Package 'psichomics'

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Title Graphical Interface for Alternative Splicing Quantification, Analysis and Visualisation

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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

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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'

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Contents

.onAttach *Print startup message*

Description

Print startup message

Usage

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

Arguments

libname	Character: library name
pkgname	Character: package name

Value

Startup message

addObjectAttrs *Set attributes to an object*

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")
psichomics:::addObjectAttrs(ll, "words"=2, "language"="English")
```

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

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 *Append new groups to already existing groups*

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 *Check if string identifies splicing events*

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 *Return the interface to display an article*

Description

Return the interface to display an article

Usage

```
articleUI(article)
```

Arguments

article	PubMed article

Value

HTML to render an article's interface

assignColours *Assign colours to groups*

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` *Basic statistics performed on data*

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` *Blend two HEX colours*

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 `((Cx * Ex) + (Cy * Ey))/(Ex + Ey)`, where:

- `Cx` and `Cy` are the contributions of a variable to principal components `x` and `y`
- `Ex` and `Ey` 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 *Checks the format of a file*

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 *Return an user interface depending on the status of the FireBrowse API*

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 *Check type of groups within file*

Description

Check type of groups within file

Usage

```
checkGroupType(file)
```

Arguments

file	Character: file path

Value

Type of group: Samples, ASevents or NULL

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

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 *Prepare survival terms in case of valid input*

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)

clusterICAset *Server logic for clustering ICA data*

Description

Server logic for clustering ICA data

Usage

```
clusterICAset(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 *Server logic for clustering PCA data*

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 *Modified colour input with 100% width*

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 `.colSums()` 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 number: Which dimensions are regarded as 'rows' or 'columns' to sum over. For `row*`, the sum or mean is over dimensions `dims+1, ...`; for `col*` it is over dimensions `1:dims`.

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("ENSG00000012048", "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 cor.test

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 geom_point() 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 geom_point() related to highlighted points
selected	Integer: index of rows/points to be coloured
selectedParams	List of parameters to pass to geom_point() related to selected points
labelled	Integer: index of rows/points to be labelled
labelledParams	List of parameters to pass to ggrepel::geom_label_repel 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

```
psichomics:::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` *Create sparkline charts to be used in a data table*

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 *Calculate statistics for each row or column of a matrix*

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))
psichomics:::customRowMeans(df)
psichomics:::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 *Set of functions to perform differential analyses*

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` *Enable or disable a tab from the* `navbar`

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 https://github.com/vastgroup/vast-tools 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` *Display characters in the command-line*

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 *Download files to a given directory*

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)
psichomics:::downloadFiles(url, "~/Pictures")

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

## End(Not run)
```

ensemblToUniprot *Convert from Ensembl to UniProt identifier*

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 *Escape symbols for use in regular expressions*

Description

Escape symbols for use in regular expressions

Usage

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

Arguments

...	Characters to be pasted with no space

Value

Escaped string

eventPlotOptions *Options for event plotting*

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 *Interactive folder selection using a native dialogue*

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 path.expand())
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. shinyBS::bsTooltip and shinyBS::bsPopover)
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 filterByExpr 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 <- readFile("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 `getSplicingEventTypes(psi)`, where `psi` is the alternative splicing quantification data; if `eventType = NULL`, 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 `unique(getSplicingEventData(psi)$subtype)`, where `psi` is the alternative splicing quantification data; if `eventSubtype = NULL`, 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 log10(PSI variance) per splicing event
maxLogVar	Numeric: maximum log10(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

psi	Data frame or matrix: alternative splicing quantification
gene	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

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

Value

Event data (or NULL if not found)

geneExprFileInput *File input for molecular data*

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 *Logic set to perform survival analysis based on gene expression cutoffs*

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 *Get global data*

Description

Get global data

Usage

```
getData()
```

Value

Variable containing all data of interest

getDataRows *Get rows of a data frame between two row indexes*

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` *Get the path to the Downloads folder*

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 <- psichomics:::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()
```

getGlobal *Get or set globally accessible elements*

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 *Get or set groups*

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 *Get GTEx data information*

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` *Get or set hidden globally accessible elements*

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` *Get or set points or regions for plots*

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

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, `c("data", "analyses")` 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 *Get available parameters for TCGA data*

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 *Matches user interface (UI) functions from a given loader*

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 *Filters the events with valid elements according to the given validator*

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))
psichomics:::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 *Create the interface for the tooltip of a plot*

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 hoverOpts
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 *Data grouping interface*

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 *Logic server to manipulate data grouping*

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 *Server function for data grouping (one call)*

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 *Plot survival curves*

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 survfit.survTerms() function
...	Arguments passed on to highcharter::hc_add_series
fun	Name of function or function used to transform the survival curve: log will put y axis on log scale, event plots cumulative events (f(y) = 1-y), cumhaz plots the cumulative hazard function (f(y) = -log(y)), and cloglog 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 highcharter::hc_add_series

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 *Import groups from a file*

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`
Interface to filter alternative splicing

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 *Get psichomics file inside a given directory*

Description

Get psichomics 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 *Check if a number is whole*

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 *Check if files exist*

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 *Check if* R*hrefhttp://firebrowse.org/api-docs/FireBrowse API is running*

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 *Check if running in RStudio Server*

Description

Check if running in RStudio Server

Usage

```
isRStudioServer()
```

Value

Boolean stating whether running in RStudio Server

joinEventsPerType *Full outer join all given events based on select columns*

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 *String used to search for matches in a junction quantification file*

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 *Label groups based on a given cutoff*

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)
psichomics:::leveneTest(vals, group)

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

---

linkToArticles *psichomics article's link interface*

Description

psichomics article's link interface

Usage

```
linkToArticles()
```

Value

HTML elements

---

linkToRunJS *Link to run arbitrary JavaScript code*

Description

Link to run arbitrary JavaScript code

Usage

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

Arguments

text	Character: text label
code	Character: JavaScript code

Value

HTML elements

---

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

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

```
psichomics:::listAllAnnotations()
```

---

listSplicingAnnotations *List alternative splicing annotations*

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 *Load alternative splicing annotation from* AnnotationHub

---

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 *Load AnnotationHub*

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

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 *Load file based on its format*

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 fread
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` *Load supported file formats*

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 *Download and load GTEx data*

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 getGtexDataTypes)
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 *Load local files*

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 *Missing information modal template*

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

Set of functions to load splicing quantification

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

Download and load SRA projects via R*hrefhttps://jhubiostatistics.shinyapps.io/recount/recount2*

Description

Download and load SRA projects via recount2

Usage

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

Arguments

project	Character: SRA project identifiers (check recount_abstract)
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 *Download and process TCGA data*

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 getDownloadsFolder())
data	Character: data to load (see getTCGAdataTypes())
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 queryFirebrowseData
	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 *Modified* tabPanel *function to show icon and title*

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` *Create a special* `selectize` *input in the navigation bar*

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 voom)?

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

---

onCollapseOpen *On collapse observer*

Description

Adds a JavaScript listener to a Bootstrap collapse panel so that when it is shown, a Shiny input value is updated with the provided label.

Usage

```
onCollapseOpen(id)
```

Arguments

`id`	The ID of the collapse panel.

Value

A `tags$script` object containing the JavaScript listener.

---

operateOnGroups *Set operations on groups*

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

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 fread
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

```
psichomics:::parseFirebrowseMetadata("Dates")
psichomics:::parseFirebrowseMetadata("Centers")
psichomics:::parseFirebrowseMetadata("HeartBeat")

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

`parseMatsEvent` *Parse alternative splicing events from MATS*

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
")
psichomics:::parseMatsEvent(event, "A3SS")
```

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

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)
psichomics:::parseMatsGeneric(junctions, strand = "+", coords, plus, minus)

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

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

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

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

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

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

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

```
psichomics:::parseMatsAFE(junctions, strand = "+")
```

`parseMisoEvent` *Parse an alternative splicing event from MISO*

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 . - .")
psichomics:::parseMisoEvent(event)
```

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

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="psichomics")
annotation <- read.delim(gff3, header=FALSE, comment.char="#")
IDcolumn <- 9
psichomics:::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 . - .")
psichomics:::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 . + .")
psichomics:::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 . - .")
psichomics:::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 . - .")
psichomics:::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 . - .")
psichomics:::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  .  -  .")
psichomics:::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  .  +  .")
psichomics:::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  .  +  .")
psichomics:::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:+")
psichomics:::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="psichomics")

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

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

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

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:-"
psichomics:::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
psichomics:::parseSuppaGeneric(junctions, strand = "+", coords, plus, minus)

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

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

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

junctions <- read.table(
    text = "169763871 169764046 169767998 169764550 169765124 169767998")
```

```
psichomics:::parseSuppaAFE(junctions, "+")

junctions <- read.table(
   text = "202060671 202068453 202068489 202073793 202060671 202072798 202072906 202073793")
psichomics:::parseSuppaMXE(junctions, "+")

junctions <- read.table(text = "169772450 169773216 169772450 169773253")
psichomics:::parseSuppaA3SS(junctions, "+")

junctions <- read.table(text = "50193276 50197008 50192997 50197008")
psichomics:::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 = "psichomics")
)

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 *Parse XML from UniProt REST service*

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 *Retrieve URLs from a response to a FireBrowse data query*

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 <- psichomics:::queryFirebrowseData(cohort = "ACC")
url <- psichomics:::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"
)
psichomics:::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")
psichomics:::parseVastToolsSE(junctions)

# these functions are vectorised!
junctions <- read.table(text = "41040823 41046768 41046903 41051785
```

```
                                58864658 58864693 58864294 58864563")
psichomics:::parseVastToolsSE(junctions)

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

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

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

`performICA` *Perform independent component analysis after processing missing values*

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 `model.frame`) containing the variables in the formula `formula`. By default the variables are taken from `environment(formula)`.
`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 `scale`.

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 scale.
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 alg.typ == "parallel" the components are extracted simultaneously (the default). if alg.typ == "deflation" 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 fun == "logcosh"
...	Arguments passed on to fastICA::fastICA

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

data	an optional data frame (or similar: see model.frame) containing the variables in the formula formula. By default the variables are taken from environment(formula).
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 scale.
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 scale.
missingValues	Integer: number of tolerated missing values per column to be replaced with the mean of the values of that same column
...	Arguments passed on to stats::prcomp

Value

PCA result in a prcomp object

See Also

Other functions to analyse principal components: calculateLoadingsContribution(), plotPCA(), plotPCAvariance()

Examples

```
performPCA(USArrests)
```

---

plotClusters *Add clusters to* highchart *object*

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` *Plot sample distribution*

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 `stats::density.default` `bw` 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.) `bw` can also be a character string giving a rule to choose the bandwidth. See `bw.nrd`. 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). The specified (or computed) value of `bw` is multiplied by `adjust`.

`adjust` the bandwidth used is actually `adjust*bw`. 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` numeric vector of non-negative observation weights, hence of same length as `x`. The default `NULL` is equivalent to `weights = rep(1/nx, nx)` where `nx` is the length of (the finite entries of) `x[]`. If `na.rm = TRUE` and there are `NA`'s in `x`, they *and* 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.
Note that weights are *not* taken into account for automatic bandwidth rules, i.e., when `bw` is a string. When the weights are proportional to true counts `cn`, `density(x = rep(x, cn))` may be used instead of `weights`.

`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, *no* density is estimated, and the 'canonical bandwidth' of the chosen `kernel` is returned instead.

`subdensity` used only when `weights` are specified which do not sum to one. When true, it indicates that a "sub-density" is desired and no warning should be signalled. By default, when false, a `warning` is signalled when the weights do not sum to one.

`warnWbw` `logical`, used only when `weights` are specified *and* `bw` is `character`, i.e., automatic bandwidth selection is chosen (as by default). When true (as by default), a `warning` 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 `fft` is used) and the final result is interpolated by `approx`. 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 `cut * bw` outside of `range(x)`.

`cut` by default, the values of `from` and `to` are `cut` bandwidths beyond the extremes of the data. This allows the estimated density to drop to approximately zero at the extremes.

`ext` a positive extension factor, `4` by default. The values `from` and `to` are further extended on both sides to `lo <- from - ext * bw` and `up <- to + ext * bw` which are then used to build the grid used for the FFT and interpolation, see `n` above. Do not change unless you know what you are doing!

`old.coords` `logical` to require pre-R 4.4.0 behaviour which gives too large values by a factor of about $(1 + 1/(2n - 2))$.

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, psi = TRUE 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 `renderBoxplot` `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* -log10(p-values) *of the results obtained after multiple group independence testing*

Description

Plot -log10(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 testGroupIndependence())
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

`ica`	Object resulting from `performICA()`
`components`	Numeric: independent components to plot
`groups`	Matrix: groups to plot indicating the index of interest of the samples (use clinical or sample groups)
`...`	Arguments passed on to `pairsD3::pairsD3` `group` a optional vector specifying the group each observation belongs to. Used for tooltips and colouring the observations. `subset` 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. `labels` the names of the variables (column names of `x` used by default). `cex` the magnification of the plotting symbol (default=3) `width` the width (and height) of the plot when viewed externally. `col` an optional (hex) colour for each of the levels in the group vector. `big` a logical parameter. Prevents inadvertent plotting of huge data sets. Default limit is 10 variables, to plot more than 10 set `big=TRUE`. `theme` a character parameter specifying whether the theme should be colour `colour` (default) or black and white `bw`. `opacity` numeric between 0 and 1. The opacity of the plotting symbols (default 0.9).

`tooltip` an optional vector with the tool tip to be displayed when hovering over an observation. You can include basic html.

`leftmar` space on the left margin

`topmar` space on the bottom margin

`diag` 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 *Plot library size*

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 *Create the explained variance plot from a PCA*

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 *Interface to modify the style of the plot points*

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 *Plot protein features*

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 log10(mean). If y = 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. log10(var)); if y = 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)
psichomics:::plotSingleICA(ica)
psichomics:::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")
psichomics:::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 <- readFile("ex_splicing_annotation.RDS")
junctionQuant <- readFile("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 *Plot transcripts*

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="psichomics")

# 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="psichomics")

# 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 `fileBrowser` `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 psichomics*

Description

Prepare user-provided files to be loaded into psichomics

Usage

```
prepareSRAmetadata(file, output = "psichomics_metadata.txt")

prepareJunctionQuant(
  ...,
  output = "psichomics_junctions.txt",
  startOffset = NULL,
  endOffset = NULL
)

prepareGeneQuant(
  ...,
  output = "psichomics_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 *Create word break opportunities (for HTML) using given characters*

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 *Preserve attributes when extracting values*

Description

Add object to class sticky

Usage

```
preserveAttributes(x)
```

Arguments

x	Object

Value

Object with class sticky

---

processButton *Style button used to initiate a process*

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 shiny::actionButton icon An optional icon() to appear on the button. width The width of the input, e.g. '400px', or '100%'; see validateCssUnit(). disabled If TRUE, the button will not be clickable. Use updateActionButton() to dynamically enable/disable the button.
class	Character: class

Value

HTML for a button

---

processDatasetNames *Process dataset names*

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 *Check if survival analyses successfully completed or returned errors*

Description

Check if survival analyses successfully completed or returned errors

Usage

```
processSurvival(session, ...)
```

Arguments

session	Shiny session
...	Arguments passed on to processSurvTerms
	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

`processSurvTerms` *Process survival curves terms to calculate survival curves*

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

`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)
group	Character: group relative to each subject
formulaStr	Character: formula to use
coxph	Boolean: fit a Cox proportional hazards regression model?
scale	Character: rescale the survival time to days, weeks, months or years
followup	Character: name of column containing follow up time
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

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)
}
```

`psichomics` *Start graphical interface of psichomics*

Description

Start graphical interface of psichomics

Usage

```
psichomics(
  ...,
  launch.browser = TRUE,
  shinyproxy = FALSE,
  testData = FALSE,
  cache = getAnnotationHubOption("CACHE")
)
```

Arguments

`...`	Arguments passed on to `shiny::runApp` `port` The TCP port that the application should listen on. If the `port` is not specified, and the `shiny.port` option is set (with `options(shiny.port = XX)`), 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 `shiny.host` 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 `shiny.testmode` 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:
psichomics()

## 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 queryPubMed 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 *Quantify alternative splicing events*

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 <- readFile("ex_splicing_annotation.RDS")
junctionQuant <- readFile("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")
psichomics:::queryEnsembl(path, query, grch37 = TRUE)

path  <- "lookup/symbol/human/BRCA2"
query <- list(expand=1)
psichomics:::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]
psichomics:::queryFirebrowseData(cohort = names(cohort),
                                 data_type = "mRNASeq")

# Querying for data from a specific date
dates <- getTCGAdates()
dates <- format(dates, psichomics:::getFirebrowseDateFormat()$query)

psichomics:::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

```
psichomics:::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"
psichomics:::queryUniprot(protein, format)

transcript <- "ENST00000488540"
format <- "xml"
psichomics:::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 *Load psichomics-specific file*

Description

Load psichomics-specific file

Usage

```
readFile(file)
```

Arguments

file	Character: path to the file

Value

Loaded file

Examples

```
junctionQuant <- readFile("ex_junctionQuant.RDS")
```

---

reduceDimensionality *Reduce dimensionality after processing missing values from data frame*

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)),
  ...
)
```

Arguments

data	Data frame: data
type	Character: dimensionality reduction technique (pca or ica)
center	either a logical value or numeric-alike vector of length equal to the number of columns of x, where 'numeric-alike' means that as.numeric(.) will be applied successfully if is.numeric(.) is not true.
scale.	Boolean: scale variables?
naTolerance	Integer: percentage of tolerated missing values per column (deprecated)
missingValues	Integer: number of tolerated missing values per column to be replaced with the mean of the values of that same column
...	Extra parameters passed to FUN

Value

PCA result in a prcomp object or ICA result object

---

renameDuplicated *Rename vector to avoid duplicated values with another vector*

Description

Renames values by adding an index to the end of duplicates. This allows to prepare unique values in two vectors before a merge, for instance.

Usage

```
renameDuplicated(check, comp)
```

Arguments

check	Character: values to rename if duplicated
comp	Character: values to compare with

Value

Character vector with renamed values if duplicated; else, it returns the usual values. It does not return the comparator values.

Examples

```
psichomics:::renameDuplicated(check = c("blue", "red"), comp = c("green",
                                                                 "blue"))
```

renameGroups *Rename duplicated names from a new group*

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 *Render boxplot*

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 *Render protein information*

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 *Replace a string with another in a list*

Description

Replace a string with another in a list

Usage

```
replaceStrInList(tag, old, new)
```

rm.null *Filter* NULL *elements from a vector or a list*

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 *Round by the given number of digits*

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` *Round down/up the minimum/maximum value*

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` *Save processed SRA data in file*

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 *Group selection*

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 *Select pre-made groups from a selected item*

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 *Set data from FireBrowse*

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 *Load local files*

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 *Perform set operations on selected groups*

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 *Create an icon based on set operations*

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 *Show or remove an alert*

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 *Sidebar without a well*

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 *Get number of significant digits*

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 *Sort coordinates for some event types*

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 *Set the status of a process to style a given button*

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` *Create, set and terminate a progress object*

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 `shiny::modalDialog`
	`easyClose` If `TRUE`, the modal dialog can be dismissed by clicking outside the dialog box, or be 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 `modalButton()`, or from a call to `removeModal()` 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^ρ 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 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.

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 righ-hand-side covariate.

Note that the ordinary log-rank test is equivalent to the score test from a Cox model, using the Breslow approximation for ties. Use the Cox model form for more complex models, e.g., time-dependent covariates.

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, Biometics, 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` *Preserve attributes of* `sticky` *objects when extracting or transposing object*

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` *Creates a* `tabPanel` *template for a* `datatable` *with a title and description*

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 *Create HTML table from data frame or matrix*

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 *Create a row for a HTML table*

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 *Multiple independence tests between reference groups and list of groups*

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:

`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

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 *Test the survival difference between groups of subjects*

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 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.

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 `processSurvTerms`
	`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 *Create script for auto-completion of text input*

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")
psichomics:::textSuggestions("textareaid", words)
```

toJSarray *Convert vector of values to JavaScript array*

Description

Convert vector of values to JavaScript array

Usage

```
toJSarray(values)
```

Arguments

values	Character vector

Value

Character with valid JavaScript array

traceInList *Find an item in list of lists and return its coordinates*

Description

Find an item in list of lists and return its coordinates

Usage

```
traceInList(ll, item)
```

transformData *Transform data in data frame*

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 *Show variable transformation(s)*

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 *Transform values as per a given type of transformation*

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 (.Machine$double.xmin) to avoid infinity values following log-transformation (may not be plotted); useful for p-values of 0

Value

Integer containing transformed values

---

trimWhitespace *Trims whitespace from a word*

Description

Trims whitespace from a word

Usage

```
trimWhitespace(word)
```

Arguments

word	Character to trim

Value

Character without whitespace

Examples

```
psichomics:::trimWhitespace("    hey   there     ")
psichomics:::trimWhitespace(c("pineapple    ", "one two three",
                              " sunken    ship   "))
```

uniqueBy *Check unique rows of a data frame based on a set of its columns*

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 *Update available clinical attributes when the clinical data changes*

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

`session`	Shiny session
`id`	Character: identifier
`...`	Additional arguments passed to `fileBrowser()`. Only used if `value = NULL`.
`value`	Character: file or directory path
`ask`	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

join	List of lists of data frame
eventType	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 correlateGEandAS()
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 stats::loess.smooth?
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 stats::loess.smooth 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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