```

### Arguments

data	One-row data frame/matrix or vector: values per sample for a single gene
match	Matrix: match between samples and subjects
clinical	Data frame or matrix: clinical dataset (only required if the subjects argument is not handed)
patients	Character: subject identifiers (only required if the clinical argument is not handed)
samples	Character: samples to use when assigning values per subject (if NULL, all samples will be used)

### Value

Values per subject

### See Also

Other functions to analyse survival: [getAttributesTime\(\)](#), [labelBasedOnCutoff\(\)](#), [optimalSurvivalCutoff\(\)](#), [plotSurvivalCurves\(\)](#), [plotSurvivalPvaluesByCutoff\(\)](#), [processSurvTerms\(\)](#), [survdiffTerms\(\)](#), [survfit.survTerms\(\)](#), [testSurvival\(\)](#)

### Examples

```
# Calculate PSI for skipped exon (SE) and mutually exclusive (MXE) events
annot <- readfile("ex_splicing_annotation.RDS")
junctionQuant <- readfile("ex_junctionQuant.RDS")

psi <- quantifySplicing(annot, junctionQuant, eventType=c("SE", "MXE"))

# Match between subjects and samples
match <- rep(paste("Subject", 1:3), 2)
names(match) <- colnames(psi)

# Assign PSI values to each subject based on the PSI of their samples
assignValuePerSubject(psi[3, ], match)
```



---

basicStats	<i>Basic statistics performed on data</i>
------------	---

---

**Description**

Variance and median of each group. If data has 2 groups, also calculates the delta variance and delta median.

**Usage**

```
basicStats(data, groups)
```

**Arguments**

data	Numeric, data frame or matrix: gene expression data or alternative splicing event quantification values (sample names are based on their names or colnames)
groups	List of sample names or vector containing the group name per data value (read Details); if NULL or a character vector of length 1, data values are considered from the same group

**Value**

HTML elements

---

blendColours	<i>Blend two HEX colours</i>
--------------	------------------------------

---

**Description**

Blend two HEX colours

**Usage**

```
blendColours(colour1, colour2, colour1Percentage = 0.5)
```

**Arguments**

colour1	Character: HEX colour
colour2	Character: HEX colour
colour1Percentage	Character: percentage of colour 1 mixed in blended colour

**Value**

Character representing an HEX colour

**Source**

Code modified from <https://stackoverflow.com/questions/5560248>

**Examples**

```
psichomics:::blendColours("#3f83a3", "#f48000")
```

---

```
browseDownloadFolderInput
```

*Browse download folder input*

---

**Description**

Browse download folder input

**Usage**

```
browseDownloadFolderInput(id)
```

**Arguments**

id                    Character: element identifier

**Value**

HTML element in character

---

```
browserHistory            Enable history navigation
```

---

**Description**

Navigate app according to the location given by the navigation bar. Code and logic adapted from <https://github.com/daattali/advanced-shiny/blob/master/navigate-history>

**Usage**

```
browserHistory(navId, input, session)
```

**Arguments**

navId                Character: identifier of the navigation bar  
input                Input object  
session              Session object

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

 calculateInclusionLevels

*Calculate inclusion levels using alternative splicing event annotation and junction quantification for many samples*

---

### Description

Calculate inclusion levels using alternative splicing event annotation and junction quantification for many samples

### Usage

```
calculateInclusionLevels(
  eventType,
  junctionQuant,
  annotation,
  minReads = 10,
  onlyReturnASeventNames = FALSE
)
```

### Arguments

eventType	Character: type of the alternative event to calculate
junctionQuant	Matrix: junction quantification with samples as columns and junctions as rows
annotation	Data.frame: alternative splicing annotation related to event type
minReads	Integer: minimum of total reads required to consider the quantification as valid

### Value

Matrix with inclusion levels

---

calculateLoadingsContribution

*Calculate the contribution of PCA loadings to the selected principal components*

---

### Description

Total contribution of a variable is calculated as per  $((C_x * E_x) + (C_y * E_y)) / (E_x + E_y)$ , where:

- $C_x$  and  $C_y$  are the contributions of a variable to principal components  $x$  and  $y$
- $E_x$  and  $E_y$  are the eigenvalues of principal components  $x$  and  $y$

### Usage

```
calculateLoadingsContribution(pca, pcX = 1, pcY = 2)
```

**Arguments**

pca	prcomp object
pcX	Character: name of the X axis of interest from the PCA
pcY	Character: name of the Y axis of interest from the PCA

**Value**

Data frame containing the correlation between variables and selected principal components and the contribution of variables to the selected principal components (both individual and total contribution)

**Source**

<http://www.sthda.com/english/articles/31-principal-component-methods-in-r-practical-guide/112-pca-principal-component-analysis-essentials/>

**See Also**

Other functions to analyse principal components: [performPCA\(\)](#), [plotPCA\(\)](#), [plotPCAvariance\(\)](#)

**Examples**

```
pca <- performPCA(USArrests)
calculateLoadingsContribution(pca)
```

---

checkFileFormat	<i>Checks the format of a file</i>
-----------------	------------------------------------

---

**Description**

Checks the format of a file

**Usage**

```
checkFileFormat(format, head, filename = "")
```

**Arguments**

format	Environment: format of the file
head	Data.frame: head of the file to check
filename	Character: name of the file

**Details**

The name of the file may also be required to be considered of a certain format.

**Value**

TRUE if the file matches the given format's attributes

---

checkFirebrowse	<i>Return an user interface depending on the status of the FireBrowse API</i>
-----------------	---

---

**Description**

If the API is working, it'll be loaded. Else, a message will appear warning the user that the API is down and that will let check again if the API is back online.

**Usage**

```
checkFirebrowse(ns)
```

**Arguments**

ns	Namespace function
----	--------------------

**Value**

HTML elements

---

checkGroupType	<i>Check type of groups within file</i>
----------------	---

---

**Description**

Check type of groups within file

**Usage**

```
checkGroupType(file)
```

**Arguments**

file	Character: file path
------	----------------------

**Value**

Type of group: Samples, ASevents or NULL

---

checkIntegrity	<i>Compute the 32-byte MD5 hashes of one or more files and check with given md5 file</i>
----------------	--

---

**Description**

Compute the 32-byte MD5 hashes of one or more files and check with given md5 file

**Usage**

```
checkIntegrity(filesToCheck, md5file)
```

**Arguments**

filesToCheck	Character: files to calculate and match MD5 hashes
md5file	Character: file containing correct MD5 hashes

**Value**

Logical vector showing TRUE for files with matching md5sums and FALSE for files with non-matching md5sums

---

checkSurvivalInput	<i>Prepare survival terms in case of valid input</i>
--------------------	--

---

**Description**

Prepare survival terms in case of valid input

**Usage**

```
checkSurvivalInput(session, input, coxph = FALSE)
```

**Arguments**

session	Shiny session
input	Shiny input
coxph	Boolean: prepare data for Cox models?

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

clusterICAs	<i>Server logic for clustering ICA data</i>
-------------	---

---

**Description**

Server logic for clustering ICA data

**Usage**

```
clusterICAs(session, input, output)
```

**Arguments**

session	Shiny session
input	Shiny input
output	Shiny output

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

clusterSet	<i>Server logic for clustering PCA data</i>
------------	---

---

**Description**

Server logic for clustering PCA data

**Usage**

```
clusterSet(session, input, output)
```

**Arguments**

session	Shiny session
input	Shiny input
output	Shiny output

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

colourInputMod	<i>Modified colour input with 100% width</i>
----------------	--

---

### Description

Modified colour input with 100% width

### Usage

```
colourInputMod(...)
```

### Arguments

... Arguments passed on to `colourpicker::colourInput`

`inputId` The input slot that will be used to access the value.

`label` Display label for the control, or 'NULL' for no label.

`value` Initial value (can be a colour name or HEX code)

`showColour` Whether to show the chosen colour as text inside the input, as the background colour of the input, or both (default).

`palette` The type of colour palette to allow the user to select colours from. `square` (default) shows a square colour palette that allows the user to choose any colour, while `limited` only gives the user a predefined list of colours to choose from.

`allowedCols` A list of colours that the user can choose from. Only applicable when `palette == "limited"`. The `limited` palette uses a default list of 40 colours if `allowedCols` is not defined. If the colour specified in `value` is not in the list, the default colour will revert to black.

`allowTransparent` If TRUE, enables a slider to choose an alpha (transparency) value for the colour. When a colour with opacity is chosen, the return value is an 8-digit HEX code.

`returnName` If TRUE, then return the name of an R colour instead of a HEX value when possible.

`closeOnClick` If TRUE, then the colour selection panel will close immediately after selecting a colour.

`width` The width of the input, e.g. "400px" or "100%"

### Value

HTML elements



---

colSums, EList-method *Sum columns using an EList-class object*

---

### Description

Sum columns using an [EList-class](#) object

### Usage

```
## S4 method for signature 'EList'  
colSums(x, na.rm = FALSE, dims = 1)
```

### Arguments

x	an array of two or more dimensions, containing numeric, complex, integer or logical values, or a numeric data frame. For <code>.colSums()</code> etc, a numeric, integer or logical matrix (or vector of length $m * n$ ).
na.rm	logical. Should missing values (including NaN) be omitted from the calculations?
dims	integer: Which dimensions are regarded as 'rows' or 'columns' to sum over. For <code>row*</code> , the sum or mean is over dimensions <code>dims+1, ...</code> ; for <code>col*</code> it is over dimensions <code>1:dims</code> .

### Value

Numeric vector with the sum of the columns

---

convertGeneIdentifiers  
*Convert gene identifiers*

---

### Description

Convert gene identifiers

### Usage

```
convertGeneIdentifiers(  
  annotation,  
  genes,  
  key = "ENSEMBL",  
  target = "SYMBOL",  
  ignoreDuplicatedTargets = TRUE  
)
```

**Arguments**

annotation	OrgDb with genome wide annotation for an organism or character with species name to query OrgDb, e.g. "Homo sapiens"
genes	Character: genes to be converted
key	Character: type of identifier used, e.g. ENSEMBL; read ?AnnotationDbi::columns
target	Character: type of identifier to convert to; read ?AnnotationDbi::columns
ignoreDuplicatedTargets	Boolean: if TRUE, identifiers that share targets with other identifiers will not be converted

**Value**

Character vector of the respective targets of gene identifiers. The previous identifiers remain other identifiers have the same target (in case ignoreDuplicatedTargets = TRUE) or if no target was found.

**See Also**

Other functions for gene expression pre-processing: [filterGeneExpr\(\)](#), [normaliseGeneExpression\(\)](#), [plotGeneExprPerSample\(\)](#), [plotLibrarySize\(\)](#), [plotRowStats\(\)](#)

**Examples**

```
# Use species name to automatically look for a OrgDb database
sp <- "Homo sapiens"
genes <- c("ENSG0000012048", "ENSG00000083093", "ENSG00000141510",
           "ENSG00000051180")
convertGeneIdentifiers(sp, genes)
convertGeneIdentifiers(sp, genes, key="ENSEMBL", target="UNIPROT")

# Alternatively, set the annotation database directly
ah <- AnnotationHub::AnnotationHub()
sp <- AnnotationHub::query(ah, c("OrgDb", "Homo sapiens"))[[1]]
columns(sp) # these attributes can be used to change the attributes

convertGeneIdentifiers(sp, genes)
convertGeneIdentifiers(sp, genes, key="ENSEMBL", target="UNIPROT")
```

---

correlateGEandAS

*Correlate gene expression data against alternative splicing quantification*

---

**Description**

Test for association between paired samples' gene expression (for any genes of interest) and alternative splicing quantification.

**Usage**

```
correlateGEandAS(geneExpr, psi, gene, ASevents = NULL, ...)
```

**Arguments**

geneExpr	Matrix or data frame: gene expression data
psi	Matrix or data frame: alternative splicing quantification data
gene	Character: gene symbol for genes of interest
ASevents	Character: alternative splicing events to correlate with gene expression of a gene (if NULL, the events will be automatically retrieved from the given gene)
...	Extra parameters passed to <a href="#">cor.test</a>

**Value**

List of correlations where each element contains:

eventID	Alternative splicing event identifier
cor	Correlation between gene expression and alternative splicing quantification of one alternative splicing event
geneExpr	Gene expression for the selected gene
psi	Alternative splicing quantification for the alternative splicing event

**See Also**

Other functions to correlate gene expression and alternative splicing: [\[.GEandAScorrelation\(\)\]](#)

**Examples**

```
annot <- readFile("ex_splicing_annotation.RDS")
junctionQuant <- readFile("ex_junctionQuant.RDS")
psi <- quantifySplicing(annot, junctionQuant, eventType=c("SE", "MXE"))

geneExpr <- readFile("ex_gene_expression.RDS")
correlateGEandAS(geneExpr, psi, "ALDOA")
```

---

createDataTab                      *Render a specific data tab (including data table and related interface)*

---

**Description**

Render a specific data tab (including data table and related interface)

**Usage**

```
createDataTab(index, data, name, session, input, output)
```

**Arguments**

index	Integer: index of the data to load
data	Data frame: data with everything to load
name	Character: name of the dataset
session	Shiny session
input	Shiny session input
output	Shiny session output

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

createDensitySparklines  
*Create density sparklines for inclusion levels*

---

**Description**

Create density sparklines for inclusion levels

**Usage**

```
createDensitySparklines(  
  data,  
  events,  
  areSplicingEvents = TRUE,  
  groups = NULL,  
  geneExpr = NULL,  
  inputID = "sparklineInput"  
)
```

**Arguments**

data	Character: HTML-formatted data series of interest
events	Character: event identifiers
areSplicingEvents	Boolean: are these splicing events (TRUE) or gene expression (FALSE)?
groups	Character: name of the groups used for differential analyses
geneExpr	Character: name of the gene expression dataset
inputID	Character: identifier of input to get attributes of clicked event (Shiny only)

**Value**

HTML element with sparkline data

---

createEventPlotting *Create plot for events*

---

**Description**

Create plot for events

**Usage**

```
createEventPlotting(
  df,
  x,
  y,
  params,
  highlightX,
  highlightY,
  highlightParams,
  selected,
  selectedParams,
  labelled,
  labelledParams,
  xlim,
  ylim
)
```

**Arguments**

df	Data frame
x	Character: name of the variable used for the X axis
y	Character: name of the variable used for the Y axis
params	List of parameters to pass to <code>geom_point()</code> related to most points
highlightX	Integer: region of points in X axis to highlight
highlightY	Integer: region of points in Y axis to highlight
highlightParams	List of parameters to pass to <code>geom_point()</code> related to highlighted points
selected	Integer: index of rows/points to be coloured
selectedParams	List of parameters to pass to <code>geom_point()</code> related to selected points
labelled	Integer: index of rows/points to be labelled
labelledParams	List of parameters to pass to <code>ggrepel::geom_label_repel</code> related to labelled points
xlim	Numeric: limits of X axis
ylim	Numeric: limits of Y axis

**Value**

List containing HTML elements and highlighted points

---

createGroup

*Prepare to create group according to specific details*

---

**Description**

Prepare to create group according to specific details

**Usage**

```
createGroup(
  session,
  input,
  output,
  id,
  type,
  selected = NULL,
  expr = NULL,
  groupNames = NULL
)
```

**Arguments**

session	Shiny session
input	Shiny input
output	Shiny output
id	Character: identifier of the group selection
type	Character: type of group to create
selected	Character: selected item
expr	Character: expression
groupNames	Character: group names

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

createGroupByAttribute

*Split elements into groups based on a given column of a dataset*

---

**Description**

Elements are identified by their respective row name.

**Usage**

```
createGroupByAttribute(col, dataset)
```

**Arguments**

col	Character: column name
dataset	Matrix or data frame: dataset

**Value**

Named list with each unique value from a given column and respective elements

**See Also**

Other functions for data grouping: [getGeneList\(\)](#), [getSampleFromSubject\(\)](#), [getSubjectFromSample\(\)](#), [groupPerElem\(\)](#), [plotGroupIndependence\(\)](#), [testGroupIndependence\(\)](#)

**Examples**

```
df <- data.frame(gender=c("male", "female"),
                 stage=paste("stage", c(1, 3, 1, 4, 2, 3, 2, 2)))
rownames(df) <- paste0("subject-", LETTERS[1:8])
createGroupByAttribute(col="stage", dataset=df)
```

---

createGroupById      *Create groups based on given row indexes or identifiers*

---

**Description**

Create groups based on given row indexes or identifiers

**Usage**

```
createGroupById(session, rows, identifiers)
```

**Arguments**

session	Shiny session
rows	Character: comma-separated row indexes or identifiers
identifiers	Character: available identifiers

**Value**

Character: values based on given row indexes or identifiers

---

createGroupFromInput      *Set new groups according to the user input*

---

**Description**

Set new groups according to the user input

**Usage**

```
createGroupFromInput(
  session,
  input,
  output,
  dataset,
  id,
  type,
  selected = NULL,
  expr = NULL,
  groupNames = NULL
)
```

**Arguments**

session	Shiny session
input	Shiny input
output	Shiny output
dataset	Data frame or matrix: dataset of interest
id	Character: identifier of the group selection
type	Character: type of group to create
selected	Character: selected item
expr	Character: expression
groupNames	Character: group names

**Value**

Matrix with the group names and respective elements

---

```
createJunctionsTemplate
  Creates a template of alternative splicing junctions
```

---

**Description**

Creates a template of alternative splicing junctions

**Usage**

```
createJunctionsTemplate(
  nrow,
  program = character(0),
  event.type = character(0),
  chromosome = character(0),
  strand = character(0),
  id = character(0)
)
```

**Arguments**

nrow	Integer: row number
program	Character: program used to get the junctions
event.type	Character: event type
chromosome	Character: chromosome
strand	Character: positive-sense (+) or negative-sense (-) strand
id	Character: event identifiers

**Value**

A data frame with the junctions coordinate names pre-filled with NA

**Examples**

```
psychomics:::createJunctionsTemplate(nrow = 8)
```



---

createOptimalSurvData *Create survival data based on a PSI cutoff*

---

### Description

Data is presented in the table for statistical analyses

### Usage

```
createOptimalSurvData(
  eventPSI,
  clinical,
  censoring,
  event,
  timeStart,
  timeStop,
  match,
  patients,
  samples
)
```

### Arguments

eventPSI	Numeric: alternative splicing quantification for multiple samples relative to a single splicing event
clinical	Data frame: clinical data
censoring	Character: censor using left, right, interval or interval2
event	Character: name of column containing time of the event of interest
timeStart	Character: name of column containing starting time of the interval or follow up time
timeStop	Character: name of column containing ending time of the interval (only relevant for interval censoring)
match	Matrix: match between samples and subjects
patients	Character: subject identifiers (only required if the clinical argument is not handed)
samples	Character: samples to use when assigning values per subject (if NULL, all samples will be used)

### Value

Survival data including optimal PSI cutoff, minimal survival p-value and HTML element required to plot survival curves

---

createSparklines	<i>Create sparkline charts to be used in a data table</i>
------------------	---

---

### Description

Create sparkline charts to be used in a data table

### Usage

```
createSparklines(
  hc,
  data,
  events,
  groups = NULL,
  geneExpr = NULL,
  inputID = "sparklineInput",
  ...
)
```

### Arguments

hc	highchart object
data	Character: HTML-formatted data series of interest
events	Character: event identifiers
groups	Character: name of the groups used for differential analyses
geneExpr	Character: name of the gene expression dataset
inputID	Character: identifier of input to get attributes of clicked event (Shiny only)
id	Character: Shiny input identifier

### Value

HTML element with sparkline data

---

customRowMeans	<i>Calculate statistics for each row or column of a matrix</i>
----------------	--

---

### Description

Calculate statistics for each row or column of a matrix

**Usage**

```

customRowMeans(mat, na.rm = FALSE, fast = FALSE)

customRowMedians(mat, na.rm = FALSE, fast = FALSE)

customRowVars(mat, na.rm = FALSE, fast = FALSE)

customRowMins(mat, na.rm = FALSE, fast = FALSE)

customRowMaxs(mat, na.rm = FALSE, fast = FALSE)

customRowRanges(mat, na.rm = FALSE, fast = FALSE)

customColMedians(mat, na.rm = FALSE, fast = FALSE)

```

**Arguments**

mat	Matrix
na.rm	Boolean: remove missing values (NA)?
fast	Boolean: use Rfast functions? They may return different results from R built-in functions

**Value**

Vector of selected statistic

**Examples**

```

df <- rbind("Gene 1"=c(3, 5, 7), "Gene 2"=c(8, 2, 4), "Gene 3"=c(9:11))
psychomics:::customRowMeans(df)
psychomics:::customRowVars(df, fast=TRUE)

```

---

diagramSplicingEvent *Prepare SVG diagram of alternative splicing events*

---

**Description**

Prepare SVG diagram of alternative splicing events

**Usage**

```

diagramSplicingEvent(
  parsed,
  type,
  class = "pull-right",
  style = NULL,
  showText = TRUE,
  showPath = TRUE,
  showAlternative1 = TRUE,
  showAlternative2 = TRUE,
  constitutiveWidth = NULL,

```

```

    alternativeWidth = NULL,
    intronWidth = NULL,
    constitutiveFill = "lightgray",
    constitutiveStroke = "darkgray",
    alternative1Fill = "#ffb153",
    alternative1Stroke = "#faa000",
    alternative2Fill = "#caa06c",
    alternative2Stroke = "#9d7039"
)

```

### Arguments

parsed	Alternative splicing event
type	Character: alternative splicing event type
class	Character: class of SVG parent tag
style	Character: style of SVG parent tag
showText	Boolean: display coordinates and length (if available)
showPath	Boolean: display alternative splicing junctions
showAlternative1	Boolean: show alternative exon 1 and respective splicing junctions and text?
showAlternative2	Boolean: show alternative exon 2 and respective splicing junctions and text? (only related with mutually exclusive exons)
constitutiveWidth	Numeric: width of constitutive exon(s)
alternativeWidth	Numeric: width of alternative exon(s)
intronWidth	Numeric: width of intron's representation
constitutiveFill	Character: fill colour of constitutive exons
constitutiveStroke	Character: stroke colour of constitutive exons
alternative1Fill	Character: fill colour of alternative exon 1
alternative1Stroke	Character: stroke colour of alternative exon 1
alternative2Fill	Character: fill colour of alternative exon 2
alternative2Stroke	Character: stroke colour of alternative exon 2

### Value

Diagrams per alternative splicing event in SVG

---

diffAnalyses      *Perform statistical analyses*

---

## Description

Perform statistical analyses

## Usage

```
diffAnalyses(
  data,
  groups = NULL,
  analyses = c("wilcoxRankSum", "ttest", "kruskal", "levene", "fligner"),
  pvalueAdjust = "BH",
  geneExpr = NULL,
  inputID = "sparklineInput"
)
```

## Arguments

data	Data frame or matrix: gene expression or alternative splicing quantification
groups	Named list of characters (containing elements belonging to each group) or character vector (containing the group of each individual sample); if NULL, sample types are used instead when available, e.g. normal, tumour and metastasis
analyses	Character: statistical tests to perform (see Details)
pvalueAdjust	Character: method used to adjust p-values (see Details)
geneExpr	Character: name of the gene expression dataset (only required for density sparklines available in the interactive mode)
inputID	Character: identifier of input to get attributes of clicked event (Shiny only)

## Details

The following statistical analyses may be performed simultaneously via the `analysis` argument:

- `ttest` - Unpaired t-test (2 groups)
- `wilcoxRankSum` - Wilcoxon Rank Sum test (2 groups)
- `kruskal` - Kruskal test (2 or more groups)
- `levene` - Levene's test (2 or more groups)
- `fligner` - Fligner-Killeen test (2 or more groups)
- `density` - Sample distribution per group (only usable through the visual interface)

The following p-value adjustment methods are supported via the `pvalueAdjust` argument:

- `none`: do not adjust p-values
- `BH`: Benjamini-Hochberg's method (false discovery rate)
- `BY`: Benjamini-Yekutieli's method (false discovery rate)
- `bonferroni`: Bonferroni correction (family-wise error rate)
- `holm`: Holm's method (family-wise error rate)
- `hochberg`: Hochberg's method (family-wise error rate)
- `hommel`: Hommel's method (family-wise error rate)

**Value**

Table of statistical analyses

**See Also**

Other functions to perform and plot differential analyses: [plotDistribution\(\)](#)

**Examples**

```
# Calculate PSI for skipped exon (SE) and mutually exclusive (MXE) events
eventType <- c("SE", "MXE")
annot <- readfile("ex_splicing_annotation.RDS")
junctionQuant <- readfile("ex_junctionQuant.RDS")

psi <- quantifySplicing(annot, junctionQuant, eventType=c("SE", "MXE"))
group <- c(rep("Normal", 3), rep("Tumour", 3))
diffAnalyses(psi, group)
```

---

diffExpressionSet      *Set of functions to perform differential analyses*

---

**Description**

Set of functions to perform differential analyses

**Usage**

```
diffExpressionSet(session, input, output)
```

**Arguments**

session	Shiny session
input	Shiny input
output	Shiny output

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

diffSplicingSet	<i>Set of functions to perform differential analyses</i>
-----------------	--

---

**Description**

Set of functions to perform differential analyses

**Usage**

```
diffSplicingSet(session, input, output)
```

**Arguments**

session	Shiny session
input	Shiny input
output	Shiny output

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

disableTab	<i>Enable or disable a tab from the navbar</i>
------------	--

---

**Description**

Enable or disable a tab from the navbar

**Usage**

```
disableTab(tab)  
enableTab(tab)
```

**Arguments**

tab	Character: tab
-----	----------------

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

discardLowCoveragePSIvalues

*Remove alternative splicing quantification values based on coverage*

---

### Description

Remove alternative splicing quantification values based on coverage

### Usage

```
discardLowCoveragePSIvalues(
  psi,
  minReads = 10,
  vasttoolsScoresToDiscard = c("VLOW", "N")
)
```

### Arguments

psi	Data frame or matrix: alternative splicing quantification
minReads	Currently this argument does nothing
vasttoolsScoresToDiscard	Character: if you are using inclusion levels from VAST-TOOLS, filter the data based on quality scores for read coverage, e.g. use vasttoolsScoresToDiscard = c("SOK", "OK", "LOW") to only keep events with good read coverage (by default, events are not filtered based on quality scores); read <a href="https://github.com/vastgroup/vast-tools">https://github.com/vastgroup/vast-tools</a> for more information on VAST-TOOLS quality scores

### Value

Alternative splicing quantification data with missing values for any values with insufficient coverage

---

discardOutsideSamplesFromGroups

*Discard grouped samples if not within a sample vector*

---

### Description

Discard grouped samples if not within a sample vector

### Usage

```
discardOutsideSamplesFromGroups(groups, samples, clean = FALSE)
```

### Arguments

groups	Named list of samples
samples	Character: vector with all available samples
clean	Boolean: clean results?



**Value**

Groups without samples not found in samples

---

display	<i>Display characters in the command-line</i>
---------	---

---

**Description**

Display characters in the command-line

**Usage**

```
display(char, timeStr = "Time difference of")
```

**Arguments**

char	Character: message
timeStr	Character: message when a difftime object is passed to the char argument

**Value**

NULL (display message in command-line)

---

downloadFiles	<i>Download files to a given directory</i>
---------------	--

---

**Description**

Download files to a given directory

**Usage**

```
downloadFiles(url, folder, download = download.file, ...)
```

**Arguments**

url	Character: download links
folder	Character: directory to store the downloaded archives
download	Function to use to download files
...	Extra parameters passed to the download function

**Value**

Invisible TRUE if every file was successfully downloaded

**Examples**

```
## Not run:
url <- paste0("https://unsplash.it/400/300/?image=", 570:572)
psychomics::downloadFiles(url, "~/Pictures")

# Download without printing to console
psychomics::downloadFiles(url, "~/Pictures", quiet = TRUE)

## End(Not run)
```

---

ensemblToUniprot	<i>Convert from Ensembl to UniProt identifier</i>
------------------	---

---

**Description**

Convert from Ensembl to UniProt identifier

**Usage**

```
ensemblToUniprot(protein)
```

**Arguments**

protein            Character: Ensembl identifier

**Value**

UniProt protein identifier

**See Also**

Other functions to retrieve external information: [plotProtein\(\)](#), [plotTranscripts\(\)](#), [queryEnsemblByGene\(\)](#)

**Examples**

```
gene <- "ENSG00000173262"
ensemblToUniprot(gene)

protein <- "ENSP00000445929"
ensemblToUniprot(protein)
```

---

escape	<i>Escape symbols for use in regular expressions</i>
--------	--

---

**Description**

Escape symbols for use in regular expressions

**Usage**

```
escape(...)
```

**Arguments**

... Characters to be pasted with no space

**Value**

Escaped string

---

eventPlotOptions	<i>Options for event plotting</i>
------------------	-----------------------------------

---

**Description**

Options for event plotting

**Usage**

```
eventPlotOptions(session, df, xAxis, yAxis, labelSortBy)
```

**Arguments**

session	Shiny session
df	Data frame
xAxis	Character: currently selected variable for the X axis
yAxis	Character: currently selected variable for the Y axis
labelSortBy	Character: currently selected variable for the selectize element to sort differentially analysis

**Value**

HTML elements

---

exportGroupsToFile     *Export groups to a file*

---

**Description**

Export groups to a file

**Usage**

```
exportGroupsToFile(groups, file, match = NULL)
```

**Arguments**

groups	Matrix with groups
file	Character: path to output file
match	Match between elements within groups

**Value**

Saves groups to file

---

export\_highcharts     *Add an exporting feature to a highcharts object*

---

**Description**

Add an exporting feature to a highcharts object

**Usage**

```
export_highcharts(hc, fill = "transparent", text = "Export")
```

**Arguments**

hc	A highcharts object
fill	Character: colour fill
text	Character: button text

**Value**

A highcharts object with an export button

---

fileBrowser	<i>Interactive folder selection using a native dialogue</i>
-------------	---

---

## Description

Interactive folder selection using a native dialogue

## Usage

```
fileBrowser(  
  default = NULL,  
  caption = NULL,  
  multiple = FALSE,  
  directory = FALSE  
)
```

## Arguments

default	Character: path to initial folder
caption	Character: caption on the selection dialogue
multiple	Boolean: allow to select multiple files?
directory	Boolean: allow to select directories instead of files?

## Details

Platform-dependent implementation:

- **Windows**: calls the `utils::choose.files` R function.
- **macOS**: uses AppleScript to display a folder selection dialogue. If `default = NA`, folder selection falls back to the default behaviour of the `choose folder` AppleScript command. Otherwise, paths are expanded with `path.expand()`.
- **Linux**: calls the `zenity` system command.

## Value

A length one character vector, character NA if 'Cancel' was selected

## Source

<https://github.com/wleepang/shiny-directory-input>

---

fileBrowserInfoInput *File browser input*

---

### Description

Input to interactively select a file or directory on the server

### Usage

```
fileBrowserInfoInput(id, label, infoContent = NULL, clearable = FALSE)
```

```
fileBrowserInput(
  id,
  label,
  value = NULL,
  placeholder = NULL,
  info = FALSE,
  infoFUN = NULL,
  infoPlacement = "right",
  infoTitle = "",
  infoContent = "",
  clearable = FALSE
)
```

### Arguments

id	Character: input identifier
label	Character: input label (if NULL, no labels are displayed)
infoContent	Character: text to show as content of information
clearable	Boolean: allow to clear selected file or directory?
value	Character: initial value (paths are expanded via <a href="#">path.expand()</a> )
placeholder	Character: placeholder when no file or folder is selected
info	Boolean: add information icon for tooltips and pop-overs
infoFUN	Function to use to provide information (e.g. <code>shinyBS::bsToolTip</code> and <code>shinyBS::bsPopover</code> )
infoPlacement	Character: placement of the information (top, bottom, right or left)
infoTitle	Character: text to show as title of information

### Details

To show the dialog for file input, the [prepareFileBrowser\(\)](#) function needs to be included in the server logic.

This widget relies on [fileBrowser\(\)](#) to present an interactive dialogue to users for selecting a directory on the local filesystem. Therefore, this widget is intended for shiny apps that are run locally - i.e. on the same system that files/directories are to be accessed - and not from hosted applications (e.g. from <https://www.shinyapps.io>).

### Value

HTML elements for a file browser input

**Source**

<https://github.com/wleepang/shiny-directory-input>

**See Also**

[updateFileBrowserInput\(\)](#) and [prepareFileBrowser\(\)](#)

---

filterGeneExpr      *Filter genes based on their expression*

---

**Description**

Uses [filterByExpr](#) to determine genes with sufficiently large counts to retain for statistical analysis.

**Usage**

```
filterGeneExpr(  
  geneExpr,  
  minMean = 0,  
  maxMean = Inf,  
  minVar = 0,  
  maxVar = Inf,  
  minCounts = 10,  
  minTotalCounts = 15  
)
```

**Arguments**

geneExpr	Data frame or matrix: gene expression
minMean	Numeric: minimum of read count mean per gene
maxMean	Numeric: maximum of read count mean per gene
minVar	Numeric: minimum of read count variance per gene
maxVar	Numeric: maximum of read count variance per gene
minCounts	Numeric: minimum number of read counts per gene for a worthwhile number of samples (check <a href="#">filterByExpr</a> for more information)
minTotalCounts	Numeric: minimum total number of read counts per gene

**Value**

Boolean vector indicating which genes have sufficiently large counts

**See Also**

Other functions for gene expression pre-processing: [convertGeneIdentifiers\(\)](#), [normaliseGeneExpression\(\)](#), [plotGeneExprPerSample\(\)](#), [plotLibrarySize\(\)](#), [plotRowStats\(\)](#)

**Examples**

```

geneExpr <- readRDS("ex_gene_expression.RDS")

# Add some genes with low expression
geneExpr <- rbind(geneExpr,
                 lowReadGene1=c(rep(4:5, 10)),
                 lowReadGene2=c(rep(5:1, 10)),
                 lowReadGene3=c(rep(10:1, 10)),
                 lowReadGene4=c(rep(7:8, 10)))

# Filter out genes with low reads across samples
geneExpr[filterGeneExpr(geneExpr), ]

```

---

filterGroups

*Filter groups with less data points than the threshold*


---

**Description**

Groups containing a number of non-missing values less than the threshold are discarded.

**Usage**

```
filterGroups(vector, group, threshold = 1)
```

**Arguments**

vector	Character: elements
group	Character: respective group of each elements
threshold	Integer: number of valid non-missing values by group

**Value**

Named vector with filtered elements from valid groups. The group of the respective element is given as an attribute.

**Examples**

```

# Removes groups with less than two elements
vec <- 1:6
names(vec) <- paste("sample", letters[1:6])
filterGroups(vec, c("A", "B", "B", "C", "D", "D"), threshold=2)

```



---

 filterPSI

*Filter alternative splicing quantification*


---

### Description

Filter alternative splicing quantification

### Usage

```
filterPSI(
  psi,
  eventType = NULL,
  eventSubtype = NULL,
  minPSI = -Inf,
  maxPSI = Inf,
  minMedian = -Inf,
  maxMedian = Inf,
  minLogVar = -Inf,
  maxLogVar = Inf,
  minRange = -Inf,
  maxRange = Inf
)
```

### Arguments

psi	Data frame or matrix: alternative splicing quantification
eventType	Character: filter data based on event type; check all event types available by using <code>getSplicingEventTypes(psi)</code> , where <code>psi</code> is the alternative splicing quantification data; if <code>eventType = NULL</code> , events are not filtered by event type
eventSubtype	Character: filter data based on event subtype; check all event subtypes available in your data by using <code>unique(getSplicingEventData(psi)\$subtype)</code> , where <code>psi</code> is the alternative splicing quantification data; if <code>eventSubtype = NULL</code> , events are not filtered by event subtype
minPSI	Numeric: minimum PSI value
maxPSI	Numeric: maximum PSI value
minMedian	Numeric: minimum median PSI per splicing event
maxMedian	Numeric: maximum median PSI per splicing event
minLogVar	Numeric: minimum $\log_{10}$ (PSI variance) per splicing event
maxLogVar	Numeric: maximum $\log_{10}$ (PSI variance) per splicing event
minRange	Numeric: minimum PSI range across samples per splicing event
maxRange	Numeric: maximum PSI range across samples per splicing event

### Value

Boolean vector indicating which splicing events pass the thresholds

**See Also**

Other functions for PSI quantification: `getSplicingEventTypes()`, `listSplicingAnnotations()`, `loadAnnotation()`, `plotRowStats()`, `quantifySplicing()`

**Examples**

```
# Calculate PSI for skipped exon (SE) and mutually exclusive (MXE) events
annot <- readfile("ex_splicing_annotation.RDS")
junctionQuant <- readfile("ex_junctionQuant.RDS")

psi <- quantifySplicing(annot, junctionQuant, eventType=c("SE", "MXE"))
# Filter PSI
psi[filterPSI(psi, minMedian=0.05, maxMedian=0.95, minRange=0.15), ]
```

---

`findASeventsFromGene` *Find splicing events based on given genes*

---

**Description**

Find splicing events based on given genes

**Usage**

```
findASeventsFromGene(psi, gene)
```

**Arguments**

<code>psi</code>	Data frame or matrix: alternative splicing quantification
<code>gene</code>	Character: gene

**Value**

Character vector containing alternative splicing events

---

`findEventData` *Look for event data in input*

---

**Description**

Check if event data can be found in data and then event. Event data has to be an object of class `eventData`

**Usage**

```
findEventData(event = NULL, data = NULL)
```

**Arguments**

<code>event</code>	Character: AS event that may contain event data in its attribute <code>eventData</code>
<code>data</code>	Data frame or matrix: either event data or data containing event data in its attributes <code>rowData</code> or <code>eventData</code>

**Value**

Event data (or NULL if not found)

---

geneExprFileInput	<i>File input for molecular data</i>
-------------------	--------------------------------------

---

**Description**

File input for molecular data

**Usage**

```
geneExprFileInput(id, clearable = FALSE)
ASquantFileInput(id, clearable = FALSE)
junctionQuantFileInput(id, clearable = FALSE)
sampleInfoFileInput(id, clearable = FALSE)
subjectInfoFileInput(id, clearable = FALSE)
```

**Arguments**

id	Character: identifier for gene expression input
clearable	Boolean: allow to clear selected file or directory?

**Value**

HTML elements

---

geneExprSurvSet	<i>Logic set to perform survival analysis based on gene expression cutoffs</i>
-----------------	--

---

**Description**

Logic set to perform survival analysis based on gene expression cutoffs

**Usage**

```
geneExprSurvSet(session, input, output)
```

**Arguments**

session	Shiny session
input	Shiny input
output	Shiny output

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

geNormalisationFilteringInterface

*Interface to normalise and filter gene expression*

---

### Description

Interface to normalise and filter gene expression

### Usage

```
geNormalisationFilteringInterface(ns)
```

### Arguments

ns                    Namespace function

### Value

HTML elements

---

getAttributesTime

*Get time values for given columns in a clinical dataset*

---

### Description

Get time values for given columns in a clinical dataset

### Usage

```
getAttributesTime(
  clinical,
  event,
  timeStart,
  timeStop = NULL,
  followup = "days_to_last_followup"
)
```

### Arguments

clinical	Data frame: clinical data
event	Character: name of column containing time of the event of interest
timeStart	Character: name of column containing starting time of the interval or follow up time
timeStop	Character: name of column containing ending time of the interval (only relevant for interval censoring)
followup	Character: name of column containing follow up time

**Value**

Data frame containing the time for the given columns

**See Also**

Other functions to analyse survival: [assignValuePerSubject\(\)](#), [labelBasedOnCutoff\(\)](#), [optimalSurvivalCutoff\(\)](#), [plotSurvivalCurves\(\)](#), [plotSurvivalPvaluesByCutoff\(\)](#), [processSurvTerms\(\)](#), [survdiffTerms\(\)](#), [survfit.survTerms\(\)](#), [testSurvival\(\)](#)

**Examples**

```
df <- data.frame(followup=c(200, 300, 400), death=c(NA, 300, NA))
rownames(df) <- paste("subject", 1:3)
getAttributesTime(df, event="death", timeStart="death", followup="followup")
```

---

getClinicalDataForSurvival

*Retrieve clinical data based on attributes required for survival analysis*

---

**Description**

Retrieve clinical data based on attributes required for survival analysis

**Usage**

```
getClinicalDataForSurvival(..., formulaStr = NULL)
```

**Arguments**

... Character: names of columns to retrieve  
 formulaStr Character: right-side of the formula for survival analysis

**Value**

Filtered clinical data

---

getClinicalMatchFrom *Get or set clinical matches from a given data type*

---

**Description**

Get or set clinical matches from a given data type

**Usage**

```
getClinicalMatchFrom(dataset, category = getCategory())
setClinicalMatchFrom(dataset, matches, category = getCategory())
```

**Arguments**

dataset	Character: data set name
category	Character: data category
matches	Vector of integers: clinical matches of dataset

**Value**

Getters return globally accessible data, whereas setters return NULL as they are only used to modify the Shiny session's state

**Note**

Needs to be called inside a reactive function

**See Also**

Other functions to get and set global variables: [getDifferentialExpression\(\)](#), [getDifferentialSplicing\(\)](#), [getGlobal\(\)](#), [getGroups\(\)](#), [getHighlightedPoints\(\)](#), [getSelectedDataPanel\(\)](#)

---

getData	<i>Get global data</i>
---------	------------------------

---

**Description**

Get global data

**Usage**

```
getData()
```

**Value**

Variable containing all data of interest

---

getDataRows	<i>Get rows of a data frame between two row indexes</i>
-------------	---

---

**Description**

Get rows of a data frame between two row indexes

**Usage**

```
getDataRows(i, data, firstRow, lastRow)
```

**Arguments**

i	Integer: current iteration
data	Data.frame: contains the data of interest
firstRow	Vector of integers: First row index of interest; value must be less than the respective last row index and less than the number of rows in the data frame
lastRow	Vector of integers: Last row index of interest; value must be higher than the respective first row index and less than the number of rows in the data frame

**Details**

For a given iteration i, returns data from firstRow[i] to lastRow[i]

**Value**

Data frame subset from two row indexes (returns NA if the first row index is NA)

---

getDifferentialExpression

*Get or set differential expression' elements for a data category*

---

**Description**

Get or set differential expression' elements for a data category

**Usage**

```
getDifferentialExpression(category = getCategory())  
setDifferentialExpression(differential, category = getCategory())  
getDifferentialExpressionFiltered(category = getCategory())  
setDifferentialExpressionFiltered(differential, category = getCategory())  
getDifferentialExpressionSurvival(category = getCategory())  
setDifferentialExpressionSurvival(survival, category = getCategory())  
getDifferentialExpressionResetPaging(category = getCategory())  
setDifferentialExpressionResetPaging(reset, category = getCategory())  
getDifferentialExpressionColumns(category = getCategory())  
setDifferentialExpressionColumns(columns, category = getCategory())
```

**Arguments**

category	Character: data category
differential	Data frame or matrix: differential analyses table
survival	Data frame or matrix: differential analyses' survival data
reset	Character: reset paging of differential analyses table?
columns	Character: differential analyses' column names

**Value**

Getters return globally accessible data, whereas setters return NULL as they are only used to modify the Shiny session's state

**Note**

Needs to be called inside a reactive function

**See Also**

Other functions to get and set global variables: [getClinicalMatchFrom\(\)](#), [getDifferentialSplicing\(\)](#), [getGlobal\(\)](#), [getGroups\(\)](#), [getHighlightedPoints\(\)](#), [getSelectedDataPanel\(\)](#)

---

getDifferentialSplicing

*Get or set differential splicing' elements for a data category*

---

**Description**

Get or set differential splicing' elements for a data category

**Usage**

```
getDifferentialSplicing(category = getCategory())
```

```
setDifferentialSplicing(differential, category = getCategory())
```

```
getDifferentialSplicingFiltered(category = getCategory())
```

```
setDifferentialSplicingFiltered(differential, category = getCategory())
```

```
getDifferentialSplicingSurvival(category = getCategory())
```

```
setDifferentialSplicingSurvival(survival, category = getCategory())
```

```
getDifferentialSplicingResetPaging(category = getCategory())
```

```
setDifferentialSplicingResetPaging(reset, category = getCategory())
```

```
getDifferentialSplicingColumns(category = getCategory())
```

```
setDifferentialSplicingColumns(columns, category = getCategory())
```



**Arguments**

category	Character: data category
differential	Data frame or matrix: differential analyses table
survival	Data frame or matrix: differential analyses' survival data
reset	Character: reset paging of differential analyses table?
columns	Character: differential analyses' column names

**Value**

Getters return globally accessible data, whereas setters return NULL as they are only used to modify the Shiny session's state

**Note**

Needs to be called inside a reactive function

**See Also**

Other functions to get and set global variables: [getClinicalMatchFrom\(\)](#), [getDifferentialExpression\(\)](#), [getGlobal\(\)](#), [getGroups\(\)](#), [getHighlightedPoints\(\)](#), [getSelectedDataPanel\(\)](#)

---

getDownloadsFolder	<i>Get the path to the Downloads folder</i>
--------------------	---

---

**Description**

Get the path to the Downloads folder

**Usage**

```
getDownloadsFolder()
```

**Value**

Path to Downloads folder

**See Also**

Other functions associated with TCGA data retrieval: [getTCGAdataTypes\(\)](#), [isFirebrowseUp\(\)](#), [loadTCGAdata\(\)](#), [parseTCGAsampleTypes\(\)](#)

Other functions associated with GTEx data retrieval: [getGtexDataTypes\(\)](#), [getGtexTissues\(\)](#), [loadGtexData\(\)](#)

Other functions associated with SRA data retrieval: [loadSRAproject\(\)](#)

**Examples**

```
getDownloadsFolder()
```

---

`getFirebrowseDateFormat`*Returns the date format used by the FireBrowse API*

---

**Description**

Returns the date format used by the FireBrowse API

**Usage**

```
getFirebrowseDateFormat()
```

**Value**

Named list with date formats from FireBrowse API

**Examples**

```
format <- psychomics::getFirebrowseDateFormat()

# date format to use in a query to FireBrowse API
format$query

# date format to parse a date in a response from FireBrowse API
format$response
```

---

`getGeneList`*Get curated, literature-based gene lists*

---

**Description**

Available gene lists:

- **Sebestyen et al., 2016:** 1350 genes encoding RNA-binding proteins, 167 of which are splicing factors

**Usage**

```
getGeneList(genes = NULL)
```

**Arguments**

`genes` Vector of characters: intersect lists with given genes (lists with no matching genes will not be returned)

**Value**

List of genes

**See Also**

Other functions for data grouping: [createGroupByAttribute\(\)](#), [getSampleFromSubject\(\)](#), [getSubjectFromSample\(\)](#), [groupPerElem\(\)](#), [plotGroupIndependence\(\)](#), [testGroupIndependence\(\)](#)

**Examples**

```
getGeneList()
```

---

<code>getGlobal</code>	<i>Get or set globally accessible elements</i>
------------------------	--

---

**Description**

Get or set globally accessible elements

**Usage**

```
getGlobal(category = getCategory(), ..., sep = "_")  
setGlobal(category = getCategory(), ..., value, sep = "_")  
setData(data)  
setDataTable(name, value, category = getCategory())  
getAutoNavigation()  
setAutoNavigation(auto)  
getCores()  
setCores(integer)  
getSignificant()  
setSignificant(integer)  
getPrecision()  
setPrecision(integer)  
getASevents()  
getAnnotationHub()  
setAnnotationHub(ah)  
getASevent()  
setASevent(event, data = NULL)
```

```
getEvent()
setEvent(event, data = NULL)
getGenes()
getCategories()
getCategory()
setCategory(category)
getCategoryData()
getActiveDataset()
setActiveDataset(dataset)
getClinicalData(attrs = NULL)
getSubjectId()
getSubjectAttributes()
getSampleInfo()
setSampleInfo(value, category = getCategory())
getSampleId()
getSampleAttributes()
getJunctionQuantification(category = getCategory())
getGeneExpression(item = NULL, category = getCategory(), EList = FALSE)
setNormalisedGeneExpression(geneExpr, category = getCategory())
getInclusionLevels()
setInclusionLevels(incLevels, category = getCategory())
getInclusionLevelsSummaryStatsCache(category = getCategory())
setInclusionLevelsSummaryStatsCache(cache, category = getCategory())
getPCA(category = getCategory())
setPCA(pca, category = getCategory())
getICA(category = getCategory())
```

```

setICA(ica, category = getCategory())
getCorrelation(category = getCategory())
setCorrelation(correlation, category = getCategory())
getGroupIndependenceTesting(category = getCategory())
setGroupIndependenceTesting(groupIndependenceTesting, category = getCategory())
getSpecies(category = getCategory())
setSpecies(species, category = getCategory())
getAssemblyVersion(category = getCategory())
setAssemblyVersion(assembly, category = getCategory())
getAnnotationName(category = getCategory())
setAnnotationName(annotName, category = getCategory())
getURLtoDownload()
setURLtoDownload(url)

```

### Arguments

category	Character: data category
...	Arguments to identify a variable
sep	Character to separate identifiers
value	Value to attribute to an element
data	Matrix or data frame: alternative splicing information
name	Character: data table name
auto	Boolean: enable automatic navigation of browser history?
integer	Integer: value of the setting
ah	AnnotationHub
event	Character: alternative splicing event
dataset	Character: dataset name
attrs	Character: name of attributes to retrieve (if NULL, the whole dataset is returned)
item	Character: name of specific item to retrieve (if NULL, the whole list is returned)
EList	Boolean: return gene expression datasets as EList if possible or as data frames?
geneExpr	Data frame or matrix: normalised gene expression
incLevels	Data frame or matrix: inclusion levels
cache	List of summary statistics
pca	prcomp object (principal component analysis)
ica	Object containing independent component analysis

correlation	prcomp object (correlation analyses)
groupIndependenceTesting	Object containing group independence testing results
species	Character: species
assembly	Character: assembly version
annotName	Character: annotation name
url	Character: URL links to download

**Value**

Getters return globally accessible data, whereas setters return NULL as they are only used to modify the Shiny session's state

**Note**

Needs to be called inside a reactive function

**See Also**

Other functions to get and set global variables: [getClinicalMatchFrom\(\)](#), [getDifferentialExpression\(\)](#), [getDifferentialSplicing\(\)](#), [getGroups\(\)](#), [getHighlightedPoints\(\)](#), [getSelectedDataPanel\(\)](#)

---

getGroups	<i>Get or set groups</i>
-----------	--------------------------

---

**Description**

Get or set groups

**Usage**

```
getGroups(
  type = c("Patients", "Samples", "ASevents", "Genes"),
  complete = FALSE,
  category = getCategory()
)
```

```
setGroups(
  type = c("Patients", "Samples", "ASevents", "Genes"),
  groups,
  category = getCategory()
)
```

**Arguments**

type	Character: type of groups (either Patients, Samples, ASevents or Genes)
complete	Boolean: return all the information on groups (TRUE) or just the group names and respective indexes (FALSE)?
category	Character: data category
groups	Matrix: groups of dataset

**Value**

Getters return globally accessible data, whereas setters return NULL as they are only used to modify the Shiny session's state

**Note**

Needs to be called inside a reactive function

**See Also**

Other functions to get and set global variables: [getClinicalMatchFrom\(\)](#), [getDifferentialExpression\(\)](#), [getDifferentialSplicing\(\)](#), [getGlobal\(\)](#), [getHighlightedPoints\(\)](#), [getSelectedDataPanel\(\)](#)

---

getGtexDataTypes	<i>Get GTEx data information</i>
------------------	----------------------------------

---

**Description**

Get GTEx data information

**Usage**

```
getGtexDataTypes()
```

```
getGtexReleases()
```

**Value**

GTEx data information

**See Also**

Other functions associated with GTEx data retrieval: [getDownloadsFolder\(\)](#), [getGtexTissues\(\)](#), [loadGtexData\(\)](#)

**Examples**

```
getGtexDataTypes()  
getGtexReleases()
```

---

getGtexDataURL                      *Get links to download GTEX data*

---

**Description**

Get links to download GTEX data

**Usage**

```
getGtexDataURL(  
    release,  
    domain = "https://storage.googleapis.com",  
    offline = FALSE  
)
```

**Arguments**

release	Numeric: GTEX data release
domain	Character: GTEX data storage domain
offline	Boolean: simulate offline behaviour

**Value**

Character with URLs to download GTEX data

---

getGtexTissues                      *Get GTEX tissues from given GTEX sample attributes*

---

**Description**

Get GTEX tissues from given GTEX sample attributes

**Usage**

```
getGtexTissues(folder = getDownloadsFolder(), release = getGtexReleases()[[1]])
```

**Arguments**

folder	Character: folder containing data
release	Numeric: GTEX data release to load

**Value**

Character: available tissues

**See Also**

Other functions associated with GTEX data retrieval: [getDownloadsFolder\(\)](#), [getGtexDataTypes\(\)](#), [loadGtexData\(\)](#)



**Examples**

```
## Not run:
getGtexTissues()

## End(Not run)
```

---

getHidden	<i>Get or set hidden globally accessible elements</i>
-----------	---

---

**Description**

Get or set hidden globally accessible elements

**Usage**

```
getHidden()

setHidden(val)
```

**Arguments**

val                    Value to attribute

**Value**

Getters return hidden globally accessible data, whereas setters return NULL as they are only used to modify the state of hidden elements

---

getHighlightedPoints	<i>Get or set points or regions for plots</i>
----------------------	---

---

**Description**

Get or set points or regions for plots

**Usage**

```
getHighlightedPoints(id, category = getCategory())

setHighlightedPoints(id, events, category = getCategory())

getZoom(id, category = getCategory())

setZoom(id, zoom, category = getCategory())

getSelectedPoints(id, category = getCategory())

setSelectedPoints(id, events, category = getCategory())

getLabelledPoints(id, category = getCategory())

setLabelledPoints(id, events, category = getCategory())
```

**Arguments**

id	Character: identifier
category	Character: data category
events	Integer: index of events
zoom	Integer: range of X and Y coordinates for zooming

**Value**

Getters return globally accessible data, whereas setters return NULL as they are only used to modify the Shiny session's state

**Note**

Needs to be called inside a reactive function

**See Also**

Other functions to get and set global variables: [getClinicalMatchFrom\(\)](#), [getDifferentialExpression\(\)](#), [getDifferentialSplicing\(\)](#), [getGlobal\(\)](#), [getGroups\(\)](#), [getSelectedDataPanel\(\)](#)

---

getNumerics	<i>Convert a column to numeric if possible and ignore given columns composed of lists</i>
-------------	---

---

**Description**

Convert a column to numeric if possible and ignore given columns composed of lists

**Usage**

```
getNumerics(table, by = NULL, toNumeric = FALSE)
```

**Arguments**

table	Data matrix: table
by	Character: column names of interest
toNumeric	Boolean: which columns to convert to numeric

**Value**

Processed data matrix

**Examples**

```

event <- read.table(text = "ABC123 + 250 300 350
                           DEF456 - 900 800 700")
names(event) <- c("Event ID", "Strand", "C1.end", "A1.end", "A1.start")

# Let's change one column to character
event[ , "C1.end"] <- as.character(event[ , "C1.end"])
is.character(event[ , "C1.end"])

event <- psichomics::getNumerics(event, by = c("Strand", "C1.end", "A1.end",
                                             "A1.start"),
                                 toNumeric = c(FALSE, TRUE, TRUE, TRUE))

# Let's check if the same column is now integer
is.numeric(event[ , "C1.end"])

```

---

getSampleFromSubject *Get samples matching the given subjects*

---

**Description**

Get samples matching the given subjects

**Usage**

```

getSampleFromSubject(
  patients,
  samples,
  clinical = NULL,
  rm.NA = TRUE,
  match = NULL,
  showMatch = FALSE
)

```

**Arguments**

patients	Character or list of characters: subject identifiers
samples	Character: sample identifiers
clinical	Data frame or matrix: clinical dataset
rm.NA	Boolean: remove missing values?
match	Integer: vector of subject index with the sample identifiers as name to save time (optional)
showMatch	Boolean: show matching subject index?

**Value**

Names of the matching samples (if showMatch = TRUE, a character with the subjects as values and their respective samples as names is returned)

**See Also**

Other functions for data grouping: [createGroupByAttribute\(\)](#), [getGeneList\(\)](#), [getSubjectFromSample\(\)](#), [groupPerElem\(\)](#), [plotGroupIndependence\(\)](#), [testGroupIndependence\(\)](#)

**Examples**

```

subjects <- c("GTEX-ABC", "GTEX-DEF", "GTEX-GHI", "GTEX-JKL", "GTEX-MNO")
samples <- paste0(subjects, "-sample")
clinical <- data.frame(samples=samples)
rownames(clinical) <- subjects
getSampleFromSubject(subjects[c(1, 4)], samples, clinical)

```

---

getSelectedDataPanel *Get or set selected panel in data section*

---

**Description**

Get or set selected panel in data section

**Usage**

```
getSelectedDataPanel()
```

```
setSelectedDataPanel(id)
```

**Value**

Getters return globally accessible data, whereas setters return NULL as they are only used to modify the Shiny session's state

**Note**

Needs to be called inside a reactive function

**See Also**

Other functions to get and set global variables: [getClinicalMatchFrom\(\)](#), [getDifferentialExpression\(\)](#), [getDifferentialSplicing\(\)](#), [getGlobal\(\)](#), [getGroups\(\)](#), [getHighlightedPoints\(\)](#)

---

getServerFunctions *Matches server functions from a given loader*

---

**Description**

Matches server functions from a given loader

**Usage**

```
getServerFunctions(loader, ..., priority = NULL)
```

**Arguments**

loader	Character: loader to run the functions
...	Extra arguments to pass to server functions
priority	Character: name of functions to prioritise by the given order; for instance, <code>c("data", "analyses")</code> would load data, then analyses and finally the remaining functions

**Value**

Invisible TRUE

---

getSplicingEventCoordinates

*Returns the coordinates of interest for a given event type*

---

**Description**

Returns the coordinates of interest for a given event type

**Usage**

```
getSplicingEventCoordinates(type, sorting = FALSE)
```

**Arguments**

type	Character: alternative splicing event type
sorting	Boolean: get coordinates used for sorting and comparison between different programs?

**Value**

Coordinates of interest according to the alternative splicing event type

---

getSplicingEventData *Get splicing event information for given alternative splicing quantification data*

---

**Description**

Get splicing event information for given alternative splicing quantification data

**Usage**

```
getSplicingEventData(psi)
```

**Arguments**

psi	Matrix or data frame: alternative splicing quantification data
-----	--

**Value**

Matrix or data frame containing splicing event information for alternative splicing events in psi (if available)

---

```
getSplicingEventFromGenes
```

*Get alternative splicing events from genes or vice-versa*

---

### Description

Get alternative splicing events from genes or vice-versa

### Usage

```
getSplicingEventFromGenes(genes, ASevents, data = NULL)
```

```
getGenesFromSplicingEvents(ASevents, data = NULL)
```

### Arguments

genes	Character: gene symbols (or TCGA-styled gene symbols)
ASevents	Character: alternative splicing events
data	Matrix or data frame: alternative splicing information

### Details

A list of alternative splicing events is required to run `getSplicingEventFromGenes`

### Value

Named character containing alternative splicing events or genes and their respective genes or alternative splicing events as names (depending on the function in use)

### Examples

```
ASevents <- c("SE_1+_201763003_201763300_201763374_201763594_NAV1",
              "SE_1+_183515472_183516238_183516387_183518343_SMG7",
              "SE_1+_183441784_183471388_183471526_183481972_SMG7",
              "SE_1+_181019422_181022709_181022813_181024361_MR1",
              "SE_1+_181695298_181700311_181700367_181701520_CACNA1E")
genes <- c("NAV1", "SMG7", "MR1", "HELLO")

# Get splicing events from genes
matchedASevents <- getSplicingEventFromGenes(genes, ASevents)

# Names of matched events are the matching input genes
names(matchedASevents)
matchedASevents

# Get genes from splicing events
matchedGenes <- getGenesFromSplicingEvents(ASevents)

# Names of matched genes are the matching input alternative splicing events
names(matchedGenes)
matchedGenes
```

---

getSplicingEventTypes *Get supported splicing event types*

---

**Description**

Get supported splicing event types

**Usage**

```
getSplicingEventTypes(psi = NULL, acronymsAsNames = FALSE)
```

**Arguments**

psi                    Data frame or matrix: alternative splicing quantification data  
acronymsAsNames        Boolean: return acronyms as names?

**Value**

Named character vector with splicing event types

**See Also**

Other functions for PSI quantification: [filterPSI\(\)](#), [listSplicingAnnotations\(\)](#), [loadAnnotation\(\)](#), [plotRowStats\(\)](#), [quantifySplicing\(\)](#)

**Examples**

```
getSplicingEventTypes()
```

---

getSubjectFromSample *Get subjects from given samples*

---

**Description**

Get subjects from given samples

**Usage**

```
getSubjectFromSample(sampleId, patientId = NULL, na = FALSE, sampleInfo = NULL)
```

**Arguments**

sampleId                Character: sample identifiers  
patientId                Character: subject identifiers to filter by (optional; if a matrix or data frame is given, its rownames will be used to infer the subject identifiers)  
na                        Boolean: return NA for samples with no matching subjects  
sampleInfo               Data frame or matrix: sample information containing the sample identifiers as rownames and a column named "Subject ID" with the respective subject identifiers

**Value**

Character: subject identifiers corresponding to the given samples

**See Also**

Other functions for data grouping: [createGroupByAttribute\(\)](#), [getGeneList\(\)](#), [getSampleFromSubject\(\)](#), [groupPerElem\(\)](#), [plotGroupIndependence\(\)](#), [testGroupIndependence\(\)](#)

**Examples**

```
samples <- paste0("GTEX-", c("ABC", "DEF", "GHI", "JKL", "MNO"), "-sample")
getSubjectFromSample(samples)

# Filter returned samples based on available subjects
subjects <- paste0("GTEX-", c("DEF", "MNO"))
getSubjectFromSample(samples, subjects)
```

---

getTCGAdataTypes	<i>Get available parameters for TCGA data</i>
------------------	---

---

**Description**

Parameters obtained via [FireBrowse](#)

**Usage**

```
getTCGAdataTypes()

getTCGAdates()

getTCGAcohorts(cohort = NULL)
```

**Arguments**

cohort            Character: filter results by cohorts (optional)

**Value**

Parsed response

**See Also**

Other functions associated with TCGA data retrieval: [getDownloadsFolder\(\)](#), [isFirebrowseUp\(\)](#), [loadTCGAdata\(\)](#), [parseTCGAsampleTypes\(\)](#)

**Examples**

```
getTCGAdataTypes()
if (isFirebrowseUp()) getTCGAdates()
if (isFirebrowseUp()) getTCGAcohorts()
```



---

getUiFunctions	<i>Matches user interface (UI) functions from a given loader</i>
----------------	--

---

**Description**

Matches user interface (UI) functions from a given loader

**Usage**

```
getUiFunctions(ns, loader, ..., priority = NULL)
```

**Arguments**

ns	Shiny function to create IDs within a namespace
loader	Character: loader to run the functions
...	Extra arguments to pass to the user interface (UI) functions
priority	Character: name of functions to prioritise by the given order; for instance, c("data", "analyses") would load data, then analyses and finally the remaining functions

**Value**

List of functions related to the given loader

---

getValidEvents	<i>Filters the events with valid elements according to the given validator</i>
----------------	--

---

**Description**

Filters the events with valid elements according to the given validator

**Usage**

```
getValidEvents(event, validator, areMultipleExonsValid = FALSE)
```

**Arguments**

event	Data.frame containing only one event with at least 7 columns as retrieved from the alternative splicing annotation files from MISO (GFF3 files)
validator	Character: valid elements for each event
areMultipleExonsValid	Boolean: consider runs of exons as valid when comparing with the validator? Default is FALSE (see details)

**Details**

areMultipleExonsValid allows to consider runs of exons (i.e. sequences where exon occurs consecutively) as valid when comparing based on the validator. For example, if validator = c("gene", "mRNA", "exon") and areMultipleExonsValid = FALSE, the event c("gene", "mRNA", "exon", "exon") is not valid as it has one additional exon. If areMultipleExonsValid = TRUE, the same event would be valid.

**Value**

Data.frame with valid events

**Examples**

```
event <- read.table(text = "
chr1 SE gene 17233 18061 . - .
chr1 SE dkfd 00000 30000 . - .
chr1 SE mRNA 17233 18061 . - .
chr1 SE exon 17233 17368 . - .
chr1 SE exon 17526 17742 . - .
chr1 SE exon 17915 18061 . - .
chr1 SE mRNA 17233 18061 . - .
chr1 SE exon 17233 17368 . - .
chr1 SE exon 17915 18061 . - .
chr1 SE gene 17233 18061 . - .
chr1 SE mRNA 17233 18061 . - .
chr1 SE exon 17233 17368 . - .
chr1 SE exon 17606 17742 . - .
chr1 SE exon 17915 18061 . - .
chr1 SE mRNA 17233 18061 . - .
chr1 SE exon 17233 17368 . - .
chr1 SE exon 17915 18061 . - .
")
validator <- c("gene", "mRNA", rep("exon", 3), "mRNA", rep("exon", 2))
psychomics::getValidEvents(event, validator)
```

---

ggplotServer

*Logic set to create an interactive [ggplot](#)*

---

**Description**

Logic set to create an interactive [ggplot](#)

**Usage**

```
ggplotServer(
  input,
  output,
  id,
  plot = NULL,
  df = NULL,
  x = NULL,
  y = NULL,
  eventData = NULL
)

ggplotAuxServer(input, output, id)
```

**Arguments**

input	Shiny input
output	Shiny output
id	Character: identifier
plot	Character: plot expression (if NULL, no plots are rendered)
df	Data frame
x	Character: name of the variable used for the X axis
y	Character: name of the variable used for the Y axis
eventData	Alternative splicing event information (if available)

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

**Note**

Insert `ggplotAuxSet` outside any observer (so it is only run once)

---

ggplotTooltip	<i>Create the interface for the tooltip of a plot</i>
---------------	---

---

**Description**

Create the interface for the tooltip of a plot

**Usage**

```
ggplotTooltip(df, hover, x, y, eventData = NULL)
```

**Arguments**

df	Data frame
hover	Mouse hover information for a given plot as retrieved from <a href="#">hoverOpts</a>
x	Character: name of the variable used for the X axis
y	Character: name of the variable used for the Y axis
eventData	Alternative splicing event information (if available)

**Value**

HTML elements

---

ggplotUI                      *Interface for interactive ggplot*

---

**Description**

Interface for interactive [ggplot](#)

**Usage**

```
ggplotUI(id)
```

**Arguments**

id                      Character: identifier

**Value**

HTML elements

---

globalSelectize              *Create a selectize input available from any page*

---

**Description**

Create a selectize input available from any page

**Usage**

```
globalSelectize(id, placeholder, ASevent = FALSE)
```

**Arguments**

id                      Character: input identifier  
placeholder            Character: input placeholder  
ASevent                Boolean: select alternative splicing events?

**Value**

HTML element for a global selectize input

---

groupByAttribute	<i>Data grouping interface</i>
------------------	--------------------------------

---

**Description**

Data grouping interface

**Usage**

```
groupByAttribute(ns, cols, id, example)
```

```
groupByPreMadeList(ns, data, id)
```

```
groupById(ns, id)
```

```
groupByExpression(ns, id)
```

```
groupByGrep(ns, cols, id)
```

**Arguments**

ns	Namespace function
cols	Character or list: name of columns to show
id	Character: identifier
example	Character: text to show as an example
data	List: list of groups with elements

**Value**

HTML elements

---

groupManipulation	<i>Logic server to manipulate data grouping</i>
-------------------	---

---

**Description**

Logic server to manipulate data grouping

**Usage**

```
groupManipulation(input, output, session, type)
```

**Arguments**

input	Shiny input
output	Shiny output
session	Shiny session
type	Character: type of data for each the interface is intended

**Value**

HTML elements

---

 groupManipulationInput
*Interface to manipulate data grouping***Description**

Interface to manipulate data grouping

**Usage**

groupManipulationInput(id, type)

**Arguments**

id                   Character: identifier

type                 Character: type of data for each the interface is intended

**Value**

HTML elements

---

 groupPerElem
*Assign one group to each element***Description**

Assign one group to each element

**Usage**

groupPerElem(groups, elem = NULL, outerGroupName = NA)

**Arguments**

groups               List of integers: groups of elements

elem                 Character: all elements available

outerGroupName     Character: name to give to outer group (if NULL, only show elements matched to their respective groups)

**Value**

Character vector where each element corresponds to the group of the respective element

**See Also**Other functions for data grouping: [createGroupByAttribute\(\)](#), [getGeneList\(\)](#), [getSampleFromSubject\(\)](#), [getSubjectFromSample\(\)](#), [plotGroupIndependence\(\)](#), [testGroupIndependence\(\)](#)

**Examples**

```
groups <- list(1:3, 4:7, 8:10)
names(groups) <- paste("Stage", 1:3)
groupPerElem(groups)
```

---

groupsServerOnce	<i>Server function for data grouping (one call)</i>
------------------	---

---

**Description**

These functions only run once instead of running for every instance of groups

**Usage**

```
groupsServerOnce(input, output, session)
```

**Arguments**

input	Shiny input
output	Shiny output
session	Shiny session

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

hchart.survfit	<i>Plot survival curves</i>
----------------	-----------------------------

---

**Description**

Plot survival curves

**Usage**

```
## S3 method for class 'survfit'
hchart(
  object,
  ...,
  fun = NULL,
  markTimes = TRUE,
  symbol = "plus",
  markerColor = "black",
  ranges = FALSE,
  rangesOpacity = 0.3
)
```

**Arguments**

object	survfit object as returned from <code>survfit.survTerms()</code> function
...	Arguments passed on to <code>highcharter:hc_add_series</code>
fun	Name of function or function used to transform the survival curve: <code>log</code> will put y axis on log scale, <code>event</code> plots cumulative events ( $f(y) = 1-y$ ), <code>cumhaz</code> plots the cumulative hazard function ( $f(y) = -\log(y)$ ), and <code>cloglog</code> creates a complimentary log-log survival plot ( $f(y) = \log(-\log(y))$ ) along with log scale for the x-axis.
markTimes	Label curves marked at each censoring time?
symbol	Symbol to use as marker
markerColor	Colour of the marker; if NULL, the respective colour of each series are used
ranges	Plot interval ranges?
rangesOpacity	Opacity of the interval ranges

**Value**

highchart object to plot survival curves

**Examples**

```
# Plot Kaplan-Meier curves
require("survival")
require("highcharter")
leukemia.surv <- survfit(Surv(time, status) ~ x, data = aml)
hchart(leukemia.surv)

# Plot the cumulative hazard function
lsurv2 <- survfit(Surv(time, status) ~ x, aml, type='fleming')
hchart(lsurv2, fun="cumhaz")

# Plot the fit of a Cox proportional hazards regression model
fit <- coxph(Surv(futime, fustat) ~ age, data = ovarian)
ovarian.surv <- survfit(fit, newdata=data.frame(age=60))
hchart(ovarian.surv, ranges = TRUE)
```

---

hc\_scatter

*Create scatter plot*

---

**Description**

Create a scatter plot using highcharter



**Usage**

```

hc_scatter(
  hc,
  x,
  y,
  z = NULL,
  label = NULL,
  showInLegend = FALSE,
  color = NULL,
  ...
)

```

**Arguments**

hc	Highchart object
x	Numeric: X axis
y	Numeric: Y axis
z	Numeric: Z axis to set the bubble size (optional)
label	Character: data label for each point (optional)
showInLegend	Boolean: show the data in the legend box?
color	Character: series colour
...	Arguments passed on to <a href="#">highcharter::hc_add_series</a>

**Value**

highcharter object containing information for a scatter plot

---

HTMLfast

*Faster version of shiny::HTML*


---

**Description**

Faster version of shiny::HTML

**Usage**

```
HTMLfast(text)
```

**Arguments**

text	Character: text
------	-----------------

**Value**

HTML element

---

importGroupsFrom	<i>Import groups from a file</i>
------------------	----------------------------------

---

**Description**

Import groups from a file

**Usage**

```
importGroupsFrom(
  file,
  uniqueElems = NULL,
  matchingElems = NULL,
  match = NULL,
  type = NULL
)
```

**Arguments**

file	Character: path to file
uniqueElems	Character: vector of unique elements (samples or alternative splicing events)
matchingElems	Character: vector of matching elements (subjects or genes)
match	Match between elements within groups

**Value**

Matrix with groups

---

inclusionLevelsFilterInterface	<i>Interface to filter alternative splicing</i>
--------------------------------	---

---

**Description**

Interface to filter alternative splicing

**Usage**

```
inclusionLevelsFilterInterface(ns)
```

**Arguments**

ns	Namespace function
----	--------------------

**Value**

HTML elements

---

inclusionLevelsInterface

*Interface to quantify alternative splicing*

---

### Description

Interface to quantify alternative splicing

### Usage

```
inclusionLevelsInterface(ns)
```

### Arguments

ns                    Namespace function

### Value

HTML elements

---

inlineDialog

*Alert in the style of a dialogue box with a button*

---

### Description

Alert in the style of a dialogue box with a button

### Usage

```
inlineDialog(  
  description,  
  ...,  
  buttonLabel = NULL,  
  buttonIcon = NULL,  
  buttonId = NULL,  
  id = NULL,  
  type = c("error", "warning"),  
  bigger = FALSE  
)  
  
errorDialog(description, ...)  
  
warningDialog(description, ...)
```

**Arguments**

description	Character: description
...	Extra parameters when creating the alert
buttonLabel	Character: button label
buttonIcon	Character: button icon
buttonId	Character: button identifier
id	Character: identifier
type	Character: type of alert (error or warning)
bigger	Boolean: wrap the description in a h4 tag?

**Value**

HTML elements

---

insideFile	<i>Get psychomics file inside a given directory</i>
------------	---

---

**Description**

Get psychomics file inside a given directory

**Usage**

```
insideFile(...)
```

**Arguments**

... character vectors, specifying subdirectory and file(s) within some package. The default, none, returns the root of the package. Wildcards are not supported.

**Value**

Loaded file

---

is.whole	<i>Check if a number is whole</i>
----------	-----------------------------------

---

**Description**

Check if a number is whole

**Usage**

```
is.whole(x, tol = .Machine$double.eps^0.5)
```

**Arguments**

x	Object to be tested
tol	Numeric: tolerance used for comparison

**Value**

TRUE if number is whole; otherwise, FALSE

---

isFile	<i>Check if files exist</i>
--------	-----------------------------

---

**Description**

Check if files exist

**Usage**

```
isFile(files)
```

**Arguments**

files	Character: vector of filepaths to check
-------	---

**Value**

Boolean vector stating whether each file exists or not

---

isFirebrowseUp	<i>Check if <a href="http://firebrowse.org/api-docs/FireBrowse_API_is_running">Rhrefhttp://firebrowse.org/api-docs/FireBrowse API is running</a></i>
----------------	--

---

**Description**

Check if **FireBrowse API** is running

**Usage**

```
isFirebrowseUp()
```

**Value**

Invisible TRUE if the **FireBrowse API** is working; otherwise, raises a warning with the status code and a brief explanation.

**See Also**

Other functions associated with TCGA data retrieval: [getDownloadsFolder\(\)](#), [getTCGAdataTypes\(\)](#), [loadTCGAdata\(\)](#), [parseTCGAsampleTypes\(\)](#)

**Examples**

```
isFirebrowseUp()
```

---

isRStudioServer	<i>Check if running in RStudio Server</i>
-----------------	---

---

**Description**

Check if running in RStudio Server

**Usage**

```
isRStudioServer()
```

**Value**

Boolean stating whether running in RStudio Server

---

joinEventsPerType	<i>Full outer join all given events based on select columns</i>
-------------------	---

---

**Description**

Full outer join all given events based on select columns

**Usage**

```
joinEventsPerType(events, types = NULL)
```

**Arguments**

events	Data frame or matrix: alternative splicing events
types	Character: alternative splicing types

**Value**

List of events joined by alternative splicing event type

---

junctionString	<i>String used to search for matches in a junction quantification file</i>
----------------	--

---

**Description**

String used to search for matches in a junction quantification file

**Usage**

```
junctionString(chr, strand, junc5, junc3, showStrand)
```

**Arguments**

chr	Character: chromosome
strand	Character: strand
junc5	Integer: 5' end junction
junc3	Integer: 3' end junction
showStrand	Boolean: include strand?

**Value**

Formatted character string

---

labelBasedOnCutoff	<i>Label groups based on a given cutoff</i>
--------------------	---

---

**Description**

Label groups based on a given cutoff

**Usage**

```
labelBasedOnCutoff(data, cutoff, label = NULL, gte = TRUE)
```

**Arguments**

data	Numeric: test data
cutoff	Numeric: test cutoff
label	Character: label to prefix group names
gte	Boolean: test using greater than or equal than cutoff (TRUE) or less than or equal than cutoff (FALSE)?

**Value**

Labelled groups

**See Also**

Other functions to analyse survival: `assignValuePerSubject()`, `getAttributesTime()`, `optimalSurvivalCutoff()`, `plotSurvivalCurves()`, `plotSurvivalPvaluesByCutoff()`, `processSurvTerms()`, `survdiffTerms()`, `survfit.survTerms()`, `testSurvival()`

**Examples**

```
labelBasedOnCutoff(data=c(1, 0, 0, 1, 0, 1), cutoff=0.5)

labelBasedOnCutoff(data=c(1, 0, 0, 1, 0, 1), cutoff=0.5, "Ratio")

# Use "greater than" instead of "greater than or equal to"
labelBasedOnCutoff(data=c(1, 0, 0, 0.5, 0, 1), cutoff=0.5, gte=FALSE)
```

---

leveneTest

*Levene's test*


---

**Description**

Performs a Levene's test to assess the equality of variances

**Usage**

```
leveneTest(x, g, centers = median)
```

**Arguments**

x	Numeric vector or list of numeric vectors: non-numeric elements of a list will be coerced with a warning
g	Vector or factor: groups of elements in x (ignored with a warning if x is a list)
centers	Function used to calculate how much values spread; for instance, median (default) or mean

**Details**

The implementation of this function is based on `car:::leveneTest.default` with a more standard result.

**Value**

A list with class "htest" containing the following components:

statistic	the value of the test statistic with a name describing it.
p.value	the p-value for the test.
method	the type of test applied.
data.name	a character string giving the names of the data.



**Examples**

```
vals <- sample(30, replace=TRUE)
group <- lapply(list("A", "B", "C"), rep, 10)
group <- unlist(group)
psychomics:::leveneTest(vals, group)

## Using Levene's test based on the mean
psychomics:::leveneTest(vals, group, mean)
```

---

linkToArticles	<i>psychomics article's link interface</i>
----------------	--

---

**Description**

psychomics article's link interface

**Usage**

```
linkToArticles()
```

**Value**

HTML elements

---

linkToRunJS	<i>Link to run arbitrary JavaScript code</i>
-------------	--

---

**Description**

Link to run arbitrary JavaScript code

**Usage**

```
linkToRunJS(text, code)
```

**Arguments**

text	Character: text label
code	Character: JavaScript code

**Value**

HTML elements

---

listAllAnnotations	<i>List alternative splicing annotation files available, as well as custom annotation</i>
--------------------	---

---

**Description**

List alternative splicing annotation files available, as well as custom annotation

**Usage**

```
listAllAnnotations(...)
```

**Arguments**

... Custom annotation loaded

**Value**

Named character vector with splicing annotation files available

**Examples**

```
psychomics:::listAllAnnotations()
```

---

listSplicingAnnotations	<i>List alternative splicing annotations</i>
-------------------------	--

---

**Description**

List alternative splicing annotations

**Usage**

```
listSplicingAnnotations(
  species = NULL,
  assembly = NULL,
  date = NULL,
  cache = getAnnotationHubOption("CACHE"),
  group = FALSE
)
```

**Arguments**

species	Character: filter results by species (regular expression)
assembly	Character: filter results by assembly (regular expression)
date	Character: filter results by date (regular expression)
cache	Character: path to AnnotationHub cache (used to load alternative splicing event annotation)
group	Boolean: group values based on data provider?

**Value**

Named character vector with splicing annotation names

**See Also**

Other functions for PSI quantification: [filterPSI\(\)](#), [getSplicingEventTypes\(\)](#), [loadAnnotation\(\)](#), [plotRowStats\(\)](#), [quantifySplicing\(\)](#)

**Examples**

```
listSplicingAnnotations() # Return all alternative splicing annotations
listSplicingAnnotations(assembly="hg19") # Search for hg19 annotation
listSplicingAnnotations(assembly="hg38") # Search for hg38 annotation
listSplicingAnnotations(date="201(7|8)") # Search for 2017 or 2018 annotation
```

---

loadAnnotation	<i>Load alternative splicing annotation from AnnotationHub</i>
----------------	--

---

**Description**

Load alternative splicing annotation from AnnotationHub

**Usage**

```
loadAnnotation(annotation, cache = getAnnotationHubOption("CACHE"))
```

**Arguments**

annotation	Character: annotation to load
cache	Character: path to AnnotationHub cache (used to load alternative splicing event annotation)

**Value**

List of data frames containing the alternative splicing annotation per event type

**See Also**

Other functions for PSI quantification: [filterPSI\(\)](#), [getSplicingEventTypes\(\)](#), [listSplicingAnnotations\(\)](#), [plotRowStats\(\)](#), [quantifySplicing\(\)](#)

**Examples**

```
human <- listSplicingAnnotations(species="Homo sapiens")[[1]]
## Not run:
annot <- loadAnnotation(human)

## End(Not run)
```

---

loadAnnotationHub	<i>Load AnnotationHub</i>
-------------------	---------------------------

---

**Description**

Load AnnotationHub

**Usage**

```
loadAnnotationHub(cache = getAnnotationHubOption("CACHE"))
```

**Arguments**

cache	Character: path to AnnotationHub cache (used to load alternative splicing event annotation)
-------	---

**Value**

AnnotationHub object with all entries

---

loadBy	<i>Check if a given function should be loaded by the calling module</i>
--------	---

---

**Description**

Check if a given function should be loaded by the calling module

**Usage**

```
loadBy(loader, FUN)
```

**Arguments**

loader	Character: name of the file responsible to load such function
FUN	Function

**Value**

Boolean vector

---

 loadCustomSplicingAnnotationSet

*Set of functions to load a custom alternative splicing annotation*


---

**Description**

Instructions to build the Shiny app

**Usage**

```
loadCustomSplicingAnnotationSet(session, input, output)
```

**Arguments**

session	Shiny session
input	Shiny input
output	Shiny output

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

loadedDataModal

*Warn user about loaded data*


---

**Description**

Warn user about loaded data

**Usage**

```
loadedDataModal(session, modalId, replaceButtonId, keepButtonId)
```

**Arguments**

session	Shiny session
modalId	Character: identifier of the modal
replaceButtonId	Character: identifier of the button to replace data
keepButtonId	Character: identifier of the button to append data

**Value**

HTML elements for a warning modal reminding data is loaded

---

loadFile	<i>Load file based on its format</i>
----------	--------------------------------------

---

**Description**

Tries to recognise the file format and parses the content of the given file accordingly.

**Usage**

```
loadFile(
  file,
  formats = loadFileFormats(),
  ...,
  verbose = FALSE,
  multiple = FALSE
)
```

**Arguments**

file	Character: file to parse
formats	List of file formats to check
...	Extra parameters passed to <a href="#">fread</a>
verbose	Boolean: detail steps while parsing
multiple	Boolean: expect more than one file?

**Details**

The resulting data frame includes the attribute `tablename` with the name of the data frame

**Value**

Data frame with the contents of the given file if the file format is recognised; otherwise, returns `NULL`

---

loadFileFormats	<i>Load supported file formats</i>
-----------------	------------------------------------

---

**Description**

Load supported file formats

**Usage**

```
loadFileFormats()
```

**Value**

Supported file formats

---

loadFirebrowseFolders *Load FireBrowse folders*

---

**Description**

Loads the files present in each folder as a data.frame.

**Usage**

```
loadFirebrowseFolders(folder, exclude = "")
```

**Arguments**

folder	Character: folder(s) in which to look for FireBrowse files
exclude	Character: files to exclude from the loading

**Value**

List with loaded data.frames

**Note**

For faster execution, this function uses the readr library. This function ignores subfolders of the given folder (which means that files inside subfolders are NOT loaded).

---

loadGeneExpressionSet *Set of functions to load splicing quantification*

---

**Description**

Instructions to build the Shiny app

**Usage**

```
loadGeneExpressionSet(session, input, output)
```

**Arguments**

session	Shiny session
input	Shiny input
output	Shiny output

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

loadGtexData	<i>Download and load GTEX data</i>
--------------	------------------------------------

---

### Description

Download and load GTEX data

### Usage

```
loadGtexData(
  folder = getDownloadsFolder(),
  data = getGtexDataTypes(),
  tissue = NULL,
  release = getGtexReleases()[[1]],
  progress = TRUE
)
```

### Arguments

folder	Character: folder containing data
data	Character: data types to load (see <code>getGtexDataTypes()</code> )
tissue	Character: tissues to load (if NULL, load all); tissue selection may speed up data loading
release	Numeric: GTEX data release to load
progress	Boolean: display progress?

### Value

List with loaded data

### See Also

Other functions associated with GTEX data retrieval: [getDownloadsFolder\(\)](#), [getGtexDataTypes\(\)](#), [getGtexTissues\(\)](#)

Other functions to load data: [loadLocalFiles\(\)](#), [loadSRaproject\(\)](#), [loadTCGAdata\(\)](#)

### Examples

```
## Not run:
# Download and load all available GTEX data
data <- loadGtexData()

# Download and load only junction quantification and sample info from GTEX
getGtexDataTypes()
data <- loadGtexData(data=c("sampleInfo", "junctionQuant"))

# Download and load only data for specific tissues
getGtexTissues()
data <- loadGtexData(tissue=c("Stomach", "Small Intestine"))

# Download and load data from a specific GTEX data release
```



```
data <- loadGtexData(tissue=c("Stomach", "Small Intestine"), release=7)
## End(Not run)
```

---

loadGtexDataShiny      *Shiny wrapper to load GTEX data*

---

**Description**

Shiny wrapper to load GTEX data

**Usage**

```
loadGtexDataShiny(session, input, replace = TRUE)
```

**Arguments**

session	Shiny session
input	Shiny input
replace	Boolean: replace loaded data?

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

loadGtexFile      *Load GTEX file*

---

**Description**

Load GTEX file

**Usage**

```
loadGtexFile(path, pattern, samples = NULL)
```

**Arguments**

path	Character: path to file
pattern	Character: pattern of the format type to load file
samples	Character: samples to filter datasets

**Value**

Loaded file as a data frame

---

loadLocalFiles	<i>Load local files</i>
----------------	-------------------------

---

### Description

Load local files

### Usage

```
loadLocalFiles(  
  folder,  
  ignore = c(".aux.", ".mage-tab."),  
  name = "Data",  
  verbose = FALSE  
)
```

### Arguments

folder	Character: path to folder or ZIP archive
ignore	Character: skip folders and filenames that match the expression
name	Character: name
verbose	Boolean: print steps?

### Value

List of data frames from valid files

### See Also

Other functions to load data: [loadGtexData\(\)](#), [loadSRAProject\(\)](#), [loadTCGadata\(\)](#)

### Examples

```
## Not run:  
folder <- "~/Downloads/ACC 2016"  
data <- loadLocalFiles(folder)  
  
ignore <- c(".aux.", ".mage-tab.", "junction quantification")  
loadLocalFiles(folder, ignore)  
  
## End(Not run)
```

---

loadRequiredData	<i>Missing information modal template</i>
------------------	---

---

**Description**

Missing information modal template

**Usage**

```
loadRequiredData(modal = NULL)

missingDataModal(session, dataType, buttonId)

missingDataGuide(dataType)
```

**Arguments**

modal	Character: modal identifier
session	Shiny session
dataType	Character: type of data missing
buttonId	Character: identifier of button to take user to load missing data

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

**Examples**

```
## Not run:
if (shiny::isRunning()) {
  session <- session$ns
  buttonInput <- "takeMeThere"
  buttonId <- ns(buttonInput)
  dataType <- "Inclusion levels"
  missingDataModal(session, buttonId, dataType)
  observeEvent(input[[buttonInput]], missingDataGuide(dataType))
}

## End(Not run)
```

---

loadSplicingQuantificationSet	<i>Set of functions to load splicing quantification</i>
-------------------------------	---

---

**Description**

Instructions to build the Shiny app

**Usage**

```
loadSplicingQuantificationSet(session, input, output)
```

**Arguments**

session	Shiny session
input	Shiny input
output	Shiny output

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

loadSRAproject	<i>Download and load SRA projects via</i>
	<i><a href="https://jhubiostatistics.shinyapps.io/recount/recount2">Rhrefhttps://jhubiostatistics.shinyapps.io/recount/recount2</a></i>

---

**Description**

Download and load SRA projects via [recount2](#)

**Usage**

```
loadSRAproject(project, outdir = getDownloadsFolder())
```

**Arguments**

project	Character: SRA project identifiers (check <a href="#">recount_abstract</a> )
outdir	Character: directory to store the downloaded files

**Value**

List with loaded projects

**See Also**

Other functions associated with SRA data retrieval: [getDownloadsFolder\(\)](#)

Other functions to load data: [loadGtexData\(\)](#), [loadLocalFiles\(\)](#), [loadTCGadata\(\)](#)

**Examples**

```
## Not run:
View(recount::recount_abstract)
sra <- loadSRAproject("SRP053101")
names(sra)
names(sra[[1]])

## End(Not run)
```

---

loadTCGAdata	<i>Download and process TCGA data</i>
--------------	---------------------------------------

---

### Description

TCGA data obtained via [FireBrowse](#)

### Usage

```
loadTCGAdata(
  folder = getDownloadsFolder(),
  data = c("clinical", "junction_quantification", "RSEM_genes"),
  exclude = c(".aux.", ".mage-tab.", "MANIFEST.txt"),
  ...,
  download = TRUE
)
```

### Arguments

folder	Character: directory to store the downloaded archives (by default, saves to <a href="#">getDownloadsFolder()</a> )
data	Character: data to load (see <a href="#">getTCGAdataTypes()</a> )
exclude	Character: files and folders to exclude from downloading and from loading into R (by default, exclude files containing .aux., .mage-tab. and MANIFEST.TXT)
...	Arguments passed on to <a href="#">queryFirebrowseData</a>
date	Character: dates of the data retrieval by FireBrowse (by default, it uses the most recent data available)
cohort	Character: abbreviation of the cohorts (by default, returns data for all cohorts)
data_type	Character: data types (optional)
tool	Character: data produced by the selected FireBrowse tools (optional)
platform	Character: data generation platforms (optional)
center	Character: data generation centres (optional)
level	Integer: data levels (optional)
protocol	Character: sample characterization protocols (optional)
page	Integer: page of the results to return (optional)
page_size	Integer: number of records per page of results (optional)
sort_by	String: column used to sort the data (by default, sort by cohort)
download	Boolean: download missing files

### Value

A list with the loaded data, unless required files are unavailable and `download = FALSE` (if so, it returns the URL of files to download)

### See Also

Other functions associated with TCGA data retrieval: [getDownloadsFolder\(\)](#), [getTCGAdataTypes\(\)](#), [isFirebrowseUp\(\)](#), [parseTCGAsampleTypes\(\)](#)

Other functions to load data: [loadGtexData\(\)](#), [loadLocalFiles\(\)](#), [loadSRAProject\(\)](#)

**Examples**

```

getTCGAcohorts()
getTCGAdataTypes()
## Not run:
loadTCGAdata(cohort = "ACC", data_type = "Clinical")

## End(Not run)

```

---

```
loadTCGAsampleMetadata
```

*Prepare TCGA sample metadata from loaded datasets*

---

**Description**

If no TCGA datasets apply, the input is returned

**Usage**

```
loadTCGAsampleMetadata(data)
```

**Arguments**

data                    List of list of data frames

**Value**

List of list of data frames

---

```
matchGroupASeventsAndGenes
```

*Match AS events and genes in a group*

---

**Description**

Match AS events and genes in a group

**Usage**

```
matchGroupASeventsAndGenes(id, group, ASevents)
```

**Arguments**

id                      Character: identifier  
group                    Data frame: group

**Value**

Data frame with groups containing matching elements

---

`matchGroupSubjectsAndSamples`*Match subjects and samples in a group*

---

**Description**

Match subjects and samples in a group

**Usage**

```
matchGroupSubjectsAndSamples(id, group)
```

**Arguments**

`id`                   Character: identifier

`group`                Data frame: group

**Value**

Data frame with groups containing matching elements

---

`matchSplicingEventsWithGenes`*Match splicing events with respective genes*

---

**Description**

Match splicing events with respective genes

**Usage**

```
matchSplicingEventsWithGenes(ASevents, data = NULL)
```

**Arguments**

`ASevents`            Character: alternative splicing events to be matched

`data`                Matrix or data frame: alternative splicing information

**Value**

Named character vector containing the splicing events and their respective gene as their name

---

modTabPanel	<i>Modified tabPanel function to show icon and title</i>
-------------	--

---

**Description**

Modified tabPanel function to show icon and title

**Usage**

```
modTabPanel(title, ..., icon = NULL, menu = FALSE)
```

**Arguments**

title	Character: title of the tab
...	HTML elements to render
icon	Character: name of the icon
menu	Boolean: create a dropdown menu-like tab?

**Value**

HTML interface

**Note**

Icon is hidden at small viewports

---

navSelectize	<i>Create a special selectize input in the navigation bar</i>
--------------	---

---

**Description**

Create a special selectize input in the navigation bar

**Usage**

```
navSelectize(id, label, placeholder = label, ASevent = FALSE)
```

**Arguments**

id	Character: input identifier
label	Character: input label
placeholder	Character: input placeholder
ASevent	Boolean: select alternative splicing events?

**Value**

HTML element to be included in a navigation bar



---

 normaliseGeneExpression

*Filter and normalise gene expression*


---

## Description

Gene expression is filtered and normalised in the following steps:

- Filter gene expression;
- Normalise gene expression with [calcNormFactors](#);
- If performVoom = FALSE, compute counts per million (CPM) using [cpm](#) and log2-transform values if log2transform = TRUE;
- If performVoom = TRUE, use [voom](#) to compute log2-CPM, quantile-normalise (if method = "quantile") and estimate mean-variance relationship to calculate observation-level weights.

## Usage

```
normaliseGeneExpression(
  geneExpr,
  geneFilter = NULL,
  method = "TMM",
  p = 0.75,
  log2transform = TRUE,
  priorCount = 0.25,
  performVoom = FALSE
)
```

```
normalizeGeneExpression(
  geneExpr,
  geneFilter = NULL,
  method = "TMM",
  p = 0.75,
  log2transform = TRUE,
  priorCount = 0.25,
  performVoom = FALSE
)
```

## Arguments

geneExpr	Matrix or data frame: gene expression
geneFilter	Boolean: filtered genes (if NULL, skip filtering)
method	Character: normalisation method, including TMM, RLE, upperquartile, none or quantile (see Details)
p	numeric value between 0 and 1 specifying which quantile of the counts should be used by method="upperquartile".
log2transform	Boolean: perform log2-transformation?
priorCount	Average count to add to each observation to avoid zeroes after log-transformation
performVoom	Boolean: perform mean-variance modelling (using <a href="#">voom</a> )?

## Details

edgeR::calcNormFactors will be used to normalise gene expression if method is TMM, RLE, upperquartile or none. If performVoom = TRUE, voom will only normalise if method = "quantile".

Available normalisation methods:

- TMM is recommended for most RNA-seq data where more than half of the genes are believed not differentially expressed between any pair of samples;
- RLE calculates the median library from the geometric mean of all columns and the median ratio of each sample to the median library is taken as the scale factor;
- upperquartile calculates the scale factors from a given quantile of the counts for each library, after removing genes with zero counts in all libraries;
- quantile forces the entire empirical distribution of each column to be identical (only performed if performVoom = TRUE).

## Value

Filtered and normalised gene expression

## See Also

Other functions for gene expression pre-processing: [convertGeneIdentifiers\(\)](#), [filterGeneExpr\(\)](#), [plotGeneExprPerSample\(\)](#), [plotLibrarySize\(\)](#), [plotRowStats\(\)](#)

## Examples

```
geneExpr <- readRDS("ex_gene_expression.RDS")
normaliseGeneExpression(geneExpr)
```

---

operateOnGroups	<i>Set operations on groups</i>
-----------------	---------------------------------

---

## Description

This function can be used on groups to merge, intersect, subtract, etc.

## Usage

```
operateOnGroups(  
  input,  
  session,  
  operation,  
  buttonId,  
  symbol = " ",  
  type,  
  sharedData = sharedData  
)
```

**Arguments**

input	Shiny input
session	Shiny session
operation	Character: set operation
buttonId	Character: ID of the button to trigger operation
symbol	Character: Unicode symbol to visually indicate the operation performed
type	Character: type of group where set operations are to be performed
sharedData	Shiny app's global variable

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

optimalSurvivalCutoff *Calculate optimal data cutoff that best separates survival curves*

---

**Description**

Uses `stats::optim` with the Brent method to test multiple cutoffs and to find the minimum log-rank p-value.

**Usage**

```
optimalSurvivalCutoff(
  clinical,
  data,
  censoring,
  event,
  timeStart,
  timeStop = NULL,
  followup = "days_to_last_followup",
  session = NULL,
  filter = TRUE,
  survTime = NULL,
  lower = NULL,
  upper = NULL
)
```

**Arguments**

clinical	Data frame: clinical data
data	Numeric: data values
censoring	Character: censor using left, right, interval or interval2
event	Character: name of column containing time of the event of interest
timeStart	Character: name of column containing starting time of the interval or follow up time
timeStop	Character: name of column containing ending time of the interval (only relevant for interval censoring)

followup	Character: name of column containing follow up time
session	Shiny session (only used for the visual interface)
filter	Boolean or numeric: elements to use (all are used by default)
survTime	survTime object: times to follow up, time start, time stop and event (optional)
lower, upper	Bounds in which to search (if NULL, bounds are set to lower = 0 and upper = 1 if all data values are within that interval; otherwise, lower = min(data, na.rm = TRUE) and upper = max(data, na.rm = TRUE))

**Value**

List containing the optimal cutoff (par) and the corresponding p-value (value)

**See Also**

Other functions to analyse survival: [assignValuePerSubject\(\)](#), [getAttributesTime\(\)](#), [labelBasedOnCutoff\(\)](#), [plotSurvivalCurves\(\)](#), [plotSurvivalPvaluesByCutoff\(\)](#), [processSurvTerms\(\)](#), [survdiffTerms\(\)](#), [survfit.survTerms\(\)](#), [testSurvival\(\)](#)

**Examples**

```
clinical <- read.table(text = "2549  NA ii  female
                             840  NA i   female
                             NA 1204 iv  male
                             NA  383 iv  female
                             1293  NA iii male
                             NA 1355 ii  male")
names(clinical) <- c("patient.days_to_last_followup",
                    "patient.days_to_death",
                    "patient.stage_event.pathologic_stage",
                    "patient.gender")
timeStart <- "days_to_death"
event     <- "days_to_death"

psi <- c(0.1, 0.2, 0.9, 1, 0.2, 0.6)
opt <- optimalSurvivalCutoff(clinical, psi, "right", event, timeStart)
```

---

optimSurvDiffSet	<i>Optimal survival difference given an inclusion level cutoff for a specific alternative splicing event</i>
------------------	--

---

**Description**

Optimal survival difference given an inclusion level cutoff for a specific alternative splicing event

**Usage**

```
optimSurvDiffSet(session, input, output)
```

**Arguments**

session	Shiny session
input	Shiny input
output	Shiny output

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

parseCategoricalGroups

*Parse categorical columns in a data frame*

---

**Description**

Retrieve elements grouped by their unique group based on each categorical column

**Usage**

```
parseCategoricalGroups(df)
```

**Arguments**

df                      Data frame

**Value**

List of lists containing values based on rownames of df

**See Also**

[testGroupIndependence\(\)](#) and [plotGroupIndependence\(\)](#)

**Examples**

```
df <- data.frame("race"=c("caucasian", "caucasian", "asian"),
                 "gender"=c("male", "female", "male"))
rownames(df) <- paste("subject", 1:3)
parseCategoricalGroups(df)
```

---

parseDateResponse

*Parse the date from a response*

---

**Description**

Parse the date from a response

**Usage**

```
parseDateResponse(string)
```

**Arguments**

string                  Character: dates

**Value**

Parsed date

---

parseFile *Parse file according to its format*

---

**Description**

Parse file according to its format

**Usage**

```
parseFile(format, file, ..., verbose = FALSE)
```

**Arguments**

format	Environment: format of the file
file	Character: file to load
...	Extra parameters passed to <a href="#">fread</a>
verbose	Boolean: detail step while parsing?

**Details**

The resulting data frame includes the attribute `tablename` with the name of the data frame

**Value**

Data frame with the loaded file

---

parseFirebrowseMetadata  
*Query the FireBrowse API for metadata*

---

**Description**

Query the FireBrowse API for metadata

**Usage**

```
parseFirebrowseMetadata(type, ...)
```

**Arguments**

type	Character: metadata to retrieve
...	Character: parameters to pass to query (optional)

**Value**

List with parsed response

**Examples**

```

psychomics:::parseFirebrowseMetadata("Dates")
psychomics:::parseFirebrowseMetadata("Centers")
psychomics:::parseFirebrowseMetadata("HeartBeat")

# Get the abbreviation and description of all cohorts available
psychomics:::parseFirebrowseMetadata("Cohorts")
# Get the abbreviation and description of the selected cohorts
psychomics:::parseFirebrowseMetadata("Cohorts", cohort = c("ACC", "BRCA"))

```

---

parseMatsEvent	<i>Parse alternative splicing events from MATS</i>
----------------	--

---

**Description**

Parse alternative splicing events from MATS

**Usage**

```
parseMatsEvent(event, event_type)
```

**Arguments**

event	Data frame row: MATS splicing event
event_type	Character: Type of event to parse (see details)

**Details**

The following event types can be parsed:

- **SE**: Skipped exon
- **MXE**: Mutually exclusive exons
- **RI**: Retained intron
- **A3SS**: Alternative 3' splice site
- **A5SS**: Alternative 5' splice site

**Value**

List containing the event attributes and junctions

**Examples**

```

# MATS event (alternative 3' splice site)
event <- read.table(text = "
  2 ENSG00000166012 TAF1D chr11 - 93466515 93466671 93466515 93466563 93467790 93467826
  5 ENSG00000166012 TAF1D chr11 - 93466515 93466671 93466515 93466585 93467790 93467826
  6 ENSG00000166012 TAF1D chr11 - 93466515 93466585 93466515 93466563 93467790 93467826
")
psychomics:::parseMatsEvent(event, "A3SS")

```

---

parseMatsGeneric	<i>Parse junctions of an alternative splicing event from MATS according to event type</i>
------------------	---

---

### Description

Parse junctions of an alternative splicing event from MATS according to event type

### Usage

```
parseMatsGeneric(junctions, strand, coords, plus_pos, minus_pos)
```

```
parseMatsSE(junctions, strand)
```

```
parseMatsMXE(junctions, strand)
```

```
parseMatsRI(junctions, strand)
```

```
parseMatsA3SS(junctions, strand)
```

```
parseMatsA5SS(junctions, strand)
```

```
parseMatsAFE(junctions, strand)
```

```
parseMatsALE(junctions, strand)
```

### Arguments

junctions	Integer: event's junctions
strand	Character: strand of the event
coords	Character: names of the alternative splicing coordinates
plus_pos	Integer: match of each junction in the respective coordinate for the plus strand
minus_pos	Integer: match of each junction in the respective coordinate for the minus strand

### Details

The following event types are ready to be parsed:

- **SE** (skipped exon)
- **MXE** (mutually exclusive exon)
- **RI** (retained intron)
- **A5SS** (alternative 5' splice site)
- **A3SS** (alternative 3' splice site)
- **AFE** (alternative first exon)
- **ALE** (alternative last exon)

You can use `parseMatsGeneric` to parse other event types.



**Value**

Data frame with parsed junctions

**See Also**

[parseMatsEvent\(\)](#)

**Examples**

```
# Parse generic event (in this case, an exon skipping event)
junctions <- read.table(text=
  "79685787 79685910 79685796 79685910 79679566 79679751")
coords <- c("A1.start", "A1.end",
           "C1.start", "C1.end",
           "C2.start", "C2.end")
plus <- c(1:6)
minus <- c(2:1, 6:3)
psychomics:::parseMatsGeneric(junctions, strand = "+", coords, plus, minus)

# Parse exon skipping event
junctions <- read.table(text=
  "79685787 79685910 79685796 79685910 79679566 79679751")
psychomics:::parseMatsSE(junctions, strand = "+")

# Parse mutually exclusive exon event
junctions <- read.table(text=
  "158282161 158282276 158282689 158282804 158281047 158281295 158283950 158284199")
psychomics:::parseMatsMXE(junctions, strand = "+")

# Parse retained intron event
junctions <- read.table(text=
  "15929853 15932100 15929853 15930016 15930687 15932100")
psychomics:::parseMatsRI(junctions, strand = "+")

# Parse alternative 3' splicing site event
junctions <- read.table(text=
  "79685787 79685910 79685796 79685910 79679566 79679751")
psychomics:::parseMatsA3SS(junctions, strand = "+")

# Parse alternative 5' splicing site event
junctions <- read.table(text=
  "102884421 102884501 102884421 102884489 102884812 102885881")
psychomics:::parseMatsA5SS(junctions, strand = "+")

# Parse alternative first exon event
junctions <- read.table(text=
  "16308723 16308879 16308967 16309119 16314269 16314426")
psychomics:::parseMatsAFE(junctions, strand = "+")

# Parse alternative last exon event
junctions <- read.table(text=
  "111858645 111858828 111851063 111851921 111850441 111850543")
psychomics:::parseMatsAFE(junctions, strand = "+")
```

---

parseMisoEvent	<i>Parse an alternative splicing event from MISO</i>
----------------	--

---

**Description**

Parse an alternative splicing event from MISO

**Usage**

```
parseMisoEvent(event)
```

**Arguments**

event	Data.frame containing only one event with at least 7 columns as retrieved from the alternative splicing annotation files from MISO (GFF3 files)
-------	---

**Details**

More information about MISO available at <http://miso.readthedocs.org>

**Value**

List with event attributes and junction positions for the exons (depends on the events)

**Examples**

```
# example of alternative splicing event: skipped exon (SE)
event <- read.table(text = "
chr1 SE gene 16854 18061 . - .
chr1 SE mRNA 16854 18061 . - .
chr1 SE exon 16854 17055 . - .
chr1 SE exon 17233 17742 . - .
chr1 SE exon 17915 18061 . - .
chr1 SE mRNA 16854 18061 . - .
chr1 SE exon 16854 17955 . - .
chr1 SE exon 17915 18061 . - .")
psychomics:::parseMisoEvent(event)
```

---

parseMisoEventID	<i>Match MISO's splicing event IDs with the IDs present in the alternative splicing annotation file and get events in a data frame</i>
------------------	--

---

**Description**

Match MISO's splicing event IDs with the IDs present in the alternative splicing annotation file and get events in a data frame

**Usage**

```
parseMisoEventID(eventID, annotation, IDcolumn)
```

**Arguments**

eventID	Character: alternative event IDs
annotation	Data.frame: alternative event annotation file
IDcolumn	Integer: index of the column with the event ID's in the alternative event annotation file

**Details**

For faster execution times, provide a vector of event IDs.

For more information about MISO, see <http://miso.readthedocs.org>.

**Value**

Data frame of the matching events (or NA when nothing matches)

**Note**

If possible, it's recommend to use smaller subsets of the alternative events' annotation instead of all data for faster runs. For example, when trying to match only skipped exons event IDs, only use the annotation of skipped exons instead of using a mega annotation with all event types.

**Examples**

```
eventID <- c("114785@uc001sok.1@uc001soj.1", "114784@uc001bxm.1@uc001bxn.1")
# the annotation is one of the GFF3 files needed to run MISO
gff3 <- system.file("extdata", "miso_AS_annot_example.gff3",
  package="psychomics")
annotation <- read.delim(gff3, header=FALSE, comment.char="#")
IDcolumn <- 9
psychomics:::parseMisoEventID(eventID, annotation, IDcolumn)
```

---

parseMisoGeneric

*Parse junctions of an event from MISO according to event type*

---

**Description**

Parse junctions of an event from MISO according to event type

**Usage**

```
parseMisoGeneric(event, validator, eventType, coord, plusIndex, minusIndex)
```

```
parseMisoSE(event)
```

```
parseMisoMXE(event)
```

```
parseMisoRI(event, strand)
```

```
parseMisoA5SS(event)
```

```
parseMisoA3SS(event, plusIndex, minusIndex)
```

```
parseMisoTandemUTR(event, minusIndex)
```

```
parseMisoAFE(event)
```

```
parseMisoALE(event)
```

### Arguments

event	Data.frame containing only one event with at least 7 columns as retrieved from the alternative splicing annotation files from MISO (GFF3 files)
validator	Character: valid elements for each event
eventType	Character: event type (see details for available events)
coord	Character: coordinate positions to fill
plusIndex	Integer: index of the coordinates for a plus strand event
minusIndex	Integer: index of the coordinates for a minus strand event
strand	Character: positive-sense (+) or negative-sense - strand

### Details

The following event types are available to be parsed:

- **SE** (exon skipping)
- **MXE** (mutually exclusive exon)
- **RI** (retained intron)
- **A5SS** (alternative 5' splice site)
- **A3SS** (alternative 3' splice site)
- **AFE** (alternative first exon)
- **ALE** (alternative last exon)
- **Tandem UTR**

### Value

List of parsed junctions

### See Also

[parseMisoEvent\(\)](#)

### Examples

```
# skipped exon event (SE)
event <- read.table(text = "
chr1 SE gene 16854 18061 . - .
chr1 SE mRNA 16854 18061 . - .
chr1 SE exon 16854 17055 . - .
chr1 SE exon 17233 17742 . - .
chr1 SE exon 17915 18061 . - .
chr1 SE mRNA 16854 18061 . - .
chr1 SE exon 16854 17955 . - .
chr1 SE exon 17915 18061 . - .")
```

```

psychomics:::parseMisoSE(event)

# mutually exclusive exon (MXE) event
event <- read.table(text = "
chr1 MXE gene 764383 788090 . + .
chr1 MXE mRNA 764383 788090 . + .
chr1 MXE exon 764383 764484 . + .
chr1 MXE exon 776580 776753 . + .
chr1 MXE exon 787307 788090 . + .
chr1 MXE mRNA 764383 788090 . + .
chr1 MXE exon 764383 764484 . + .
chr1 MXE exon 783034 783186 . + .
chr1 MXE exon 787307 788090 . + .")
psychomics:::parseMisoMXE(event)

# retained intron (RI) event
event <- read.table(text = "
chr1 RI gene 17233 17742 . - .
chr1 RI mRNA 17233 17742 . - .
chr1 RI exon 17233 17742 . - .
chr1 RI mRNA 17233 17742 . - .
chr1 RI exon 17233 17364 . - .
chr1 RI exon 17601 17742 . - .")
psychomics:::parseMisoRI(event)

# alternative 5' splice site (A5SS) event
event <- read.table(text = "
chr1 A5SS gene 17233 17742 . - .
chr1 A5SS mRNA 17233 17742 . - .
chr1 A5SS exon 17233 17368 . - .
chr1 A5SS exon 17526 17742 . - .
chr1 A5SS mRNA 17233 17742 . - .
chr1 A5SS exon 17233 17368 . - .
chr1 A5SS exon 17606 17742 . - .")
psychomics:::parseMisoA5SS(event)

# alternative 3' splice site (A3SS) event
event <- read.table(text = "
chr1 A3SS gene 15796 16765 . - .
chr1 A3SS mRNA 15796 16765 . - .
chr1 A3SS exon 15796 15947 . - .
chr1 A3SS exon 16607 16765 . - .
chr1 A3SS mRNA 15796 16765 . - .
chr1 A3SS exon 15796 15942 . - .
chr1 A3SS exon 16607 16765 . - .")
psychomics:::parseMisoA3SS(event)

# Tandem UTR event
event <- read.table(text = "
chr19 TandemUTR gene 10663759 10664625 . - .
chr19 TandemUTR mRNA 10663759 10664625 . - .
chr19 TandemUTR exon 10663759 10664625 . - .
chr19 TandemUTR mRNA 10664223 10664625 . - .
chr19 TandemUTR exon 10664223 10664625 . - .")
psychomics:::parseMisoTandemUTR(event)

# alternative first exon (AFE) event

```

```

event <- read.table(text = "
chr12 AFE gene 57916659 57920171 . + .
chr12 AFE mRNA 57919131 57920171 . + .
chr12 AFE exon 57919131 57920171 . + .
chr12 AFE mRNA 57916659 57918199 . + .
chr12 AFE exon 57916659 57916794 . + .
chr12 AFE exon 57917812 57917875 . + .
chr12 AFE exon 57918063 57918199 . + .")
psychomics:::parseMisoAFE(event)

# alternative last exon (ALE) event
event <- read.table(text = "
chr6 ALE gene 30620579 30822593 . + .
chr6 ALE mRNA 30822190 30822593 . + .
chr6 ALE exon 30822190 30822593 . + .
chr6 ALE mRNA 30620579 30620982 . + .
chr6 ALE exon 30620579 30620982 . + .")
psychomics:::parseMisoALE(event)

```

---

parseMisoId

*Parse MISO's alternative splicing event identifier*

---

## Description

Parse MISO's alternative splicing event identifier

## Usage

```
parseMisoId(id)
```

## Arguments

id                    Character: MISO alternative splicing event identifier

## Value

Character with the parsed ID

## Examples

```

id <- paste0(
  "ID=ENSMUSG00000026150.chr1:82723803:82723911:+@chr1:82724642:82724813:",
  "+@chr1:82725791:82726011:+.B;Parent=ENSMUSG00000026150.chr1:82723803:",
  "82723911:+@chr1:82724642:82724813:+@chr1:82725791:82726011:+")
psychomics:::parseMisoId(id)

```

---

parseSplicingEvent      *Parse alternative splicing event identifier*

---

### Description

Parse alternative splicing event identifier

### Usage

```
parseSplicingEvent(
  event,
  char = FALSE,
  pretty = FALSE,
  extra = NULL,
  coords = FALSE,
  data = NULL
)
```

### Arguments

event	Character: event identifier
char	Boolean: return character vector instead of list with parsed values?
pretty	Boolean: return a prettier name of the event identifier?
extra	Character: extra information to add (such as species and assembly version); only used if pretty = TRUE and char = TRUE
coords	Boolean: display extra coordinates regarding the alternative and constitutive regions of alternative splicing events? Only used if char = FALSE
data	Matrix or data frame: alternative splicing information

### Value

Data.frame containing type of event, chromosome, strand, gene and position of alternative splicing events or character with that same information (depending on what is available)

### Examples

```
events <- c(
  "A3SS_15+_63353138_63353912_63353397_TPM1",
  "A3SS_11_-_61118463_61117115_61117894_CYB561A3",
  "A5SS_21+_48055675_48056459_48056808_PRMT2",
  "A5SS_1_-_1274742_1274667_1274033_DVL1",
  "AFE_9+_131902430_131901928_131904724_PPP2R4",
  "AFE_5_-_134686513_134688636_134681747_H2AFY",
  "ALE_12+_56554104_56554410_56555171_MYL6",
  "ALE_8_-_38314874_38287466_38285953_FGFR1",
  "SE_9+_6486925_6492303_6492401_6493826_UHRF2",
  "SE_19_-_5218431_5216778_5216731_5215606_PTPRS",
  "MXE_15+_63335142_63335905_63336030_63336226_63336351_63349184_TPM1",
  "MXE_17_-_74090495_74087316_74087224_74086478_74086410_74085401_EXOC7")
parseSplicingEvent(events)
```

---

parseSuppaAnnotation *Parse events from alternative splicing annotation*

---

## Description

Parse events from alternative splicing annotation

## Usage

```

parseSuppaAnnotation(
  folder,
  types = c("SE", "AF", "AL", "MX", "A5", "A3", "RI"),
  genome = "hg19"
)

parseVastToolsAnnotation(
  folder,
  types = c("ALT3", "ALT5", "COMBI", "IR", "MERGE3m", "MIC", "EXSK", "MULTI"),
  genome = "Hsa",
  complexEvents = FALSE
)

parseMisoAnnotation(
  folder,
  types = c("SE", "AFE", "ALE", "MXE", "A5SS", "A3SS", "RI", "TandemUTR"),
  genome = "hg19"
)

parseMatsAnnotation(
  folder,
  types = c("SE", "AFE", "ALE", "MXE", "A5SS", "A3SS", "RI"),
  genome = "fromGTF",
  novelEvents = TRUE
)

```

## Arguments

folder	Character: path to folder
types	Character: type of events to retrieve (depends on the program of origin; see details)
genome	Character: genome of interest (for instance, hg19; depends on the program of origin)
complexEvents	Boolean: should complex events in A3SS and A5SS be parsed?
novelEvents	Boolean: parse events detected due to novel splice sites

## Details

Type of parsable events:

- Alternative 3' splice site



- Alternative 5' splice site
- Alternative first exon
- Alternative last exon
- Skipped exon (may include skipped micro-exons)
- Mutually exclusive exon
- Retained intron
- Tandem UTR

**Value**

Retrieve data frame with events based on a given alternative splicing annotation

**See Also**

Other functions to prepare alternative splicing annotations: [prepareAnnotationFromEvents\(\)](#)

**Examples**

```
# Load sample files
folder <- "extdata/eventsAnnotSample/suppa_output/suppaEvents"
suppaOutput <- system.file(folder, package="psychomics")

suppa <- parseSuppaAnnotation(suppaOutput)
# Load sample files
folder <- "extdata/eventsAnnotSample/VASTDB/Hsa/TEMPLATES"
vastToolsOutput <- system.file(folder, package="psychomics")

vast <- parseVastToolsAnnotation(vastToolsOutput)
# Load sample files
folder <- "extdata/eventsAnnotSample/miso_annotation"
misoOutput <- system.file(folder, package="psychomics")

miso <- parseMisoAnnotation(misoOutput)
# Load sample files
folder <- "extdata/eventsAnnotSample/mats_output/ASEvents"
matsOutput <- system.file(folder, package="psychomics")

mats <- parseMatsAnnotation(matsOutput)

# Do not parse novel events
mats <- parseMatsAnnotation(matsOutput, novelEvents=FALSE)
```

---

parseSuppaEvent

*Parses splicing events of a specific event type from SUPPA*

---

**Description**

Parses splicing events of a specific event type from SUPPA

**Usage**

```
parseSuppaEvent(event)
```

**Arguments**

event                      Character vector: Splicing event attributes and junction positions

**Details**

More information about SUPPA available at <https://bitbucket.org/regulatorygenomicsupf/suppa>

The following event types are available to be parsed:

- **SE** (skipped exon)
- **RI** (retained intron)
- **MX** (mutually exclusive exons)
- **A5** (alternative 5' splice site)
- **A3** (alternative 3' splice site)
- **AL** (alternative last exon)
- **AF** (alternative first exon)

**Value**

List with the event attributes (chromosome, strand, event type and the position of the exon boundaries)

**Note**

It only allows to parse one event type at once.

**Examples**

```
event <- "ENSG00000000419;A3:20:49557492-49557642:49557470-49557642:-"
psychomics:::parseSuppaEvent(event)
```

---

parseSuppaGeneric            *Parse junctions of an event from SUPPA*

---

**Description**

Parse junctions of an event from SUPPA

**Usage**

```
parseSuppaGeneric(junctions, strand, coords, plus_pos, minus_pos)
```

```
parseSuppaSE(junctions, strand)
```

```
parseSuppaRI(junctions, strand)
```

```
parseSuppaALE(junctions, strand)
```

```
parseSuppaAFE(junctions, strand)
```

```
parseSuppaMXE(junctions, strand)
```

```
parseSuppaA3SS(junctions, strand)
```

```
parseSuppaA5SS(junctions, strand)
```

### Arguments

junctions	List of integers: exon-exon junctions of an event
strand	Character: positive-sense (+) or negative-sense (-) strand
coords	Character: coordinate positions to fill
plus_pos	Integer: index of the coordinates for a plus strand event
minus_pos	Integer: index of the coordinates for a minus strand event

### Details

The following event types are available to be parsed:

- **SE** (exon skipping)
- **RI** (retained intron)
- **MXE** (mutually exclusive exons)
- **A5SS** (alternative 5' splice site)
- **A3SS** (alternative 3' splice site)
- **ALE** (alternative last exon)
- **AFE** (alternative first exon)

### Value

Data frame of parsed junctions

### See Also

[parseSuppaEvent\(\)](#)

### Examples

```
# Parse generic event (in this case, an exon skipping event)
junctions <- read.table(text = "169768099 169770024 169770112 169771762")
coords <- c("C1.end", "A1.start", "A1.end", "C2.start")
plus <- 1:4
minus <- 1:4
psychomics:::parseSuppaGeneric(junctions, strand = "+", coords, plus, minus)

junctions <- read.table(text = "169768099 169770024 169770112 169771762")
psychomics:::parseSuppaSE(junctions, "+")

junctions <- read.table(text = "196709749 196709922 196711005 196711181")
psychomics:::parseSuppaRI(junctions, "+")

junctions <- read.table(
  text = "24790610 24792494 24792800 24790610 24795476 24795797")
psychomics:::parseSuppaALE(junctions, "+")
```

```
junctions <- read.table(  
  text = "169763871 169764046 169767998 169764550 169765124 169767998")  
psychomics:::parseSuppaAFE(junctions, "+")  
  
junctions <- read.table(  
  text = "202060671 202068453 202068489 202073793 202060671 202072798 202072906 202073793")  
psychomics:::parseSuppaMXE(junctions, "+")  
  
junctions <- read.table(text = "169772450 169773216 169772450 169773253")  
psychomics:::parseSuppaA3SS(junctions, "+")  
  
junctions <- read.table(text = "50193276 50197008 50192997 50197008")  
psychomics:::parseSuppaA5SS(junctions, "+")
```

---

parseTCGAsampleTypes *Parse sample information from TCGA sample identifiers*

---

## Description

Parse sample information from TCGA sample identifiers

## Usage

```
parseTCGAsampleTypes(  
  samples,  
  filename = system.file("extdata", "TCGAsampleType.RDS", package = "psychomics")  
)  
  
parseTCGAsampleInfo(samples, match = NULL)
```

## Arguments

samples	Character: sample identifiers
filename	Character: path to RDS file containing corresponding types
match	Integer: match between samples and subjects (NULL by default; performs the match)

## Value

Metadata associated with each TCGA sample

## See Also

Other functions associated with TCGA data retrieval: [getDownloadsFolder\(\)](#), [getTCGAdataTypes\(\)](#), [isFirebrowseUp\(\)](#), [loadTCGAdata\(\)](#)

**Examples**

```

parseTCGAsampleTypes(c("TCGA-01A-Tumour", "TCGA-10B-Normal"))
samples <- c("TCGA-3C-AAAU-01A-11R-A41B-07", "TCGA-3C-AALI-01A-11R-A41B-07",
            "TCGA-3C-AALJ-01A-31R-A41B-07", "TCGA-3C-AALK-01A-11R-A41B-07",
            "TCGA-4H-AAAK-01A-12R-A41B-07", "TCGA-5L-AAT0-01A-12R-A41B-07")

parseTCGAsampleInfo(samples)

```

---

parseUniprotXML	<i>Parse XML from UniProt REST service</i>
-----------------	--

---

**Description**

Parse XML from UniProt REST service

**Usage**

```
parseUniprotXML(xml)
```

**Arguments**

xml                      response from UniProt

**Value**

List containing protein length and data frame of protein features

---

parseUrlsFromFirebrowseResponse	<i>Retrieve URLs from a response to a FireBrowse data query</i>
---------------------------------	---

---

**Description**

Retrieve URLs from a response to a FireBrowse data query

**Usage**

```
parseUrlsFromFirebrowseResponse(res)
```

**Arguments**

res                      Response from httr::GET to a FireBrowse data query

**Value**

Named character with URLs

**Examples**

```

res <- psychomics:::queryFirebrowseData(cohort = "ACC")
url <- psychomics:::parseUrlsFromFirebrowseResponse(res)

```

---

parseVastToolsEvent     *Parses an alternative splicing event from VAST-TOOLS*

---

### Description

Parses an alternative splicing event from VAST-TOOLS

### Usage

```
parseVastToolsEvent(event)
```

### Arguments

event                    Data.frame: VAST-TOOLS event containing gene symbol, event ID, length, junctions coordinates, event type and inclusion levels for both samples

### Details

Junctions are parsed from

### Value

List with the event attributes (chromosome, strand, event type and the position of the exon boundaries)

### Note

Only supports to parse one event at a time.

### Examples

```
event <- read.table(text =
"NFYA HsaEX0042823 chr6:41046768-41046903 136 chr6:41040823,41046768-41046903,41051785 C2 0 N 0 N"
)
psychomics:::parseVastToolsEvent(event)
```

---

parseVastToolsSE             *Parse junctions of an event from VAST-TOOLS according to event type*

---

### Description

Parse junctions of an event from VAST-TOOLS according to event type

### Usage

```
parseVastToolsSE(junctions)
```

```
parseVastToolsRI(junctions, strand)
```

```
parseVastToolsA3SS(junctions)
```

```
parseVastToolsA5SS(junctions)
```

**Arguments**

junctions	Data.frame or matrix: exon-exon junctions of alternative splicing events (it must have 4 columns)
strand	Character: positive (+) or negative (-) strand

**Details**

The following event types are available to be parsed:

- **SE** (skipped exon)
- **RI** (retained intron)
- **A5SS** (alternative 5' splice site)
- **A3SS** (alternative 3' splice site)

**Value**

List of parsed junctions

**See Also**

[parseVastToolsEvent\(\)](#)

**Examples**

```
junctions <- read.table(text = "41040823 41046768 41046903 41051785")
psychomics:::parseVastToolsSE(junctions)

# these functions are vectorised!
junctions <- read.table(text = "41040823 41046768 41046903 41051785
                               58864658 58864693 58864294 58864563")
psychomics:::parseVastToolsSE(junctions)

junctions <- read.table(text = "58864658 58864693 58864294 58864563")
psychomics:::parseVastToolsRI(junctions, strand = "+")

junctions <- rbind(
  c(36276385, list(c(36277798, 36277315)), 36277974),
  c(7133604, 7133377, list(c(7133474, 7133456)))
)
psychomics:::parseVastToolsA3SS(junctions)

junctions <- rbind(
  c(74650610, list(c(74650654, 74650658)), 74650982),
  c(list(c(49557666, 49557642), 49557746, 49557470))
)
psychomics:::parseVastToolsA5SS(junctions)
```

---

performICA	<i>Perform independent component analysis after processing missing values</i>
------------	---

---

### Description

Perform independent component analysis after processing missing values

### Usage

```
performICA(
  data,
  n.comp = min(5, ncol(data)),
  center = TRUE,
  scale. = FALSE,
  missingValues = round(0.05 * nrow(data)),
  alg.typ = c("parallel", "defaltion"),
  fun = c("logcosh", "exp"),
  alpha = 1,
  ...
)
```

### Arguments

data	an optional data frame (or similar: see <a href="#">model.frame</a> ) containing the variables in the formula formula. By default the variables are taken from <code>environment(formula)</code> .
n.comp	number of components to be extracted
center	a logical value indicating whether the variables should be shifted to be zero centered. Alternately, a vector of length equal the number of columns of x can be supplied. The value is passed to <code>scale</code> .
scale.	a logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is FALSE for consistency with S, but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of x can be supplied. The value is passed to <code>scale</code> .
missingValues	Integer: number of tolerated missing values per column to be replaced with the mean of the values of that same column
alg.typ	if <code>alg.typ == "parallel"</code> the components are extracted simultaneously (the default). if <code>alg.typ == "deflation"</code> the components are extracted one at a time.
fun	the functional form of the $G$ function used in the approximation to neg-entropy (see 'details').
alpha	constant in range [1, 2] used in approximation to neg-entropy when <code>fun == "logcosh"</code>
...	Arguments passed on to <code>fastICA::fastICA</code>

### Value

ICA result in a `prcomp` object



**See Also**

Other functions to analyse independent components: [plotICA\(\)](#)

**Examples**

```
performICA(USArrests)
```

---

```
performPCA
```

*Perform principal component analysis after processing missing values*

---

**Description**

Perform principal component analysis after processing missing values

**Usage**

```
performPCA(
  data,
  center = TRUE,
  scale. = FALSE,
  missingValues = round(0.05 * nrow(data)),
  ...
)
```

**Arguments**

<code>data</code>	an optional data frame (or similar: see <a href="#">model.frame</a> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>center</code>	a logical value indicating whether the variables should be shifted to be zero centered. Alternately, a vector of length equal the number of columns of <code>x</code> can be supplied. The value is passed to <code>scale</code> .
<code>scale.</code>	a logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is <code>FALSE</code> for consistency with <code>S</code> , but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of <code>x</code> can be supplied. The value is passed to <a href="#">scale</a> .
<code>missingValues</code>	Integer: number of tolerated missing values per column to be replaced with the mean of the values of that same column
<code>...</code>	Arguments passed on to <code>stats::prcomp</code>

**Value**

PCA result in a `prcomp` object

**See Also**

Other functions to analyse principal components: [calculateLoadingsContribution\(\)](#), [plotPCA\(\)](#), [plotPCVariance\(\)](#)

**Examples**

```
performPCA(USArrests)
```

---

plotClusters	<i>Add clusters to highchart object</i>
--------------	---

---

**Description**

Clusters are added as coloured polygons.

**Usage**

```
plotClusters(hc, data, clustering)
```

**Arguments**

hc	highchart object
data	Data frame
clustering	Character: group of each sample

**Value**

highcharter object

---

plotDistribution	<i>Plot sample distribution</i>
------------------	---------------------------------

---

**Description**

The tooltip shows the median, variance, maximum, minimum and number of non-NA samples of each data series, as well as sample names if available.

**Usage**

```
plotDistribution(
  data,
  groups = NULL,
  rug = length(data) < 500,
  vLine = TRUE,
  ...,
  title = NULL,
  subtitle = NULL,
  type = c("density", "boxplot", "violin"),
  invertAxes = FALSE,
  psi = NULL,
  rugLabels = FALSE,
  rugLabelsRotation = 0,
  legend = TRUE,
  valueLabel = NULL
)
```

**Arguments**

data	Numeric, data frame or matrix: gene expression data or alternative splicing event quantification values (sample names are based on their names or colnames)
groups	List of sample names or vector containing the group name per data value (read Details); if NULL or a character vector of length 1, data values are considered from the same group
rug	Boolean: show rug plot?
vLine	Boolean: plot vertical lines (including descriptive statistics for each group)?
...	Arguments passed on to <code>stats::density.default</code>
bw	<p>the smoothing bandwidth to be used. The kernels are scaled such that this is the standard deviation of the smoothing kernel. (Note this differs from the reference books cited below, and from S-PLUS.)</p> <p>bw can also be a character string giving a rule to choose the bandwidth. See <code>bw.nrd</code>.</p> <p>The default, "nrd0", has remained the default for historical and compatibility reasons, rather than as a general recommendation, where e.g., "SJ" would rather fit, see also Venables and Ripley (2002).</p> <p>The specified (or computed) value of bw is multiplied by adjust.</p>
adjust	the bandwidth used is actually <code>adjust*bw</code> . This makes it easy to specify values like 'half the default' bandwidth.
kernel,window	a character string giving the smoothing kernel to be used. This must partially match one of "gaussian", "rectangular", "triangular", "epanechnikov", "biweight", "cosine" or "optcosine", with default "gaussian", and may be abbreviated to a unique prefix (single letter). "cosine" is smoother than "optcosine", which is the usual 'cosine' kernel in the literature and almost MSE-efficient. However, "cosine" is the version used by S.
weights	<p>numeric vector of non-negative observation weights, hence of same length as x. The default NULL is equivalent to <code>weights = rep(1/nx, nx)</code> where nx is the length of (the finite entries of) <code>x[]</code>. If <code>na.rm = TRUE</code> and there are NA's in x, they <i>and</i> the corresponding weights are removed before computations. In that case, when the original weights have summed to one, they are re-scaled to keep doing so.</p> <p>Note that weights are <i>not</i> taken into account for automatic bandwidth rules, i.e., when bw is a string. When the weights are proportional to true counts <code>cn</code>, <code>density(x = rep(x, cn))</code> may be used instead of weights.</p>
width	this exists for compatibility with S; if given, and bw is not, will set bw to width if this is a character string, or to a kernel-dependent multiple of width if this is numeric.
give.Rkern	logical; if true, <i>no</i> density is estimated, and the 'canonical bandwidth' of the chosen kernel is returned instead.
subdensity	<p>used only when weights are specified which do not sum to one.</p> <p>When true, it indicates that a "sub-density" is desired and no warning should be signalled. By default, when false, a <b>warning</b> is signalled when the weights do not sum to one.</p>
warnWbw	logical, used only when weights are specified <i>and</i> bw is character, i.e., automatic bandwidth selection is chosen (as by default). When true (as by default), a <b>warning</b> is signalled to alert the user that automatic bandwidth selection will not take the weights into account and hence may be suboptimal.

n	the number of equally spaced points at which the density is to be estimated. When $n > 512$ , it is rounded up to a power of 2 during the calculations (as <code>fft</code> is used) and the final result is interpolated by <code>approx</code> . So it almost always makes sense to specify $n$ as a power of two.
from, to	the left and right-most points of the grid at which the density is to be estimated; the defaults are <code>cut * bw</code> outside of <code>range(x)</code> .
cut	by default, the values of <code>from</code> and <code>to</code> are cut bandwidths beyond the extremes of the data. This allows the estimated density to drop to approximately zero at the extremes.
title	Character: plot title
subtitle	Character: plot subtitle
type	Character: density, boxplot or violin plot
invertAxes	Boolean: plot X axis as Y and vice-versa?
psi	Boolean: are data composed of PSI values? If NULL, <code>psi = TRUE</code> if all data values are between 0 and 1
rugLabels	Boolean: plot sample names in the rug?
rugLabelsRotation	Numeric: rotation (in degrees) of rug labels; this may present issues at different zoom levels and depending on the proximity of data values
legend	Boolean: show legend?
valueLabel	Character: label for the value (by default, either Inclusion levels or Gene expression)

## Details

Argument groups can be either:

- a list of sample names, e.g. `list("Group 1"=c("Sample A", "Sample B"), "Group 2"=c("Sample C"))`
- a character vector with the same length as `data`, e.g. `c("Sample A", "Sample C", "Sample B")`.

## Value

highchart object with density plot

## See Also

Other functions to perform and plot differential analyses: `diffAnalyses()`

## Examples

```
data <- sample(20, rep=TRUE)/20
groups <- paste("Group", c(rep("A", 10), rep("B", 10)))
names(data) <- paste("Sample", seq(data))
plotDistribution(data, groups)

# Using colours
attr(groups, "Colour") <- c("Group A"="pink", "Group B"="orange")
plotDistribution(data, groups)
```

---

plotGeneExprPerSample *Plot distribution of gene expression per sample*

---

### Description

Plot distribution of gene expression per sample

### Usage

```
plotGeneExprPerSample(geneExpr, ...)
```

### Arguments

geneExpr	Data frame or matrix: gene expression
...	Arguments passed on to <a href="#">renderBoxplot</a>
data	Data frame or matrix
outliers	Boolean: draw outliers?
sortByMedian	Boolean: sort box plots based on ascending median?
showXlabels	Boolean: show labels in X axis?

### Value

Gene expression distribution plots

### See Also

Other functions for gene expression pre-processing: [convertGeneIdentifiers\(\)](#), [filterGeneExpr\(\)](#), [normaliseGeneExpression\(\)](#), [plotLibrarySize\(\)](#), [plotRowStats\(\)](#)

### Examples

```
df <- data.frame(geneA=c(2, 4, 5),
                 geneB=c(20, 3, 5),
                 geneC=c(5, 10, 21))
colnames(df) <- paste("Sample", 1:3)
plotGeneExprPerSample(df)
```

---

plotGroupIndependence *Plot  $-\log_{10}$ (p-values) of the results obtained after multiple group independence testing*

---

### Description

Plot  $-\log_{10}$ (p-values) of the results obtained after multiple group independence testing

**Usage**

```
plotGroupIndependence(
  groups,
  top = 50,
  textSize = 10,
  colourLow = "lightgrey",
  colourMid = "blue",
  colourHigh = "orange",
  colourMidpoint = 150
)
```

**Arguments**

groups	multiGroupIndependenceTest object (obtained after running <a href="#">testGroupIndependence()</a> )
top	Integer: number of attributes to render
textSize	Integer: size of the text
colourLow	Character: name or HEX code of colour for lower values
colourMid	Character: name or HEX code of colour for middle values
colourHigh	Character: name or HEX code of colour for higher values
colourMidpoint	Numeric: midpoint to identify middle values

**Value**

ggplot object

**See Also**

[parseCategoricalGroups\(\)](#) and [testGroupIndependence\(\)](#)

Other functions for data grouping: [createGroupByAttribute\(\)](#), [getGeneList\(\)](#), [getSampleFromSubject\(\)](#), [getSubjectFromSample\(\)](#), [groupPerElem\(\)](#), [testGroupIndependence\(\)](#)

**Examples**

```
elements <- paste("subjects", 1:50)
ref <- elements[10:50]
groups <- list(race=list(asian=elements[1:3],
                        white=elements[4:7],
                        black=elements[8:10]),
              region=list(european=elements[c(4, 5, 9)],
                          african=elements[c(6:8, 10:50)]))
groupTesting <- testGroupIndependence(ref, groups, elements)
plotGroupIndependence(groupTesting)
```

plotICA

*Create multiple scatterplots from ICA***Description**

Create multiple scatterplots from ICA

**Usage**

```
plotICA(ica, components = seq(10), groups = NULL, ...)
```

**Arguments**

<code>ica</code>	Object resulting from <a href="#">performICA()</a>
<code>components</code>	Numeric: independent components to plot
<code>groups</code>	Matrix: groups to plot indicating the index of interest of the samples (use clinical or sample groups)
<code>...</code>	Arguments passed on to <a href="#">pairsD3::pairsD3</a>
<code>group</code>	a optional vector specifying the group each observation belongs to. Used for tooltips and colouring the observations.
<code>subset</code>	an optional vector specifying a subset of observations to be used for plotting. Useful when you have a large number of observations, you can specify a random subset.
<code>labels</code>	the names of the variables (column names of <code>x</code> used by default).
<code>cex</code>	the magnification of the plotting symbol (default=3)
<code>width</code>	the width (and height) of the plot when viewed externally.
<code>col</code>	an optional (hex) colour for each of the levels in the group vector.
<code>big</code>	a logical parameter. Prevents inadvertent plotting of huge data sets. Default limit is 10 variables, to plot more than 10 set <code>big=TRUE</code> .
<code>theme</code>	a character parameter specifying whether the theme should be colour colour (default) or black and white bw.
<code>opacity</code>	numeric between 0 and 1. The opacity of the plotting symbols (default 0.9).
<code>tooltip</code>	an optional vector with the tool tip to be displayed when hovering over an observation. You can include basic html.
<code>leftmar</code>	space on the left margin
<code>topmar</code>	space on the bottom margin
<code>diag</code>	logical, whether or not the main diagonal is plotted (scatter plot of variables against themselves).

**Value**

Multiple scatterplots as a `pairsD3` object

**See Also**

Other functions to analyse independent components: [performICA\(\)](#)

**Examples**

```

data <- scale(USArrests)
ica <- fastICA::fastICA(data, n.comp=4)
plotICA(ica)

# Colour by groups
groups <- NULL
groups$sunny <- c("California", "Hawaii", "Florida")
groups$ozEntrance <- c("Kansas")
groups$novel <- c("New Mexico", "New York", "New Hampshire", "New Jersey")
plotICA(ica, groups=groups)

```

---

plotLibrarySize	<i>Plot library size</i>
-----------------	--------------------------

---

**Description**

Plot library size

**Usage**

```

plotLibrarySize(
  data,
  log10 = TRUE,
  title = "Library size distribution across samples",
  subtitle = "Library size: total number of mapped reads",
  colour = "orange"
)

```

**Arguments**

data	Data frame or matrix: gene expression
log10	Boolean: log10-transform data?
title	Character: plot title
subtitle	Character: plot subtitle
colour	Character: data colour

**Value**

Library size distribution

**See Also**

Other functions for gene expression pre-processing: [convertGeneIdentifiers\(\)](#), [filterGeneExpr\(\)](#), [normaliseGeneExpression\(\)](#), [plotGeneExprPerSample\(\)](#), [plotRowStats\(\)](#)

**Examples**

```

df <- data.frame(geneA=c(2, 4, 5),
                 geneB=c(20, 3, 5),
                 geneC=c(5, 10, 21))
colnames(df) <- paste("Sample", 1:3)
plotLibrarySize(df)

```



---

plotPCA *Create a scatterplot from a PCA object*

---

### Description

Create a scatterplot from a PCA object

### Usage

```
plotPCA(  
  pca,  
  pcX = 1,  
  pcY = 2,  
  groups = NULL,  
  individuals = TRUE,  
  loadings = FALSE,  
  nLoadings = NULL  
)
```

### Arguments

pca	prcomp object
pcX	Character: name of the X axis of interest from the PCA
pcY	Character: name of the Y axis of interest from the PCA
groups	Matrix: groups to plot indicating the index of interest of the samples (use clinical or sample groups)
individuals	Boolean: plot PCA individuals
loadings	Boolean: plot PCA loadings/rotations
nLoadings	Integer: Number of variables to plot, ordered by those that most contribute to selected principal components (this allows for faster performance as only the most contributing variables are rendered); if NULL, all variables are plotted

### Value

Scatterplot as an highchart object

### See Also

Other functions to analyse principal components: [calculateLoadingsContribution\(\)](#), [performPCA\(\)](#), [plotPCAVariance\(\)](#)

### Examples

```
pca <- prcomp(USArrests, scale=TRUE)  
plotPCA(pca)  
plotPCA(pca, pcX=2, pcY=3)  
  
# Plot both individuals and loadings  
plotPCA(pca, pcX=2, pcY=3, loadings=TRUE)  
  
# Only plot loadings  
plotPCA(pca, pcX=2, pcY=3, loadings=TRUE, individuals=FALSE)
```

---

plotPCAvariance	<i>Create the explained variance plot from a PCA</i>
-----------------	--

---

**Description**

Create the explained variance plot from a PCA

**Usage**

```
plotPCAvariance(pca)
```

**Arguments**

pca                    prcomp object

**Value**

Plot variance as an highchart object

**See Also**

Other functions to analyse principal components: [calculateLoadingsContribution\(\)](#), [performPCA\(\)](#), [plotPCA\(\)](#)

**Examples**

```
pca <- prcomp(USArrests)
plotPCAvariance(pca)
```

---

plotPointsStyle	<i>Interface to modify the style of the plot points</i>
-----------------	---

---

**Description**

Interface to modify the style of the plot points

**Usage**

```
plotPointsStyle(
  ns,
  id,
  description,
  help = NULL,
  size = 2,
  colour = "black",
  alpha = 1
)
```

**Arguments**

ns	Namespace function
id	Character: identifier
description	Character: display text for user
help	Character: extra text to help the user
size	Integer: default size
colour	Character: default colour
alpha	Numeric: default transparency value

**Value**

HTML elements

---

plotProtein	<i>Plot protein features</i>
-------------	------------------------------

---

**Description**

Plot protein features

**Usage**

```
plotProtein(molecule)
```

**Arguments**

molecule	Character: UniProt protein or Ensembl transcript identifier
----------	---

**Value**

highcharter object

**See Also**

Other functions to retrieve external information: [ensemblToUniprot\(\)](#), [plotTranscripts\(\)](#), [queryEnsemblByGene\(\)](#)

**Examples**

```
protein <- "P38398"  
plotProtein(protein)  
  
transcript <- "ENST00000488540"  
plotProtein(transcript)
```

---

plotRowStats

*Plot row-wise statistics*


---

### Description

Scatter plot to compare between the row-wise mean, median, variance or range from a data frame or matrix. Also supports transformations of those variables, such as  $\log_{10}(\text{mean})$ . If  $y = \text{NULL}$ , a density plot is rendered instead.

### Usage

```
plotRowStats(
  data,
  x,
  y = NULL,
  subset = NULL,
  xmin = NULL,
  xmax = NULL,
  ymin = NULL,
  ymax = NULL,
  xlim = NULL,
  ylim = NULL,
  cache = NULL,
  verbose = FALSE,
  data2 = NULL,
  legend = FALSE,
  legendLabels = c("Original", "Highlighted")
)
```

### Arguments

data	Data frame or matrix containing samples per column and, for instance, gene or alternative splicing event per row
x, y	Character: statistic to calculate and display in the plot per row; choose between mean, median, var or range (or transformations of those variables, e.g. $\log_{10}(\text{var})$ ); if $y = \text{NULL}$ , the density of $x$ will be plot instead
subset	Boolean or integer: data points to highlight
xmin, xmax, ymin, ymax	Numeric: minimum and maximum X and Y values to draw in the plot
xlim, ylim	Numeric: X and Y axis range
cache	List of summary statistics for data previously calculated to avoid repeating calculations (output also returns cache in attribute named cache with appropriate data)
verbose	Boolean: print messages of the steps performed
data2	Same as data argument but points in data2 are highlighted (unless data2 = NULL)
legend	Boolean: show legend?
legendLabels	Character: legend labels

**Value**

Plot of data

**See Also**

Other functions for gene expression pre-processing: [convertGeneIdentifiers\(\)](#), [filterGeneExpr\(\)](#), [normaliseGeneExpression\(\)](#), [plotGeneExprPerSample\(\)](#), [plotLibrarySize\(\)](#)

Other functions for PSI quantification: [filterPSI\(\)](#), [getSplicingEventTypes\(\)](#), [listSplicingAnnotations\(\)](#), [loadAnnotation\(\)](#), [quantifySplicing\(\)](#)

**Examples**

```
library(ggplot2)

# Plotting gene expression data
geneExpr <- readfile("ex_gene_expression.RDS")
plotRowStats(geneExpr, "mean", "var^(1/4)") +
  ggtitle("Mean-variance plot") +
  labs(y="Square Root of the Standard Deviation")

# Plotting alternative splicing quantification
annot <- readfile("ex_splicing_annotation.RDS")
junctionQuant <- readfile("ex_junctionQuant.RDS")
psi <- quantifySplicing(annot, junctionQuant, eventType=c("SE", "MXE"))

medianVar <- plotRowStats(psi, x="median", y="var", xlim=c(0, 1)) +
  labs(x="Median PSI", y="PSI variance")
medianVar

rangeVar <- plotRowStats(psi, x="range", y="log10(var)", xlim=c(0, 1)) +
  labs(x="PSI range", y="log10(PSI variance)")
rangeVar
```

---

plotSingleICA

*Create a scatterplot for ICA*


---

**Description**

Create a scatterplot for ICA

**Usage**

```
plotSingleICA(ica, icX = 1, icY = 2, groups = NULL)
```

**Arguments**

ica	Object containing an ICA
icX	Character: name of the X axis
icY	Character: name of the Y axis
groups	Matrix: groups to plot indicating the index of interest of the samples (use clinical or sample groups)

**Value**

Scatterplot as an highcharter object

**Examples**

```
ica <- performICA(USArrests, scale=TRUE)
psychomics:::plotSingleICA(ica)
psychomics:::plotSingleICA(ica, icX=2, icY=3)

# Colour by groups
groups <- NULL
groups$sunny <- c("California", "Hawaii", "Florida")
groups$ozEntrance <- c("Kansas")
groups$novel <- c("New Mexico", "New York", "New Hampshire", "New Jersey")
psychomics:::plotSingleICA(ica, groups=groups)
```

---

plotSplicingEvent      *Plot diagram of alternative splicing events*

---

**Description**

Plot diagram of alternative splicing events

**Usage**

```
plotSplicingEvent(
  ASevent,
  data = NULL,
  showText = TRUE,
  showPath = TRUE,
  showAlternative1 = TRUE,
  showAlternative2 = TRUE,
  constitutiveWidth = NULL,
  alternativeWidth = NULL,
  intronWidth = NULL,
  constitutiveFill = "lightgray",
  constitutiveStroke = "darkgray",
  alternative1Fill = "#ffb153",
  alternative1Stroke = "#faa000",
  alternative2Fill = "#caa06c",
  alternative2Stroke = "#9d7039",
  class = NULL,
  style = NULL
)
```

**Arguments**

ASevent	Character: alternative splicing event identifiers
data	Matrix or data frame: alternative splicing information
showText	Boolean: display coordinates and length (if available)
showPath	Boolean: display alternative splicing junctions

```

showAlternative1
    Boolean: show alternative exon 1 and respective splicing junctions and text?
showAlternative2
    Boolean: show alternative exon 2 and respective splicing junctions and text?
    (only related with mutually exclusive exons)
constitutiveWidth
    Numeric: width of constitutive exon(s)
alternativeWidth
    Numeric: width of alternative exon(s)
intronWidth
    Numeric: width of intron's representation
constitutiveFill
    Character: fill colour of constitutive exons
constitutiveStroke
    Character: stroke colour of constitutive exons
alternative1Fill
    Character: fill colour of alternative exon 1
alternative1Stroke
    Character: stroke colour of alternative exon 1
alternative2Fill
    Character: fill colour of alternative exon 2
alternative2Stroke
    Character: stroke colour of alternative exon 2
class
    Character: class of SVG parent tag
style
    Character: style of SVG parent tag

```

**Value**

List of SVG (one for each alternative splicing event)

**Examples**

```

events <- c(
  "A3SS_15+_63353138_63353912_63353397_TPM1",
  "A3SS_11_-_61118463_61117115_61117894_CYB561A3",
  "A5SS_21+_48055675_48056459_48056808_PRMT2",
  "A5SS_1_-_1274742_1274667_1274033_DVL1",
  "AFE_9+_131902430_131901928_131904724_PPP2R4",
  "AFE_5_-_134686513_134688636_134681747_H2AFY",
  "ALE_12+_56554104_56554410_56555171_MYL6",
  "ALE_8_-_38314874_38287466_38285953_FGFR1",
  "SE_9+_6486925_6492303_6492401_6493826_UHRF2",
  "SE_19_-_5218431_5216778_5216731_5215606_PTPRS",
  "MXE_15+_63335142_63335905_63336030_63336226_63336351_63349184_TPM1",
  "MXE_17_-_74090495_74087316_74087224_74086478_74086410_74085401_EXOC7")
diagram <- plotSplicingEvent(events)

## Not run:
diagram[["A3SS_3_-_145796903_145794682_145795711_PLOD2"]]
diagram[[6]]
diagram

## End(Not run)

```

---

plotSurvivalCurves      *Plot survival curves*

---

### Description

Plot survival curves

### Usage

```
plotSurvivalCurves(  
  surv,  
  mark = TRUE,  
  interval = FALSE,  
  pvalue = NULL,  
  title = "Survival analysis",  
  scale = NULL,  
  auto = TRUE  
)
```

### Arguments

surv	Survival object
mark	Boolean: mark times?
interval	Boolean: show interval ranges?
pvalue	Numeric: p-value of the survival curves
title	Character: plot title
scale	Character: time scale (default is days)
auto	Boolean: return the plot automatically prepared (TRUE) or only the bare minimum (FALSE)?

### Value

Plot of survival curves

### See Also

Other functions to analyse survival: [assignValuePerSubject\(\)](#), [getAttributesTime\(\)](#), [labelBasedOnCutoff\(\)](#), [optimalSurvivalCutoff\(\)](#), [plotSurvivalPvaluesByCutoff\(\)](#), [processSurvTerms\(\)](#), [survdiffTerms\(\)](#), [survfit.survTerms\(\)](#), [testSurvival\(\)](#)

### Examples

```
require("survival")  
fit <- survfit(Surv(time, status) ~ x, data = aml)  
plotSurvivalCurves(fit)
```



---

```
plotSurvivalPvaluesByCutoff
```

*Plot p-values of survival difference between groups based on multiple cutoffs*

---

## Description

Plot p-values of survival difference between groups based on multiple cutoffs

## Usage

```
plotSurvivalPvaluesByCutoff(  
  clinical,  
  data,  
  censoring,  
  event,  
  timeStart,  
  timeStop = NULL,  
  followup = "days_to_last_followup",  
  significance = 0.05,  
  cutoffs = seq(0, 0.99, 0.01)  
)
```

## Arguments

clinical	Data frame: clinical data
data	Numeric: elements of interest to test against the cutoff
censoring	Character: censor using left, right, interval or interval2
event	Character: name of column containing time of the event of interest
timeStart	Character: name of column containing starting time of the interval or follow up time
timeStop	Character: name of column containing ending time of the interval (only relevant for interval censoring)
followup	Character: name of column containing follow up time
significance	Numeric: significance threshold
cutoffs	Numeric: cutoffs to test

## Value

p-value plot

## See Also

Other functions to analyse survival: [assignValuePerSubject\(\)](#), [getAttributesTime\(\)](#), [labelBasedOnCutoff\(\)](#), [optimalSurvivalCutoff\(\)](#), [plotSurvivalCurves\(\)](#), [processSurvTerms\(\)](#), [survdiffTerms\(\)](#), [survfit.survTerms\(\)](#), [testSurvival\(\)](#)

**Examples**

```

clinical <- read.table(text = "2549  NA ii  female
                             840  NA i   female
                             NA 1204 iv  male
                             NA  383 iv  female
                             1293  NA iii male")
names(clinical) <- c("patient.days_to_last_followup",
                    "patient.days_to_death",
                    "patient.stage_event.pathologic_stage",
                    "patient.gender")
clinical <- do.call(rbind, rep(list(clinical), 5))
rownames(clinical) <- paste("Subject", seq(nrow(clinical)))

# Calculate PSI for skipped exon (SE) and mutually exclusive (MXE) events
annot <- readRDS("ex_splicing_annotation.RDS")
junctionQuant <- readRDS("ex_junctionQuant.RDS")

psi <- quantifySplicing(annot, junctionQuant, eventType=c("SE", "MXE"))

# Match between subjects and samples
match <- c("Cancer 1"="Subject 3",
           "Cancer 2"="Subject 17",
           "Cancer 3"="Subject 21")

eventData <- assignValuePerSubject(psi[3, ], match)

event      <- "days_to_death"
timeStart  <- "days_to_death"
plotSurvivalPvaluesByCutoff(clinical, eventData, censoring="right",
                             event=event, timeStart=timeStart)

```

---

plottableXranges      *HTML code to plot a X-ranges series*

---

**Description**

HTML code to plot a X-ranges series

**Usage**

```
plottableXranges(hc, shiny = FALSE)
```

**Arguments**

hc	highcharter object
shiny	Boolean: is the function running in a Shiny session?

**Value**

HTML elements

---

plotTranscripts	<i>Plot transcripts</i>
-----------------	-------------------------

---

## Description

Plot transcripts

## Usage

```
plotTranscripts(  
  info,  
  eventPosition = NULL,  
  event = NULL,  
  eventData = NULL,  
  shiny = FALSE  
)
```

## Arguments

info	Information retrieved from Ensembl
eventPosition	Numeric: coordinates of the alternative splicing event (ignored if event is set)
event	Character: identifier of the alternative splicing event to plot
eventData	Object containing event information to be parsed
shiny	Boolean: is the function running in a Shiny session?

## Value

NULL (function is only used to modify the Shiny session's state or internal variables)

## See Also

Other functions to retrieve external information: [ensemblToUniprot\(\)](#), [plotProtein\(\)](#), [queryEnsemblByGene\(\)](#)

## Examples

```
event <- "SE_12_-_7985318_7984360_7984200_7982602_SLC2A14"  
info <- queryEnsemblByEvent(event, species="human", assembly="hg19")  
## Not run:  
plotTranscripts(info, event=event)  
  
## End(Not run)
```

---

`prepareAnnotationFromEvents`*Prepare annotation from alternative splicing events*

---

### Description

In case more than one data frame with alternative splicing events is given, the events are cross-referenced according to the chromosome, strand and relevant coordinates per event type (see details).

### Usage

```
prepareAnnotationFromEvents(...)
```

### Arguments

... Data frame(s) of alternative splicing events to include in the annotation

### Details

Events from two or more data frames are cross-referenced based on each event's chromosome, strand and specific coordinates relevant for each event type:

- Skipped exon: constitutive exon 1 end, alternative exon (start and end) and constitutive exon 2 start
- Mutually exclusive exon: constitutive exon 1 end, alternative exon 1 and 2 (start and end) and constitutive exon 2 start
- Alternative 5' splice site: constitutive exon 1 end, alternative exon 1 end and constitutive exon 2 start
- Alternative first exon: same as alternative 5' splice site
- Alternative 3' splice site: constitutive exon 1 end, alternative exon 1 start and constitutive exon 2 start
- Alternative last exon: same as alternative 3' splice site

### Value

List of data frames with the annotation from different data frames joined by event type

### Note

When cross-referencing events, gene information is discarded.

### See Also

Other functions to prepare alternative splicing annotations: [parseSuppaAnnotation\(\)](#)

**Examples**

```
# Load sample files (SUPPA annotation)
folder <- "extdata/eventsAnnotSample/suppa_output/suppaEvents"
suppaOutput <- system.file(folder, package="psychomics")

# Parse and prepare SUPPA annotation
suppa <- parseSuppaAnnotation(suppaOutput)
annot <- prepareAnnotationFromEvents(suppa)

# Load sample files (rMATS annotation)
folder <- "extdata/eventsAnnotSample/mats_output/ASEvents/"
matsOutput <- system.file(folder, package="psychomics")

# Parse rMATS annotation and prepare combined annotation from rMATS and SUPPA
mats <- parseMatsAnnotation(matsOutput)
annot <- prepareAnnotationFromEvents(suppa, mats)
```

---

```
prepareEventPlotOptions
```

*Prepare event plot options*

---

**Description**

Prepare event plot options

**Usage**

```
prepareEventPlotOptions(id, ns, labelsPanel = NULL)
```

**Arguments**

id	Character: identifier
ns	Namespace identifier
labelsPanel	Tab panel containing options to label points

**Value**

HTML elements

---

```
prepareFileBrowser
```

*Prepare file browser dialogue and update the input's value accordingly to selected file or directory*

---

**Description**

Prepare file browser dialogue and update the input's value accordingly to selected file or directory

**Usage**

```
prepareFileBrowser(session, input, id, modalId = "modal", ...)
```

**Arguments**

session	Shiny session
input	Shiny input
id	Character: input identifier
modalId	Character: modal window identifier
...	Arguments passed on to <a href="#">fileBrowser</a>
default	Character: path to initial folder
caption	Character: caption on the selection dialogue
multiple	Boolean: allow to select multiple files?
directory	Boolean: allow to select directories instead of files?

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

```
prepareFirebrowseArchives
```

*Prepares FireBrowse archives in a given directory*

---

**Description**

Checks FireBrowse archives' integrity using the MD5 files, extracts the content of the archives, moves the content to newly-created folders and removes the original downloaded archives.

**Usage**

```
prepareFirebrowseArchives(archive, md5, folder, outdir)
```

**Arguments**

archive	Character: path to downloaded archives
md5	Character: path to MD5 files of each archive
folder	Character: master directory where every archive will be extracted
outdir	Character: subdirectories where to move the extracted content

**Value**

Invisible TRUE if successful

**Examples**

```
file <- paste0(
  "~/Downloads",
  "ACC/20151101/gdac.broadinstitute.org_ACC.",
  "Merge_Clinical.Level_1.2015110100.0.0.tar.gz")
md5 <- paste0(file, ".md5")
## Not run:
prepareFirebrowseArchives(archive = file, md5 = paste0(file, ".md5"))

## End(Not run)
```

---

```
prepareGenePresentation
```

*Prepare presentation of multiple genes for the same splicing event*

---

### Description

Prepare presentation of multiple genes for the same splicing event

### Usage

```
prepareGenePresentation(gene, collapse = "/")
```

### Arguments

gene	Character: gene
collapse	Character: character string to separate in case of more than one gene

### Value

Same object with items collapsed

---

```
prepareJunctionQuantSTAR
```

*Prepare user-provided files to be loaded into psichomics*

---

### Description

Prepare user-provided files to be loaded into psichomics

### Usage

```
prepareJunctionQuantSTAR(..., startOffset = -1, endOffset = +1)

prepareGeneQuantSTAR(
  ...,
  strandedness = c("unstranded", "stranded", "stranded (reverse)")
)
```

### Arguments

...	Character: path of (optionally named) input files (see Examples)
startOffset	Numeric: value to offset start position
endOffset	Numeric: value to offset end position
strandedness	Character: strandedness of RNA-seq protocol; may be one of the following: unstraded, stranded or stranded (reverse)

### Value

Prepared file (if output != NULL) and object

**Examples**

```
## Not run:
prepareJunctionQuant("Control rep1"=junctionFile1,
                    "Control rep2"=junctionFile2,
                    "KD rep1"=junctionFile3,
                    "KD rep2"=junctionFile4)

## End(Not run)
## Not run:
prepareGeneQuant("Control rep1"=geneCountFile1,
                "Control rep2"=geneCountFile2,
                "KD rep1"=geneCountFile3,
                "KD rep2"=geneCountFile4)

## End(Not run)
```

---

```
preparePreMadeGroupForSelection
```

*Prepare list of pre-made groups for a selectize element*

---

**Description**

Prepare list of pre-made groups for a selectize element

**Usage**

```
preparePreMadeGroupForSelection(groups)
```

**Arguments**

groups            List of list of characters

**Value**

List

---

```
prepareSRAMetadata
```

*Prepare user-provided files to be loaded into psychomics*

---

**Description**

Prepare user-provided files to be loaded into psychomics



**Usage**

```

prepareSRAMetadata(file, output = "psychomics_metadata.txt")

prepareJunctionQuant(
  ...,
  output = "psychomics_junctions.txt",
  startOffset = NULL,
  endOffset = NULL
)

prepareGeneQuant(
  ...,
  output = "psychomics_gene_counts.txt",
  strandedness = c("unstranded", "stranded", "stranded (reverse)")
)

```

**Arguments**

file	Character: path to file
output	Character: path of output file (if NULL, only returns the data without saving it to a file)
...	Character: path of (optionally named) input files (see Examples)
startOffset	Numeric: value to offset start position
endOffset	Numeric: value to offset end position
strandedness	Character: strandedness of RNA-seq protocol; may be one of the following: unstraded, stranded or stranded (reverse)

**Value**

Prepared file (if output != NULL) and object

**Examples**

```

## Not run:
prepareJunctionQuant("Control rep1"=junctionFile1,
                    "Control rep2"=junctionFile2,
                    "KD rep1"=junctionFile3,
                    "KD rep2"=junctionFile4)

## End(Not run)
## Not run:
prepareGeneQuant("Control rep1"=geneCountFile1,
                "Control rep2"=geneCountFile2,
                "KD rep1"=geneCountFile3,
                "KD rep2"=geneCountFile4)

## End(Not run)

```

---

prepareWordBreak	<i>Create word break opportunities (for HTML) using given characters</i>
------------------	--

---

**Description**

Create word break opportunities (for HTML) using given characters

**Usage**

```
prepareWordBreak(  
    str,  
    pattern = c(".", "-", "\\ ", "/", "_", ",", " ", "+", "="),  
    html = TRUE  
)
```

**Arguments**

str	Character: text
pattern	Character: pattern(s) of interest to be used as word break opportunities
html	Boolean: convert to HTML?

**Value**

String containing HTML elements

---

preserveAttributes	<i>Preserve attributes when extracting values</i>
--------------------	---

---

**Description**

Add object to class sticky

**Usage**

```
preserveAttributes(x)
```

**Arguments**

x	Object
---	--------

**Value**

Object with class sticky

---

processButton	<i>Style button used to initiate a process</i>
---------------	--

---

**Description**

Style button used to initiate a process

**Usage**

```
processButton(id, label, ..., class = "btn-primary")
```

**Arguments**

id	Character: button identifier
label	Character: label
...	Arguments passed on to <a href="#">shiny::actionButton</a>
icon	An optional <a href="#">icon()</a> to appear on the button.
width	The width of the input, e.g. '400px', or '100%'; see <a href="#">validateCssUnit()</a> .
class	Character: class

**Value**

HTML for a button

---

processDatasetNames	<i>Process dataset names</i>
---------------------	------------------------------

---

**Description**

Process dataset names

**Usage**

```
processDatasetNames(data)
```

**Arguments**

data	List of lists of data frames
------	------------------------------

**Details**

Avoid duplicated names and append the technology used for junction quantification

**Value**

Processed list of lists of data frames

---

processSRAdata      *Process SRA quantification data*

---

**Description**

Process SRA quantification data

**Usage**

```
processSRAdata(files, data, IDcolname)
```

**Arguments**

files	Character: path to SRA quantification files
data	Data frame: processed quantification data
IDcolname	Character: name of the column containing the identifiers

**Value**

Process file

---

processSurvData      *Process survival data to calculate survival curves*

---

**Description**

Process survival data to calculate survival curves

**Usage**

```
processSurvData(
  event,
  timeStart,
  timeStop,
  followup,
  group,
  clinical,
  survTime = NULL
)
```

**Arguments**

event	Character: name of column containing time of the event of interest
timeStart	Character: name of column containing starting time of the interval or follow up time
timeStop	Character: name of column containing ending time of the interval (only relevant for interval censoring)
followup	Character: name of column containing follow up time
group	Character: group relative to each subject
clinical	Data frame: clinical data
survTime	survTime object: Times to follow up, time start, time stop and event (optional)

**Details**

The event time is only used to determine whether the event has occurred (1) or not (0) in case of missing values.

If survTime = NULL, survival times are obtained from the clinical dataset according to the names given in timeStart, timeStop, event and followup. This may become quite slow when used in a loop. If the aforementioned variables are constant, consider running `getAttributesTime()` outside the loop and using its output via the survTime argument of this function (see Examples).

**Value**

Data frame with terms needed to calculate survival curves

---

processSurvival	<i>Check if survival analyses successfully completed or returned errors</i>
-----------------	---

---

**Description**

Check if survival analyses successfully completed or returned errors

**Usage**

```
processSurvival(session, ...)
```

**Arguments**

session	Shiny session
...	Arguments passed on to <a href="#">processSurvTerms</a>
censoring	Character: censor using left, right, interval or interval2
scale	Character: rescale the survival time to days, weeks, months or years
formulaStr	Character: formula to use
coxph	Boolean: fit a Cox proportional hazards regression model?
survTime	survTime object: times to follow up, time start, time stop and event (optional)
group	Character: group relative to each subject
clinical	Data frame: clinical data
event	Character: name of column containing time of the event of interest
timeStart	Character: name of column containing starting time of the interval or follow up time
timeStop	Character: name of column containing ending time of the interval (only relevant for interval censoring)
followup	Character: name of column containing follow up time

**Value**

List with survival analysis results

---

<code>processSurvTerms</code>	<i>Process survival curves terms to calculate survival curves</i>
-------------------------------	---

---

**Description**

Process survival curves terms to calculate survival curves

**Usage**

```
processSurvTerms(
  clinical,
  censoring,
  event,
  timeStart,
  timeStop = NULL,
  group = NULL,
  formulaStr = NULL,
  coxph = FALSE,
  scale = "days",
  followup = "days_to_last_followup",
  survTime = NULL
)
```

**Arguments**

<code>clinical</code>	Data frame: clinical data
<code>censoring</code>	Character: censor using left, right, interval or interval2
<code>event</code>	Character: name of column containing time of the event of interest
<code>timeStart</code>	Character: name of column containing starting time of the interval or follow up time
<code>timeStop</code>	Character: name of column containing ending time of the interval (only relevant for interval censoring)
<code>group</code>	Character: group relative to each subject
<code>formulaStr</code>	Character: formula to use
<code>coxph</code>	Boolean: fit a Cox proportional hazards regression model?
<code>scale</code>	Character: rescale the survival time to days, weeks, months or years
<code>followup</code>	Character: name of column containing follow up time
<code>survTime</code>	survTime object: times to follow up, time start, time stop and event (optional)

**Details**

The event time is only used to determine whether the event has occurred (1) or not (0) in case of missing values.

If `survTime = NULL`, survival times are obtained from the clinical dataset according to the names given in `timeStart`, `timeStop`, `event` and `followup`. This may become quite slow when used in a loop. If the aforementioned variables are constant, consider running `getAttributesTime()` outside the loop and using its output via the `survTime` argument of this function (see Examples).

**Value**

A list with a formula object and a data frame with terms needed to calculate survival curves

**See Also**

Other functions to analyse survival: [assignValuePerSubject\(\)](#), [getAttributesTime\(\)](#), [labelBasedOnCutoff\(\)](#), [optimalSurvivalCutoff\(\)](#), [plotSurvivalCurves\(\)](#), [plotSurvivalPvaluesByCutoff\(\)](#), [survdiffTerms\(\)](#), [survfit.survTerms\(\)](#), [testSurvival\(\)](#)

**Examples**

```
clinical <- read.table(text = "2549  NA ii  female
                             840  NA i   female
                             NA 1204 iv  male
                             NA  383 iv  female
                             1293  NA iii male
                             NA 1355 ii  male")
names(clinical) <- c("patient.days_to_last_followup",
                    "patient.days_to_death",
                    "patient.stage_event.pathologic_stage",
                    "patient.gender")
timeStart <- "days_to_death"
event <- "days_to_death"
formulaStr <- "patient.stage_event.pathologic_stage + patient.gender"
survTerms <- processSurvTerms(clinical, censoring="right", event, timeStart,
                              formulaStr=formulaStr)

# If running multiple times, consider calculating survTime only once
survTime <- getAttributesTime(clinical, event, timeStart)
for (i in seq(5)) {
  survTerms <- processSurvTerms(clinical, censoring="right", event,
                                timeStart, formulaStr=formulaStr,
                                survTime=survTime)
}
```

---

psychomics

*Start graphical interface of psychomics*

---

**Description**

Start graphical interface of psychomics

**Usage**

```
psychomics(
  ...,
  launch.browser = TRUE,
  shinyproxy = FALSE,
  testData = FALSE,
  cache = getAnnotationHubOption("CACHE")
)
```

**Arguments**

...	Arguments passed on to <code>shiny::runApp</code>
port	The TCP port that the application should listen on. If the port is not specified, and the <code>shiny.port</code> option is set (with <code>options(shiny.port = XX)</code> ), then that port will be used. Otherwise, use a random port between 3000:8000, excluding ports that are blocked by Google Chrome for being considered unsafe: 3659, 4045, 5060, 5061, 6000, 6566, 6665:6669 and 6697. Up to twenty random ports will be tried.
host	The IPv4 address that the application should listen on. Defaults to the <code>shiny.host</code> option, if set, or "127.0.0.1" if not. See Details.
workerId	Can generally be ignored. Exists to help some editions of Shiny Server Pro route requests to the correct process.
quiet	Should Shiny status messages be shown? Defaults to FALSE.
display.mode	The mode in which to display the application. If set to the value "showcase", shows application code and metadata from a DESCRIPTION file in the application directory alongside the application. If set to "normal", displays the application normally. Defaults to "auto", which displays the application in the mode given in its DESCRIPTION file, if any.
test.mode	Should the application be launched in test mode? This is only used for recording or running automated tests. Defaults to the <code>shiny.testmode</code> option, or FALSE if the option is not set.
launch.browser	If true, the system's default web browser will be launched automatically after the app is started. Defaults to true in interactive sessions only. The value of this parameter can also be a function to call with the application's URL.
shinyproxy	Boolean: prepare visual interface to run in Shinyproxy?
testData	Boolean: load with test data
cache	Character: path to AnnotationHub cache (used to load alternative splicing event annotation)

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

**Examples**

```
## Not run:
psychomics()

## End(Not run)
```

---

pubmedUI

*Return the interface of relevant PubMed articles for a given gene*


---

**Description**

Return the interface of relevant PubMed articles for a given gene

**Usage**

```
pubmedUI(ns, gene, ...)
```



**Arguments**

ns	Namespace function
gene	Character: gene
...	Arguments passed on to <a href="#">queryPubMed</a>
top	Numeric: number of articles to retrieve
field	Character: field of interest where to look for terms (abstract by default)
sort	Character: sort by a given parameter (relevance by default)

**Value**

HTML interface of relevant PubMed articles

---

quantifySplicing	<i>Quantify alternative splicing events</i>
------------------	---

---

**Description**

Quantify alternative splicing events

**Usage**

```
quantifySplicing(
  annotation,
  junctionQuant,
  eventType = c("SE", "MXE", "ALE", "AFE", "A3SS", "A5SS"),
  minReads = 10,
  genes = NULL
)
```

**Arguments**

annotation	List of data frames: annotation for each alternative splicing event type
junctionQuant	Data frame: junction quantification
eventType	Character: splicing event types to quantify
minReads	Integer: values whose number of total supporting read counts is below minReads are returned as NA
genes	Character: gene symbols for which to quantify splicing events (if NULL, events from all genes are quantified)

**Value**

Data frame with the quantification of the alternative splicing events

**See Also**

Other functions for PSI quantification: [filterPSI\(\)](#), [getSplicingEventTypes\(\)](#), [listSplicingAnnotations\(\)](#), [loadAnnotation\(\)](#), [plotRowStats\(\)](#)

**Examples**

```
# Calculate PSI for skipped exon (SE) and mutually exclusive (MXE) events
annot <- readRDS("ex_splicing_annotation.RDS")
junctionQuant <- readRDS("ex_junctionQuant.RDS")

quantifySplicing(annot, junctionQuant, eventType=c("SE", "MXE"))
```

---

quantifySplicingSet     *Set of functions to quantify alternative splicing*

---

**Description**

Instructions to build the Shiny app

**Usage**

```
quantifySplicingSet(session, input)
```

**Arguments**

session	Shiny session
input	Shiny input

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

queryEnsembl     *Query the Ensembl REST API*

---

**Description**

Query the Ensembl REST API

**Usage**

```
queryEnsembl(path, query, grch37 = TRUE)
```

**Arguments**

path	Character: API path
query	Character: API query
grch37	Boolean: query the Ensembl GRCh37 API? if FALSE, query the most recent API

**Value**

Parsed response or NULL if no response

## Examples

```
path <- "overlap/region/human/7:140424943-140624564"
query <- list(feature = "gene")
psychomics:::queryEnsembl(path, query, grch37 = TRUE)
```

```
path <- "lookup/symbol/human/BRCA2"
query <- list(expand=1)
psychomics:::queryEnsembl(path, query, grch37 = TRUE)
```

---

queryEnsemblByGene      *Query information from Ensembl*

---

## Description

Query information from Ensembl

## Usage

```
queryEnsemblByGene(gene, species = NULL, assembly = NULL)
```

```
queryEnsemblByEvent(event, species = NULL, assembly = NULL, data = NULL)
```

## Arguments

gene	Character: gene
species	Character: species (may be NULL for an Ensembl identifier)
assembly	Character: assembly version (may be NULL for an Ensembl identifier)
event	Character: alternative splicing event
data	Matrix or data frame: alternative splicing information

## Value

Information from Ensembl

## See Also

Other functions to retrieve external information: [ensemblToUniprot\(\)](#), [plotProtein\(\)](#), [plotTranscripts\(\)](#)

## Examples

```
queryEnsemblByGene("BRCA1", "human", "hg19")
queryEnsemblByGene("ENSG00000139618")
event <- "SE_17_-_41251792_41249306_41249261_41246877_BRCA1"
queryEnsemblByEvent(event, species="human", assembly="hg19")
```

---

queryFirebrowseData     *Query the FireBrowse API for TCGA data*

---

### Description

Query the FireBrowse API for TCGA data

### Usage

```
queryFirebrowseData(
  format = "json",
  date = NULL,
  cohort = NULL,
  data_type = NULL,
  tool = NULL,
  platform = NULL,
  center = NULL,
  level = NULL,
  protocol = NULL,
  page = NULL,
  page_size = NULL,
  sort_by = NULL
)
```

### Arguments

format	Character: response format as JSON, CSV or TSV
date	Character: dates of the data retrieval by FireBrowse (by default, it uses the most recent data available)
cohort	Character: abbreviation of the cohorts (by default, returns data for all cohorts)
data_type	Character: data types (optional)
tool	Character: data produced by the selected FireBrowse tools (optional)
platform	Character: data generation platforms (optional)
center	Character: data generation centres (optional)
level	Integer: data levels (optional)
protocol	Character: sample characterization protocols (optional)
page	Integer: page of the results to return (optional)
page_size	Integer: number of records per page of results (optional)
sort_by	String: column used to sort the data (by default, sort by cohort)

### Value

Response from the FireBrowse API (it needs to be parsed)

**Examples**

```

cohort <- getTCGAcohorts()[1]
psychomics:::queryFirebrowseData(cohort = names(cohort),
                                  data_type = "mRNASeq")

# Querying for data from a specific date
dates <- getTCGAdates()
dates <- format(dates, psychomics:::getFirebrowseDateFormat())$query

psychomics:::queryFirebrowseData(date = dates[2], cohort = names(cohort))

```

---

queryPubMed

*Query the PubMed REST API*


---

**Description**

Query the PubMed REST API

**Usage**

```
queryPubMed(primary, ..., top = 3, field = "abstract", sort = "relevance")
```

**Arguments**

primary	Character: primary search term
...	Character: other relevant search terms
top	Numeric: number of articles to retrieve
field	Character: field of interest where to look for terms (abstract by default)
sort	Character: sort by a given parameter (relevance by default)

**Value**

Parsed response

**Examples**

```
psychomics:::queryPubMed("BRCA1", "cancer", "adrenocortical carcinoma")
```

---

queryUniprot                      *Query the UniProt REST API*

---

**Description**

Query the UniProt REST API

**Usage**

```
queryUniprot(molecule, format = "xml")
```

**Arguments**

molecule	Character: protein or transcript to query
format	Character: format of the response

**Value**

Parsed response

**Examples**

```
protein <- "P51587"
format <- "xml"
psychomics:::queryUniprot(protein, format)

transcript <- "ENST00000488540"
format <- "xml"
psychomics:::queryUniprot(transcript, format)
```

---

readAnnot                      *Read custom or remote annotation*

---

**Description**

Instructions to build the Shiny app

**Usage**

```
readAnnot(session, annotation, showProgress = FALSE)
```

**Arguments**

session	Shiny session
annotation	Character: chosen annotation
showProgress	Boolean: show progress?

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

readFile	<i>Load psychomics-specific file</i>
----------	--------------------------------------

---

**Description**

Load psychomics-specific file

**Usage**

```
readFile(file)
```

**Arguments**

file            Character: path to the file

**Value**

Loaded file

**Examples**

```
junctionQuant <- readFile("ex_junctionQuant.RDS")
```

---

reduceDimensionality	<i>Reduce dimensionality after processing missing values from data frame</i>
----------------------	--

---

**Description**

Reduce dimensionality after processing missing values from data frame

**Usage**

```
reduceDimensionality(  
  data,  
  type = c("pca", "ica"),  
  center = TRUE,  
  scale. = FALSE,  
  naTolerance = NULL,  
  missingValues = round(0.05 * ncol(data)),  
  ...  
)
```





---

renameGroups	<i>Rename duplicated names from a new group</i>
--------------	---

---

**Description**

Rename duplicated names from a new group

**Usage**

```
renameGroups(new, old)
```

**Arguments**

new	Matrix: new groups
old	Matrix: pre-existing groups

**Value**

Character with no duplicated group names

**Note**

The names of pre-existing groups are not modified.

---

renderBoxplot	<i>Render boxplot</i>
---------------	-----------------------

---

**Description**

Render boxplot

**Usage**

```
renderBoxplot(  
  data,  
  outliers = FALSE,  
  sortByMedian = TRUE,  
  showXlabels = TRUE,  
  title = NULL,  
  seriesName = "Gene expression"  
)
```

**Arguments**

data	Data frame or matrix
outliers	Boolean: draw outliers?
sortByMedian	Boolean: sort box plots based on ascending median?
showXlabels	Boolean: show labels in X axis?

**Value**

Box plot

**Examples**

```
psichomics:::renderBoxplot(data.frame(a=1:10, b=10:19, c=45:54))
```

---

```
renderDataTableSparklines
```

*Render a data table with sparkline HTML elements*

---

**Description**

Render a data table with sparkline HTML elements

**Usage**

```
renderDataTableSparklines(..., options = NULL)
```

**Arguments**

... Arguments passed on to [shiny::renderDataTable](#)

expr An expression that returns a data frame or a matrix.

searchDelay The delay for searching, in milliseconds (to avoid too frequent search requests).

callback A JavaScript function to be applied to the DataTable object. This is useful for DataTables plug-ins, which often require the DataTable instance to be available.

quoted If it is TRUE, then the [quote\(\)](#)ed value of expr will be used when expr is evaluated. If expr is a quosure and you would like to use its expression as a value for expr, then you must set quoted to TRUE.

outputArgs A list of arguments to be passed through to the implicit call to [dataTableOutput\(\)](#) when [renderDataTable\(\)](#) is used in an interactive R Markdown document.

options List of options to pass to [renderDataTable\(\)](#)

**Details**

This slightly modified version of [renderDataTable\(\)](#) calls a JavaScript function to convert the sparkline HTML elements to an interactive highchart object

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

renderGeneticInfo     *Render genetic information*

---

**Description**

Render genetic information

**Usage**

```
renderGeneticInfo(  
  output,  
  info,  
  species = NULL,  
  assembly = NULL,  
  grch37 = FALSE,  
  eventDiagram = NULL,  
  gene = NULL  
)
```

**Arguments**

output	Shiny output
info	Information as retrieved from Ensembl
species	Character: species name
assembly	Character: assembly version
grch37	Boolean: use version GRCh37 of the genome?
eventDiagram	Diagram of selected alternative splicing event
ns	Namespace function

**Value**

HTML elements to render gene, protein and transcript annotation

---

renderGroupInterface     *Render group interface*

---

**Description**

Render group interface

**Usage**

```
renderGroupInterface(ns, multiFisherTests = TRUE)
```

**Arguments**

ns	Namespace function
multiFisherTests	Boolean: allow to perform multiple Fisher exact test between groups

**Value**

HTML elements

---

renderProteinInfo	<i>Render protein information</i>
-------------------	-----------------------------------

---

**Description**

Render protein information

**Usage**

```
renderProteinInfo(protein, transcript, species, assembly)
```

**Arguments**

protein	Character: protein identifier
transcript	Character: Ensembl identifier of the protein's respective transcript
species	Character: species
assembly	Character: assembly

**Value**

HTML elements

---

replaceStrInList	<i>Replace a string with another in a list</i>
------------------	--

---

**Description**

Replace a string with another in a list

**Usage**

```
replaceStrInList(tag, old, new)
```

---

rm.null	<i>Filter NULL elements from a vector or a list</i>
---------	---

---

**Description**

Filter NULL elements from a vector or a list

**Usage**

```
rm.null(v)
```

**Arguments**

v	Vector or list
---	----------------

**Value**

Filtered vector or list with no NULL elements; if v is a vector composed of NULL elements, returns a NULL; if v is a list of NULL elements, returns an empty list

---

roundDigits	<i>Round by the given number of digits</i>
-------------	--

---

**Description**

Round by the given number of digits

**Usage**

```
roundDigits(n)
```

**Arguments**

n	Numeric: number to round
---	--------------------------

**Value**

Formatted number with a given numeric precision

---

roundMinDown	<i>Round down/up the minimum/maximum value</i>
--------------	--

---

**Description**

Round down/up the minimum/maximum value

**Usage**

```
roundMinDown(x, digits = 0)
```

```
roundMaxUp(x, digits = 0)
```

**Arguments**

x	Numeric: values
---	-----------------

digits	Numeric: number of maximum digits
--------	-----------------------------------

**Value**

Rounded numeric value

---

saveProcessedSRAdata	<i>Save processed SRA data in file</i>
----------------------	--

---

**Description**

Save processed SRA data in file

**Usage**

```
saveProcessedSRAdata(data, output = NULL)
```

**Arguments**

data	Object to save
------	----------------

output	Character: output filename (if NULL, no file is saved)
--------	--

**Value**

If output = NULL, save input to a file and return it as invisible; otherwise, just return the input

---

selectGroupsUI	<i>Group selection</i>
----------------	------------------------

---

**Description**

Group selection interface and logic

**Usage**

```
selectGroupsUI(
  id,
  label,
  type,
  placeholder = "Type to search groups",
  noGroupsLabel = NULL,
  groupsLabel = NULL,
  maxItems = NULL,
  returnAllDataLabel = NULL,
  returnAllDataValue = FALSE
)

selectGroupsServer(session, id, type, preference = NULL)

getSelectedGroups(input, id, type, filter = NULL)
```

**Arguments**

id	Character: identifier
label	Character: selectize label
type	Character: type of groups (either Patients, Samples, ASevents or Genes)
placeholder	Character: selectize placeholder
noGroupsLabel	Character: label to explicitly allow to select no groups (if NULL, this option is not displayed to the user)
groupsLabel	Character: label to explicitly allow to select groups (only required if noGroupsLabel is not NULL)
maxItems	Numeric: maximum number of groups to select
returnAllDataLabel	Character: label to allow to return data outside selected groups as belonging to an outside group (if NULL, this option is not displayed to the user)
returnAllDataValue	Boolean: default value to whether return all data or not (only required if returnAllDataLabel is not NULL)
session	Shiny session
preference	Character: name of groups to pre-select, when available (if NULL, all groups will be pre-selected)
input	Shiny input
filter	Character: get groups only if they are present in this argument (if TCGA-styled gene symbols, they will be "converted" to gene symbols alone)

**Value**

selectGroupsUI: Interface for group selection  
 selectGroupsServer: Server logic for group selection  
 getSelectedGroups: List with selected groups (or NULL when no groups are selected)

**Note**

To allow the user to (explicitly) select no groups, pass the noGroupsLabel and groupsLabel arguments.

---

selectizeGeneInput      *Create input to select a gene*

---

**Description**

Create input to select a gene

**Usage**

```
selectizeGeneInput(
  id,
  label = "Gene",
  choices = NULL,
  multiple = FALSE,
  ...,
  placeholder = "Type to search for a gene..."
)
```

**Arguments**

id	Character: identifier
label	Display label for the control, or NULL for no label.
choices	List of values to select from. If elements of the list are named, then that name — rather than the value — is displayed to the user. It's also possible to group related inputs by providing a named list whose elements are (either named or unnamed) lists, vectors, or factors. In this case, the outermost names will be used as the group labels (leveraging the <optgroup> HTML tag) for the elements in the respective sublist. See the example section for a small demo of this feature.
multiple	Is selection of multiple items allowed?
...	Arguments passed to the options list of selectizeInput()
placeholder	Character: placeholder

**Value**

HTML elements



---

selectPreMadeGroup	<i>Select pre-made groups from a selected item</i>
--------------------	--

---

**Description**

Select pre-made groups from a selected item

**Usage**

```
selectPreMadeGroup(groups, selected, genes = NULL)
```

**Arguments**

groups	List of list of characters
selected	Character: selected item

**Value**

Elements of selected item

---

setFirebrowseData	<i>Set data from FireBrowse</i>
-------------------	---------------------------------

---

**Description**

Set data from FireBrowse

**Usage**

```
setFirebrowseData(input, output, session, replace = TRUE)
```

**Arguments**

input	Shiny input
output	Shiny output
session	Shiny session
replace	Boolean: replace loaded data?

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

setLocalData	<i>Load local files</i>
--------------	-------------------------

---

**Description**

Load local files

**Usage**

```
setLocalData(input, output, session, replace = TRUE)
```

```
setMultipleFilesData(input, output, session, replace = TRUE)
```

**Arguments**

input	Shiny input
output	Shiny output
session	Shiny session
replace	Boolean: replace loaded data?

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

setOperation	<i>Perform set operations on selected groups</i>
--------------	--

---

**Description**

Perform set operations on selected groups

**Usage**

```
setOperation(  
  operation,  
  groups,  
  selected,  
  symbol = " ",  
  groupName = NULL,  
  first = NULL,  
  second = NULL,  
  matches = NULL,  
  type = "Samples",  
  assignColoursToGroups = FALSE  
)
```

**Arguments**

operation	Character: set operation
groups	Matrix: groups
selected	Integer: index of rows regarding selected groups
symbol	Character: Unicode symbol to visually indicate the operation performed
groupName	Character: group name (automatically created if NULL or "")
first	Character: identifiers of the first element (required when performing the complement operation)
second	Character: identifiers of the second element (required when performing the complement operation)
matches	Character: match between samples (as names) and subjects (as values)
type	Character: type of group where set operations are to be performed
assignColoursToGroups	Boolean: assign colours to new groups?

**Value**

Matrix containing groups (new group is in the first row)

---

setOperationIcon	<i>Create an icon based on set operations</i>
------------------	---

---

**Description**

Based on the [icon\(\)](#) function

**Usage**

```
setOperationIcon(name, class = NULL, ...)
```

**Arguments**

name	Character: icon name
class	Character: additional classes to customise the icon element
...	Extra arguments for the icon HTML element

**Value**

Icon element

---

showAlert	<i>Show or remove an alert</i>
-----------	--------------------------------

---

**Description**

Show or remove an alert

**Usage**

```
showAlert(  
  session,  
  ...,  
  title,  
  style = NULL,  
  dismissible = TRUE,  
  alertId = "alert",  
  iconName = NULL,  
  caller = NULL  
)  
  
successAlert(  
  session,  
  ...,  
  title = NULL,  
  dismissible = TRUE,  
  alertId = "success",  
  caller = NULL  
)  
  
errorAlert(  
  session,  
  ...,  
  title = NULL,  
  dismissible = TRUE,  
  alertId = "alert",  
  caller = NULL  
)  
  
warningAlert(  
  session,  
  ...,  
  title = NULL,  
  dismissible = TRUE,  
  alertId = "alert",  
  caller = NULL  
)  
  
removeAlert(output, alertId = "alert")
```

**Arguments**

session	Shiny session
---------	---------------

...	Arguments to render as elements of alert
title	Character: title
style	Character: style (error, warning or NULL)
dismissible	Boolean: is the alert dismissible?
alertId	Character: identifier
iconName	Character: icon name
caller	Character: caller module identifier
output	Shiny output

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

**See Also**

[showModal\(\)](#)

---

showGroupsTable      *Present groups table*

---

**Description**

Present groups table

**Usage**

```
showGroupsTable(type)
```

**Arguments**

type                  Character: type of groups (either Patients, Samples, ASevents or Genes)

**Value**

Matrix with groups ordered (or NULL if there are no groups)

---

sidebar	<i>Sidebar without a well</i>
---------	-------------------------------

---

**Description**

Modified version of `shiny::sidebarPanel` without a well

**Usage**

```
sidebar(..., width = 4)
```

**Arguments**

...	Output elements to include in the sidebar/main panel.
width	The width of the sidebar and main panel. By default, the sidebar takes up 1/3 of the width, and the main panel 2/3. The total width must be 12 or less.

**Value**

HTML elements

---

signifDigits	<i>Get number of significant digits</i>
--------------	---

---

**Description**

Get number of significant digits

**Usage**

```
signifDigits(n)
```

**Arguments**

n	Numeric: number to round
---	--------------------------

**Value**

Formatted number with a given number of significant digits

---

singleDiffAnalyses     *Perform statistical analysis on a given splicing event*

---

## Description

Perform statistical analyses on a given vector containing elements from different groups

## Usage

```
singleDiffAnalyses(  
  vector,  
  group,  
  threshold = 1,  
  step = 100,  
  analyses = c("wilcoxRankSum", "ttest", "kruskal", "levene", "fligner")  
)
```

## Arguments

vector	Numeric
group	Character: group of each element in the vector
threshold	Integer: minimum number of values per group
step	Numeric: number of events before the progress bar is updated (a bigger number allows for a faster execution)
analyses	Character: analyses to perform (see Details)

## Details

The following statistical analyses may be performed by including the respective string in the analysis argument:

- ttest - Unpaired t-test (2 groups)
- wilcoxRankSum - Wilcoxon Rank Sum test (2 groups)
- kruskal - Kruskal test (2 or more groups)
- levene - Levene's test (2 or more groups)
- fligner - Fligner-Killeen test (2 or more groups)

## Value

A row from a data frame with the results

---

sortCoordinates	<i>Sort coordinates for some event types</i>
-----------------	--

---

**Description**

Some programs sort the coordinates of specific event types differently. To make them all comparable across programs, the coordinates are ordered by increasing (plus strand) or decreasing order (minus strand)

**Usage**

```
sortCoordinates(events)
```

**Arguments**

events	List of data frames with alternative splicing events for a given program
--------	--

**Value**

List of data frames with alternative splicing events for a given program

---

startProcess	<i>Set the status of a process to style a given button</i>
--------------	--

---

**Description**

- startProcess: Style button to show a process is in progress
- endProcess: Style button to show a process finished; also, closes the progress bar (if closeProgressBar = TRUE) and prints the difference between the current time and time

**Usage**

```
startProcess(id)
```

```
endProcess(id, time = NULL, closeProgressBar = TRUE)
```

**Arguments**

id	Character: button identifier
time	POSIXct object: start time needed to show the interval time (if NULL, the time interval is not displayed)
closeProgressBar	Boolean: close progress bar?

**Value**

startProcess returns the start time of the process (may be used as the time argument to endProcess), whereas endProcess returns the difference between current time and time (or NULL if time is not specified)



---

startProgress	<i>Create, set and terminate a progress object</i>
---------------	--

---

**Description**

Create, set and terminate a progress object

**Usage**

```
startProgress(  
  message,  
  divisions,  
  global = if (isRunning()) sharedData else getHidden()  
)  
  
updateProgress(  
  message = "Loading...",  
  value = NULL,  
  max = NULL,  
  detail = NULL,  
  divisions = NULL,  
  global = if (isRunning()) sharedData else getHidden(),  
  console = TRUE  
)  
  
closeProgress(  
  message = NULL,  
  global = if (isRunning()) sharedData else getHidden()  
)
```

**Arguments**

message	Character: progress message
divisions	Integer: number of divisions in the progress bar
global	Shiny's global variable
value	Integer: current progress value
max	Integer: maximum progress value
detail	Character: detailed message
console	Boolean: print message to console?

**Details**

If divisions is not NULL, a progress bar starts with the given divisions. If value = NULL, the progress bar increments one unit; otherwise, the progress bar increments value.

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

 styleModal
 

---



---

*Create a modal window*


---

### Description

Create a modal window

### Usage

```
styleModal(
  session,
  title,
  ...,
  style = NULL,
  iconName = "exclamation-circle",
  footer = NULL,
  echo = FALSE,
  size = "medium",
  dismissButton = TRUE,
  caller = NULL
)
```

```
errorModal(session, title, ..., size = "small", footer = NULL, caller = NULL)
```

```
warningModal(session, title, ..., size = "small", footer = NULL, caller = NULL)
```

```
infoModal(session, title, ..., size = "small", footer = NULL, caller = NULL)
```

### Arguments

session	Shiny session
title	Character: title
...	Arguments passed on to <a href="#">shiny::modalDialog</a>
easyClose	If TRUE, the modal dialog can be dismissed by clicking outside the dialog box, or by pressing the Escape key. If FALSE (the default), the modal dialog can't be dismissed in those ways; instead it must be dismissed by clicking on a <code>modalButton()</code> , or from a call to <code>removeModal()</code> on the server.
fade	If FALSE, the modal dialog will have no fade-in animation (it will simply appear rather than fade in to view).
style	Character: style (NULL, warning, error or info)
iconName	Character: icon name
footer	HTML elements to use in footer
echo	Boolean: print to console?
size	Character: size of the modal (small, medium or large)
dismissButton	Boolean: show dismiss button in footer?
caller	Character: caller module identifier

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

**See Also**

[showAlert\(\)](#)

---

subjectMultiMatchWarning

*Helper text to explain what happens when a subject matches multiple samples when performing survival analysis*

---

**Description**

Helper text to explain what happens when a subject matches multiple samples when performing survival analysis

**Usage**

```
subjectMultiMatchWarning()
```

**Value**

Character

---

subsetGeneExpressionFromMatchingGenes

*Subset gene expression based on (full or partial) matching genes*

---

**Description**

Subset gene expression based on (full or partial) matching genes

**Usage**

```
subsetGeneExpressionFromMatchingGenes(geneExpr, gene)
```

**Arguments**

geneExpr	Data frame or matrix: gene expression
gene	Character: genes to look for

**Value**

Gene expression subset for the input genes

survdiffTerms

*Test Survival Curve Differences***Description**

Tests if there is a difference between two or more survival curves using the  $G^\rho$  family of tests, or for a single curve against a known alternative.

**Usage**

```
survdiffTerms(survTerms, ...)
```

**Arguments**

survTerms	survTerms object: survival terms obtained after running processSurvTerms (see examples)
...	Arguments passed on to <code>survival::survdiff</code>
	subset expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating which observation numbers are to be included (or excluded if negative), or a character vector of row names to be included. All observations are included by default.
	na.action a missing-data filter function. This is applied to the model.frame after any subset argument has been used. Default is <code>options()\$na.action</code> .
	rho a scalar parameter that controls the type of test.
	timefix process times through the <code>aeqSurv</code> function to eliminate potential roundoff issues.

**Value**

survfit object. See `survfit.object` for details. Methods defined for `survfit` objects are `print`, `plot`, `lines`, and `points`.

**Description**

This function implements the G-rho family of Harrington and Fleming (1982), with weights on each death of  $S(t)^\rho$ , where  $S(t)$  is the Kaplan-Meier estimate of survival. With  $\rho = 0$  this is the log-rank or Mantel-Haenszel test, and with  $\rho = 1$  it is equivalent to the Peto & Peto modification of the Gehan-Wilcoxon test.

Peto and Peto show that the Gehan-Wilcoxon test can be badly biased if the two groups have different censoring patterns, and proposed an alternative. Prentice and Marek later showed an actual example where this issue occurs. For most data sets the Gehan-Wilcoxon and Peto-Peto-Prentice variant will hardly differ, however.

If the right hand side of the formula consists only of an offset term, then a one sample test is done. To cause missing values in the predictors to be treated as a separate group, rather than being omitted, use the `factor` function with its `exclude` argument to recode the right-hand-side covariate.

## References

Harrington, D. P. and Fleming, T. R. (1982). A class of rank test procedures for censored survival data. *Biometrika*, 553-566.

Peto R. Peto and Peto, J. (1972) Asymptotically efficient rank invariant test procedures (with discussion), *JRSSA*, 185-206.

Prentice, R. and Marek, P. (1979) A qualitative discrepancy between censored data rank tests, *Biometrics*, 861-867.

## See Also

Other functions to analyse survival: [assignValuePerSubject\(\)](#), [getAttributesTime\(\)](#), [labelBasedOnCutoff\(\)](#), [optimalSurvivalCutoff\(\)](#), [plotSurvivalCurves\(\)](#), [plotSurvivalPvaluesByCutoff\(\)](#), [processSurvTerms\(\)](#), [survfit.survTerms\(\)](#), [testSurvival\(\)](#)

## Examples

```
clinical <- read.table(text = "2549  NA ii  female
                             840  NA i   female
                             NA 1204 iv  male
                             NA  383 iv  female
                             1293  NA iii male
                             NA 1355 ii  male")
names(clinical) <- c("patient.days_to_last_followup",
                    "patient.days_to_death",
                    "patient.stage_event.pathologic_stage",
                    "patient.gender")
timeStart <- "days_to_death"
event <- "days_to_death"
formulaStr <- "patient.stage_event.pathologic_stage + patient.gender"
survTerms <- processSurvTerms(clinical, censoring="right", event, timeStart,
                              formulaStr=formulaStr)
survdiffTerms(survTerms)
```

---

survfit.survTerms      *Create survival curves*

---

## Description

Create survival curves

## Usage

```
## S3 method for class 'survTerms'
survfit(formula, ...)
```

## Arguments

formula      survTerms object: survival terms obtained after running processSurvTerms (see examples)

...          Arguments passed on to [survival::survdiff](#)

`subset` expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating which observation numbers are to be included (or excluded if negative), or a character vector of row names to be included. All observations are included by default.

`na.action` a missing-data filter function. This is applied to the `model.frame` after any subset argument has been used. Default is `options()$na.action`.

`rho` a scalar parameter that controls the type of test.

`timefix` process times through the `aeqSurv` function to eliminate potential roundoff issues.

## Details

A survival curve is based on a tabulation of the number at risk and number of events at each unique death time. When time is a floating point number the definition of "unique" is subject to interpretation. The code uses `factor()` to define the set. For further details see the documentation for the appropriate method, i.e., `?survfit.formula` or `?survfit.coxph`.

A `survfit` object may contain a single curve, a set of curves (vector), a matrix of curves, or even a 3 way array: `dim(fit)` will reveal the dimensions. Predicted curves from a `coxph` model have one row for each stratum in the Cox model fit and one column for each specified covariate set. Curves from a multi-state model have one row for each stratum and a column for each state, the strata correspond to predictors on the right hand side of the equation. The default printing and plotting order for curves is by column, as with other matrices.

## Value

`survfit` object. See `survfit.object` for details. Methods defined for `survfit` objects are `print`, `plot`, `lines`, and `points`.

## See Also

Other functions to analyse survival: `assignValuePerSubject()`, `getAttributesTime()`, `labelBasedOnCutoff()`, `optimalSurvivalCutoff()`, `plotSurvivalCurves()`, `plotSurvivalPvaluesByCutoff()`, `processSurvTerms()`, `survdiffTerms()`, `testSurvival()`

## Examples

```
library("survival")
clinical <- read.table(text = "2549  NA ii  female
                             840  NA i   female
                             NA 1204 iv  male
                             NA  383 iv  female
                             1293  NA iii male
                             NA 1355 ii  male")
names(clinical) <- c("patient.days_to_last_followup",
                    "patient.days_to_death",
                    "patient.stage_event.pathologic_stage",
                    "patient.gender")
timeStart <- "days_to_death"
event <- "days_to_death"
formulaStr <- "patient.stage_event.pathologic_stage + patient.gender"
survTerms <- processSurvTerms(clinical, censoring="right", event, timeStart,
                              formulaStr=formulaStr)
```

```
survfit(survTerms)
```

---

t.sticky	<i>Preserve attributes of sticky objects when extracting or transposing object</i>
----------	--

---

### Description

Most attributes - with the exception of names, dim, dimnames, class and row.names - are preserved in simple transformations of objects from class sticky

### Usage

```
## S3 method for class 'sticky'
t(x)

## S3 method for class 'sticky'
x[i, j, ...]
```

### Arguments

x	Object
i, j, ...	Numeric or character: indices of elements to extract

### Value

Transformed object with most attributes preserved

---

tabDataset	<i>Creates a tabPanel template for a datatable with a title and description</i>
------------	---

---

### Description

Creates a tabPanel template for a datatable with a title and description

### Usage

```
tabDataset(
  ns,
  title,
  tableId,
  columns,
  visCols,
  data,
  description = NULL,
  icon = NULL
)
```

**Arguments**

ns	Namespace function
title	Character: tab title
tableId	Character: id of the datatable
columns	Character: column names of the datatable
visCols	Boolean: visible columns
data	Data frame: dataset of interest
description	Character: description of the table (optional)
icon	Character: list containing an item named symbol (FontAwesome icon name) and another one named colour (background colour)

**Value**

HTML elements

---

table2html	<i>Create HTML table from data frame or matrix</i>
------------	--

---

**Description**

Create HTML table from data frame or matrix

**Usage**

```
table2html(
  data,
  rownames = TRUE,
  colnames = TRUE,
  class = NULL,
  style = NULL,
  thead = FALSE
)
```

**Arguments**

data	Data frame or matrix
rownames	Boolean: print row names?
colnames	Boolean: print column names?
class	Character: table class
style	Character: table style
thead	Boolean: add a thead tag to the first row?

**Value**

HTML elements



---

tableRow	<i>Create a row for a HTML table</i>
----------	--------------------------------------

---

**Description**

Create a row for a HTML table

**Usage**

```
tableRow(..., th = FALSE)
```

**Arguments**

...	Elements to include in the row
th	Boolean: is this row the table head?

**Value**

HTML elements

---

testGroupIndependence	<i>Multiple independence tests between reference groups and list of groups</i>
-----------------------	--

---

**Description**

Test multiple contingency tables comprised by two groups (one reference group and another containing remaining elements) and provided groups.

**Usage**

```
testGroupIndependence(ref, groups, elements, pvalueAdjust = "BH")
```

**Arguments**

ref	List of character: list of groups where each element contains the identifiers of respective elements
groups	List of characters: list of groups where each element contains the identifiers of respective elements
elements	Character: all available elements (if a data frame is given, its rownames will be used)
pvalueAdjust	Character: method used to adjust p-values (see Details)

**Details**

The following methods for p-value adjustment are supported by using the respective string in the `pvalueAdjust` argument:

- `none`: Do not adjust p-values
- `BH`: Benjamini-Hochberg's method (false discovery rate)
- `BY`: Benjamini-Yekutieli's method (false discovery rate)
- `bonferroni`: Bonferroni correction (family-wise error rate)
- `holm`: Holm's method (family-wise error rate)
- `hochberg`: Hochberg's method (family-wise error rate)
- `hommel`: Hommel's method (family-wise error rate)

**Value**

`multiGroupIndependenceTest` object, a data frame containing:

<code>attribute</code>	Name of the original groups compared against the reference groups
<code>table</code>	Contingency table used for testing
<code>pvalue</code>	Fisher's exact test's p-value

**See Also**

[parseCategoricalGroups\(\)](#) and [plotGroupIndependence\(\)](#)

Other functions for data grouping: [createGroupByAttribute\(\)](#), [getGeneList\(\)](#), [getSampleFromSubject\(\)](#), [getSubjectFromSample\(\)](#), [groupPerElem\(\)](#), [plotGroupIndependence\(\)](#)

**Examples**

```
elements <- paste("subjects", 1:10)
ref       <- elements[5:10]
groups   <- list(race=list(asian=elements[1:3],
                          white=elements[4:7],
                          black=elements[8:10]),
                region=list(european=elements[c(4, 5, 9)],
                            african=elements[c(6:8, 10)]))
groupTesting <- testGroupIndependence(ref, groups, elements)
# View(groupTesting)
```

---

`testSingleIndependence`

*Multiple independence tests between a reference group and list of groups*

---

**Description**

Uses Fisher's exact test.

**Usage**

```
testSingleIndependence(ref, groups, elements, pvalueAdjust = "BH")
```

**Arguments**

ref	Character: identifier of elements in reference group
groups	List of characters: list of groups where each element contains the identifiers of respective elements
elements	Character: all subject identifiers
pvalueAdjust	Character: method used to adjust p-values (see Details)

**Details**

The following methods for p-value adjustment are supported by using the respective string in the pvalueAdjust argument:

- none: Do not adjust p-values
- BH: Benjamini-Hochberg's method (false discovery rate)
- BY: Benjamini-Yekutieli's method (false discovery rate)
- bonferroni: Bonferroni correction (family-wise error rate)
- holm: Holm's method (family-wise error rate)
- hochberg: Hochberg's method (family-wise error rate)
- hommel: Hommel's method (family-wise error rate)

**Value**

Returns a groupIndependenceTest object: a list where each element is a list containing:

attribute	Name of the original groups compared against the reference groups
table	Contingency table used for testing
pvalue	Fisher's exact test's p-value

---

testSurvival	<i>Test the survival difference between groups of subjects</i>
--------------	--

---

**Description**

Test the survival difference between groups of subjects

**Usage**

```
testSurvival(survTerms, ...)
```

**Arguments**

survTerms	survTerms object: survival terms obtained after running processSurvTerms (see examples)
...	Arguments passed on to <a href="#">survival::survdiff</a>

`subset` expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating which observation numbers are to be included (or excluded if negative), or a character vector of row names to be included. All observations are included by default.

`na.action` a missing-data filter function. This is applied to the `model.frame` after any `subset` argument has been used. Default is `options()$na.action`.

`rho` a scalar parameter that controls the type of test.

`timefix` process times through the `aeqSurv` function to eliminate potential roundoff issues.

### Value

p-value of the survival difference or NA

### Note

Instead of raising errors, returns NA

### See Also

Other functions to analyse survival: [assignValuePerSubject\(\)](#), [getAttributesTime\(\)](#), [labelBasedOnCutoff\(\)](#), [optimalSurvivalCutoff\(\)](#), [plotSurvivalCurves\(\)](#), [plotSurvivalPvaluesByCutoff\(\)](#), [processSurvTerms\(\)](#), [survdiffTerms\(\)](#), [survfit.survTerms\(\)](#)

### Examples

```
require("survival")
data <- aml
timeStart <- "event"
event <- "event"
followup <- "time"
data$event <- NA
data$event[aml$status == 1] <- aml$time[aml$status == 1]
censoring <- "right"
formulaStr <- "x"
survTerms <- processSurvTerms(data, censoring=censoring, event=event,
                             timeStart=timeStart, followup=followup,
                             formulaStr=formulaStr)

testSurvival(survTerms)
```

---

testSurvivalCutoff      *Test the survival difference between two survival groups given a cutoff*

---

### Description

Test the survival difference between two survival groups given a cutoff

**Usage**

```
testSurvivalCutoff(
  cutoff,
  data,
  filter = TRUE,
  clinical,
  ...,
  session = NULL,
  survivalInfo = FALSE
)
```

**Arguments**

cutoff	Numeric: Cutoff of interest
data	Numeric: elements of interest to test against the cutoff
filter	Boolean or numeric: elements to use (all are used by default)
clinical	Data frame: clinical data
...	Arguments passed on to <a href="#">processSurvTerms</a>
censoring	Character: censor using left, right, interval or interval2
scale	Character: rescale the survival time to days, weeks, months or years
formulaStr	Character: formula to use
coxph	Boolean: fit a Cox proportional hazards regression model?
survTime	survTime object: times to follow up, time start, time stop and event (optional)
event	Character: name of column containing time of the event of interest
timeStart	Character: name of column containing starting time of the interval or follow up time
timeStop	Character: name of column containing ending time of the interval (only relevant for interval censoring)
followup	Character: name of column containing follow up time
session	Shiny session
survivalInfo	Boolean: return extra survival information

**Value**

p-value of the survival difference

---

textSuggestions	<i>Create script for auto-completion of text input</i>
-----------------	--

---

**Description**

Uses the JavaScript library `jquery.textcomplete`

**Usage**

```
textSuggestions(id, words, novalue = "No matching value", char = " ")
```

**Arguments**

id	Character: input ID
words	Character: words to suggest
novalue	Character: string when there's no matching values
char	Character to succeed accepted word

**Value**

HTML string with the JavaScript script prepared to run

**Examples**

```
words <- c("tumor_stage", "age", "gender")
psychomics:::textSuggestions("textareaid", words)
```

---

toJSarray	<i>Convert vector of values to JavaScript array</i>
-----------	---

---

**Description**

Convert vector of values to JavaScript array

**Usage**

```
toJSarray(values)
```

**Arguments**

values	Character vector
--------	------------------

**Value**

Character with valid JavaScript array

---

traceInList	<i>Find an item in list of lists and return its coordinates</i>
-------------	---

---

**Description**

Find an item in list of lists and return its coordinates

**Usage**

```
traceInList(ll, item)
```

---

transformData	<i>Transform data in data frame</i>
---------------	-------------------------------------

---

**Description**

Transform data in data frame

**Usage**

```
transformData(input, df, x, y)
```

**Arguments**

input	Shiny input
df	Data frame
x	Character: column name
y	Character: column name

**Value**

Data frame with transformed data in new columns and respective name of created columns

---

transformOptions	<i>Show variable transformation(s)</i>
------------------	--

---

**Description**

Show variable transformation(s)

**Usage**

```
transformOptions(label, type = NULL)
```

**Arguments**

label	Character: label to display
type	Character: show the variable transformation for the chosen type; if NULL, show all variable transformations

**Value**

Character labelling variable transformation(s)

---

transformValues	<i>Transform values as per a given type of transformation</i>
-----------------	---

---

**Description**

Transform values as per a given type of transformation

**Usage**

```
transformValues(val, type, avoidZero = TRUE)
```

**Arguments**

val	Integer: values to transform
type	Character: type of transformation
avoidZero	Boolean: add the smallest non-zero number available ( <code>.Machine\$double.xmin</code> ) to avoid infinity values following log-transformation (may not be plotted); useful for p-values of 0

**Value**

Integer containing transformed values

---

trimWhitespace	<i>Trims whitespace from a word</i>
----------------	-------------------------------------

---

**Description**

Trims whitespace from a word

**Usage**

```
trimWhitespace(word)
```

**Arguments**

word	Character to trim
------	-------------------

**Value**

Character without whitespace

**Examples**

```
psychomics::trimWhitespace(" hey there ")
psychomics::trimWhitespace(c("pineapple ", "one two three",
                             " sunken ship "))
```



---

uniqueBy	<i>Check unique rows of a data frame based on a set of its columns</i>
----------	--

---

**Description**

Check unique rows of a data frame based on a set of its columns

**Usage**

```
uniqueBy(data, ...)
```

**Arguments**

data	Data frame or matrix
...	Name of columns

**Value**

Data frame with unique values based on set of columns

---

updateClinicalParams	<i>Update available clinical attributes when the clinical data changes</i>
----------------------	--

---

**Description**

Update available clinical attributes when the clinical data changes

**Usage**

```
updateClinicalParams(session, attrs)
```

**Arguments**

session	Shiny session
attrs	Character: subject attributes

**Value**

NULL (function is only used to modify the Shiny session's state or internal variables)

---

```
updateFileBrowserInput
```

*Change the value of a `fileBrowserInput()` on the client*

---

### Description

Change the value of a `fileBrowserInput()` on the client

### Usage

```
updateFileBrowserInput(session, id, ..., value = NULL, ask = FALSE)
```

### Arguments

<code>session</code>	Shiny session
<code>id</code>	Character: identifier
<code>...</code>	Additional arguments passed to <code>fileBrowser()</code> . Only used if <code>value = NULL</code> .
<code>value</code>	Character: file or directory path
<code>ask</code>	Boolean: ask user to pick a file using file browser?

### Details

Sends a message to the client, telling it to change the value of the input object. For `fileBrowserInput()` objects, this changes the value displayed in the text-field and triggers a client-side change event. A directory selection dialogue is not displayed.

### Value

NULL (function is only used to modify the Shiny session's state or internal variables)

### Source

<https://github.com/wleepang/shiny-directory-input>

---

```
vennEvents
```

*Compare the number of events from the different programs in a Venn diagram*

---

### Description

Compare the number of events from the different programs in a Venn diagram

### Usage

```
vennEvents(join, eventType)
```

### Arguments

<code>join</code>	List of lists of data frame
<code>eventType</code>	Character: type of event

**Value**

Venn diagrams for a given event type

---

wilcox

*Perform and display statistical analysis*

---

**Description**

Includes interface containing the results

**Usage**

```
wilcox(data, groups, stat = NULL)
```

```
ttest(data, groups, stat = NULL)
```

```
levene(data, groups, stat = NULL)
```

```
fligner(data, groups, stat = NULL)
```

```
kruskal(data, groups, stat = NULL)
```

```
fisher(data, groups)
```

```
spearman(data, groups)
```

**Arguments**

data	Numeric, data frame or matrix: gene expression data or alternative splicing event quantification values (sample names are based on their names or colnames)
groups	List of sample names or vector containing the group name per data value (read Details); if NULL or a character vector of length 1, data values are considered from the same group
stat	Data frame or matrix: values of the analyses to be performed (if NULL, the analyses will be performed)

**Details**

- ttest: unpaired t-test
- wilcox: Wilcoxon test
- levene: Levene's test
- fligner: Fligner-Killeen test
- kruskal: Kruskal test
- fisher: Fisher's exact test
- spearman: Spearman's test

**Value**

HTML elements

---

[.GEandAScorrelation *Display results of correlation analyses*

---

### Description

Plot, print and display as table the results of gene expression and alternative splicing

### Usage

```
## S3 method for class 'GEandAScorrelation'
x[genes = NULL, ASevents = NULL]
```

```
## S3 method for class 'GEandAScorrelation'
plot(
  x,
  autoZoom = FALSE,
  loessSmooth = TRUE,
  loessFamily = c("gaussian", "symmetric"),
  colour = "black",
  alpha = 0.2,
  size = 1.5,
  loessColour = "red",
  loessAlpha = 1,
  loessWidth = 0.5,
  fontSize = 12,
  ...,
  colourGroups = NULL,
  legend = FALSE,
  showAllData = TRUE,
  density = FALSE,
  densityColour = "blue",
  densityWidth = 0.5
)
```

```
## S3 method for class 'GEandAScorrelation'
print(x, ...)
```

```
## S3 method for class 'GEandAScorrelation'
as.table(x, pvalueAdjust = "BH", ...)
```

### Arguments

x	GEandAScorrelation object obtained after running <a href="#">correlateGEandAS()</a>
genes	Character: genes
ASevents	Character: AS events
autoZoom	Boolean: automatically set the range of PSI values based on available data? If FALSE, the axis relative to PSI values will range from 0 to 1
loessSmooth	Boolean: plot a smooth curve computed by <code>stats::loess.smooth?</code>
loessFamily	Character: if gaussian, loess fitting is by least-squares, and if symmetric, a re-descending M estimator is used

colour	Character: points' colour
alpha	Numeric: points' alpha
size	Numeric: points' size
loessColour	Character: loess line's colour
loessAlpha	Numeric: loess line's opacity
loessWidth	Numeric: loess line's width
fontSize	Numeric: plot font size
...	Arguments passed on to <code>stats::loess.smooth</code> span smoothness parameter for loess. degree degree of local polynomial used. evaluation number of points at which to evaluate the smooth curve.
colourGroups	List of characters: sample colouring by group
legend	Boolean: show legend for sample colouring?
showAllData	Boolean: show data outside selected groups as a single group (coloured based on the colour argument)
density	Boolean: contour plot of a density estimate
densityColour	Character: line colour of contours
densityWidth	Numeric: line width of contours
pvalueAdjust	Character: method used to adjust p-values (see Details)

### Details

The following methods for p-value adjustment are supported by using the respective string in the `pvalueAdjust` argument:

- none: do not adjust p-values
- BH: Benjamini-Hochberg's method (false discovery rate)
- BY: Benjamini-Yekutieli's method (false discovery rate)
- bonferroni: Bonferroni correction (family-wise error rate)
- holm: Holm's method (family-wise error rate)
- hochberg: Hochberg's method (family-wise error rate)
- hommel: Hommel's method (family-wise error rate)

### Value

Plots, summary tables or results of correlation analyses

### See Also

Other functions to correlate gene expression and alternative splicing: [correlateGEandAS\(\)](#)

Other functions to correlate gene expression and alternative splicing: [correlateGEandAS\(\)](#)

**Examples**

```
annot <- readfile("ex_splicing_annotation.RDS")
junctionQuant <- readfile("ex_junctionQuant.RDS")
psi <- quantifySplicing(annot, junctionQuant, eventType=c("SE", "MXE"))

geneExpr <- readfile("ex_gene_expression.RDS")
corr <- correlateGEandAS(geneExpr, psi, "ALDOA")

# Quick display of the correlation results per splicing event and gene
print(corr)

# Table summarising the correlation analysis results
as.table(corr)

# Correlation analysis plots
colourGroups <- list(Normal=paste("Normal", 1:3),
                    Tumour=paste("Cancer", 1:3))
attr(colourGroups, "Colour") <- c(Normal="#00C65A", Tumour="#EEE273")
plot(corr, colourGroups=colourGroups, alpha=1)
```

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