Package ‘psichomics’

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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

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

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

Value
Object with attributes set

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

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

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)

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)"
appServer

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

```r
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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<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

Description

Check if string identifies splicing events

Usage

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

Arguments

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<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>char</td>
<td>Character vector</td>
</tr>
<tr>
<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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</table>

Value

TRUE if first elements are splicing events; FALSE, otherwise
articleUI  
*Return the interface to display an article*

**Description**

Return the interface to display an article

**Usage**

articleUI(article)

**Arguments**

- **article**  
  PubMed article

**Value**

HTML to render an article’s interface

---

assignColours  
*Assign colours to groups*

**Description**

Assign colours to groups

**Usage**

assignColours(new, groups = NULL)

**Arguments**

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

**Value**

Groups with an added column to state the colour
assignValuePerSubject

Assign average sample values to their corresponding subjects

Description
Assign average sample values to their corresponding subjects

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

Arguments

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

Value
Values per subject

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

Examples
# Calculate PSI for skipped exon (SE) and mutually exclusive (MXE) events
annot <- readFile("ex_splicing_annotation.RDS")
junctionQuant <- readFile("ex_junctionQuant.RDS")
psi <- quantifySplicing(annot, junctionQuant, eventType=c("SE", "MXE"))

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

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

### basicStats

**Basic statistics performed on data**

**Description**

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

**Usage**

basicStats(data, groups)

**Arguments**

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

**Value**

HTML elements

### blendColours

**Blend two HEX colours**

**Description**

Blend two HEX colours

**Usage**

blendColours(colour1, colour2, colour1Percentage = 0.5)

**Arguments**

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

**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")
```

---

**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

Description

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

Usage

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

Arguments

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

Value

Matrix with inclusion levels
calculateLoadingsContribution

Calculate the contribution of PCA loadings to the selected principal components

Description

Total contribution of a variable is calculated as per \[
\frac{(C_x \times E_x) + (C_y \times E_y)}{E_x + E_y}
\], 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

\[
\text{calculateLoadingsContribution}(\text{pca}, \text{pcX} = 1, \text{pcY} = 2)
\]

Arguments

- \text{pca} \hspace{1cm} \text{prcomp object}
- \text{pcX} \hspace{1cm} \text{Character: name of the X axis of interest from the PCA}
- \text{pcY} \hspace{1cm} \text{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


See Also

Other functions to analyse principal components: \text{performPCA()}.\text{plotPCA()}.\text{plotPCAvariance()}

Examples

\[
pca <- \text{performPCA}(\text{USArrests})
\text{calculateLoadingsContribution}(\text{pca})
\]
checkFileFormat  Checks the format of a file

Description
Checks the format of a file

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

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

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

Value
TRUE if the file matches the given format’s attributes

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

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

Usage
checkFirebrowse(ns)

Arguments
ns Namespace function

Value
HTML elements
checkGroupType  

Check type of groups within file

Description
Check type of groups within file

Usage
checkGroupType(file)

Arguments

file Character: file path

Value
Type of group: Samples, ASevents or NULL

checkIntegrity  

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

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

Usage
checkIntegrity(filesToCheck, md5file)

Arguments

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

Value
Logical vector showing TRUE for files with matching md5sums and FALSE for files with non-matching md5sums
checkSurvivalInput  
*Prepare survival terms in case of valid input*

**Description**
Prepare survival terms in case of valid input

**Usage**
```r
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**
```r
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

```r
## 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**

```r
convertGeneIdentifiers(
  annotation,
  genes,
  key = "ENSEML",
  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()`
createDataTab

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

`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 `geom_point()` related to most points
- **highlightX**: Integer: region of points in X axis to highlight
- **highlightY**: Integer: region of points in Y axis to highlight
- **highlightParams**: List of parameters to pass to `geom_point()` related to highlighted points
- **selected**: Integer: index of rows/points to be coloured
- **selectedParams**: List of parameters to pass to `geom_point()` related to selected points
- **labelled**: Integer: index of rows/points to be labelled
- **labelledParams**: List of parameters to pass to `ggrepel::geom_label_repel` related to labelled points
- **xlim**: Numeric: limits of X axis
- **ylim**: Numeric: limits of Y axis

Value

List containing HTML elements and highlighted points

---

**createGroup** | **Prepare to create group according to specific details**

Description

Prepare to create group according to specific details

Usage

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

Create groups based on given row indexes or identifiers

Description
Create groups based on given row indexes or identifiers

Usage
createGroupId(session, rows, identifiers)

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

Value
Character: values based on given row indexes or identifiers

createGroupFromInput
Set new groups according to the user input

Description
Set new groups according to the user input

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

Create 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

createJunctionsTemplate

Creates a template of alternative splicing junctions

Description

Creates a template of alternative splicing junctions

Usage

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

Arguments

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

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

Examples

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

createOptimalSurvData  
Create survival data based on a PSI cutoff

Description

Data is presented in the table for statistical analyses

Usage

```r
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)
createSparklines

Create sparkline charts to be used in a data table

Description

Create sparkline charts to be used in a data table

Usage

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

Arguments

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

Value

HTML element with sparkline data
customRowMeans

Calculate statistics for each row or column of a matrix

Description

Calculate statistics for each row or column of a matrix

Usage

customRowMeans(mat, na.rm = FALSE, fast = FALSE)
customRowMedians(mat, na.rm = FALSE, fast = FALSE)
customRowVars(mat, na.rm = FALSE, fast = FALSE)
customRowMins(mat, na.rm = FALSE, fast = FALSE)
customRowMaxs(mat, na.rm = FALSE, fast = FALSE)
customRowRanges(mat, na.rm = FALSE, fast = FALSE)
customColMedians(mat, na.rm = FALSE, fast = FALSE)

Arguments

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

Value

Vector of selected statistic

Examples

df <- rbind("Gene 1"=c(3, 5, 7), "Gene 2"=c(8, 2, 4), "Gene 3"=c(9:11))
psychomics:::customRowMeans(df)
psychomics:::customRowVars(df, fast=TRUE)
diagramSplicingEvent  Prepare SVG diagram of alternative splicing events

Description
Prepare SVG diagram of alternative splicing events

Usage
diagramSplicingEvent(
  parsed,
  type,
  class = "pull-right",
  style = NULL,
  showText = TRUE,
  showPath = TRUE,
  showAlternative1 = TRUE,
  showAlternative2 = TRUE,
  constitutiveWidth = NULL,
  alternativeWidth = NULL,
  intronWidth = NULL,
  constitutiveFill = "lightgray",
  constitutiveStroke = "darkgray",
  alternative1Fill = "#ff0b33",
  alternative1Stroke = "#fa0000",
  alternative2Fill = "#ca06c",
  alternative2Stroke = "#9d7039"
)

Arguments
  parsed  Alternative splicing event
  type    Character: alternative splicing event type
  class   Character: class of SVG parent tag
  style   Character: style of SVG parent tag
  showText Boolean: display coordinates and length (if available)
  showPath Boolean: display alternative splicing junctions
  showAlternative1 Boolean: show alternative exon 1 and respective splicing junctions and text?
  showAlternative2 Boolean: show alternative exon 2 and respective splicing junctions and text?
                    (only related with mutually exclusive exons)
  constitutiveWidth Numeric: width of constitutive exon(s)
alternativeWidth
  Numeric: width of alternative exon(s)

intronWidth
  Numeric: width of intron’s representation

constitutiveFill
  Character: fill colour of constitutive exons

constitutiveStroke
  Character: stroke colour of constitutive exons

alternative1Fill
  Character: fill colour of alternative exon 1

alternative1Stroke
  Character: stroke colour of alternative exon 1

alternative2Fill
  Character: fill colour of alternative exon 2

alternative2Stroke
  Character: stroke colour of alternative exon 2

Value

Diagrams per alternative splicing event in SVG

diffAnalyses

Perform statistical analyses

Description

Perform statistical analyses

Usage

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

Arguments

data          Data frame or matrix: gene expression or alternative splicing quantification

groups        Named list of characters (containing elements belonging to each group) or character vector (containing the group of each individual sample): if NULL, sample types are used instead when available, e.g. normal, tumour and metastasis

analyses      Character: statistical tests to perform (see Details)
pvalueAdjust  Character: method used to adjust p-values (see Details)
geneExpr  Character: name of the gene expression dataset (only required for density sparklines available in the interactive mode)
inputID   Character: identifier of input to get attributes of clicked event (Shiny only)

Details

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

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

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

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

Value

Table of statistical analyses

See Also

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

Examples

```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

Usage

diffExpressionSet(session, input, output)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>session</td>
<td>Shiny session</td>
</tr>
<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)

diffSplicingSet

Set of functions to perform differential analyses

Usage

diffSplicingSet(session, input, output)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>session</td>
<td>Shiny session</td>
</tr>
<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)
**disableTab**

*Enable or disable a tab from the navbar*

**Description**

Enable or disable a tab from the navbar

**Usage**

```
disableTab(tab)
```

```
enableTab(tab)
```

**Arguments**

- **tab**  
  Character: tab

**Value**

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

---

**discardLowCoveragePSIvalues**

*Remove alternative splicing quantification values based on coverage*

**Description**

Remove alternative splicing quantification values based on coverage

**Usage**

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

**Arguments**

- **psi**  
  Data frame or matrix: alternative splicing quantification

- **minReads**  
  Currently this argument does nothing

- **vasttoolsScoresToDiscard**  
  Character: if you are using inclusion levels from VAST-TOOLS, filter the data based on quality scores for read coverage, e.g. use `vasttoolsScoresToDiscard = c("SOK", "OK", "LOW")` to only keep events with good read coverage (by default, events are not filtered based on quality scores); read [https://github.com/vastgroup/vast-tools](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 diff object is passed to the char argument

Value

NULL (display message in command-line)
downloadFiles

Description

Download files to a given directory

Usage

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

Arguments

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

Value

Invisible TRUE if every file was successfully downloaded

Examples

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

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

## End(Not run)

ensemblToUniprot

Description

Convert from Ensembl to UniProt identifier

Usage

ensemblToUniprot(protein)
escape

Arguments

protein Character: Ensembl identifier

Value

UniProt protein identifier

See Also

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

Examples

gene <- "ENSG00000173262"
ensemblToUniprot(gene)

protein <- "ENSP00000445929"
ensemblToUniprot(protein)

---

escape Escape symbols for use in regular expressions

Description

Escape symbols for use in regular expressions

Usage

escape(...)

Arguments

... Characters to be pasted with no space

Value

Escaped string
eventPlotOptions  

**Options for event plotting**

**Description**

Options for event plotting

**Usage**

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

**Arguments**

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

**Value**

HTML elements

---

exportGroupsToFile  

**Export groups to a file**

**Description**

Export groups to a file

**Usage**

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

**Arguments**

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

**Value**

Saves groups to file
**export_highcharts**

Add an exporting feature to a highcharts object

**Description**

Add an exporting feature to a highcharts object

**Usage**

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

**Arguments**

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

**Value**

A highcharts object with an export button

---

**fileBrowser**

Interactive folder selection using a native dialogue

**Description**

Interactive folder selection using a native dialogue

**Usage**

```r
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
**Arguments**

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

**Details**

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

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

**Value**

HTML elements for a file browser input

**Source**

[https://github.com/wleepang/shiny-directory-input](https://github.com/wleepang/shiny-directory-input)

**See Also**

`updateFileBrowserInput()` and `prepareFileBrowser()`

---

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

**Description**

Uses `filterByExpr` to determine genes with sufficiently large counts to retain for statistical analysis.
Usage

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

Arguments

- **geneExpr**: Data frame or matrix: gene expression
- **minMean**: Numeric: minimum of read count mean per gene
- **maxMean**: Numeric: maximum of read count mean per gene
- **minVar**: Numeric: minimum of read count variance per gene
- **maxVar**: Numeric: maximum of read count variance per gene
- **minCounts**: Numeric: minimum number of read counts per gene for a worthwhile number of samples (check `filterByExpr` for more information)
- **minTotalCounts**: Numeric: minimum total number of read counts per gene

Value

Boolean vector indicating which genes have sufficiently large counts

See Also

Other functions for gene expression pre-processing: `convertGeneIdentifiers()`, `normaliseGeneExpression()`, `plotGeneExprPerSample()`, `plotLibrarySize()`, `plotRowStats()`

Examples

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

Arguments

psi | Data frame or matrix: alternative splicing quantification
eventType | Character: filter data based on event type; check all event types available by using getSplicingEventTypes(psi), where psi is the alternative splicing quantification data; if eventType = NULL, events are not filtered by event type
eventSubtype | Character: filter data based on event subtype; check all event subtypes available in your data by using unique(getSplicingEventData(psi)$subtype), where psi is the alternative splicing quantification data; if eventSubtype = NULL, events are not filtered by event subtype
minPSI | Numeric: minimum PSI value
maxPSI | Numeric: maximum PSI value
minMedian | Numeric: minimum median PSI per splicing event
maxMedian | Numeric: maximum median PSI per splicing event
minLogVar | Numeric: minimum log10(PSI variance) per splicing event
maxLogVar | Numeric: maximum log10(PSI variance) per splicing event
minRange | Numeric: minimum PSI range across samples per splicing event
maxRange | Numeric: maximum PSI range across samples per splicing event

Value

Boolean vector indicating which splicing events pass the thresholds

See Also

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

Examples

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

psi <- quantifySplicing(annot, junctionQuant, eventType=c("SE", "MXE"))
# Filter PSI
psi[filterPSI(psi, minMedian=0.05, maxMedian=0.95, minRange=0.15), ]
findASeventsFromGene  Find splicing events based on given genes

Description
Find splicing events based on given genes

Usage
findASeventsFromGene(psi, gene)

Arguments
psi  Data frame or matrix: alternative splicing quantification
gene  Character: gene

Value
Character vector containing alternative splicing events

findEventData  Look for event data in input

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

Usage
findEventData(event = NULL, data = NULL)

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

Value
Event data (or NULL if not found)
**geneExprFileInput**  
*File input for molecular data*

**Description**
File input for molecular data

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

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

**Value**
HTML elements

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

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

**Usage**
geneExprSurvSet(session, input, output)

**Arguments**
- **session** Shiny session
- **input** Shiny input
- **output** Shiny output
geNormalisationFilteringInterface

Interface to normalise and filter gene expression

Description

Interface to normalise and filter gene expression

Usage

geNormalisationFilteringInterface(ns)

Arguments

ns Namespace function

Value

HTML elements

getAttributesTime Get time values for given columns in a clinical dataset

Description

Get time values for given columns in a clinical dataset

Usage

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

Arguments

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

Value

Data frame containing the time for the given columns

See Also

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

Examples

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

c getClinicalDataForSurvival

Retrieve clinical data based on attributes required for survival analysis

Usage

getClinicalDataForSurvival(..., formulaStr = NULL)

Arguments

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

Value

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

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

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

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

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

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

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

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

---

**getDifferentialExpression**  
*Get or set differential expression’ elements for a data category*

**Description**  
Get or set differential expression’ elements for a data category

**Usage**  
`getDifferentialExpression(category = getCategory())`

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

`getDifferentialExpressionFiltered(category = getCategory())`

`setDifferentialExpressionFiltered(differential, category = getCategory())`
**differentialSplicing**

```r
differentialExpressionSurvival(category = getCategory())
differentialExpressionSurvival(survival, category = getCategory())
differentialExpressionResetPaging(category = getCategory())
differentialExpressionResetPaging(reset, category = getCategory())
differentialExpressionColumns(category = getCategory())
differentialExpressionColumns(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`

---

**differentialSplicing**

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

**Description**

Get or set differential splicing’ elements for a data category.
Usage

generateDifferentialSplicing(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: generateClinicalMatchFrom().generateDifferentialExpression().generateGlobal().generateGroups().generateHighlightedPoints().generateSelectedDataPanel()
getDownloadsFolder

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

getGeneList

Get curated, literature-based gene lists

Description

Available gene lists:

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

Usage

getGeneList(genes = NULL)

Arguments

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

Value

List of genes

See Also

Other functions for data grouping: `createGroupByAttribute()`, `getSampleFromSubject()`, `getSubjectFromSample()`, `groupPerElem()`, `plotGroupIndependence()`, `testGroupIndependence()`

Examples

getGeneList()
getGlobal

Get or set globally accessible elements

Description
Get or set globally accessible elements

Usage
getGlobal(category = getCategory(), ..., sep = "_")
setGlobal(category = getCategory(), ..., value, sep = "_")

setData(data)

setDataTable(name, value, category = getCategory())

getAutoNavigation()

setAutoNavigation(auto)

gCores()

setCores(integer)

gSignificant()

setSignificant(integer)

gPrecision()

setPrecision(integer)

getASevents()

gAnnotationHub()

setAnnotationHub(ah)

getASevent()

setASevent(event, data = NULL)

gEvent()

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

cache List of summary statistics
pca prcomp object (principal component analysis)
ica Object containing independent component analysis
correlation prcomp object (correlation analyses)
groupIndependenceTesting Object containing group independence testing results

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

Note
Needs to be called inside a reactive function

See Also
Other functions to get and set global variables: getClinicalMatchFrom(), getDifferentialExpression(), getDifferentialSplicing(), getGroups(), getHighlightedPoints(), getSelectedDataPanel()

---

getGroups Get or set groups

Description
Get or set groups

Usage

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

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

Arguments

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

Value

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

Note

Needs to be called inside a reactive function

See Also

Other functions to get and set global variables: `getClinicalMatchFrom()`, `getDifferentialExpression()`, `getDifferentialSplicing()`, `getGlobal()`, `getHighlightedPoints()`, `getSelectedDataPanel()`

---

getGtexDataTypes  
*Get GTEx data information*

Description

Get GTEx data information

Usage

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

Value

GTEx data information

See Also

Other functions associated with GTEx retrieval: `getDownloadsFolder()`, `getGtexTissues()`, `loadGtexData()`

Examples

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

## End(Not run)
```

---

**getHidden**

*Get or set hidden globally accessible elements*

**Description**

Get or set hidden globally accessible elements

**Usage**

```r
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

generateNumbers(table, by = NULL, toNumeric = FALSE)

Arguments

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

Value

Processed data matrix

Examples

event <- read.table(text = "ABC123 + 250 300 350
DEFG6 - 900 800 700")

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

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

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

getSampleFromSubject Get samples matching the given subjects

Description

Get samples matching the given subjects

Usage

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

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)
**getServerFunctions**

*Matches server functions from a given loader*

**Note**

Needs to be called inside a reactive function

**See Also**

Other functions to get and set global variables: `getClinicalMatchFrom()`, `getDifferentialExpression()`, `getDifferentialSplicing()`, `getGlobal()`, `getGroups()`, `getHighlightedPoints()`

---

**getServerFunctions**

**Description**

Matches server functions from a given loader

**Usage**

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

**Arguments**

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

**Value**

Invisible TRUE

---

**getSplicingEventCoordinates**

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

**Description**

Returns the coordinates of interest for a given event type

**Usage**

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

```r
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**

```r
getSplicingEventFromGenes(genes, ASevents, data = NULL)
getGenesFromSplicingEvents(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_201763374_201763594_NAV1",
"SE_1_+_183515472_183516238_183516387_183518343_SMG7",
"SE_1_+_183441784_183471388_183471526_183481972_SMG7",
"SE_1_+_181019422_181022709_181022813_181024361_MR1",
"SE_1_+_181695298_181700311_181700367_181701520_CACNA1E")
genes <- c("NAV1", "SMG7", "MR1", "HELLO")

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

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

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

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

getSplicingEventTypes  Get supported splicing event types

Description

Get supported splicing event types

Usage

getSplicingEventTypes(psi = NULL, acronymsAsNames = FALSE)
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

getSplicingEventTypes()

getSubjectFromSample  Get subjects from given samples

Description

Get subjects from given samples

Usage

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

Arguments

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

Value

Character: subject identifiers corresponding to the given samples

See Also

Other functions for data grouping: createGroupByAttribute(), getGeneList(), getSampleFromSubject(), groupPerElem(), plotGroupIndependence(), testGroupIndependence()
getTCGAd ataTypes

Examples

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

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

go
getTCGAd ataTypes

Get available parameters for TCGA data

Description

Parameters obtained via FireBrowse

Usage

getTCGAd ataTypes()

getTCGAd ates()

getTCGAc ohorts(cohort = NULL)

Arguments

cohort Character: filter results by cohorts (optional)

Value

Parsed response

See Also

Other functions associated with TCGA data retrieval: getDownloadsFolder(), isFirebrowseUp(), loadTCGAd ata(), parseTCGAsampleTypes()

Examples

getTCGAd ataTypes()
if (isFirebrowseUp()) getTCGAd ates()
if (isFirebrowseUp()) getTCGAc ohorts()
getUiFunctions  

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

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

**Usage**

```r
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**

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

**Arguments**

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

- **validator**  
  Character: valid elements for each event

- **areMultipleExonsValid**  
  Boolean: consider runs of exons as valid when comparing with the validator? Default is FALSE (see details)
Details

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

Value

Data.frame with valid events

Examples

event <- read.table(text = "
chr1 SE gene 17233 18061 . - .
chr1 SE dkfd 00000 30000 . - .
chr1 SE mRNA 17233 18061 . - .
chr1 SE exon 17233 17368 . - .
chr1 SE exon 17526 17742 . - .
chr1 SE exon 17915 18061 . - .
chr1 SE mRNA 17233 18061 . - .
chr1 SE exon 17233 17368 . - .
chr1 SE exon 17915 18061 . - .
chr1 SE gene 17233 18061 . - .
chr1 SE mRNA 17233 18061 . - .
chr1 SE exon 17233 17368 . - .
chr1 SE exon 17606 17742 . - .
chr1 SE mRNA 17233 18061 . - .
chr1 SE exon 17233 17368 . - .
chr1 SE exon 17915 18061 . - .
chr1 SE exon 17233 17368 . - .
chr1 SE exon 17915 18061 . - .
")
psychomics:::getValidEvents(event, validator)
ggplotTooltip(df, hover, x, y, eventData = NULL)

Argument

- **df**: Data frame
- **hover**: Mouse hover information for a given plot as retrieved from `hoverOpts`
- **x**: Character: name of the variable used for the X axis
- **y**: Character: name of the variable used for the Y axis
- **eventData**: Alternative splicing event information (if available)

Value

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 `hoverOpts`
- **x**: Character: name of the variable used for the X axis
- **y**: Character: name of the variable used for the Y axis
- **eventData**: Alternative splicing event information (if available)
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, ASevent = FALSE)
```

**Arguments**

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

**Value**

HTML element for a global selectize input
groupByAttribute  Data grouping interface

Description

Data grouping interface

Usage

groupByAttribute(ns, cols, id, example)
groupByPreMadeList(ns, data, id)
groupById(ns, id)
groupByExpression(ns, id)
groupByGrep(ns, cols, id)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ns</td>
<td>Namespace function</td>
</tr>
<tr>
<td>cols</td>
<td>Character or list: name of columns to show</td>
</tr>
<tr>
<td>id</td>
<td>Character: identifier</td>
</tr>
<tr>
<td>example</td>
<td>Character: text to show as an example</td>
</tr>
<tr>
<td>data</td>
<td>List: list of groups with elements</td>
</tr>
</tbody>
</table>

Value

HTML elements

groupManipulation  Logic server to manipulate data grouping

Description

Logic server to manipulate data grouping

Usage

groupManipulation(input, output, session, type)
Arguments

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

Value

HTML elements

groupManipulationInput

*Interface to manipulate data grouping*

Description

Interface to manipulate data grouping

Usage

groupManipulationInput(id, type)

Arguments

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

Value

HTML elements

groupPerElem

*Assign one group to each element*

Description

Assign one group to each element

Usage

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

groups List of integers: groups of elements

elem Character: all elements available

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

Value

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

See Also

Other functions for data grouping: `createGroupByAttribute()`, `getGeneList()`, `getSampleFromSubject()`, `getSubjectFromSample()`, `plotGroupIndependence()`, `testGroupIndependence()`

Examples

```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)
**Usage**

```r
## 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)
ovoan.surv <- survfit(fit, newdata=data.frame(age=60))
hchart(ovoan.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`
**HTMLfast**

Faster version of `shiny::HTML`

**Description**

Faster version of `shiny::HTML`

**Usage**

```r
HTMLfast(text)
```

**Arguments**

- `text` Character: text

**Value**

HTML element

---

**importGroupsFrom**

Import groups from a file

**Description**

Import groups from a file

**Usage**

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

**Arguments**

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

inclusionLevelsFilterInterface

*Interface to filter alternative splicing*

Description
Interface to filter alternative splicing

Usage
inclusionLevelsFilterInterface(ns)

Arguments
ns Namespace function

Value
HTML elements

inclusionLevelsInterface

*Interface to quantify alternative splicing*

Description
Interface to quantify alternative splicing

Usage
inclusionLevelsInterface(ns)

Arguments
ns Namespace function

Value
HTML elements
inlineDialog

**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 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(), getTCGAdatasetTypes(), loadTCGAdataset(), parseTCGAsampleTypes()

Examples
isFirebrowseUp()
**isRStudioServer**  
*Check if running in RStudio Server*

**Description**
Check if running in RStudio Server

**Usage**
```r
isRStudioServer()
```

**Value**
Boolean stating whether running in RStudio Server

---

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

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

**Usage**
```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

**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

**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)?
leveneTest

Value

Labelled groups

See Also

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

Examples

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

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

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

leveneTest

Levene's test

Description

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

Usage

leveneTest(x, g, centers = median)

Arguments

x Numeric vector or list of numeric vectors: non-numeric elements of a list will be coerced with a warning

g Vector or factor: groups of elements in x (ignored with a warning if x is a list)

centers Function used to calculate how much values spread; for instance, median (default) or mean

Details

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

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

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

Examples

```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)
```

Description

psichomics article’s link interface

Usage

`linkToArticles()`

Value

HTML elements

Description

Link to run arbitrary JavaScript code

Usage

`linkToRunJS(text, code)`
**listSplicingAnnotations**

**Arguments**

- `text` Character: text label
- `code` Character: JavaScript code

**Value**

HTML elements

---

```r
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**

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

**Arguments**

... Custom annotation loaded

**Value**

Named character vector with splicing annotation files available

**Examples**

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

---

```r
listSplicingAnnotations  List alternative splicing annotations
```

**Description**

List alternative splicing annotations
Usage

```r
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

```r
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

```r
loadAnnotation(consultation, cache = getAnnotationHubOption("CACHE"))
```
Arguments

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

Value

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

See Also

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

Examples

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

```r
loadAnnotationHub
```

Description

Load AnnotationHub

Usage

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

Arguments

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

Value

AnnotationHub object with all entries
**loadBy**

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

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

## Usage
```
loadBy(loader, FUN)
```

### Arguments
- **loader**
  - Character: name of the file responsible to load such function
- **FUN**
  - Function

### Value
Boolean vector

---

**loadCustomSplicingAnnotationSet**

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

## Description
Instructions to build the Shiny app

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

### Arguments
- **session**
  - Shiny session
- **input**
  - Shiny input
- **output**
  - Shiny output

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

Load file based on its format

Description

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

Usage

loadFile(
  file,
  formats = loadFileFormats(),
  ...
)

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?

loadDataModal

Warn user about loaded data

Description

Warn user about loaded data

Usage

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

loadFileFormats

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

loadFirebrowseFolders

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 = getGtexReleases()[[1]],
  progress = TRUE
)
```

**Arguments**

- `folder`  
  Character: folder containing data

- `data`  
  Character: data types to load (see `getGtexDataTypes`)

- `tissue`  
  Character: tissues to load (if NULL, load all); tissue selection may speed up data loading

- `release`  
  Numeric: GTEx data release to load

- `progress`  
  Boolean: display progress?
loadGtexDataShiny

Value
List with loaded data

See Also
Other functions associated with GTEx data retrieval: getDownloadsFolder(), getGtexDataTypes(), getGtexTissues()
Other functions to load data: loadLocalFiles(), loadSRAProject(), loadTCGAdata()

Examples
## Not run:
# Download and load all available GTEx data
data <- loadGtexData()

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

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

# Download and load data from a specific GTEx data release
data <- loadGtexData(tissue=c("Stomach", "Small Intestine"), release=7)

## End(Not run)

loadGtexDataShiny     Shiny wrapper to load GTEx data

Description
Shiny wrapper to load GTEx data

Usage
loadGtexDataShiny(session, input, replace = TRUE)

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

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

Description

Load local files

Usage

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

Arguments

folder | Character: path to folder or ZIP archive
ignore | Character: skip folders and filenames that match the expression
name | Character: name
verbose | Boolean: print steps?
Value
List of data frames from valid files

See Also
Other functions to load data: 

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

```r
## 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())`
loadTCGAdatadownload and process TCGA data

Description

TCGA data obtained via FireBrowse

Usage

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

Arguments

folder Character: directory to store the downloaded archives (by default, saves to getDownloadsFolder())
data Character: data to load (see getTCGAdataTypes())
exclude Character: files and folders to exclude from downloading and from loading into R (by default, exclude files containing .aux., .mage-tab. and MANIFEST.TXT)
Arguments passed on to `queryFirebrowseData`

- `date` Character: dates of the data retrieval by FireBrowse (by default, it uses the most recent data available)
- `cohort` Character: abbreviation of the cohorts (by default, returns data for all cohorts)
- `data_type` Character: data types (optional)
- `tool` Character: data produced by the selected FireBrowse tools (optional)
- `platform` Character: data generation platforms (optional)
- `center` Character: data generation centres (optional)
- `level` Integer: data levels (optional)
- `protocol` Character: sample characterization protocols (optional)
- `page` Integer: page of the results to return (optional)
- `page_size` Integer: number of records per page of results (optional)
- `sort_by` String: column used to sort the data (by default, sort by cohort)
- `download` Boolean: download missing files

**Value**

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

**See Also**

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

Other functions to load data: `loadGtexData()`, `loadLocalFiles()`, `loadSRAproject()

**Examples**

```r
getTCGACohorts()
getcGAdataTypes()
## Not run:
loadTCGAdataset(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
matchGroupASeventsAndGenes

Usage
loadTCGAsampleMetadata(data)

Arguments
data List of list of data frames

Value
List of list of data frames

matchGroupASeventsAndGenes

Match AS events and genes in a group

Description
Match AS events and genes in a group

Usage
matchGroupASeventsAndGenes(id, group, ASevents)

Arguments
id Character: identifier
group Data frame: group

Value
Data frame with groups containing matching elements

matchGroupSubjectsAndSamples

Match subjects and samples in a group

Description
Match subjects and samples in a group

Usage
matchGroupSubjectsAndSamples(id, group)
Arguments

- **id**
  - Character: identifier

- **group**
  - Data frame: group

Value

Data frame with groups containing matching elements

---

**matchSplicingEventsWithGenes**

*Match splicing events with respective genes*

**Description**

Match splicing events with respective genes

**Usage**

```r
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**

```r
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

---

**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

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

Available normalisation methods:

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

Value

Filtered and normalised gene expression

See Also

Other functions for gene expression pre-processing: `convertGeneIdentifiers()`, `filterGeneExpr()`, `plotGeneExprPerSample()`, `plotLibrarySize()`, `plotRowStats()`

Examples

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

---

**Description**

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

**Usage**

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

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>input</td>
<td>Shiny input</td>
</tr>
<tr>
<td>session</td>
<td>Shiny session</td>
</tr>
<tr>
<td>operation</td>
<td>Character: set operation</td>
</tr>
<tr>
<td>buttonId</td>
<td>Character: ID of the button to trigger operation</td>
</tr>
<tr>
<td>symbol</td>
<td>Character: Unicode symbol to visually indicate the operation performed</td>
</tr>
<tr>
<td>type</td>
<td>Character: type of group where set operations are to be performed</td>
</tr>
<tr>
<td>sharedData</td>
<td>Shiny app’s global variable</td>
</tr>
</tbody>
</table>

**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

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>clinical</td>
<td>Data frame: clinical data</td>
</tr>
<tr>
<td>data</td>
<td>Numeric: data values</td>
</tr>
<tr>
<td>censoring</td>
<td>Character: censor using left, right, interval or interval2</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>
<tr>
<td>session</td>
<td>Shiny session (only used for the visual interface)</td>
</tr>
<tr>
<td>filter</td>
<td>Boolean or numeric: elements to use (all are used by default)</td>
</tr>
<tr>
<td>survTime</td>
<td>survTime object: times to follow up, time start, time stop and event (optional)</td>
</tr>
<tr>
<td>lower, upper</td>
<td>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))</td>
</tr>
</tbody>
</table>
**optimSurvDiffSet**

**Value**

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

**See Also**

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

**Examples**

```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**

```r
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**

```r
code
```

**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**

```r
code
```

**Arguments**

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

**Value**

List with parsed response
Examples

```r
parsichomics:::parseFirebrowseMetadata("Dates")
parsichomics:::parseFirebrowseMetadata("Centers")
parsichomics:::parseFirebrowseMetadata("HeartBeat")
```

# Get the abbreviation and description of all cohorts available
parsichomics:::parseFirebrowseMetadata("Cohorts")

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

---

**parseMatsEvent**

*Parse alternative splicing events from MATS*

**Description**

Parse alternative splicing events from MATS

**Usage**

```r
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**

```r
# 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
"
) parsichomics:::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.
parseMatsGeneric

Value

Data frame with parsed junctions

See Also

parseMatsEvent()

Examples

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

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

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

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

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

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

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

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

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

parseMisoEvent Parse an alternative splicing event from MISO

Description

Parse an alternative splicing event from MISO

Usage

parseMisoEvent(event)

Arguments

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

Details

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

Value

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

Examples

# example of alternative splicing event: skipped exon (SE)

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

psichomics::parseMisoEvent(event)
```

parseMisoEventID  

**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**

```r
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](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**

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

Parse junctions of an event from MISO according to event type

Description

Parse junctions of an event from MISO according to event type

Usage

parseMisoGeneric(event, validator, eventType, coord, plusIndex, minusIndex)
parseMisoSE(event)
parseMisoMXE(event)
parseMisoRI(event, strand)
parseMisoA5SS(event)
parseMisoA3SS(event, plusIndex, minusIndex)
parseMisoTandemUTR(event, minusIndex)
parseMisoAFE(event)
parseMisoALE(event)

Arguments

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

Details

The following event types are available to be parsed:

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

**Value**
List of parsed junctions

**See Also**
- `parseMisoEvent()`

**Examples**

```r
# 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 17915 18061 . - .")
psichomics:::parseMisoSE(event)

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

# retained intron (RI) event
event <- read.table(text = "
  chr1 RI gene 17233 17742 . - .
  chr1 RI mRNA 17233 17742 . - .
  chr1 RI exon 17233 17742 . - .
  chr1 RI mRNA 17233 17742 . - .
  chr1 RI exon 17233 17364 . - .
  chr1 RI exon 17601 17742 . - .")
psichomics:::parseMisoRI(event)
```
# alternative 5' splice site (A5SS) event
event <- read.table(text = "
chr1 A5SS gene 17233 17742 . - .
chr1 A5SS mRNA 17233 17742 . - .
chr1 A5SS exon 17233 17368 . - .
chr1 A5SS exon 17526 17742 . - .
chr1 A5SS mRNA 17233 17742 . - .
chr1 A5SS exon 17233 17368 . - .
chr1 A5SS exon 17606 17742 . - .")
psichomics:::parseMisoA5SS(event)

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

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

# alternative first exon (AFE) event
event <- read.table(text = "
chr12 AFE gene 57916659 57920171 . + .
chr12 AFE mRNA 57919131 57920171 . + .
chr12 AFE exon 57919131 57920171 . + .
chr12 AFE mRNA 57919165 57918199 . + .
chr12 AFE exon 57917812 57917875 . + .
chr12 AFE exon 57918063 57918199 . + .")
psichomics:::parseMisoAFE(event)

# alternative last exon (ALE) event
event <- read.table(text = "
chr6 ALE gene 30620579 30822593 . + .
chr6 ALE mRNA 30822190 30822593 . + .
chr6 ALE exon 30822190 30822593 . + .
chr6 ALE mRNA 30620579 30620982 . + .
chr6 ALE exon 30620579 30620982 . + .")
psichomics:::parseMisoALE(event)
parseMisoId  
*Parse MISO's alternative splicing event identifier*

**Description**

Parse MISO's alternative splicing event identifier

**Usage**

`parseMisoId(id)`

**Arguments**

- **id**
  - Character: MISO alternative splicing event identifier

**Value**

Character with the parsed ID

**Examples**

```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:+")
psichomics:::parseMisoId(id)
```

parseSplicingEvent  
*Parse alternative splicing event identifier*

**Description**

Parse alternative splicing event identifier

**Usage**

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

Parse events from alternative splicing annotation

Description

Parse events from alternative splicing annotation

Usage

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

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
PARSEUPPAEvent

See Also

Other functions to prepare alternative splicing annotations: prepareAnnotationFromEvents()

Examples

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

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

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

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

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

parseSuppaEvent

Parses splicing events of a specific event type from SUPPA

Description

Parses splicing events of a specific event type from SUPPA

Usage

parseSuppaEvent(event)

Arguments

event Character vector: Splicing event attributes and junction positions

Details

More information about SUPPA available at https://bitbucket.org/regulatorygenomicsupf/suppa
The following event types are available to be parsed:
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)

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

Note
It only allows to parse one event type at once.

Examples

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

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)

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

# Parse RI event
juncitions <- read.table(text = "169768099 169770024 169770112 169771762")
psichomics:::parseSuppaRI(junctions, "+")

# Parse ALE event
juncitions <- read.table(text = "169763871 169764046 169767998 169764550 169765124 169767998")
psichomics:::parseSuppaALE(junctions, "+")
```

parseTCGAsampleTypes  
Parse sample information from TCGA sample identifiers

Description
Parse sample information from TCGA sample identifiers

Usage

parseTCGAsampleTypes(
  samples,
  filename = system.file("extdata", "TCGAsampleType.RDS", package = "psichomics")
)

parseTCGAsampleInfo(samples, match = NULL)

Arguments

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

Value
Metadata associated with each TCGA sample

See Also
Other functions associated with TCGA data retrieval: getDownloadsFolder(), getTCGAdatasetTypes(), isFirebrowseUp(), loadTCGAdataset()
Examples

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

parseUniprotXML

Parse XML from UniProt REST service

Description

Parse XML from UniProt REST service

Usage

parseUniprotXML(xml)

Arguments

xml response from UniProt

Value

List containing protein length and data frame of protein features

parseUrlsFromFirebrowseResponse

Retrieve URLs from a response to a FireBrowse data query

Description

Retrieve URLs from a response to a FireBrowse data query

Usage

parseUrlsFromFirebrowseResponse(res)

Arguments

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

Value

Named character with URLs
parseVastToolsEvent

Parses an alternative splicing event from VAST-TOOLS

Description

Parses an alternative splicing event from VAST-TOOLS

Usage

parseVastToolsEvent(event)

Arguments

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

Details

Junctions are parsed from

Value

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

Note

Only supports to parse one event at a time.

Examples

event <- read.table(text =
"NFYA HsaEX0042823 chr6:41046768-41046903 136 chr6:41040823,41046768-41046903,41051785 C2 0 N 0 N"
)
pischomics::parseVastToolsEvent(event)
parseVastToolsSE  Parse junctions of an event from VAST-TOOLS according to event type

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

Usage
parseVastToolsSE(junctions)
parseVastToolsRI(junctions, strand)
parseVastToolsA3SS(junctions)
parseVastToolsA5SS(junctions)

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

Details
The following event types are available to be parsed:

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

Value
List of parsed junctions

See Also
parseVastToolsEvent()

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

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

psichomics::parseVastToolsSE(junctions)

junctions <- read.table(text = "58864658 58864693 58864294 58864563")

psichomics::parseVastToolsRI(junctions, strand = "+")

ejunctions <- rbind(
  c(36276385, list(c(36277798, 36277315)), 36277974),
  c(7133604, 7133377, list(c(7133474, 7133456)))
)

psichomics::parseVastToolsA3SS(junctions)

ejunctions <- rbind(
  c(74650610, list(c(74650654, 74650658)), 74650982),
  c(list(c(49557666, 49557642), 49557746, 49557470))
)

psichomics::parseVastToolsA5SS(junctions)

--

performICA  Perform independent component analysis after processing missing values

---

Description

Perform independent component analysis after processing missing values

Usage

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

Arguments

data an optional data frame (or similar: see \code{model.frame}) containing the variables in the formula \code{formula}. By default the variables are taken from \code{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 \code{x} can be supplied. The value is passed to \code{scale}. 
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

missingValues
Integer: number of tolerated missing values per column to be replaced with the mean of the values of that same column

alg.typ

alg.typ
if alg.typ == "parallel" the components are extracted simultaneously (the default). if alg.typ == "deflation" the components are extracted one at a time.

fun

fun
the functional form of the G function used in the approximation to neg-entropy (see ‘details’).

alpha

alpha
constant in range [1, 2] used in approximation to neg-entropy when fun == "logcosh"

... 

... 
Arguments passed on to fastICA::fastICA

Value

Value
ICA result in a prcomp object

See Also

See Also
Other functions to analyse independent components: plotICA()

Examples

Examples
performICA(USArrests)

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

performPCA

performPCA
Perform principal component analysis after processing missing values

Description

Description
Perform principal component analysis after processing missing values

Usage

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

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

**Value**

PCA result in a `prcomp` object

**See Also**

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

**Examples**

```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
plotDistribution

Plot sample distribution

Description

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

Usage

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

Arguments

data Numeric, data frame or matrix: gene expression data or alternative splicing event quantification values (sample names are based on their names or colnames)

groups List of sample names or vector containing the group name per data value (read Details); if NULL or a character vector of length 1, data values are considered from the same group

rug Boolean: show rug plot?

vLine Boolean: plot vertical lines (including descriptive statistics for each group)?

... Arguments passed on to stats::density.default

bw the smoothing bandwidth to be used. The kernels are scaled such that this is the standard deviation of the smoothing kernel. (Note this differs from the reference books cited below, 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?
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

```r
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)
```

Description

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

Usage

```r
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

```r
elements <- paste("subjects", 1:50)
ref <- elements[10:50]
groups <- list(race=list(american=elements[1:3],
                        white=elements[4:7],
                        african=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 a optional vector specifying the group each observation belongs to. Used for tooltips and colouring the observations.
subset an optional vector specifying a subset of observations to be used for plotting. Useful when you have a large number of observations, you can specify a random subset.
labels the names of the variables (column names of x used by default).
cex the magnification of the plotting symbol (default=3)
width the width (and height) of the plot when viewed externally.
col an optional (hex) colour for each of the levels in the group vector.
big a logical parameter. Prevents inadvertent plotting of huge data sets. Default limit is 10 variables, to plot more than 10 set `big=TRUE`.
theme a character parameter specifying whether the theme should be colour (`colour`) or black and white (`bw`).
opacity numeric between 0 and 1. The opacity of the plotting symbols (default 0.9).
tooltip an optional vector with the tool tip to be displayed when hovering over an observation. You can include basic html.
leftmar space on the left margin
topmar space on the bottom margin
diag logical, whether or not the main diagonal is plotted (scatter plot of variables against themselves).

Value

Multiple scatterplots as a `pairsD3` object

See Also

Other functions to analyse independent components: `performICA()`

Examples

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

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

---

**plotLibrarySize**

*Plot library size*

**Description**

Plot library size

**Usage**

```r
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**

```r
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**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pca</td>
<td>prcomp object</td>
</tr>
<tr>
<td>pcX</td>
<td>Character: name of the X axis of interest from the PCA</td>
</tr>
<tr>
<td>pcY</td>
<td>Character: name of the Y axis of interest from the PCA</td>
</tr>
<tr>
<td>groups</td>
<td>Matrix: groups to plot indicating the index of interest of the samples (use clinical or sample groups)</td>
</tr>
<tr>
<td>individuals</td>
<td>Boolean: plot PCA individuals</td>
</tr>
<tr>
<td>loadings</td>
<td>Boolean: plot PCA loadings/rotations</td>
</tr>
<tr>
<td>nLoadings</td>
<td>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</td>
</tr>
</tbody>
</table>

**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)
```

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**

```r
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**

```r
plotProtein(molecule)
```
**plotRowStats**

**Arguments**

molecule  
Character: UniProt protein or Ensembl transcript identifier

**Value**

highchart 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 log10(mean). If `y = 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")
)
```
plotRowStats

Arguments

data Data frame or matrix containing samples per column and, for instance, gene or alternative splicing event per row

x, y Character: statistic to calculate and display in the plot per row; choose between mean, median, var or range (or transformations of those variables, e.g. log10(var)); if y = NULL, the density of x will be plot instead

subset Boolean or integer: data points to highlight

xmin, xmax, ymin, ymax Numeric: minimum and maximum X and Y values to draw in the plot

xlim, ylim Numeric: X and Y axis range

cache List of summary statistics for data previously calculated to avoid repeating calculations (output also returns cache in attribute named cache with appropriate data)

verbose Boolean: print messages of the steps performed

data2 Same as data argument but points in data2 are highlighted (unless data2 = NULL)

legend Boolean: show legend?

legendLabels Character: legend labels

Value

Plot of data

See Also

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

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

Examples

library(ggplot2)

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

# Plotting alternative splicing quantification
annot <- readFile("ex_splicing_annotation.RDS")
junctionQuant <- readFile("ex_junctionQuant.RDS")
psi <- quantifySplicing(annot, junctionQuant, eventType=c("SE", "MXE"))

medianVar <- plotRowStats(psi, x="median", y="var", xlim=c(0, 1)) +
  labs(x="Median PSI", y="PSI variance")
medianVar

rangeVar <- plotRowStats(psi, x="range", y="log10(var)", xlim=c(0, 1)) +
  labs(x="PSI range", y="log10(PSI variance)"
rangeVar

---

**plotSingleICA**  
Create a scatterplot for ICA

**Description**

Create a scatterplot for ICA

**Usage**

`plotSingleICA(ica, icX = 1, icY = 2, groups = NULL)`

**Arguments**

- `ica` Object containing an ICA  
- `icX` Character: name of the X axis  
- `icY` Character: name of the Y axis  
- `groups` Matrix: groups to plot indicating the index of interest of the samples (use clinical or sample groups)

**Value**

Scatterplot as an highcharter object

**Examples**

ica <- performICA(USArrests, scale=TRUE)  
psichomics:::plotSingleICA(ica)  
psichomics:::plotSingleICA(ica, icX=2, icY=3)

# Colour by groups  
groups <- NULL  
groups$sunny <- c("California", "Hawaii", "Florida")  
groups$ozEntrance <- c("Kansas")  
groups$novel <- c("New Mexico", "New York", "New Hampshire", "New Jersey")  
psichomics:::plotSingleICA(ica, groups=groups)
plotSplicingEvent  
Plot diagram of alternative splicing events

Description
Plot diagram of alternative splicing events

Usage
plotSplicingEvent(
  ASevent,
  data = NULL,
  showText = TRUE,
  showPath = TRUE,
  showAlternative1 = TRUE,
  showAlternative2 = TRUE,
  constitutiveWidth = NULL,
  alternativeWidth = NULL,
  intronWidth = NULL,
  constitutiveFill = "lightgray",
  constitutiveStroke = "darkgray",
  alternative1Fill = "#ffcb153",
  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

```
data <- c("A3SS_15_+_63353138_63353912_63353397_TPM1",
          "A3SS_11_-_61118463_61117115_61117894_CYB561A3",
          "A5SS_21_+_48055675_48056459_48056808_PRMT2",
          "A5SS_1_->_1274742_1274667_1274933_DVL1",
          "AFE_9_+_131902430_131901928_131904724_PPP2R4",
          "AFE_5_->_134686513_13468636_134681747_H2AFY",
          "ALE_12_+_56554104_56554410_5655171_MYL6",
          "ALE_8_->_38314874_38287466_38285953_FGFR1",
          "SE_9_+_6486925_6492303_6492401_6493826_UHRF2",
          "SE_19_->_5218431_5216778_5216731_5215606_PTPRS",
          "MXE_15_+_63335142_63335905_63336030_63336226_63336351_63349184_TPM1",
          "MXE_17_->_74090495_74087316_74087224_74086478_74086410_74085401_EXOC7")
diagram <- plotSplicingEvent(data)
## Not run:
diagram["A3SS_3_->_145796903_145794682_145795711_PLOD2"]
diagram[[6]]
diagram
## End(Not run)
```

plotSurvivalCurves  Plot survival curves

Description
Plot survival curves
Usage

plotSurvivalCurves(
  surv,
  mark = TRUE,
  interval = FALSE,
  pvalue = NULL,
  title = "Survival analysis",
  scale = NULL,
  auto = TRUE
)

Arguments

surv    Survival object
mark    Boolean: mark times?
interval Boolean: show interval ranges?
pvalue   Numeric: p-value of the survival curves
title    Character: plot title
scale    Character: time scale (default is days)
auto    Boolean: return the plot automatically prepared (TRUE) or only the bare minimum (FALSE)?

Value

Plot of survival curves

See Also

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

Examples

require("survival")
fit <- survfit(Surv(time, status) ~ x, data = aml)
plotSurvivalCurves(fit)

plotSurvivalPvaluesByCutoff

Plot p-values of survival difference between groups based on multiple cutoffs

Description

Plot p-values of survival difference between groups based on multiple cutoffs
Usage

plotSurvivalPvaluesByCutoff(
  clinical,
  data,
  censoring,
  event,
  timeStart,
  timeStop = NULL,
  followup = "days_to_last_followup",
  significance = 0.05,
  cutoffs = seq(0, 0.99, 0.01)
)

Arguments

- **clinical**: Data frame: clinical data
- **data**: Numeric: elements of interest to test against the cutoff
- **censoring**: Character: censor using left, right, interval or interval2
- **event**: Character: name of column containing time of the event of interest
- **timeStart**: Character: name of column containing starting time of the interval or follow up time
- **timeStop**: Character: name of column containing ending time of the interval (only relevant for interval censoring)
- **followup**: Character: name of column containing follow up time
- **significance**: Numeric: significance threshold
- **cutoffs**: Numeric: cutoffs to test

Value

p-value plot

See Also

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

Examples

```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")
names(clinical) <- c("patient.days_to_last_followup", "patient.days_to_death", "patient.stage_event.pathologic_stage",
```
\begin{verbatim}
plottableXranges

"patient.gender"
clinical <- do.call(rbind, rep(list(clinical), 5))
rownames(clinical) <- paste("Subject", seq(nrow(clinical)))

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

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

# Match between subjects and samples
match <- c("Cancer 1"="Subject 3",
          "Cancer 2"="Subject 17",
          "Cancer 3"="Subject 21")

eventData <- assignValuePerSubject(psi[3, ], match)

event <- "days_to_death"
timeStart <- "days_to_death"
plotSurvivalPvaluesByCutoff(clinical, eventData, censoring="right",
                           event=event, timeStart=timeStart)
\end{verbatim}

\textit{plottableXranges} \hspace{1cm} \textit{HTML code to plot a X-ranges series}

\textbf{Description}

HTML code to plot a X-ranges series

\textbf{Usage}

plottableXranges(hc, shiny = FALSE)

\textbf{Arguments}

\begin{itemize}
  \item \texttt{hc} \hspace{1cm} highcharter object
  \item \texttt{shiny} \hspace{1cm} Boolean: is the function running in a Shiny session?
\end{itemize}

\textbf{Value}

HTML elements
Description

Plot transcripts

Usage

plotTranscripts(
  info, 
  eventPosition = NULL, 
  event = NULL, 
  eventData = NULL, 
  shiny = FALSE 
)

Arguments

  info          Information retrieved from Ensembl
  eventPosition Numeric: coordinates of the alternative splicing event (ignored if event is set)
  event         Character: identifier of the alternative splicing event to plot
  eventData     Object containing event information to be parsed
  shiny         Boolean: is the function running in a Shiny session?

Value

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

See Also

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

Examples

  event <- "SE_12_-_7985318_7984360_7984200_7982602_SLC2A14"
  info <- queryEnsemblByEvent(event, species="human", assembly="hg19")
  ## Not run:
  plotTranscripts(info, event=event)
  ## End(Not run)
prepareAnnotationFromEvents

Prepare annotation from alternative splicing events

Description

In case more than one data frame with alternative splicing events is given, the events are cross-referenced according to the chromosome, strand and relevant coordinates per event type (see details).

Usage

prepareAnnotationFromEvents(...)

Arguments

... Data frame(s) of alternative splicing events to include in the annotation

Details

Events from two or more data frames are cross-referenced based on each event’s chromosome, strand and specific coordinates relevant for each event type:

- Skipped exon: constitutive exon 1 end, alternative exon (start and end) and constitutive exon 2 start
- Mutually exclusive exon: constitutive exon 1 end, alternative exon 1 and 2 (start and end) and constitutive exon 2 start
- Alternative 5’ splice site: constitutive exon 1 end, alternative exon 1 end and constitutive exon 2 start
- Alternative first exon: same as alternative 5’ splice site
- Alternative 3’ splice site: constitutive exon 1 end, alternative exon 1 start and constitutive exon 2 start
- Alternative last exon: same as alternative 3’ splice site

Value

List of data frames with the annotation from different data frames joined by event type

Note

When cross-referencing events, gene information is discarded.

See Also

Other functions to prepare alternative splicing annotations: parseSuppaAnnotation()
Examples

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

# Parse and prepare SUPPA annotation
suppa <- parseSuppaAnnotation(suppaOutput)
annot <- prepareAnnotationFromEvents(suppa)

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

# Parse rMATS annotation and prepare combined annotation from rMATS and SUPPA
mats <- parseMatsAnnotation(matsOutput)
annot <- prepareAnnotationFromEvents(suppa, mats)

prepareEventPlotOptions

Prepare event plot options

Description

Prepare event plot options

Usage

prepareEventPlotOptions(id, ns, labelsPanel = NULL)

Arguments

id Character: identifier
ns Namespace identifier
labelsPanel Tab panel containing options to label points

Value

HTML elements
**prepareFileBrowser**

Prepare file browser dialogue and update the input’s value accordingly to selected file or directory

**Description**

Prepare file browser dialogue and update the input’s value accordingly to selected file or directory

**Usage**

```r
default 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**

```r
prepareFirebrowseArchives(archive, md5, folder, outdir)
```
Arguments

archive  Character: path to downloaded archives
md5      Character: path to MD5 files of each archive
folder   Character: master directory where every archive will be extracted
outdir   Character: subdirectories where to move the extracted content

Value

Invisible TRUE if successful

Examples

```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

## Not run:
prepareJunctionQuant("Control rep1"=junctionFile1,
                      "Control rep2"=junctionFile2,
                      "KD rep1"=junctionFile3,
                      "KD rep2"=junctionFile4)

## End(Not run)
## Not run:
prepareGeneQuant("Control rep1"=geneCountFile1,
                 "Control rep2"=geneCountFile2,
                 "KD rep1"=geneCountFile3,
                 "KD rep2"=geneCountFile4)

## End(Not run)
preparePreMadeGroupForSelection

Prepare list of pre-made groups for a selectize element

Description
Prepare list of pre-made groups for a selectize element

Usage
preparePreMadeGroupForSelection(groups)

Arguments
- groups: List of list of characters

Value
List

prepareSRAmetadata
Prepare user-provided files to be loaded into psichomics

Description
Prepare user-provided files to be loaded into psichomics

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

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

prepareGeneQuant(...,
    output = "psichomics_gene_counts.txt",
    strandedness = c("unstranded", "stranded", "stranded (reverse)"
)
**Arguments**

- **file** Character: path to file
- **output** Character: path of output file (if NULL, only returns the data without saving it to a file)
- **...** Character: path of (optionally named) input files (see Examples)
- **startOffset** Numeric: value to offset start position
- **endOffset** Numeric: value to offset end position
- **strandedness** Character: strandedness of RNA-seq protocol; may be one of the following: unstraded, stranded or stranded (reverse)

**Value**

Prepared file (if output != NULL) and object

**Examples**

```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)
```

---

**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**  
*Preserve attributes when extracting values*

**Description**
Add object to class sticky

**Usage**
```
preserveAttributes(x)
```

**Arguments**
- `x` Object

**Value**
Object with class sticky

---

**processButton**  
*Style button used to initiate a process*

**Description**
Style button used to initiate a process

**Usage**
```
processButton(id, label, ..., class = "btn-primary")
```

**Arguments**
- `id` Character: button identifier
- `label` Character: label
- `...` Arguments passed on to `shiny::actionButton`
  - `icon` An optional `icon()` to appear on the button.
  - `width` The width of the input, e.g. '400px', or '100%'; see `validateCssUnit()`.
- `class` Character: class

---

**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
Value

HTML for a button

---

**processDatasetNames**  *Process dataset names*

**Description**

Process dataset names

**Usage**

`processDatasetNames(data)`

**Arguments**

- `data`: List of lists of data frames

**Details**

Avoid duplicated names and append the technology used for junction quantification

**Value**

Processed list of lists of data frames

---

**processSRAdata**  *Process SRA quantification data*

**Description**

Process SRA quantification data

**Usage**

`processSRAdata(files, data, IDcolname)`

**Arguments**

- `files`: Character: path to SRA quantification files
- `data`: Data frame: processed quantification data
- `IDcolname`: Character: name of the column containing the identifiers

**Value**

Process file
processSurvData

**Process survival data to calculate survival curves**

**Description**

Process survival data to calculate survival curves

**Usage**

```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

Description

Process survival curves terms 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

clinical Data frame: clinical data
censoring Character: censor using left, right, interval or interval2
event Character: name of column containing time of the event of interest
timeStart Character: name of column containing starting time of the interval or follow up time
timeStop Character: name of column containing ending time of the interval (only relevant for interval censoring)
group Character: group relative to each subject
formulaStr Character: formula to use
coxph Boolean: fit a Cox proportional hazards regression model?
scale Character: rescale the survival time to days, weeks, months or years
followup Character: name of column containing follow up time
survTime survTime object: times to follow up, time start, time stop and event (optional)

Details

The event time is only used to determine whether the event has occurred (1) or not (0) in case of missing values.

If survTime = NULL, survival times are obtained from the clinical dataset according to the names given in timeStart, timeStop, event and followup. This may become quite slow when used in a loop. If the aforementioned variables are constant, consider running getAttributesTime() outside the loop and using its output via the survTime argument of this function (see Examples).

Value

A list with a formula object and a data frame with terms needed to calculate survival curves
See Also

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

Examples

```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"
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)
}
```

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)
```
pubmedUI

Return the interface of relevant PubMed articles for a given gene

Description

Return the interface of relevant PubMed articles for a given gene

Usage

pubmedUI(ns, gene, ...)

Arguments

ns
Namespace function
gene
Character: gene
...
Arguments passed on to queryPubMed
top
Numeric: number of articles to retrieve
field
Character: field of interest where to look for terms (abstract by default)
sort
Character: sort by a given parameter (relevance by default)

Value

HTML interface of relevant PubMed articles

quantifySplicing

Quantify alternative splicing events

Description

Quantify alternative splicing events

Usage

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

Set of functions to quantify alternative splicing

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
queryEnsembl(path, query, grch37 = TRUE)

Arguments
- path: Character: API path
- query: Character: API query
- grch37: Boolean: query the Ensembl GRCh37 API? if FALSE, query the most recent API

Value
Parsed response or NULL if no response

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

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

queryEnsemblByGene

Query information from Ensembl

Description
Query information from Ensembl

Usage
queryEnsemblByGene(gene, species = NULL, assembly = NULL)
queryEnsemblByEvent(event, species = NULL, assembly = NULL, data = NULL)
**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**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>gene</td>
<td>Character</td>
<td>gene</td>
</tr>
<tr>
<td>species</td>
<td>Character</td>
<td>species (may be NULL for an Ensembl identifier)</td>
</tr>
<tr>
<td>assembly</td>
<td>Character</td>
<td>assembly version (may be NULL for an Ensembl identifier)</td>
</tr>
<tr>
<td>event</td>
<td>Character</td>
<td>alternative splicing event</td>
</tr>
<tr>
<td>data</td>
<td>Matrix or data frame</td>
<td>alternative splicing information</td>
</tr>
</tbody>
</table>

**Value**

Information from Ensembl

**See Also**

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

**Examples**

```r
queryEnsemblByGene("BRCA1", "human", "hg19")
queryEnsemblByGene("ENSG00000139618")
event <- "SE_17_-_41251792_41249306_41249261_41246877_BRCA1"
queryEnsemblByEvent(event, species="human", assembly="hg19")
```
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>format</td>
<td>Character: response format as JSON, CSV or TSV</td>
</tr>
<tr>
<td>date</td>
<td>Character: dates of the data retrieval by FireBrowse (by default, it uses the most recent data available)</td>
</tr>
<tr>
<td>cohort</td>
<td>Character: abbreviation of the cohorts (by default, returns data for all cohorts)</td>
</tr>
<tr>
<td>data_type</td>
<td>Character: data types (optional)</td>
</tr>
<tr>
<td>tool</td>
<td>Character: data produced by the selected FireBrowse tools (optional)</td>
</tr>
<tr>
<td>platform</td>
<td>Character: data generation platforms (optional)</td>
</tr>
<tr>
<td>center</td>
<td>Character: data generation centres (optional)</td>
</tr>
<tr>
<td>level</td>
<td>Integer: data levels (optional)</td>
</tr>
<tr>
<td>protocol</td>
<td>Character: sample characterization protocols (optional)</td>
</tr>
<tr>
<td>page</td>
<td>Integer: page of the results to return (optional)</td>
</tr>
<tr>
<td>page_size</td>
<td>Integer: number of records per page of results (optional)</td>
</tr>
<tr>
<td>sort_by</td>
<td>String: column used to sort the data (by default, sort by cohort)</td>
</tr>
</tbody>
</table>

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")
```

---

*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)
```

```r
transcript <- "ENST00000488540"
format <- "xml"
psichomics:::queryUniprot(transcript, format)
```
readAnnot  \hspace{1cm} \textit{Read custom or remote annotation}

\section*{Description}
Instructions to build the Shiny app

\section*{Usage}
\texttt{readAnnot(session, annotation, showProgress = FALSE)}

\section*{Arguments}
- \texttt{session} \hspace{1cm} \textit{Shiny session}
- \texttt{annotation} \hspace{1cm} \textit{Character: chosen annotation}
- \texttt{showProgress} \hspace{1cm} \textit{Boolean: show progress?}

\section*{Value}
\texttt{NULL} (function is only used to modify the Shiny session’s state or internal variables)

---

readFile  \hspace{1cm} \textit{Load psichomics-specific file}

\section*{Description}
Load psichomics-specific file

\section*{Usage}
\texttt{readFile(file)}

\section*{Arguments}
- \texttt{file} \hspace{1cm} \textit{Character: path to the file}

\section*{Value}
Loaded file

\section*{Examples}
\texttt{junctionQuant <- readFile("ex_junctionQuant.RDS")}
reduceDimensionality

Reduce dimensionality after processing missing values from data frame

Description

Reduce dimensionality after processing missing values from data frame

Usage

reduceDimensionality(
  data,
  type = c("pca", "ica"),
  center = TRUE,
  scale. = FALSE,
  naTolerance = NULL,
  missingValues = round(0.05 * ncol(data)),
  ...
)

Arguments

data Data frame: data

type Character: dimensionality reduction technique (pca or ica)

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

scale. Boolean: scale variables?

naTolerance Integer: percentage of tolerated missing values per column (deprecated)

missingValues Integer: number of tolerated missing values per column to be replaced with the mean of the values of that same column

... Extra parameters passed to FUN

Value

PCA result in a prcomp object or ICA result object
renameDuplicated

* Rename vector to avoid duplicated values with another vector *

**Description**

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

**Usage**

`renameDuplicated(check, comp)`

**Arguments**

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

**Value**

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

**Examples**

```r
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

- **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?
- **title**: NULL
- **seriesName**: "Gene expression"

Value

Box plot

Examples

```r
psychomics::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

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

Description
Replace a string with another in a list

Usage
replaceStrInList(tag, old, new)
**rm.null**

Filter NULL elements from a vector or a list

**Description**

Filter NULL elements from a vector or a list

**Usage**

`rm.null(v)`

**Arguments**

- `v` Vector or list

**Value**

Filtered vector or list with no NULL elements; if `v` is a vector composed of NULL elements, returns a NULL; if `v` is a list of NULL elements, returns an empty list

---

**roundDigits**

Round by the given number of digits

**Description**

Round by the given number of digits

**Usage**

`roundDigits(n)`

**Arguments**

- `n` Numeric: number to round

**Value**

Formatted number with a given numeric precision
roundMinDown  
*Round down/up the minimum/maximum value*

**Description**

Round down/up the minimum/maximum value

**Usage**

`roundMinDown(x, digits = 0)`

`roundMaxUp(x, digits = 0)`

**Arguments**

- `x`  
  Numeric: values

- `digits`  
  Numeric: number of maximum digits

**Value**

Rounded numeric value

---

saveProcessedSRAdata  
*Save processed SRA data in file*

**Description**

Save processed SRA data in file

**Usage**

`saveProcessedSRAdata(data, output = NULL)`

**Arguments**

- `data`  
  Object to save

- `output`  
  Character: output filename (if NULL, no file is saved)

**Value**

If `output = NULL`, save input to a file and return it as invisible; otherwise, just return the input
selectGroupsUI

**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

```r
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**  
Select pre-made groups from a selected item

### Description
Select pre-made groups from a selected item

### Usage
```
selectPreMadeGroup(groups, selected, genes = NULL)
```

### Arguments
- **groups**  
  List of list of characters
- **selected**  
  Character: selected item

### Value
Elements of selected item

---

**setFirebrowseData**  
Set data from FireBrowse

### Description
Set data from FireBrowse

### Usage
```
setFirebrowseData(input, output, session, replace = TRUE)
```

### Arguments
- **input**  
  Shiny input
- **output**  
  Shiny output
- **session**  
  Shiny session
- **replace**  
  Boolean: replace loaded data?
Value

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

---

**setLocalData**

*Load local files*

Description

Load local files

Usage

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

Arguments

- `input`: Shiny input
- `output`: Shiny output
- `session`: Shiny session
- `replace`: Boolean: replace loaded data?

Value

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

---

**setOperation**

*Perform set operations on selected groups*

Description

Perform set operations on selected groups

Usage

```r
setOperation(
    operation,
    groups,
    selected,
    symbol = "\n",
    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

`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
singleDiffAnalyses(
  vector,
  group,
  threshold = 1,
  step = 100,
  analyses = c("wilcoxRankSum", "ttest", "kruskal", "levene", "fligner")
)

Arguments
- **vector** Numeric
- **group** Character: group of each element in the vector
- **threshold** Integer: minimum number of values per group
- **step** Numeric: number of events before the progress bar is updated (a bigger number allows for a faster execution)
- **analyses** Character: analyses to perform (see Details)

Details
The following statistical analyses may be performed by including the respective string in the analysis argument:

- **ttest** - Unpaired t-test (2 groups)
- **wilcoxRankSum** - Wilcoxon Rank Sum test (2 groups)
- **kruskal** - Kruskal test (2 or more groups)
- **levene** - Levene’s test (2 or more groups)
- **fligner** - Fligner-Killeen test (2 or more groups)

Value
A row from a data frame with the results
**sortCoordinates**  
*Sort coordinates for some event types*

**Description**  
Some programs sort the coordinates of specific event types differently. To make them all comparable across programs, the coordinates are ordered by increasing (plus strand) or decreasing order (minus strand).

**Usage**  
```r
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**  
```r
startProcess(id)
endProcess(id, time = NULL, closeProgressBar = TRUE)
```

**Arguments**  
- `id`  
  Character: button identifier
- `time`  
  POSIXct object: start time needed to show the interval time (if NULL, the time interval is not displayed)
- `closeProgressBar`  
  Boolean: close progress bar?
Value

StartProcess returns the start time of the process (may be used as the time argument to endProcess), whereas endProcess returns the difference between current time and time (or NULL if time is not specified)

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>message</td>
<td>Character: progress message</td>
</tr>
<tr>
<td>divisions</td>
<td>Integer: number of divisions in the progress bar</td>
</tr>
<tr>
<td>global</td>
<td>Shiny’s global variable</td>
</tr>
<tr>
<td>value</td>
<td>Integer: current progress value</td>
</tr>
<tr>
<td>max</td>
<td>Integer: maximum progress value</td>
</tr>
<tr>
<td>detail</td>
<td>Character: detailed message</td>
</tr>
<tr>
<td>console</td>
<td>Boolean: print message to console?</td>
</tr>
</tbody>
</table>
Details

If divisions is not NULL, a progress bar starts with the given divisions. If value = NULL, the progress bar increments one unit; otherwise, the progress bar increments value.

Value

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

styleModal

Create a modal window

Description

Create a modal window

Usage

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

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

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

infoModal(session, title, ..., size = "small", footer = NULL, caller = NULL)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>session</td>
<td>Shiny session</td>
</tr>
<tr>
<td>title</td>
<td>Character: title</td>
</tr>
<tr>
<td>...</td>
<td>Arguments passed on to shiny::modalDialog</td>
</tr>
<tr>
<td>easyClose</td>
<td>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.</td>
</tr>
</tbody>
</table>
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()

Description

Helper text to explain what happens when a subject matches multiple samples when performing survival analysis

Usage

subjectMultiMatchWarning()

Value

Character
subsetGeneExpressionFromMatchingGenes

Subset gene expression based on (full or partial) matching genes

Description

Subset gene expression based on (full or partial) matching genes

Usage

subsetGeneExpressionFromMatchingGenes(geneExpr, gene)

Arguments

geneExpr: Data frame or matrix: gene expression
gene: Character: genes to look for

Value

Gene expression subset for the input genes

survdiffTerms

Test Survival Curve Differences

Description

Tests if there is a difference between two or more survival curves using the $G^p$ family of tests, or for a single curve against a known alternative.

Usage

survdiffTerms(survTerms, ...)

Arguments

survTerms: survTerms object: survival terms obtained after running processSurvTerms (see examples)
...: Arguments passed on to survival::survdiff
subset: expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating which observation numbers are to be included (or excluded if negative), or a character vector of row names to be included. All observations are included by default.
na.action a missing-data filter function. This is applied to the model.frame after any subset argument has been used. Default is `options()$na.action`.

rho a scalar parameter that controls the type of test.

timefix process times through the `aeqSurv` function to eliminate potential roundoff issues.

Value

`survfit` object. See `survfit.object` for details. Methods defined for `survfit` objects are `print`, `plot`, `lines`, and `points`.

Description

This function implements the G-rho family of Harrington and Fleming (1982), with weights on each death of \( S(t)^\rho \), where \( S(t) \) is the Kaplan-Meier estimate of survival. With \( \rho = 0 \) this is the log-rank or Mantel-Haenszel test, and with \( \rho = 1 \) it is equivalent to the Peto & Peto modification of the Gehan-Wilcoxon test.

Peto and Peto show that the Gehan-Wilcoxon test can be badly biased if the two groups have different censoring patterns, and proposed an alternative. Prentice and Marek later showed an actual example where this issue occurs. For most data sets the Gehan-Wilcoxon and Peto-Peto-Prentice variant will hardly differ, however.

If the right hand side of the formula consists only of an offset term, then a one sample test is done. To cause missing values in the predictors to be treated as a separate group, rather than being omitted, use the `factor` function with its `exclude` argument to recode the right-hand-side covariate.

References


See Also

Other functions to analyse survival: `assignValuePerSubject()`, `getAttributesTime()`, `labelBasedOnCutoff()`, `optimalSurvivalCutoff()`, `plotSurvivalCurves()`, `plotSurvivalPvaluesByCutoff()`, `processSurvTerms()`, `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",
"otherColumnInfo")
```

survfit.survTerms

Create survival curves

Description

Create survival curves

Usage

```r
## S3 method for class 'survTerms'
survfit(formula, ...)
```

Arguments

- `formula`: survTerms object: survival terms obtained after running `processSurvTerms` (see examples)
- `...`: Arguments passed on to `survival::survdiff`
- `subset`: expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating which observation numbers are to be included (or excluded if negative), or a character vector of row names to be included. All observations are included by default.
- `na.action`: a missing-data filter function. This is applied to the `model.frame` after any `subset` argument has been used. Default is `options()$na.action`.
- `rho`: a scalar parameter that controls the type of test.
- `timefix`: process times through the `aeqSurv` function to eliminate potential roundoff issues.

Details

A survival curve is based on a tabulation of the number at risk and number of events at each unique death time. When time is a floating point number the definition of "unique" is subject to interpretation. The code uses `factor()` to define the set. For further details see the documentation for the appropriate method, i.e., `?survfit.formula` or `?survfit.coxph`.

A `survfit` object may contain a single curve, a set of curves (vector), a matrix of curves, or even a 3 way array: `dim(fit)` will reveal the dimensions. Predicted curves from a `coxph` model have one
row for each stratum in the Cox model fit and one column for each specified covariate set. Curves from a multi-state model have one row for each stratum and a column for each state, the strata correspond to predictors on the right hand side of the equation. The default printing and plotting order for curves is by column, as with other matrices.

**Value**

survfit object. See survfit.object for details. Methods defined for survfit objects are print, plot, lines, and points.

**See Also**

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

**Examples**

```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)
```

---

**t.sticky**

Preserve attributes of sticky objects when extracting or transposing object

**Description**

Most attributes - with the exception of names, dim, dimnames, class and row.names - are preserved in simple transformations of objects from class sticky.
Usage

```r
## S3 method for class 'sticky'
t(x)
```

```r
## S3 method for class 'sticky'
x[i, j, ...]
```

Arguments

- `x` Object
- `i, j, ...` Numeric or character: indices of elements to extract

Value

Transformed object with most attributes preserved

---

**tabDataset**

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

Description

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

Usage

```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

tableRow(..., th = FALSE)

Arguments

... Elements to include in the row
th Boolean: is this row the table head?

Value

HTML elements

testGroupIndependence

Multiple independence tests between reference groups and list of groups

Description

Test multiple contingency tables comprised by two groups (one reference group and another containing remaining elements) and provided groups.

Usage

testGroupIndependence(ref, groups, elements, pvalueAdjust = "BH")

Arguments

ref List of character: list of groups where each element contains the identifiers of respective elements
groups List of characters: list of groups where each element contains the identifiers of respective elements
elements Character: all available elements (if a data frame is given, its rownames will be used)
pvalueAdjust Character: method used to adjust p-values (see Details)
Details

The following methods for p-value adjustment are supported by using the respective string in the `pvalueAdjust` argument:

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

Value

`multiGroupIndependenceTest` object, a data frame containing:

- `attribute`: Name of the original groups compared against the reference groups
- `table`: Contingency table used for testing
- `pvalue`: Fisher’s exact test’s p-value

See Also

`parseCategoricalGroups()` and `plotGroupIndependence()`

Other functions for data grouping: `createGroupByAttribute()`, `getGeneList()`, `getSampleFromSubject()`, `getSubjectFromSample()`, `groupPerElem()`, `plotGroupIndependence()`

Examples

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

Multiple independence tests between a reference group and list of
groups

Description

Uses Fisher’s exact test.

Usage

testSingleIndependence(ref, groups, elements, pvalueAdjust = "BH")

Arguments

ref Character: identifier of elements in reference group

groups List of characters: list of groups where each element contains the identifiers of
respective elements

elements Character: all subject identifiers

pvalueAdjust Character: method used to adjust p-values (see Details)

Details

The following methods for p-value adjustment are supported by using the respective string in the
pvalueAdjust argument:

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

Value

Returns a groupIndependenceTest object: a list where each element is a list containing:

attribute Name of the original groups compared against the reference groups

table Contingency table used for testing

pvalue Fisher’s exact test’s p-value
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 aoeSurv function to eliminate potential roundoff issues.

Value

- p-value of the survival difference or NA

Note

Instead of raising errors, returns NA

See Also

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

```r
require("survival")
data <- aml
timeStart <- "event"
event <- "event"
followup <- "time"
data$event <- NA
data$event[aml$status == 1] <- aml$time[aml$status == 1]
censoring <- "right"
formulaStr <- "x"
survTerms <- processSurvTerms(data, censoring=censoring, event=event,
                             timeStart=timeStart, followup=followup,
                             formulaStr=formulaStr)
testSurvival(survTerms)
```

testSurvivalCutoff

Test the survival difference between two survival groups given a cutoff

Description

Test the survival difference between two survival groups given a cutoff

Usage

```r
testSurvivalCutoff(
cutoff, 
data,  
filter = TRUE,  
clinical, ...
,  
session = NULL,  
survivalInfo = FALSE
)
```

Arguments

- `cutoff` Numeric: Cutoff of interest
- `data` Numeric: elements of interest to test against the cutoff
- `filter` Boolean or numeric: elements to use (all are used by default)
- `clinical` Data frame: clinical data
- `...` Arguments passed on to `processSurvTerms`
- `censoring` Character: censor using left, right, interval or interval2
- `scale` Character: rescale the survival time to days, weeks, months or years
- `formulaStr` Character: formula to use
- `coxph` Boolean: fit a Cox proportional hazards regression model?
survTime  survTime object: times to follow up, time start, time stop and event (optional)

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

followup  Character: name of column containing follow up time

session  Shiny session

survivalInfo  Boolean: return extra survival information

Value

p-value of the survival difference

---

textSuggestions  

Create script for auto-completion of text input

Description

Uses the JavaScript library jquery.textcomplete

Usage

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

Arguments

id  Character: input ID
words  Character: words to suggest
novalue  Character: string when there’s no matching values
char  Character to succeed accepted word

Value

HTML string with the JavaScript script prepared to run

Examples

words <- c("tumorStage", "age", "gender")
psichomics:::textSuggestions("textareaid", words)
### toJSarray

**Convert vector of values to JavaScript array**

#### Description
Convert vector of values to JavaScript array

#### Usage

```javascript
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

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

### transformData

**Transform data in data frame**

#### Description
Transform data in data frame

#### Usage

```javascript
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)
Arguments

val  Integer: values to transform

type  Character: type of transformation

avoidZero  Boolean: add the smallest non-zero number available (.Machine$double.xmin) to avoid infinity values following log-transformation (may not be plotted); useful for p-values of 0

Value

Integer containing transformed values

---

`trimWhitespace`  
Trims whitespace from a word

Description

Trims whitespace from a word

Usage

`trimWhitespace(word)`

Arguments

word  Character to trim

Value

Character without whitespace

Examples

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

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

**Description**

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

**Usage**

uniqueBy(data, ...)

**Arguments**

data Data frame or matrix
...
Name of columns

**Value**

Data frame with unique values based on set of columns

---

**updateClinicalParams**

*Update available clinical attributes when the clinical data changes*

**Description**

Update available clinical attributes when the clinical data changes

**Usage**

updateClinicalParams(session, attrs)

**Arguments**

session Shiny session
attrs Character: subject attributes

**Value**

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

*Change the value of a fileBrowserInput() on the client*

**Description**

Change the value of a fileBrowserInput() on the client

**Usage**

```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

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

Display results of correlation analyses

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

Usage

## S3 method for class 'GEandAScorrelation'
x[genes = NULL, ASevents = NULL]

## S3 method for class 'GEandAScorrelation'
plot(
x,  
  autoZoom = FALSE,  
  loessSmooth = TRUE,  
  loessFamily = c("gaussian", "symmetric"),  
  colour = "black",  
  alpha = 0.2,  
  size = 1.5,  
  loessColour = "red",  
  loessAlpha = 1,  
  loessWidth = 0.5,  
  fontSize = 12,  
  ...,
  colourGroups = NULL,  
  legend = FALSE,  
  showAllData = TRUE,  
  density = FALSE,  
  densityColour = "blue",  
  densityWidth = 0.5
## S3 method for class 'GEandAScorrelation'
print(x, ...)

## S3 method for class 'GEandAScorrelation'
as.table(x, pvalueAdjust = "BH", ...)

**Arguments**

- `x` GEandAScorrelation object obtained after running `correlateGEandAS()`
- `genes` Character: genes
- `ASevents` Character: AS events
- `autoZoom` Boolean: automatically set the range of PSI values based on available data? If FALSE, the axis relative to PSI values will range from 0 to 1
- `loessSmooth` Boolean: plot a smooth curve computed by `stats::loess.smooth`?
- `loessFamily` Character: if gaussian, loess fitting is by least-squares, and if symmetric, a re-descending M estimator is used
- `colour` Character: points’ colour
- `alpha` Numeric: points’ alpha
- `size` Numeric: points’ size
- `loessColour` Character: loess line’s colour
- `loessAlpha` Numeric: loess line’s opacity
- `loessWidth` Numeric: loess line’s width
- `fontSize` Numeric: plot font size
- `...` Arguments passed on to `stats::loess.smooth`
  - `span` smoothness parameter for loess.
  - `degree` degree of local polynomial used.
  - `evaluation` number of points at which to evaluate the smooth curve.
- `colourGroups` List of characters: sample colouring by group
- `legend` Boolean: show legend for sample colouring?
- `showAllData` Boolean: show data outside selected groups as a single group (coloured based on the colour argument)
- `density` Boolean: contour plot of a density estimate
- `densityColour` Character: line colour of contours
- `densityWidth` Numeric: line width of contours
- `pvalueAdjust` Character: method used to adjust p-values (see Details)
Details

The following methods for p-value adjustment are supported by using the respective string in the `pvalueAdjust` argument:

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

Value

Plots, summary tables or results of correlation analyses

See Also

Other functions to correlate gene expression and alternative splicing: `correlateGEandAS()`

Examples

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