Package ‘psichomics’

March 7, 2024

Title  Graphical Interface for Alternative Splicing Quantification, Analysis and Visualisation

Version  1.28.1

Encoding  UTF-8

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

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

License  MIT + file LICENSE

LazyData  true

RoxygenNote  7.3.1

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

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

LinkingTo  Rcpp

VignetteBuilder  knitr

Collate  'RcppExports.R' 'utils.R' 'globalAccess.R' 'app.R' 'analysis.R' 'analysis.correlation.R'
R topics documented:

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Date/Publication  2024-03-06
Author  Nuno Saraiva-Agostinho [aut, cre]
        (https://orcid.org/0000-0002-5549-105X),
        Nuno Luís Barbosa-Morais [aut, led, ths]
        (https://orcid.org/0000-0002-1215-0538),
        André Falcão [ths],
        Lina Gallego Paez [ctb],
        Marie Bordone [ctb],
        Teresa Maia [ctb],
        Mariana Ferreira [ctb],
        Ana Carolina Leote [ctb],
        Bernardo de Almeida [ctb]
Maintainer  Nuno Saraiva-Agostinho <nunodanielagostinho@gmail.com>

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

Arguments

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

Value
Object with attributes set

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

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)
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)`
areSplicingEvents

gtexDataUI(id, panel)
inclusionLevelsUI(id, panel)
inclusionLevelsFilterUI(id, panel)
localDataUI(id, panel)
recountDataUI(id, panel)
groupsUI(id, tab)
helpUI(id, tab)

Arguments

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<th>Description</th>
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<tr>
<td>id</td>
<td>Character: identifier</td>
</tr>
<tr>
<td>tab</td>
<td>Function to process HTML elements</td>
</tr>
<tr>
<td>panel</td>
<td>Function to enclose interface</td>
</tr>
</tbody>
</table>

Value

HTML elements

---

areSplicingEvents \(\text{Check if string identifies splicing events}\)

Description

Check if string identifies splicing events

Usage

\(\text{areSplicingEvents}(\text{char}, \text{data} = \text{NULL}, \text{num} = 6)\)

Arguments

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<td>data</td>
<td>Object containing event data</td>
</tr>
<tr>
<td>num</td>
<td>Integer: number of elements to check</td>
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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
```r
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**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>data</code></td>
<td>Numeric, data frame or matrix: gene expression data or alternative splicing event quantification values (sample names are based on their names or <code>colnames</code>)</td>
</tr>
<tr>
<td><code>groups</code></td>
<td>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</td>
</tr>
</tbody>
</table>

**Value**

HTML elements

---

### blendColours

**Blend two HEX colours**

**Description**

Blend two HEX colours

**Usage**

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

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>colour1</code></td>
<td>Character: HEX colour</td>
</tr>
<tr>
<td><code>colour2</code></td>
<td>Character: HEX colour</td>
</tr>
<tr>
<td><code>colour1Percentage</code></td>
<td>Character: percentage of colour 1 mixed in blended colour</td>
</tr>
</tbody>
</table>
**Value**

Character representing an HEX colour

**Source**

Code modified from [https://stackoverflow.com/questions/5560248](https://stackoverflow.com/questions/5560248)

**Examples**

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

---

**browseDownloadFolderInput**

*Browse download folder input*

---

**Description**

Browse download folder input

**Usage**

```r
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](https://github.com/daattali/advanced-shiny/blob/master/navigate-history)

**Usage**

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

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

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
- `onlyReturnASeventNames` : Boolean

Value

Matrix with inclusion levels
calculateLoadingsContribution

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

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

Usage

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

Arguments

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

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

Source

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**

```r
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**

```r
checkFirebrowse(ns)
```

**Arguments**

- `ns`  
  *Namespace function*

**Value**

HTML elements
checkGroupType  

Description

Check type of groups within file

Usage

checkGroupType(file)

Arguments

file  Character: file path

Value

Type of group: Samples, ASevents or NULL

checkIntegrity  

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: 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

```r
# Use species name to automatically look for a OrgDb database
sp <- "Homo sapiens"

genes <- c("ENSG00000012048", "ENSG00000083093", "ENSG00000141510", "ENSG00000051180")

convertGeneIdentifiers(sp, genes)
```
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

```r
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**

```r
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
)
createGroup

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 \texttt{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 \texttt{geom_point()} related to highlighted points
selected Integer: index of rows/points to be coloured
selectedParams List of parameters to pass to \texttt{geom_point()} related to selected points
labelled Integer: index of rows/points to be labelled
labelledParams List of parameters to pass to \texttt{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 \hspace{1cm} \textit{Prepare to create group according to specific details}

Description
Prepare to create group according to specific details

Usage

\begin{verbatim}
createGroup(
    session, input, output, id, type, selected = NULL, expr = NULL,
    groupNames = NULL
)\end{verbatim}
createGroupByAttribute

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

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

Description

Creates a template of alternative splicing junctions

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
createOptimalSurvData

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

Examples

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

---

createOptimalSurvData  Create survival data based on a PSI cutoff

Description
Data is presented in the table for statistical analyses

Usage

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

Arguments

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

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

---

**createSparklines**

*Create sparkline charts to be used in a data table*

---

**Description**

Create sparkline charts to be used in a data table

**Usage**

```r
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**

```r
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**

```r
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**

```r
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 = "#faa000",
    alternative1Fill = "#faa000",
    alternative1Stroke = "lightgray",
    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)
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**

```r
# 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**

```r
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**

```r
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](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

**Description**

Download files to a given directory

**Usage**

```r
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**

```r
## 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

**Description**

Convert from Ensembl to UniProt identifier

**Usage**

```r
ensembleToUniprot(protein)
```
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

Arguments

protein Character: Ensembl identifier

Value

UniProt protein identifier

See Also

Other functions to retrieve external information: plotProtein(), plotTranscripts(), queryEnsemblByGene()
**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**

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

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

Arguments

- **id**: Character: input identifier
- **label**: Character: input label (if \textsc{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 \texttt{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. \texttt{shinyBS::bsTooltip} and \texttt{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 \texttt{prepareFileBrowser()} function needs to be included in the server logic.

This widget relies on \texttt{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 \url{https://www.shinyapps.io}).

Value

HTML elements for a file browser input

Source

\url{https://github.com/wleepang/shiny-directory-input}

See Also

\texttt{updateFileBrowserInput()} and \texttt{prepareFileBrowser()}

---

**filterGeneExpr**  
*Filter genes based on their expression*

Description

Uses \texttt{filterByExpr} to determine genes with sufficiently large counts to retain for statistical analysis.
filterGeneExpr

Usage

```r
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

```r
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**

```r
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**

```r
# 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**

```r
filterPSI(
  psi,
  eventType = NULL,
  eventSubtype = NULL,
  minPSI = -Inf,
  maxPSI = Inf,
  minMedian = -Inf,
)```
filterPSI

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**

```r
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**

```r
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
**geNormalisationFilteringInterface**

*Interface to normalise and filter gene expression*

**Value**

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

**Description**

Interface to normalise and filter gene expression

**Usage**

```r
geneNormalisationFilteringInterface(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**

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>clinical</td>
<td>Data frame: clinical data</td>
</tr>
<tr>
<td>event</td>
<td>Character: name of column containing time of the event of interest</td>
</tr>
<tr>
<td>timeStart</td>
<td>Character: name of column containing starting time of the interval or follow up time</td>
</tr>
<tr>
<td>timeStop</td>
<td>Character: name of column containing ending time of the interval (only relevant for interval censoring)</td>
</tr>
<tr>
<td>followup</td>
<td>Character: name of column containing follow up time</td>
</tr>
</tbody>
</table>

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

```r
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")
```

---

catchClinicalDataForSurvival

Retrieve clinical data based on attributes required for survival analysis

Usage

```r
catchClinicalDataForSurvival(..., formulaStr = NULL)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>...</td>
<td>Character: names of columns to retrieve</td>
</tr>
<tr>
<td>formulaStr</td>
<td>Character: right-side of the formula for survival analysis</td>
</tr>
</tbody>
</table>

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**

```r
getClinicalMatchFrom(dataset, category = getCategory())
```

```r
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**

```r
data()```

**Value**

Variable containing all data of interest
**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())

---

**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)
getDifferentialSplicing

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()
Usage

getDifferentialSplicing(category = getCategory())

setDifferentialSplicing(differential, category = getCategory())

generateDifferentialSplicingFiltered(category = getCategory())

setDifferentialSplicingFiltered(differential, category = getCategory())

generateDifferentialSplicingSurvival(category = getCategory())

setDifferentialSplicingSurvival(survival, category = getCategory())

generateDifferentialSplicingResetPaging(category = getCategory())

setDifferentialSplicingResetPaging(reset, category = getCategory())

generateDifferentialSplicingColumns(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
getGeneList

Examples

```r
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**

```r
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**

```r
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
getGroups

Description
Get or set groups

Usage

```r
groups <- getGroups()
setGroups(groups = groups)
```
getGtexDataTypes

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>Character: type of groups (either Patients, Samples, ASevents or Genes)</td>
</tr>
<tr>
<td>complete</td>
<td>Boolean: return all the information on groups (TRUE) or just the group names and respective indexes (FALSE)?</td>
</tr>
<tr>
<td>category</td>
<td>Character: data category</td>
</tr>
<tr>
<td>groups</td>
<td>Matrix: groups of dataset</td>
</tr>
</tbody>
</table>

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()

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

**Arguments**
- `folder` Character: folder containing data
- `release` Numeric: GTEx data release to load

**Value**
Character: available tissues
getHidden

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

generateSampleFromSubject

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")

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

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

generateSampleFromSubject(
    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

```r
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

```r
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
**getServerFunctions**

**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()`

---

### Description

Matches server functions from a given loader

#### Usage

```r
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

---

### Description

Returns the coordinates of interest for a given event type

#### Usage

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

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)

genesFromSplicingEvents(ASevents, data = NULL)
getSplicingEventTypes

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_201763774_201763594_NAV1", 
"SE_1_+_183515472_183516238_183516387_183518343_SMG7", 
"SE_1_+_183447184_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) = genes

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

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

getSplicingEventTypes Get supported splicing event types

Description

Get supported splicing event types

Usage

getSplicingEventTypes(psi = NULL, acronymsAsNames = FALSE)
getSubjectFromSample

**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**

```r
getSplicingEventTypes()
```

---

**getSubjectFromSample**  
*Get subjects from given samples*

**Description**

Get subjects from given samples

**Usage**

```r
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

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

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

getTCGAdates()
gwgetTCGAcohorts(cohort = NULL)

Arguments

- cohort: Character: filter results by cohorts (optional)

Value

Parsed response

See Also

Other functions associated with TCGA data retrieval: `getDownloadsFolder()`, `isFirebrowseUp()`, `loadTCGAdat()`, `parseTCGAsampleTypes()`

Examples

```r
getTCGAdates()
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

```r
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 mRNA 17233 18061 . - .
chr1 SE exon 17233 17368 . - .
chr1 SE exon 17915 18061 . - .
")
psychomics:::getValidEvents(event, validator)
```

---

**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**

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

**Arguments**

- **df**  Data frame
- **hover**  Mouse hover information for a given plot as retrieved from hoverOpt
- **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)
ggplotUI

**Value**

HTML elements

---

**ggplotUI** *Interface for interactive ggplot*

---

**Description**

Interface for interactive ggplot

**Usage**

```r
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**

```r
globalSelectize(id, placeholder, AEvent = FALSE)
```

**Arguments**

- `id` Character: input identifier
- `placeholder` Character: input placeholder
- `AEvent` Boolean: select alternative splicing events?

**Value**

HTML element for a global selectize input
**groupByAttribute**  
*Data grouping interface*

**Description**  
Data grouping interface

**Usage**

```plaintext
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**

```plaintext
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

```r
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

```r
# 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**

```r
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
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**

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

```r
errorDialog(description, ...)
```

```r
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**
```r
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**
```r
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 [FireBrowse API](http://firebrowse.org/api-docs/) 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()`, `getTCGADATA()`, `loadTCGADATA()`, `parseTCGASampleTypes()`

**Examples**

isFirebrowseUp()
### isRStudioServer

**Description**

Check if running in RStudio Server

**Usage**

```r
isRStudioServer()
```

**Value**

Boolean stating whether running in RStudio Server

---

### joinEventsPerType

**Description**

Full outer join all given events based on select columns

**Usage**

```r
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

```r
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, 0.5, 0, 1), cutoff=0.5, gte=FALSE)
```

---

**leveneTest**

*Levene’s test*

Description

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

Usage

```r
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

```r
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**  
*psychomics article's link interface*

Description

*psychomics article’s link interface*

Usage

```r
linkToArticles()
```

Value

HTML elements

------

**linkToRunJS**  
*Link to run arbitrary JavaScript code*

Description

Link to run arbitrary JavaScript code

Usage

```r
linkToRunJS(text, code)
```
Arguments

<table>
<thead>
<tr>
<th>text</th>
<th>Character: text label</th>
</tr>
</thead>
<tbody>
<tr>
<td>code</td>
<td>Character: JavaScript code</td>
</tr>
</tbody>
</table>

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"))
```
loadAnnotationHub

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

<table>
<thead>
<tr>
<th>loader</th>
<th>Character: name of the file responsible to load such function</th>
</tr>
</thead>
<tbody>
<tr>
<td>FUN</td>
<td>Function</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>session</th>
<th>Shiny session</th>
</tr>
</thead>
<tbody>
<tr>
<td>input</td>
<td>Shiny input</td>
</tr>
<tr>
<td>output</td>
<td>Shiny output</td>
</tr>
</tbody>
</table>

Value

NULL (function is only used to modify the Shiny session’s state or internal variables)
**loadDataModal**  
*Warn user about loaded data*

**Description**

Warn user about loaded data

**Usage**

```r
loadDataModal(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**

```r
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**

```r
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**

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

**Arguments**

- `folder` Character: folder containing data
- `data` Character: data types to load (see `getGtxDataTypes`)
- `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?
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  

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  

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?
loadRequiredData

Value

List of data frames from valid files

See Also

Other functions to load data: loadGtexData(), loadSRAproject(), loadTCGAdataset()

Examples

```r
## 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

```r
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)
loadSRAproject

## 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 [recount2](https://jhubiostatistics.shinyapps.io/recount/recount2)

Description
Download and load SRA projects via recount2

Usage
loadSRAproject(project, outdir = getDownloadsFolder())
**loadTCGAdatasets**

**Download and process TCGA data**

**Description**

TCGA data obtained via FireBrowse

**Usage**

```r
loadTCGAdatasets(
  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 `getTCGAdatasets()`)
- **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)

**Examples**

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

```r
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**

loadTCGA_sampleMetadata(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?
**navSelectize**

**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

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

```r
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

dgerR::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).
operateOnGroups

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)

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()`, `getAttributeTime()`, `labelBasedOnCutoff()`, `plotSurvivalCurves()`, `plotSurvivalPvaluesByCutoff()`, `processSurvTerms()`, `survdiffTerms()`, `survfit.survTerms()`, `testSurvival()`

Examples

```r
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
parseMatsEvent

Examples

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

# Get the abbreviation and description of all cohorts available
parseMatsEvent::parseFirebrowseMetadata("Cohorts")
# Get the abbreviation and description of the selected cohorts
parseMatsEvent::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"
"
parseMatsEvent::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)
psychomics:::parseMatsGeneric(junctions, strand = "+", coords, plus, minus)

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

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

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

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

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

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

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

parseMiso55S(event)

parseMisoA3SS(event, plusIndex, minusIndex)

parseMisoTandemUTR(event, minusIndex)

parseMisoAFE(event)

parseMisoALE(event)

Arguments

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

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 exon 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 17742 . - .
  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 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**

```r
parseMisoId(id)
```

**Arguments**

- `id` Character: MISO alternative splicing event identifier

**Value**

Character with the parsed ID

**Examples**

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

psychomics::parseMisoId(id)
```

**parseSplicingEvent**

**Parse alternative splicing event identifier**

**Description**

Parse alternative splicing event identifier

**Usage**

```r
parseSplicingEvent(
  event,
  char = FALSE,
  pretty = FALSE,
  extra = NULL,
  coords = TRUE,
  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

```r
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)
```

Description

Parse events from alternative splicing annotation

Usage

```r
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,
  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
parseSuppaEvent

Parses splicing events of a specific event type from SUPPA

**Description**

Parses splicing events of a specific event type from SUPPA

**Usage**

```r
parseSuppaEvent(event)
```

**Arguments**

- `event`  
  Character vector: Splicing event attributes and junction positions

**Details**

More information about SUPPA available at [https://bitbucket.org/regulatorygenomicsupf/suppa](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:-"
pseichomics::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

```r
# Parse generic event (in this case, an exon skipping event)
junctions <- read.table(text = "169768099 169770024 169770112 169771762")
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 24795476 24795797")
psichomics:::parseSuppaALE(junctions, "+")

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

```r
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)
```

parseUniprotXMLParse XML from UniProt REST service

Description
Parse XML from UniProt REST service

Usage
```r
parseUniprotXML(xml)
```

Arguments

xml
response from UniProt

Value
List containing protein length and data frame of protein features

parseUrlsFromFirebrowseResponseRetrieve URLs from a response to a FireBrowse data query

Description
Retrieve URLs from a response to a FireBrowse data query

Usage
```r
parseUrlsFromFirebrowseResponse(res)
```

Arguments

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

Value
Named character with URLs
parseVastToolsEvent

Parses a variation event from VAST-TOOLS

### Examples
```r
res <- psichomics:::queryFirebrowseData(cohort = "ACC")
url <- psichomics:::parseUrlsFromFirebrowseResponse(res)

parseVastToolsEvent(event)
```

### Description
Parses an alternative splicing event from VAST-TOOLS

### Usage
```r
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
```r
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")
psychomics::parseVastToolsSE(junctions)

# these functions are vectorised!
junctions <- read.table(text = "41040823 41046768 41046903 41051785"
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.
Perform principal component analysis after processing missing values

Usage

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

Value

ICA result in a prcomp object

See Also

Other functions to analyse independent components: plotICA()

Examples

performICA(USArrests)
plotClusters

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

```r
performPCA(USArrests)
```

---

plotClusters  

**Add clusters to highchart object**

Description

Clusters are added as coloured polygons.

Usage

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

Arguments

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

Value

highcharter object
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, and from S-PLUS.)
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.

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?
plotGeneExprPerSample

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, ...)
plotGroupIndependence

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
)
plotICA

Create multiple scatterplots from ICA

Description

Create multiple scatterplots from ICA

Usage

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

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)
**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** an 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 (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**

```R
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")
```
plotLibrarySize

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

```r
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

```r
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**

```r
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**

```r
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)
**plotRowStats**

**Arguments**

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

**Value**

- highcharter object

**See Also**

- Other functions to retrieve external information: `ensemblToUniprot()`, `plotTranscripts()`, `queryEnsemblByGene()`

**Examples**

```r
protein <- "P38398"
plotProtein(protein)

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

---

**Description**

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

**Usage**

```r
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**

```r
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 = "#ffbb53",
  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

```r
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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>surv</td>
<td>Survival object</td>
</tr>
<tr>
<td>mark</td>
<td>Boolean: mark times?</td>
</tr>
<tr>
<td>interval</td>
<td>Boolean: show interval ranges?</td>
</tr>
<tr>
<td>pvalue</td>
<td>Numeric: p-value of the survival curves</td>
</tr>
<tr>
<td>title</td>
<td>Character: plot title</td>
</tr>
<tr>
<td>scale</td>
<td>Character: time scale (default is days)</td>
</tr>
<tr>
<td>auto</td>
<td>Boolean: return the plot automatically prepared (TRUE) or only the bare minimum (FALSE)?</td>
</tr>
</tbody>
</table>

Value

Plot of survival curves

See Also

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

Examples

```r
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.days_to_event", 
                      "patient.days_to_first_followup")
plottableXranges

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()
# 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)
prepareGenePresentation

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

```r
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

```r
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: unstranded, stranded or stranded (reverse)

Value

Prepared file (if output != NULL) and object

Examples

```r
## 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**

```r
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**

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

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

```r
prepareGeneQuant(...,
  output = "psichomics_gene_counts.txt",
  strandedness = c("unstranded", "stranded", "stranded (reverse)"))
```
prepareWordBreak

Create word break opportunities (for HTML) using given characters

Description

Create word break opportunities (for HTML) using given characters

Usage

```r
prepareWordBreak(
  str,
  pattern = c(".", "-", "/", "\", ",", ",", ",", "+", ",="),
  html = TRUE
)
```
### preserveAttributes

**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

---

### processButton

**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()`.
- **class**  
  Character: class
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

processSRAdataset  Process SRA quantification data

Description
Process SRA quantification data

Usage
processSRAdataset(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**

```r
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
processSurvTerms

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

cclinical 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

```r
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"
etvent  <- "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)
}
```

Start graphical interface of psychomics

**Description**

Start graphical interface of psychomics

**Usage**

```r
psychomics(
  ..., 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

```r
## Not run:
psichomics()
```

## End(Not run)
quantifySplicing

quantifySplicing

quantifySplicing

Description

Quantify alternative splicing events

Usage

quantifySplicing(
  annotation,
  junctionQuant,
  eventType = c("SE", "MXE", "ALE", "AFE", "A3SS", "A5SS"),
  minReads = 10,
  genes = NULL
)
quantifySplicingSet

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

```r
# 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**

```r
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**

```r
path <- "overlap/region/human/7:140424943-140624564"
query <- list(feature = "gene")
psychomics:::queryEnsembl(path, query, grch37 = TRUE)

path <- "lookup/symbol/human/BRCA2"
query <- list(expand=1)
psychomics:::queryEnsembl(path, query, grch37 = TRUE)
```

**queryEnsemblByGene**

*Query information from Ensembl*

**Description**

Query information from Ensembl

**Usage**

```r
queryEnsemblByGene(gene, species = NULL, assembly = NULL)
queryEnsemblByEvent(event, species = NULL, assembly = NULL, data = NULL)
```
queryFirebrowseData

Query the FireBrowse API for TCGA data

Description

Query the FireBrowse API for TCGA data

Usage

```r
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

```r
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")
queryUniprot

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

```r
psichomics:::queryPubMed("BRCA1", "cancer", "adrenocortical carcinoma")
```

queryUniprot

Query the UniProt REST API

Description

Query the UniProt REST API

Usage

```r
queryUniprot(molecule, format = "xml")
```

Arguments

molecule Character: protein or transcript to query
format Character: format of the response

Value

Parsed response

Examples

```r
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

_\texttt{type}         Character: dimensionality reduction technique (pca or ica)

\_\texttt{center}        either a logical value or numeric-alike vector of length equal to the number of columns of \texttt{x}, where 'numeric-alike' means that \texttt{as.numeric(.)} will be applied successfully if \texttt{is.numeric(.)} is not true.

\_\texttt{scale.}        Boolean: scale variables?

\_\texttt{naTolerance}    Integer: percentage of tolerated missing values per column (deprecated)

\_\texttt{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 \texttt{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**

```r
renderBoxplot(
  data,  
  outliers = FALSE,  
  sortByMedian = TRUE,  
  showXlabels = TRUE,  
  title = NULL,  
  seriesName = "Gene expression"
)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>data</code></td>
<td>Data frame or matrix</td>
</tr>
<tr>
<td><code>outliers</code></td>
<td>Boolean: draw outliers?</td>
</tr>
<tr>
<td><code>sortByMedian</code></td>
<td>Boolean: sort box plots based on ascending median?</td>
</tr>
<tr>
<td><code>showXlabels</code></td>
<td>Boolean: show labels in X axis?</td>
</tr>
</tbody>
</table>

**Value**

Box plot

**Examples**

```r
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**

```r
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)
replaceStrInList

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**

\[ \text{rm.null}(v) \]

**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**

\[ \text{roundDigits}(n) \]

**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

selectGroupsUI  Group selection

**Description**

Group selection interface and logic

**Usage**

```r
selectGroupsUI(
  id,
  label,
  type,
  placeholder = "Type to search groups",
  noGroupsLabel = NULL,
  groupsLabel = NULL,
  maxItems = NULL,
  returnAllDataLabel = NULL,
  returnAllDataValue = FALSE
)
```

```r
selectGroupsServer(session, id, type, preference = NULL)
```

```r
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
selectizeGeneInput

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.
selectPreMadeGroup

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?
setLocalData

Load local files

Usage

setLocalData(input, output, session, replace = TRUE)
setMultipleFilesData(input, output, session, replace = TRUE)

Arguments

input
output
session
replace

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
)
setOperationIcon

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)

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**

```r
showAlert(
  session,
  ..., 
  title,
  style = NULL,
  dismissible = TRUE,
  alertId = "alert",
  iconName = NULL,
  caller = NULL
)
```

```r
successAlert(
  session,
  ..., 
  title = NULL,
  dismissible = TRUE,
  alertId = "success",
  caller = NULL
)
```

```r
errorAlert(
  session,
  ..., 
  title = NULL,
  dismissible = TRUE,
  alertId = "alert",
  caller = NULL
)
```

```r
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**

```r
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**

```r
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**

```r
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

```r
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 `analyses` 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)

dropProcess(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?
startProgress

Value

startProgress 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

```r
styleModal(
  session,
  title,
  ...,
  style = NULL,
  iconName = "exclamation-circle",
  footer = NULL,
  echo = FALSE,
  size = "medium",
  dismissButton = TRUE,
  caller = NULL
)
```

```r
errorModal(session, title, ..., size = "small", footer = NULL, caller = NULL)
```

```r
warningModal(session, title, ..., size = "small", footer = NULL, caller = NULL)
```

```r
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 by pressing the Escape key. If FALSE (the default), the modal dialog can't be dismissed in those ways; instead it must be dismissed by clicking on a `modalButton()`, or from a call to `removeModal()` on the server.
subjectMultiMatchWarning

- **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**

```r
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 $G^p$ family of tests, or for a single curve against a known alternative.

**Usage**

```r
survdiffTerms(survTerms, ...)
```

**Arguments**

- `survTerms` (survTerms object: survival terms obtained after running processSurvTerms (see examples))
- `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 right-hand-side covariate.

References


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", "sex", "status", "group")

summary(survfit(survdiffTerms ~ factor(group), data = clinical))

plot(survfit(survdiffTerms ~ factor(group), data = clinical), conf.int = TRUE, xlab = "Time", ylab = "Survival")
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

...  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 char-
acter 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 inter-
pretation. 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

```r
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)
```

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'

\[ x[i, j, \ldots] \]

Arguments

- \( x \): Object
- \( i, j, \ldots \): 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

```r
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**

Create HTML table from data frame or matrix

**Usage**

```r
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**

```r
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**

```r
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

```r
elements <- paste("subjects", 1:10)
ref <- elements[5:10]
groups <- list(race=list(asiyan=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)
```
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()
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?
textSuggestions

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

Description

Uses the JavaScript library jquery.textcomplete

Usage

textSuggestions(id, words, novalue = "No matching value", char = " ")

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>Character: input ID</td>
</tr>
<tr>
<td>words</td>
<td>Character: words to suggest</td>
</tr>
<tr>
<td>novalue</td>
<td>Character: string when there's no matching values</td>
</tr>
<tr>
<td>char</td>
<td>Character to succeed accepted word</td>
</tr>
</tbody>
</table>

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)
transformOptions

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)
trimWhitespace

Arguments

val    Integer: values to transform

Type  Character: type of transformation

avoidZero  Boolean: add the smallest non-zero number available (.Machine$double$x.min) 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**

```r
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**

```r
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**

```r
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](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**

```r
vennEvents(join, eventType)
```
**Arguments**

- `join` List of lists of data frame
- `eventType` Character: type of event

**Value**

Venn diagrams for a given event type

**Description**

Includes interface containing the results

**Usage**

```r
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

Description

Plot, print and display as table the results of gene expression and alternative splicing

Usage

```r
## 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()

Examples

```r
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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