

Package ‘clinDataReview’

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Type Package

Title Clinical Data Review Tool

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Description Creation of interactive tables, listings and figures ('TLFs') and associated report for exploratory analysis of data in a clinical trial, e.g. for clinical oversight activities.
Interactive figures include sunburst, treemap, scatterplot, line plot and barplot of counts data.
Interactive tables include table of summary statistics (as counts of adverse events, enrollment table) and listings.
Possibility to compare data (summary table or listing) across two data batches/sets.
A clinical data review report is created via study-specific configuration files and template 'R Markdown' reports contained in the package.

Imports bookdown, clinUtils, crosstalk, data.table, ggplot2, haven, htmltools, htmlwidgets, knitr, jsonlite, jsonvalidate, methods, plotly, plyr, rmarkdown, stats, stringr, utils, tools, yaml

Suggests countrycode, inTextSummaryTable (>= 2.19.0), pander, patientProfilesVis (>= 0.12.0), reshape2, testthat, xml2, DT

SystemRequirements pandoc (to create a clinical data review report)

URL <https://github.com/openanalytics/clinDataReview>

BugReports <https://github.com/openanalytics/clinDataReview/issues>

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VignetteBuilder knitr

RoxygenNote 7.1.1

NeedsCompilation no

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R topics documented:

addDateOfReportRun	3
addFacetPanel	4
addReferenceLinesClinDataPlot	5
annotateData	6
barplotClinData	9
boxplotClinData	13
checkAvailabilityMetadata	16
checkConfigFile	17
checkReportTitles	18
checkTemplatesName	18
checkValueType	19
clinDataReview-common-args	20
clinDataReview-common-args-report	21
clinDataReview-common-args-summaryStatsVis	22
clinDataReview-templates	23
collapseHtmlContent	28
convertMdToHtml	29
createClinDataReviewReportSkeleton	30
createExampleMetadata	31
createMainConfigSkeleton	31
createPatientProfileVar	32
createRedirectPage	33
createTemplateDoc	33
exportSessionInfoToMd	34
filterData	35
filterDataSingle	38
forceParams	39
formatDataForPlotClinData	40
formatHoverText	41
formatPathDateInfoMetadata	41
formatPlotlyClinData	42
formatToHierarchicalData	43
getAxisLimPlot	44
getDataReferenceLines	45
getDimGgplot	46
getFacetVars	46
getFctTypeReferenceLines	47
getJsDepClinDataReview	47
getMdFromConfig	48
getMdHeader	49
getMetadata	50

getParamsFromConfig	51
getParFctReferenceLines	52
getPathHyperlink	53
getPathTemplate	53
getPlotTableVars	54
getSizePlotClinData	55
gitbook_clinDataReview_report	56
html_clinDataReview_report	57
JSONSchToRd	58
knitPrintClinDataReview	59
knit_print.clinDataReview	60
knit_print.clinDataReviewMetadata	60
merge.sessionInfo	61
moveSkeletonFiles	62
moveXpt	62
plotCountClinData	63
processData	65
renamePathDateInfoMetadata	66
renderInNewSession	66
render_clinDataReviewReport	67
scatterplotClinData	69
setFacetLayoutWrap	74
setPaletteStaticScatterplotClinData	75
staticScatterplotClinData	76
sunburstClinData	78
tableClinData	81
timeProfileIntervalPlot	83
transformData	86
treemapClinData	87
varToFm	90
zipClinDataReview	91

Index	92
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addDateOfReportRun *Add date of report running*

Description

Add the today's date of when the report runs to the info of the metadata.

Usage

```
addDateOfReportRun(summaryInfo)
```

Arguments

summaryInfo matrix, see output from [getMetadata](#).

Value

A matrix, same as input summaryInfo with an extra row with the date of today.

addFacetPanel	<i>Add facet-panel to single plotly plot.</i>
---------------	---

Description

Add facet-panel to single plotly plot.

Usage

```
addFacetPanel(
  pl,
  panelLab,
  panelWidth = 20,
  fontSize = 15,
  side = c("top", "right")
)
```

Arguments

pl	a plotly object to which to add a single facet panel
panelLab	text to be shown in the facet panel
panelWidth	thickness of the panel in pixels.
fontSize	fontsize of facetText
side	the side of the plot to show the panel (currently only right panels are implemented.)

Details

plot title clipping.

Incase case side = 'top', the plot title (eg. layout(title = "title")) will clip with the top pannel.

Resolve this with the following configutations: (once all the subplots have already been combined)
 layout(title = list(text = "title", yref = "container", y = 1)) # place the title at absolute
 top of the page margin = list(t = panelWidth + heightTitleTextInPixels) # If font size =
 15 roughly equal to 20 pixels.

Value

plotly object with the facet panel added.

Author(s)

lennart tuijnder

`addReferenceLinesClinDataPlot`

Add reference (horizontal/vertical/diagonal) lines to a clinical data plot

Description

Add reference (horizontal/vertical/diagonal) lines to a clinical data plot

Usage

```
addReferenceLinesClinDataPlot(  
  gg,  
  data,  
  xVar,  
  yVar,  
  xLim = NULL,  
  yLim = NULL,  
  refLinePars = NULL,  
  facetPars = NULL  
)
```

Arguments

<code>gg</code>	<code>ggplot</code> object.
<code>data</code>	Data.frame with data.
<code>xVar</code>	String with column of data containing x-variable.
<code>yVar</code>	String with column of data containing y-variable.
<code>xLim</code>	Numeric vector of length 2 with limits for the x/y axes.
<code>yLim</code>	Numeric vector of length 2 with limits for the x/y axes.
<code>refLinePars</code>	(optional) Nested list, with parameters for each reference line(s). Each sublist (a.k.a reference line) contains: <ul style="list-style-type: none">• aesthetic value(s) or variable(s) for the lines (in this case column names of data) for reference lines. The line position is controlled by the aesthetics supported in <code>geom_vline</code>, <code>geom_hline</code> and <code>geom_abline</code>.• 'label': (optional) Logical specifying if the line should be annotated (FALSE to not annotate the line) or string with annotation label. By default, the value of the position of the horizontal/vertical line or the equation of the diagonal line is displayed.
<code>facetPars</code>	List with facetting parameters, passed to the facetting function. Variables should be specified as character or formula. For 'wrap' facetting (<code>facetType</code> is 'wrap'), if the layout is not specified via <code>nrow/ncol</code> , 2 columns are used by default.

Value

Updated `ggplot` object.

Author(s)

Laure Cougnaud

annotateData	<i>Annotate a SDTM dataset.</i>
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Description

Standard annotation variables are available via the parameter `annotType`. Custom dataset/variables of interest are specified via the `annotDataset/annotVar` parameters.

Usage

```
annotateData(
  data,
  dataPath = ".",
  annotations,
  subjectVar = "USUBJID",
  verbose = FALSE,
  labelVars = NULL,
  labelData = "data"
)
```

Arguments

<code>data</code>	Data.frame with input data to annotate.
<code>dataPath</code>	String with path to the data.
<code>annotations</code>	Annotations (or list of those) either as a: <ul style="list-style-type: none"> • string with standard annotation type, among: <ul style="list-style-type: none"> – demographics: standard variables from the demographics data (DM or ADSL) are extracted – exposed_subjects: a logical variable: EXFL is added to data, identifying exposed subjects, i.e. subjects included in the exposure dataset (EX/ADEX) dataset and with non empty and non missing start date ('EXSTDTC', 'STDY' or 'ASTDY') – functional_groups_lab: a character variable: 'LBFCTGRP' is added to data based on standard naming of the parameter code ('PARAMCD' or 'LBTESTCD' variable) • list of custom annotation, with: <ul style="list-style-type: none"> – (optional) annotation dataset, either:

- * 'dataset': String with name of the annotation dataset, e.g. 'ex' to import data from the file: '[dataset].sas7bdat' in dataPath
 - * 'data': Data.frame with annotation dataset
- The input data is used if 'data' and 'dataset' are not specified.
- 'vars': Either:
 - * Character vector with variables of interest from annotation dataset. If not specified, all variables of the dataset are considered.
 - * String with new variable name computed from varFct
 - 'varFct': (optional) Either:
 - * function of data or string containing such function (e.g. 'function(data) ...')
 - * string containing manipulations from column names of data (e.g. 'col1 + col2')
 used to create a new variable specified in vars.
 - 'filters': (optional) Filters for the **annotation dataset**, see filters parameter of `filterData`.
The annotation dataset is first filtered, before being combined to the input data, such as only the records retained in the annotation dataset will be annotated in the output data. Other records will have missing values in the annotated variables.
 - 'varLabel': (optional) label for new variable in case varFct is specified.
 - 'varsBy': (optional) Character vector with variables used to merge input data and the annotation dataset. If not specified:
 - * if an external dataset (dataset/data) is specified: subjectVar is used
 - * otherwise: annotation dataset and input data are merged by rows IDs

subjectVar	String with subject ID variable, 'USUBJID' by default.
verbose	Logical, if TRUE (FALSE by default) progress messages are printed in the current console. For the visualizations, progress messages during download of subject-specific report are displayed in the browser console.
labelVars	Named character vector containing variable labels of data. This will be updated with the labels of the extra annotation variables (in <code>attr(output, 'labelVars')</code>).
labelData	(optional) String with label for input data, that will be included in progress messages.

Value

Annotated data. If labelVars is specified, the output contains an extra attribute: 'labelVars' containing updated labelVars (accessible via: `in attr(output, 'labelVars')`).

Examples

```
library(clinUtils)

data(dataADaMCDISCP01)
```

```

dataLB <- dataADaMCDISCP01$ADLBC
dataDM <- dataADaMCDISCP01$ADSL
dataAE <- dataADaMCDISCP01$ADAE

labelVars <- attr(dataADaMCDISCP01, "labelVars")

# standard annotations:
# path to dataset should be specified via: 'pathData'
## Not run:
annotateData(dataLB, annotations = "demographics", pathData = ...)

## End(Not run)

# add all variables in annotation data (if not already available)
head(annotateData(dataLB, annotations = list(data = dataDM)), 1)

# only variables of interest
head(annotateData(dataLB, annotations = list(data = dataDM, vars = c("ARM", "ETHNIC"))), 1)

# filter annotation dataset
dataAnnotated <- annotateData(dataLB,
  annotations = list(
    data = dataDM,
    vars = c("ARM", "ETHNIC"),
    filters = list(var = "ARM", value = "Placebo")
  )
)
head(subset(dataAnnotated, ARM == "Placebo"), 1)
head(subset(dataAnnotated, is.na(ARM)), 1)

# worst-case scenario: add a new variable based on filtering condition
dataAE$AESEV <- factor(dataAE$AESEV, levels = c('MILD', 'MODERATE', 'SEVERE'))
dataAEWC <- annotateData(
  data = dataAE,
  annotations = list(
    vars = "WORSTINT",
    # create new variable: 'WORSTINT'
    # with TRUE if maximum toxicity grade per subject/test
    # (if multiple, they are all retained)
    filters = list(
      var = "AESEV",
      # max will take latest level in a factor
      # (so 'MODERATE' if 'MILD'/'MODERATE' are available)
      valueFct = function(x) x[which.max(as.numeric(x))],
      varsBy = c("USUBJID", "AEDECOD"),
      keepNA = FALSE,
      varNew = "WORSTINT",
      labelNew = "worst-case"
    )
  ),
  labelVars = labelVars,
  verbose = TRUE

```



```

)
attr(dataAESC, "labelVars")["WORSTINT"]

# add a new variable based on a combination of variables:
dataLB <- annotateData(dataLB,
  annotations = list(vars = "HILORATIO", varFct = "A1HI / A1LO")
)

# add a new variable based on extraction of a existing variable
# Note: slash should be doubled when the function is specified as text
dataLB <- annotateData(dataLB,
  annotations = list(vars = "PERIOD", varFct = "sub('.* Week (.+)', 'Week \\\\1', AVISIT)")
)

# multiple annotations:
dataAnnotated <- annotateData(dataLB,
  annotations = list(
    list(data = dataDM, vars = c("ARM", "ETHNIC")),
    list(data = dataAE, vars = c("AESEV"))
  )
)
head(dataAnnotated, 1)

```

barplotClinData

Barplot interactive plot.

Description

Barplot interactive plot.

Usage

```

barplotClinData(
  data,
  xVar,
  yVar,
  xLab = getLabelVar(xVar, labelVars = labelVars),
  yLab = getLabelVar(yVar, labelVars = labelVars),
  colorVar = NULL,
  colorLab = getLabelVar(colorVar, labelVars = labelVars),
  colorPalette = NULL,
  barmode = "group",
  titleExtra = NULL,
  title = paste(paste(yLab, "vs", xLab, titleExtra), collapse = "<br>"),
  labelVars = NULL,
  width = NULL,
  height = NULL,
  hoverVars,
  hoverLab,

```

```

textVar = NULL,
pathVar = NULL,
pathLab = getLabelVar(pathVar, labelVars = labelVars),
table = FALSE,
tableVars,
tableLab,
tableButton = TRUE,
tablePars = list(),
id = paste0("plotClinData", sample.int(n = 1000, size = 1)),
verbose = FALSE
)

```

Arguments

data	Data.frame with data.
xVar	String with column of data containing x-variable.
yVar	String with column of data containing y-variable.
xLab	String with label for xVar.
yLab	String with label for xVar.
colorVar	(optional) String with color variable.
colorLab	String with label for colorVar.
colorPalette	(optional) Named character vector with color palette. If not specified, the viridis color palette is used. See clinColors .
barmode	String with type of barplot, either: 'group' or 'stack' (see parameter in layout).
titleExtra	String with extra title for the plot (appended after title).
title	String with title for the plot.
labelVars	Named character vector containing variable labels.
width	Numeric, width of the plot in pixels, 700 by default.
height	Numeric, height of the plot in pixels, 700 by default.
hoverVars	Character vector with variable(s) to be displayed in the hover, by default any position and aesthetic variables displayed in the plot.
hoverLab	Named character vector with labels for hoverVars.
textVar	(optional) String with a text variable, that will be displayed outside of each bar.
pathVar	String with variable of data containing hyperlinks with path to the subject-specific report, formatted as:

```
<a href="/path-to-report">label</a>
```

.

If multiple, they should be separated by: ', '.

The report(s) will be:

- compressed to a zip file and downloaded if the user clicks on the 'p' (a.k.a 'profile') key when hovering on a point of the plot

	<ul style="list-style-type: none"> included in a collapsible row, and clickable with hyperlinks in the table
pathLab	String with label for pathVar, included in the collapsible row in the table.
table	Logical, if TRUE (FALSE by default) returns also a datatable containing the plot data. (The plot and the table are not linked.)
tableVars	Character vector with variables to be included in the table.
tableLab	Named character vector with labels for each tableVars.
tableButton	Logical, if TRUE (by default) the table is included within an HTML button.
tablePars	List with parameters passed to the getClinDT function.
id	String with general id for the plot: <ul style="list-style-type: none"> 'id' is used as group for the SharedData 'button:[id]' is used as button ID if table is TRUE <p>If not specified, a random id, as 'plotClinData[X]' is used.</p>
verbose	Logical, if TRUE (FALSE by default) progress messages are printed in the current console. For the visualizations, progress messages during download of subject-specific report are displayed in the browser console.

Value

Either:

- if table is requested a `clinDataReview` object, a.k.a a list with the 'plot' ([plotly](#) object) and 'table' ([datatable](#) object)
- otherwise: [plotly](#) object

Author(s)

Laure Cougnaud

See Also

Other visualizations of summary statistics for clinical data: [boxplotClinData\(\)](#), [plotCountClinData\(\)](#), [sunburstClinData\(\)](#), [treemapClinData\(\)](#)

Examples

```
library(clinUtils)

data(dataADaMCDISCP01)
labelVars <- attr(dataADaMCDISCP01, "labelVars")

dataAE <- dataADaMCDISCP01$ADAE
dataDM <- dataADaMCDISCP01$ADSL

## example of basic barplot:

# treemap takes as input table with counts
library(inTextSummaryTable)
```

```

# total counts: Safety Analysis Set (patients with start date for the first treatment)
dataTotal <- subset(dataDM, RFSTDTC != "")

# compute adverse event table
tableAE <- computeSummaryStatisticsTable(
  data = dataAE,
  rowVar = c("AEBODSYS", "AEDECOD"),
  dataTotal = dataTotal,
  labelVars = labelVars,
  stats = getStats("count")
)

dataPlot <- subset(tableAE, AEDECOD != "Total")

dataPlot$n <- as.numeric(dataPlot$n)

# create plot
barplotClinData(
  data = dataPlot,
  xVar = "AEDECOD",
  yVar = "n", yLab = "Number of patients with adverse events",
  labelVars = labelVars
)
# add number on top of the bars
barplotClinData(
  data = dataPlot,
  xVar = "AEDECOD",
  yVar = "n", yLab = "Number of patients with adverse events",
  textVar = "n",
  labelVars = labelVars
)

# display percentage of events per severity
tableAEBySeverity <- computeSummaryStatisticsTable(
  data = dataAE,
  rowVar = c("AEDECOD", "AESEV"),
  dataTotal = dataTotal,
  labelVars = labelVars,
  statsPerc = "statm",
  stats = getStats("%m"),
  dataTotalPerc = dataAE,
  rowVarTotalPerc = "AEDECOD"
)
barplotClinData(
  data = tableAEBySeverity,
  xVar = "AEDECOD",
  yVar = "statPercm", yLab = "Percentage of adverse events",
  labelVars = labelVars,
  colorVar = "AESEV", bargmode = "stack",
  hoverVar = c("AEDECOD", "AESEV", "statN", "statm", "statPercm"),
  hoverLab = c(
    labelVars["AEDECOD"],

```

```

labelVars["AESEV"],
statN = "Number of patients",
statm = "Number of events",
statPercm = "Percentage of events"
),
textVar = "%m",
)

```

boxplotClinData	<i>Boxplot interactive plot.</i>
-----------------	----------------------------------

Description

Boxplot interactive plot.

Usage

```

boxplotClinData(
  data,
  xVar,
  yVar,
  xLab = getLabelVar(xVar, labelVars = labelVars),
  yLab = getLabelVar(yVar, labelVars = labelVars),
  colorVar = NULL,
  colorLab = getLabelVar(colorVar, labelVars = labelVars),
  colorPalette = NULL,
  facetVar = NULL,
  facetLab = getLabelVar(facetVar, labelVars = labelVars),
  ncol = 1L,
  titleExtra = NULL,
  title = paste(paste(yLab, "vs", xLab, titleExtra), collapse = "<br>"),
  labelVars = NULL,
  width = NULL,
  height = NULL,
  hoverVars,
  hoverLab,
  pathVar = NULL,
  pathLab = getLabelVar(pathVar, labelVars = labelVars),
  idVar = "USUBJID",
  idLab = getLabelVar(idVar, labelVars = labelVars),
  table = FALSE,
  tableVars,
  tableLab,
  tableButton = TRUE,
  tablePars = list(),
  id = paste0("plotClinData", sample.int(n = 1000, size = 1)),
  verbose = FALSE
)

```

Arguments

<code>data</code>	Data.frame with data.
<code>xVar</code>	String with column of data containing x-variable.
<code>yVar</code>	String with column of data containing y-variable.
<code>xLab</code>	String with label for xVar.
<code>yLab</code>	String with label for xVar.
<code>colorVar</code>	(optional) String with color variable.
<code>colorLab</code>	String with label for colorVar.
<code>colorPalette</code>	(optional) Named character vector with color palette. If not specified, the viridis color palette is used. See clinColors .
<code>facetVar</code>	(optional) String with facet variable.
<code>facetLab</code>	String with label for facetVar.
<code>ncol</code>	single-length integer denoting the number of columns for the facetting.
<code>titleExtra</code>	String with extra title for the plot (appended after title).
<code>title</code>	String with title for the plot.
<code>labelVars</code>	Named character vector containing variable labels.
<code>width</code>	Numeric, width of the plot in pixels, 700 by default.
<code>height</code>	Numeric, height of the plot in pixels, 700 by default.
<code>hoverVars</code>	Character vector with variable(s) to be displayed in the hover, by default any position and aesthetic variables displayed in the plot.
<code>hoverLab</code>	Named character vector with labels for hoverVars.
<code>pathVar</code>	String with variable of data containing hyperlinks with path to the subject-specific report, formatted as: <pre>label</pre>
	.
	If multiple, they should be separated by: ', '.
	The report(s) will be:
	<ul style="list-style-type: none"> • compressed to a zip file and downloaded if the user clicks on the 'p' (a.k.a 'profile') key when hovering on a point of the plot • included in a collapsible row, and clickable with hyperlinks in the table
<code>pathLab</code>	String with label for pathVar, included in the collapsible row in the table.
<code>idVar</code>	String with variable containing subject ID.
<code>idLab</code>	String with label for idVar.
<code>table</code>	Logical, if TRUE (FALSE by default) returns also a datatable containing the plot data. (The plot and the table are not linked.)
<code>tableVars</code>	Character vector with variables to be included in the table.
<code>tableLab</code>	Named character vector with labels for each tableVars.

tableButton	Logical, if TRUE (by default) the table is included within an HTML button.
tablePars	List with parameters passed to the getClinDT function.
id	String with general id for the plot: <ul style="list-style-type: none"> • 'id' is used as group for the SharedData • 'button:[id]' is used as button ID if table is TRUE If not specified, a random id, as 'plotClinData[X]' is used.
verbose	Logical, if TRUE (FALSE by default) progress messages are printed in the current console. For the visualizations, progress messages during download of subject-specific report are displayed in the browser console.

Value

Either:

- if table is requested a `clinDataReview` object, a.k.a a list with the 'plot' ([plotly](#) object) and 'table' ([datatable](#) object)
- otherwise: [plotly](#) object

Author(s)

Lennart Tuijnder

See Also

Other visualizations of summary statistics for clinical data: [barplotClinData\(\)](#), [plotCountClinData\(\)](#), [sunburstClinData\(\)](#), [treemapClinData\(\)](#)

Examples

```
library(clinUtils)

data(dataADaMCDISCP01)
labelVars <- attr(dataADaMCDISCP01, "labelVars")

## example of basic barplot:

data <- subset(dataADaMCDISCP01$ADVS,
PARAMCD == "DIABP" & ANL01FL == "Y" &
AVISIT %in% c("Baseline", "Week 2", "Week 4", "Week 6", "Week 8")
)

## example of basic boxplot:

# With color var and facet:
boxplotClinData(
data = data,
xVar = "AVISIT",
yVar = "AVAL",
colorVar = "TRTA",
```

```

facetVar = "ATPT",
title = "Diastolic Blood Pressure distribution by actual visit and analysis timepoint",
yLab = "Actual value of the Diastolic Blood Pressure parameter (mmHg)",
labelVars = labelVars
)

# Control number of facet columns:
boxplotClinData(
data = data,
xVar = "AVISIT",
yVar = "AVAL",
colorVar = "TRTA",
facetVar = "ATPT",
ncol = 2,
title = "Diastolic Blood Pressure distribution by actual visit and analysis timepoint",
yLab = "Actual value of the Diastolic Blood Pressure parameter (mmHg)",
labelVars = labelVars
)

# Facet or color is optional:
boxplotClinData(
data = data,
xVar = "AVISIT",
yVar = "AVAL",
colorVar = "TRTA",
title = "Diastolic Blood Pressure distribution by actual visit and analysis timepoint",
yLab = "Actual value of the Diastolic Blood Pressure parameter (mmHg)",
labelVars = labelVars
)

boxplotClinData(
data = data,
xVar = "AVISIT",
yVar = "AVAL",
facetVar = "ATPT",
ncol = 2,
title = "Diastolic Blood Pressure distribution by actual visit and analysis timepoint",
yLab = "Actual value of the Diastolic Blood Pressure parameter (mmHg)",
labelVars = labelVars
)

```

checkAvailabilityMetadata

Check availability of arguments in list

Description

Check availability of arguments in list

Usage

```
checkAvailabilityMetadata(paramsList, subListName)
```

Arguments

paramsList	A named list.
subListName	String indicating which of the sublist names to check for existence.

Value

The content of the sublist. If not available, returns "Not Available".

checkConfigFile	<i>Check a configuration file (in _YAML_format) based on a requirement file in JSON Schema format.</i>
-----------------	--

Description

Check a configuration file (in _YAML_ format) based on a requirement file in JSON Schema format.

Usage

```
checkConfigFile(configFile, configSpecFile)
```

Arguments

configFile	String with name of the config file of interest in YAML format.
configSpecFile	String with name of the config file containing requirements in JSON Schema format.

Value

No returned value, an error message is printed in the console if the configuration file doesn't comply to the specified specifications.

Author(s)

Laure Cougnaud

checkReportTitles *Check report titles*

Description

Check uniqueness of report titles across the config files. If not unique titles are provided, an error is returned.

Usage

```
checkReportTitles(
  configFiles,
  configDir = file.path(inputDir, "config"),
  inputDir = "."
)
```

Arguments

configFiles Character vector with config file names
 configDir String with directory with config files, ('config' by default)
 inputDir String with input directory, working directory by default.

Value

A named vector with the report titles and the corresponding config file

Author(s)

Michela Pasetto

See Also

Other clinical data reporting: [convertMdToHtml\(\)](#), [forceParams\(\)](#), [getMdHeader\(\)](#), [getParamsFromConfig\(\)](#), [gitbook_clinDataReview_report\(\)](#), [html_clinDataReview_report\(\)](#), [knitPrintClinDataReview\(\)](#), [render_clinDataReviewReport\(\)](#)

checkTemplatesName *Checks of config files template.*

Description

Check if the templates specified in the input config files don't originate from multiple sources (e.g. custom and R package via the parameter `templatePackage`). If so, the corresponding config files are not considered.

Usage

```
checkTemplatesName(
  configFiles,
  configDir = file.path(inputDir, "config"),
  inputDir = ".")
)
```

Arguments

configFiles	Character vector with name or path of the config file(s).
configDir	String with directory with config files, by default a 'config' folder in inputDir. It should contain a general 'config.yml' file and dedicated 'config-[X].yml' for each chapter. The order of each chapter is specified in the 'config' slot in the general 'config.yml'.
inputDir	String with input directory, working directory by default.

Value

Updated configFiles

Author(s)

Laure Cougnaud

checkValueType	<i>Check if the specified valueType parameter can be passed to the branchvalues of the <code>plot_ly</code> treemap/sunburst visualizations.</i>
----------------	--

Description

If this parameter is set to 'total' and the sum of the counts of the the children nodes is not bigger than the parent node, an empty plot is created. In this case, this function set this parameter to: 'relative'.

Usage

```
checkValueType(data, vars, valueVar, valueType = "total", labelVars = NULL)
```

Arguments

data	Data.frame with data.
vars	Character vector with variables of data containing plot nodes. If multiple, they should be specified in hierarchical order (from parent to child node).
valueVar	String with numeric variable of data containing node value, and associated label.

valueType	String with type of values in valueVar (branchvalues of the <code>plot_ly</code> function), among others: 'total' (default, only if <code>sum(child) <=</code> to parent) or 'relative'.
labelVars	Named character vector containing variable labels.

Value

If the condition is fulfilled: updated valueType and warning; otherwise input valueType.

Author(s)

Laure Cougnaud

clinDataReview-common-args

Common arguments for the functions of the clinDataReview package

Description

Common arguments for the functions of the clinDataReview package

Arguments

data	Data.frame with data.
verbose	Logical, if TRUE (FALSE by default) progress messages are printed in the current console. For the visualizations, progress messages during download of subject-specific report are displayed in the browser console.
gg	<code>ggplot</code> object.
xVar	String with column of data containing x-variable.
yVar	String with column of data containing y-variable.
xLab	String with label for xVar.
yLab	String with label for xVar.
xLim, yLim	Numeric vector of length 2 with limits for the x/y axes.
idVar	String with variable containing subject ID.
idLab	String with label for idVar.
width	Numeric, width of the plot in pixels, 700 by default.
height	Numeric, height of the plot in pixels, 700 by default.
facetPars	List with facetting parameters, passed to the facetting function. Variables should be specified as character or formula. For 'wrap' facetting (facetType is 'wrap'), if the layout is not specified via <code>nrow/ncol</code> , 2 columns are used by default.
lineVars	List with parameters for the reference lines.
hoverVars	Character vector with variable(s) to be displayed in the hover, by default any position and aesthetic variables displayed in the plot.

hoverLab	Named character vector with labels for hoverVars.
pathExpand	Logical, should the variable in pathExpand be included in a collapsible row or as hyperlink in the table? Should be TRUE for if multiple paths are included for each idVar, FALSE otherwise (by default).
table	Logical, if TRUE (FALSE by default) returns also a datatable containing the plot data. The plot and table are linked when included in a Rmarkdown document: when clicking on an plot element, only the corresponding records are retained in the associated table; when some records are selected in the table, they are highlighted in the associated table.
refLinePars	(optional) Nested list, with parameters for each reference line(s). Each sublist (a.k.a reference line) contains: <ul style="list-style-type: none"> • aesthetic value(s) or variable(s) for the lines (in this case column names of data) for reference lines. The line position is controlled by the aesthetics supported in geom_vline, geom_hline and geom_abline. • 'label': (optional) Logical specifying if the line should be annotated (FALSE to not annotate the line) or string with annotation label. By default, the value of the position of the horizontal/vertical line or the equation of the diagonal line is displayed.
labelVars	Named character vector containing variable labels.
id	String with general id for the plot: <ul style="list-style-type: none"> • 'id' is used as group for the SharedData • 'button:[id]' is used as button ID if table is TRUE <p>If not specified, a random id, as 'plotClinData[X]' is used.</p>
title	String with title for the plot.
titleExtra	String with extra title for the plot (appended after title).
colorPalette	(optional) Named character vector with color palette. If not specified, the viridis color palette is used. See clinColors .

Value

No return value, used for the documentation of the functions of the package.

clinDataReview-common-args-report

Common parameters for the clinical data reporting function

Description

Common parameters for the clinical data reporting function

Arguments

indexPath	String with path to the index file, by default 'index.Rmd' in inputDir.
configDir	String with directory with config files, by default a 'config' folder in inputDir. It should contain a general 'config.yml' file and dedicated 'config-[X].yml' for each chapter. The order of each chapter is specified in the 'config' slot in the general general 'config.yml'.
inputDir	String with input directory, working directory by default.
outputDir	String with output directory, ('report' by default).
intermediateDir	String with intermediate directory ('interim' by default), where markdown files and rds file specifying Js libraries (with knit_meta) for each sub report are stored.

Value

No return value, used for the documentation of the clinical data reporting functions of the package.

clinDataReview-common-args-summaryStatsVis

Common arguments for the plotting functions summary statistics of the clinDataReview package

Description

Common arguments for the plotting functions summary statistics of the clinDataReview package

Arguments

vars	Character vector with variables of data containing plot nodes. If multiple, they should be specified in hierarchical order (from parent to child node).
varsLab	Named character vector with labels for vars.
valueVar, valueLab	String with numeric variable of data containing node value, and associated label.
valueType	String with type of values in valueVar (branchvalues of the <code>plot_ly</code> function), among others: 'total' (default, only if <code>sum(child) <= to parent</code>) or 'relative'.
pathVar	String with variable of data containing hyperlinks with path to the subject-specific report, formatted as: <pre>label</pre> <p>.</p> <p>If multiple, they should be separated by: ', '.</p> <p>The report(s) will be:</p>

	<ul style="list-style-type: none"> • compressed to a zip file and downloaded if the user clicks on the 'p' (a.k.a 'profile') key when hovering on a point of the plot • included in a collapsible row, and clickable with hyperlinks in the table
pathLab	String with label for pathVar, included in the collapsible row in the table.
table	Logical, if TRUE (FALSE by default) returns also a datatable containing the plot data. (The plot and the table are not linked.)

Value

No return value, used for the documentation of the plotting functions of summary statistics of the package.

clinDataReview-templates

Rmarkdown templates for clinical data

Description

Template reports with standard visualizations/tables available in the package are described here.

Details

For each template, required parameters are indicated in **bold**.

Value

No return value, used for the documentation of the Rmarkdown template reports contained in the package.

Parameter type

Please note that the type mentioned below corresponds to the type in the config file (in YAML/JSON format).The mapping to R data type is as followed:

- string: character vector of length 1
- integer: integer vector of length 1
- array: vector/list without names
- object: list with names

Clinical data template for a visualization of count data : countsVisualizationTemplate

This report compute counts of variable(s) of interest (with the inTextSummaryTable package) and visualize them with a treemap and/or sunburst.

The following parameters are available:

- template: string set to: 'countsVisualizationTemplate.Rmd' , name of the template report

- `templatePackage`: string set to: 'clinDataReview' , package from which the template should be extracted
- `reportTitle`: string , header title
- `reportTitleLevel`: (optional) integer , header level, 1 by default (1: 'chapter', '2': 'section', '3': subsection, ...)
- `dataFileName`: string , name of the data file of interest
- `dataProcessing`: (optional) array , data processing parameters, passed to [processData](#)
- `dataTotalFileName`: (optional) string , filename of the total dataset
- `dataTotalProcessing`: (optional) array , data processing parameters for 'dataTotalFileName', passed to [processData](#)
- `countVar`: string , variable of data to count on
- `parentVar`: (optional) string or array , parent variable(s) of the counting variable, used for grouping
- `colorVar`: (optional) string or object , numeric variable(s) to consider for coloring, named by count/parent variable if different for each variable
- `colorRange`: (optional) array of number(s) of length: minimum 2, maximum 2 , range of the color variable for the visualization
- `loopingVar`: (optional) array or string , data variable(s) to loop over, for which each output should be created
- `loopingNMax`: (optional) integer , maximum number of elements of `loopingVar` to include in the report
- `loopingTotal`: (optional) boolean , should the total also be computed by `loopingVar` (TRUE by default)?
- `typePlot`: (optional) array or string of string(s)
- `startup`: (optional) array or string , R commands that should be run at the start of the report

Clinical data template to create a report division : `divisionTemplate`

This report includes a division, i.e. extra chapter, section of subsection in the report.
The following parameters are available:

- `template`: string set to: 'divisionTemplate.Rmd' , name of the template report
- `templatePackage`: string set to: 'clinDataReview' , package from which the template should be extracted
- `reportTitle`: string , header title
- `reportTitleLevel`: (optional) integer , header level, 1 by default (1: 'chapter', '2': 'section', '3': subsection, ...)
- `content`: (optional) string , any content that should be included after the title

Clinical data template to create a listing : listingTemplate

This report displays a listing of the variables and data of interest, displayed in an interactive table. This table can contains comparison with a previous batch ('comparisonTable' parameters).

The following parameters are available:

- `template`: string set to: 'listingTemplate.Rmd' , name of the template report
- `templatePackage`: string set to: 'clinDataReview' , package from which the template should be extracted
- `reportTitle`: string , header title
- `reportTitleLevel`: (optional) integer , header level, 1 by default (1: 'chapter', '2': 'section', '3': subsection, ...)
- `dataFileName`: string , name of the data file of interest
- `dataProcessing`: (optional) array , data processing parameters, passed to [processData](#)
- `dataTotalFileName`: (optional) string , filename of the total dataset
- `dataTotalProcessing`: (optional) array , data processing parameters for 'dataTotalFileName', passed to [processData](#)
- `tableParams`: (optional) object , parameters to create the table, passed to [tableClinData](#)
- `comparisonTableType`: (optional) string among: 'none', 'newData-diff-interactive', 'table-comparison-interactive' , output type of the comparison table
- `comparisonTableParams`: (optional) object , parameters for the comparison table, passed to [compareTables](#)
- `loopingVar`: (optional) array or string , data variable(s) to loop over, for which each output should be created
- `loopingNMax`: (optional) integer , maximum number of elements of `loopingVar` to include in the report
- `listingDocx`: (optional) boolean , export listing to Word

Clinical data template for the creation of patient profiles : patientProfilesTemplate

This report creates the specified patient profiles (with the `patientProfilesVis` package) by subject, and export them to a specified directory.

The following parameters are available:

- `template`: string set to: 'patientProfilesTemplate.Rmd' , name of the template report
- `templatePackage`: string set to: 'clinDataReview' , package from which the template should be extracted
- `reportTitle`: string , header title
- `reportTitleLevel`: (optional) integer , header level, 1 by default (1: 'chapter', '2': 'section', '3': subsection, ...)
- `createPatientProfiles`: (optional) boolean , Should the patient profiles be created or only loaded from a previous execution?
- `patientProfilesGeneralParams`: (optional) object , set of parameters used for all patient profiles modules. These parameters are passed to all `subjectProfile[]Plot` functions.

- patientProfilesParams: array of object(s)
The following parameters are available:
 - typePlot: string among: 'text', 'line', 'interval', 'event' , plot type, used to get the appropriate plot module function:
 - * 'text': [subjectProfileTextPlot](#)
 - * 'line': [subjectProfileLinePlot](#)
 - * 'interval': [subjectProfileIntervalPlot](#)
 - * 'event': [subjectProfileEventPlot](#)
 - dataFileName: string , name of the data file of interest
 - dataProcessing: (optional) array , data processing parameters, passed to [processData](#)
 - plotParams: object , parameters for the plotting function. Parameters depending on the dataset of interest can be specified as:
[parameterName]: !r-lazy [dataI]
 , parameters for each patient profile module
- patientProfilesCreateReportParams: (optional) object , parameters for the creation of the patient profile report(s), passed to [createSubjectProfileReport](#)
- tableParams: (optional) object , parameters specifying a table containing data of interest and links to created patient profiles
- startup: (optional) array or string , R commands that should be run at the start of the report

Clinical data generic template for visualization : plotTemplate

This report visualizes input data with a function of the clinical data review package. The data can be compared to the data of a previous batch, in the table associated to the plot ('comparisonTable' parameters).

The following parameters are available:

- template: string set to: 'plotTemplate.Rmd' , name of the template report
- templatePackage: string set to: 'clinDataReview' , package from which the template should be extracted
- reportTitle: string , header title
- reportTitleLevel: (optional) integer , header level, 1 by default (1: 'chapter', '2': 'section', '3': subsection, ...)
- dataFileName: string , name of the data file of interest
- dataProcessing: (optional) array , data processing parameters, passed to [processData](#)
- plotFunction: string among: 'timeProfileIntervalPlot', 'scatterplotClinData', 'boxplot-ClinData' , plotting function of the package to consider
- plotParams: object , parameters for the plotting function. Parameters depending on the dataset of interest can be specified as:
[parameterName]: !r-lazy [dataI]
- comparisonTableType: (optional) string among: 'none', 'newData-diff' , output type of the comparison table. If specified, an additional column: 'Comparison Type' is included in the table attached to the plot.

- `comparisonTableParams`: (optional) object , parameters for the comparison table, passed to [compareTables](#). If `referenceVars` is not specified, all variables displayed in the plot are used.
- `loopingVar`: (optional) array or string , data variable(s) to loop over, for which each output should be created
- `loopingNMax`: (optional) integer , maximum number of elements of `loopingVar` to include in the report
- `startup`: (optional) array or string , R commands that should be run at the start of the report

Clinical data template for visualization of summarized data : `summaryPlotTemplate`

This report summarizes the data of interest (with the `inTextSummaryTable` package) and visualize it with any clinical data review plot function.

The following parameters are available:

- `template`: string set to: `'summaryPlotTemplate.Rmd'` , name of the template report
- `templatePackage`: string set to: `'clinDataReview'` , package from which the template should be extracted
- `reportTitle`: string , header title
- `reportTitleLevel`: (optional) integer , header level, 1 by default (1: `'chapter'`, `'2'`: `'section'`, `'3'`: `'subsection, ...'`)
- `dataFileName`: string , name of the data file of interest
- `dataProcessing`: (optional) array , data processing parameters, passed to [processData](#)
- `dataTotalFileName`: (optional) string , filename of the total dataset
- `dataTotalProcessing`: (optional) array , data processing parameters for `'dataTotalFileName'`, passed to [processData](#)
- `tableParams`: object , parameters to summarize the data in a table, passed to [computeSummaryStatisticsTable](#)
- `tableProcessing`: (optional) array , data processing parameters for the summary table, passed to [processData](#)
- `plotFunction`: string among: `'timeProfileIntervalPlot'`, `'scatterplotClinData'`, `'sunburst-ClinData'`, `'treemapClinData'`, `'barplotClinData'` , plotting function to visualize summary data
- `plotParams`: object , parameters for the plotting function
- `loopingVar`: (optional) array or string , data variable(s) to loop over, for which each output should be created
- `loopingNMax`: (optional) integer , maximum number of elements of `loopingVar` to include in the report
- `loopingTotal`: (optional) boolean , should the total also be computed by `loopingVar` (TRUE by default)?
- `startup`: (optional) array or string , R commands that should be run at the start of the report

Clinical data template for a summary table of the data : `summaryTableTemplate`

This report summarizes the data of interest (with the `inTextSummaryTable` package). This table is displayed with an interactive table in the report, and exported to a docx file. This table can be compared to a summary table of a previous batch (`'comparisonTable'` parameters).

The following parameters are available:

- `template`: string set to: `'summaryTableTemplate.Rmd'` , name of the template report
- `templatePackage`: string set to: `'clinDataReview'` , package from which the template should be extracted
- `reportTitle`: string , header title
- `reportTitleLevel`: (optional) integer , header level, 1 by default (1: `'chapter'`, '2': `'section'`, '3': `'subsection, ...'`)
- `dataFileName`: string , name of the data file of interest
- `dataProcessing`: (optional) array , data processing parameters, passed to [processData](#)
- `dataTotalFileName`: (optional) string , filename of the total dataset
- `dataTotalProcessing`: (optional) array , data processing parameters for `'dataTotalFileName'`, passed to [processData](#)
- `tableParams`: object , parameters to summarize the data in a table, passed to [computeSummaryStatisticsTable](#)
- `tableParamsDocx`: (optional) object , parameters to format the table to the docx format, passed to [exportSummaryStatisticsTable](#)
- `tableParamsDT`: (optional) object , parameters to format the table to the DT interactive table included in the report, passed to [exportSummaryStatisticsTable](#)
- `comparisonTableType`: (optional) string among: `'none'`, `'table-comparison-interactive'`, `'newData-diff'` , output type of the comparison table
- `comparisonTableParams`: (optional) object , parameters for the comparison table, passed to [compareTables](#). By default, statistics variables are compared across row and column elements.
- `loopingVar`: (optional) array or string , data variable(s) to loop over, for which each output should be created
- `loopingNMax`: (optional) integer , maximum number of elements of `loopingVar` to include in the report
- `loopingTotal`: (optional) boolean , should the total also be computed by `loopingVar` (TRUE by default)?

collapseHtmlContent *Function to create collapsible HTML content*

Description

Please note that the button is of class: `'hideshow'`, defined in the `'input.hideshow.js'` js file included in the package.

Usage

```
collapseHtmlContent(input, title = "Click to show or hide")
```

Arguments

input	Object to be collapse, e.g. datatable.
title	String with button title.

Value

tag object

Author(s)

Laure Cougnaud

convertMdToHtml

Convert clinical data Markdown files to HTML

Description

This consists of:

1. importing the general config file ('config'.yaml) to identify each report of interest ('config' tag)
2. for each report of interest: checking if the associated Markdown and rds file (list of Js dependencies) are available in intermediateDir
3. combining all Rmarkdown reports to a single document: main.md
4. converting main.md to an HTML document

Usage

```
convertMdToHtml(  
  outputDir = "./report",  
  inputDir = ".",  
  configDir = file.path(inputDir, "config"),  
  indexPath = file.path(inputDir, "index.Rmd"),  
  intermediateDir = "./interim",  
  mdFiles = NULL  
)
```

Arguments

outputDir	String with output directory, ('report' by default).
inputDir	String with input directory, working directory by default.
configDir	String with directory with config files, by default a 'config' folder in inputDir. It should contain a general 'config.yml' file and dedicated 'config-[X].yml' for each chapter. The order of each chapter is specified in the 'config' slot in the general 'config.yml'.
indexPath	String with path to the index file, by default 'index.Rmd' in inputDir.
intermediateDir	String with intermediate directory ('interim' by default), where markdown files and rds file specifying Js libraries (with knit_meta) for each sub report are stored.
mdFiles	(optional) Path to the Markdown files that should be converted. If specified, the specified config files in configDir are ignored.

Value

String with path to the front page of the clinical data report.

Author(s)

Laure Cougnaud

See Also

Other clinical data reporting: [checkReportTitles\(\)](#), [forceParams\(\)](#), [getMdHeader\(\)](#), [getParamsFromConfig\(\)](#), [gitbook_clinDataReview_report\(\)](#), [html_clinDataReview_report\(\)](#), [knitPrintClinDataReview\(\)](#), [render_clinDataReviewReport\(\)](#)

createClinDataReviewReportSkeleton

Create the skeleton of a report

Description

Creates the skeleton of a report to start running the analyses.

Usage

```
createClinDataReviewReportSkeleton(dir = ".")
```

Arguments

dir	String with the path of the directory where the skeleton should be created. The current working directory is used as default.
-----	---

Details

This function is meant to get familiar with the use of the package and the necessary files to create a report.

It will create a ready-to-use report with example data from the `clinUtils` package. After getting use to the file structure, the user can substitute the example data with custom data sets and add specific configuration files.

Value

The files to run a report are written in the specified directory. To run the report, the user can call the [render_clinDataReviewReport](#).

`createExampleMetadata` *Create an example metadata file*

Description

Create an example of metadata file for the [createClinDataReviewReportSkeleton](#).

Usage

```
createExampleMetadata(dir)
```

Arguments

`dir` String, path to the directory.

Value

Nothing, the example metadata file is created in the specified directory.

`createMainConfigSkeleton`
Create the config file for the skeleton

Description

This function creates the main config file for the [createClinDataReviewReportSkeleton](#) with the directory where the data are stored.

Usage

```
createMainConfigSkeleton(dir, dirData)
```

Arguments

dir String, path to the directory.
 dirData String, path to the directory of the data.

Value

No return value, a file `_config.yml` is created in the specified directory.

createPatientProfileVar

Create link to patient profile

Description

Create a link to a patient profile directory (where the patient profile files are saved) by adding an extra column with the link in the data. The path to the patient profile is built as: `[patientProfilePath]/subjectProfile-[subjectID].pdf`, where `'/'` are replaced with `'-'` in the subject identifier (`subjectVar`).

Usage

```
createPatientProfileVar(
  data,
  patientProfilePath,
  subjectVar = "USUBJID",
  checkExist = TRUE
)
```

Arguments

data a data.frame
 patientProfilePath string indicating the directory where the patient profiles are stored.
 subjectVar string indicating which column in the data represents the unique subject identifier, "USUBJID" by default.
 checkExist Logical, if TRUE (by default) the patientProfilePath is checked for existence, and an error is returned if this directory doesn't exist.

Value

A data.frame with two extra columns: `patientProfilePath` and `patientProfileLink` with the path to the patient profile and an hyperlink to it, respectively.

Author(s)

Michela Pasetto

Examples

```
# Typical CDISC dataset contains universal subject ID (USUBJID)
data <- data.frame(USUBJID = c("subj1", "subj2", "subj3"))
dataWithPatientProfileVar <- createPatientProfileVar(
  data = data,
  patientProfilePath = "pathProfiles",
  checkExist = FALSE
)
# path and HTML link are included in the output dataset
head(dataWithPatientProfileVar[, c("USUBJID", "patientProfilePath", "patientProfileLink")])
```

createRedirectPage *Create a redirect page*

Description

Create an html page that redirects to the "1-introduction.html" page of the clinical data report available in a directory. See output from [render_clinDataReviewReport](#).

Usage

```
createRedirectPage(redirectPage = "report.html", dir = "report_dependencies")
```

Arguments

redirectPage	String with the path of the html file that redirects to the "1-introduction.html" page of the report.
dir	String for the path where the "1-introduction.html" is stored.

Value

The html file is created.

createTemplateDoc *Create documentation for clinical data template reports available in the 'template' folder of the package.*

Description

If a JSON schema file available, the information relative to the template is extracted from this file with the function JSONSchToRd.

Usage

```
createTemplateDoc(
  templatePath = system.file("template", package = "clinDataReview")
)
```

Arguments

templatePath string with path where the template Rmd reports and associated JSON schema files are stored, by default path of the installed version of the package. This parameter is only for expert use of the package.

Value

Character vector with Rd code containing description for all template documents.

Author(s)

Laure Cougnaud

References

[JSON schema specification](#)

exportSessionInfoToMd *Combine all session informations across all clinical data reports and export them into a dedicated Markdown document*

Description

Combine all session informations across all clinical data reports and export them into a dedicated Markdown document

Usage

```
exportSessionInfoToMd(sessionInfos, mdFiles, intermediateDir = "interim")
```

Arguments

sessionInfos List with [sessionInfo](#) objects

mdFiles Character vector with Markdown files

intermediateDir String with intermediate directory ('interim' by default), where markdown files and rds file specifying Js libraries (with `knit_meta`) for each sub report are stored.

Value

String with path to Markdown file containing the session information, NULL if no session information(s) are provided.

Author(s)

Laure Cougnaud

filterData	<i>Filter dataset based on specified filters.</i>
------------	---

Description

A dataset can be filtered:

- based:
 - on a specific value of interest)
 - on a function of the variable (valueFct parameter), e.g. maximum of the variable)
 - to retain only non missing values of a variable (keepNA set to FALSE)
- by groups (varsBy parameter)

****Note that by default, missing values in the filtering variable are retained (which differs from the default behaviour in R)**.** To filter missing records, please set the keepNA parameter to FALSE.

Usage

```
filterData(
  data,
  filters,
  keepNA = TRUE,
  returnAll = FALSE,
  verbose = FALSE,
  labelVars = NULL,
  labelData = "data"
)
```

Arguments

- | | |
|---------|--|
| data | Data.frame with data. |
| filters | Unique filter or list of filters. Each filter should be a list containing: <ul style="list-style-type: none"> • 'var': String with variable from data to filter on. • 'value': (optional) Character vector with values from var to consider. • 'valueFct': (optional) Function (or string wit this function) to be applied on var to extract value to consider • 'op': (optional) String with operator used to retain records from value. If not specified, the inclusion operator: '%in%' is considered, a.k.a records with var in value are retained. • 'rev': (optional) Logical, if TRUE (FALSE by default), filtering condition based on value/valueFct is reversed. • 'keepNA': (optional) Logical, if TRUE (by default), missing values in var are retained. If not specified, keepNA general parameter is used. • 'varsBy': (optional) Character vector with variables in data containing groups to filter by |

- 'varNew': (optional) String with name for the new variable created
- 'labelNew': (optional) String with label for varNew

If a list of filters is specified, the logical operator (see [Logic](#)) linking the different conditions can be specified between the two conditions, e.g.: `list(list(var = "SEX", value = "F"), "&", list(var = "COUNTRY", value = "DEU"))`.

keepNA	Logical, if TRUE (by default) missing values in var are retained. If set to FALSE, missing values are ignored for all filters. The specification within filters prevails on this parameter.
returnAll	Logical: <ul style="list-style-type: none"> • if FALSE (by default): the data for only the filtered records is returned. • if TRUE: the full data is returned. Records are flagged based on the filters condition, in a new column: varNew (if specified), or 'keep' otherwise; containing TRUE if the record fulfill all conditions, FALSE otherwise
verbose	Logical, if TRUE (FALSE by default) progress messages are printed in the current console. For the visualizations, progress messages during download of subject-specific report are displayed in the browser console.
labelVars	Named character vector containing variable labels.
labelData	(optional) String with label for input data, that will be included in progress messages.

Value

Filtered data if returnAll is FALSE (by default). Otherwise data with additional column: keep or varNew (if specified), containing TRUE for records which fulfill the specified condition(s) and FALSE otherwise.

Author(s)

Laure Cougnaud

Examples

```
library(clinUtils)

data(dataADaMCDISCP01)
labelVars <- attr(dataADaMCDISCP01, "labelVars")

dataDM <- dataADaMCDISCP01$ADSL

## single filter

# filter with inclusion criteria:
filterData(
  data = dataDM,
  filters = list(var = "SEX", value = "M"),
  verbose = TRUE
)
```

```
# filter with non-inclusion criteria
filterData(
  data = dataDM,
  filters = list(var = "SEX", value = "M", rev = TRUE),
  verbose = TRUE
)

# filter based on inequality operator
filterData(
  data = dataDM,
  filters = list(var = "AGE", value = 75, op = "<="),
  verbose = TRUE
)

# missing values are retained by default!
dataDMNA <- dataDM
dataDMNA[1 : 2, "AGE"] <- NA
filterData(
  data = dataDMNA,
  filters = list(var = "AGE", value = 75, op = "<="),
  verbose = TRUE
)

# filter missing values on variable
filterData(
  data = dataDMNA,
  filters = list(var = "AGE", value = 75, op = "<=", keepNA = FALSE),
  verbose = TRUE
)

# retain only missing values
filterData(
  data = dataDMNA,
  filters = list(var = "AGE", value = NA, keepNA = TRUE),
  verbose = TRUE
)

# filter missing values
filterData(
  data = dataDMNA,
  filters = list(var = "AGE", keepNA = FALSE),
  verbose = TRUE
)

## multiple filters

# by default the records fulfilling all conditions are retained ('AND')
filterData(
  data = dataDM,
  filters = list(
    list(var = "AGE", value = 75, op = "<="),
    list(var = "SEX", value = "M")
  )
)
```

```

),
verbose = TRUE
)

# custom operator:
filterData(
  data = dataDM,
  filters = list(
    list(var = "AGE", value = 75, op = "<="),
    "|",
    list(var = "SEX", value = "M")
  ),
  verbose = TRUE
)

```

filterDataSingle *Filter data for a single filter*

Description

Filter data for a single filter

Usage

```

filterDataSingle(
  data,
  filters,
  keepNA = TRUE,
  returnAll = FALSE,
  labelVars = NULL,
  labelData = "data"
)

```

Arguments

data	Data.frame with data.
filters	Unique filter or list of filters.
keepNA	Logical, if TRUE (by default) missing values in var are retained. If set to FALSE, missing values are ignored for all filters. The specification within filters prevails on this parameter.
returnAll	Logical: <ul style="list-style-type: none"> if FALSE (by default): the data for only the filtered records is returned. if TRUE: the full data is returned. Records are flagged based on the filters condition, in a new column: varNew (if specified), or 'keep' otherwise; containing TRUE if the record fulfill all conditions, FALSE otherwise
labelVars	Named character vector containing variable labels.
labelData	(optional) String with label for input data, that will be included in progress messages.

Value

Updated data.

Author(s)

Laure Cougnaud

forceParams	<i>Force the evaluation of the parameters from config file.</i>
-------------	---

Description

This function is only useful if some parameters should be lazy-evaluated in the report. These parameters should have the class: `r-lazy`. A typical use case is a parameter that consists of a R expression depending on objects created in a template report (typically data). Parameters are searched in the environment in which this function is called from.

Usage

```
forceParams(params)
```

Arguments

`params` List of parameters as obtained via the [getParamsFromConfig](#) function.

Value

Input parameter list, with object(s) of class `r-lazy` evaluated.

Author(s)

Laure Cougnaud

See Also

[getParamsFromConfig](#)

Other clinical data reporting: [checkReportTitles\(\)](#), [convertMdToHtml\(\)](#), [getMdHeader\(\)](#), [getParamsFromConfig\(\)](#), [gitbook_clinDataReview_report\(\)](#), [html_clinDataReview_report\(\)](#), [knitPrintClinDataReview\(\)](#), [render_clinDataReviewReport\(\)](#)

Examples

```
data <- mtcars
params <- list(label = "Cars dataset", nrow = structure("nrow(data)", class = "r-lazy"))
str(params)
str(forceParams(params))
```

```
formatDataForPlotClinData
```

Format data for interactive plot for clinical data

Description

Format data for interactive plot for clinical data

Usage

```
formatDataForPlotClinData(
  data,
  hoverVars = NULL,
  hoverLab = getLabelVar(hoverVars, labelVars = labelVars),
  hoverByVar = NULL,
  keyVar = NULL,
  id = paste0("plotClinData", sample.int(n = 1000, size = 1)),
  labelVars = NULL
)
```

Arguments

data	Data.frame with data.
hoverVars	Character vector with variable(s) to be displayed in the hover, by default any position and aesthetic variables displayed in the plot.
hoverLab	Named character vector with labels for hoverVars.
hoverByVar	Character vector with variables identifying unique elements in the plot, usually x, y, facet variables. These variables are used to identify records with the same position in the plot, their information are combined in the hover.
keyVar	String with unique key variable, identifying unique group for which the link between the table and the plot should be done.
id	String with general id for the plot: <ul style="list-style-type: none"> • 'id' is used as group for the SharedData • 'button:[id]' is used as button ID if table is TRUE If not specified, a random id, as 'plotClinData[X]' is used.
labelVars	Named character vector containing variable labels.

Value

Updated [SharedData](#) with:

- extra column: 'hover' with combined info from hoverVars

Author(s)

Laure Cougnaud

formatHoverText	<i>Format hover text for use in plotly interactive plots. The labels are wrapped to multiple lines if exceed the width of the plotly hover box, e.g. in case labels for points with same x/y coordinates overlap, and corresponding labels are truncated.</i>
-----------------	---

Description

Format hover text for use in plotly interactive plots. The labels are wrapped to multiple lines if exceed the width of the plotly hover box, e.g. in case labels for points with same x/y coordinates overlap, and corresponding labels are truncated.

Usage

```
formatHoverText(x, label, width = 50)
```

Arguments

x	Vector with hover text information.
label	Label for the variable
width	Integer, number of characters at which the hover text should be cut at to multiple lines.

Value

String with formatted hover label.

Author(s)

Laure Cougnaud

formatPathDateInfoMetadata	<i>Format the info on paths from metadata</i>
----------------------------	---

Description

Format the info on paths from metadata

Usage

```
formatPathDateInfoMetadata(summaryInfo, namesInfo)
```

Arguments

summaryInfo matrix, see output from [getMetadata](#).
 namesInfo Named vector to rename the final output.

Value

A kable object, to be printed.

formatPlotlyClinData *Format interactive plot, with possibility to download patient profiles on a click event.*

Description

Format interactive plot, with possibility to download patient profiles on a click event.

Usage

```
formatPlotlyClinData(
  pl,
  data,
  idVar = "USUBJID",
  pathVar = NULL,
  pathDownload = TRUE,
  idFromDataPlot = FALSE,
  idVarPlot = "key",
  labelVarPlot = NULL,
  highlightOn = "plotly_click",
  highlightOff = "plotly_doubleclick",
  id = paste0("plotClinData", sample.int(n = 1000, size = 1)),
  verbose = FALSE
)
```

Arguments

pl [ggplotly](#) object.
 data Data.frame with data.
 idVar String with variable of data containing plot element.
 pathVar String with variable of data containing path to a subject-specific report (e.g. patient profiles).
 pathDownload Logical, if TRUE (by default) the subject-specific report(s) are downloaded in a zip compressed file. If FALSE (only available if unique report per idVarPlot), each report is opened in a new window.
 idFromDataPlot Logical, if TRUE (by default) idVarPlot is extracted from the data of the plot output object (e.g. if this plot was created from [ggplotly](#)), otherwise directly from the plot object (if the plot was created from [plot_ly](#) directly).

idVarPlot	String with variable in the plotly output containing IDs.
labelVarPlot	String with plotly variable used to extract label to build the file name of the zip compressed file containing patient report. If not specified, the label are extracted based on the idVarPlot of the selected plot element.
highlightOn	String with event to turn on the selection (on parameter of highlight), 'plotly_click' by default.
highlightOff	String with event to turn off the selection (off parameter of highlight), 'plotly_doubleclick' by default.
id	String with general id for the plot: <ul style="list-style-type: none"> • 'id' is used as group for the SharedData • 'button:[id]' is used as button ID if table is TRUE If not specified, a random id, as 'plotClinData[X]' is used.
verbose	Logical, if TRUE report progress messages during execution (included in the browser 'Console').

Value

Updated [plotly](#) object.

Author(s)

Laure Cougnaud

formatToHierarchicalData

Format data to a hierarchical data, in the format as required by the plotly sunburst and treemap.

Description

Note that new variables are created for each variable of interest (the variables are not overwritten) to avoid issues with cases where the value in the child and parent variables are the same.

Usage

```
formatToHierarchicalData(data, vars, valueVar)
```

Arguments

data	Data.frame with data.
vars	Character vector with variables of data containing plot nodes. If multiple, they should be specified in hierarchical order (from parent to child node).
valueVar	String with numeric variable of data containing node value, and associated label.

Value

Updated data.frame with vars in hierarchical format, with extra attributes (in 'metadat'):

- 'varID': String with column of output containing ID of specific element.
This is a combination from the specified vars, or 'Overall' for the grand total.
- 'varParent': String with column of output containing ID of the parent element
- 'varLabel': String with column of output containing the label to display.
This is usually the name of the child element.

Author(s)

Laure Cougnaud

getAxisLimPlot

Get axis limits for a [ggplot](#) plot from the input dataset.

Description

Get axis limits for a [ggplot](#) plot from the input dataset.

Usage

```
getAxisLimPlot(
  data,
  xVar,
  yVar,
  xLim = NULL,
  yLim = NULL,
  facetPars = NULL,
  refLineData = NULL
)
```

Arguments

data	Data.frame with data.
xVar	String with column of data containing x-variable.
yVar	String with column of data containing y-variable.
xLim	Numeric vector of length 2 with limits for the x/y axes.
yLim	Numeric vector of length 2 with limits for the x/y axes.
facetPars	List with faceting parameters, passed to the faceting function. Variables should be specified as character or formula. For 'wrap' faceting (facetType is 'wrap'), if the layout is not specified via nrow/ncol, 2 columns are used by default.
refLineData	Data used for the reference lines, as output of the getDataReferenceLines function.

Value

Data.frame with limits of the:

- x-axis: 'xmin'/'xmax'
- y-axis: 'ymin'/'ymax'

for each element of the facetting variable (if any).

getDataReferenceLines *Extract data for the reference lines*

Description

This function especially extracts the data if an aesthetic variable is specified in the reference line parameters.

Usage

```
getDataReferenceLines(refLinePars, data, facetPars = NULL)
```

Arguments

- | | |
|-------------|--|
| refLinePars | (optional) Nested list, with parameters for each reference line(s). Each sublist (a.k.a reference line) contains: <ul style="list-style-type: none"> • aesthetic value(s) or variable(s) for the lines (in this case column names of data) for reference lines. The line position is controlled by the aesthetics supported in geom_vline, geom_hline and geom_abline. • 'label': (optional) Logical specifying if the line should be annotated (FALSE to not annotate the line) or string with annotation label. By default, the value of the position of the horizontal/vertical line or the equation of the diagonal line is displayed. |
| data | Data.frame with data. |
| facetPars | List with facetting parameters, passed to the facetting function. Variables should be specified as character or formula. For 'wrap' facetting (facetType is 'wrap'), if the layout is not specified via nrow/ncol, 2 columns are used by default. |

Value

List of data for the lines

Author(s)

Laure Cougnaud

getDimGgplot *Get plot dimensions*

Description

Get plot dimensions

Usage

```
getDimGgplot(gg)
```

Arguments

gg [ggplot](#)

Value

Numeric vector with number of rows ('nrow') and columns ('ncol') of the plot

Author(s)

Laure Cougnaud

getFacetVars *Get facetting variables from facet parameters.*

Description

Get facetting variables from facet parameters.

Usage

```
getFacetVars(facetPars = list())
```

Arguments

facetPars List with facetting parameters, passed to the facetting function. Variables should be specified as character or formula. For 'wrap' facetting (facetType is 'wrap'), if the layout is not specified via nrow/ncol, 2 columns are used by default.

Value

Character vector with facetting variable

Author(s)

Laure Cougnaud

`getFctTypeReferenceLines`*Get the names of the `ggplot` function to use for the reference lines*

Description

Get the names of the `ggplot` function to use for the reference lines

Usage

```
getFctTypeReferenceLines(refLinePars)
```

Arguments

- `refLinePars` (optional) Nested list, with parameters for each reference line(s). Each sublist (a.k.a reference line) contains:
- aesthetic value(s) or variable(s) for the lines (in this case column names of data) for reference lines. The line position is controlled by the aesthetics supported in `geom_vline`, `geom_hline` and `geom_abline`.
 - 'label': (optional) Logical specifying if the line should be annotated (FALSE to not annotate the line) or string with annotation label. By default, the value of the position of the horizontal/vertical line or the equation of the diagonal line is displayed.

Value

List of type of each reference lines, among: 'vline', 'hline' and 'abline'.

Author(s)

Laure Cougnaud

`getJsDepClinDataReview`*Get Javascript custom scripts required for specific clinical data functionalities.*

Description

Get Javascript custom scripts required for specific clinical data functionalities.

Usage

```
getJsDepClinDataReview(  
  type = c("collapsibleButton", "patientProfiles"),  
  dep = NULL  
)
```

Arguments

type	(optional) Character vector with type of dependencies, either: 'collapsibleButton' or 'patientProfiles'.
dep	(optional) Character vector with names of Javascript dependencies By default, all dependencies are included.

Value

List of [htmlDependency](#). To include this dependency in a report e.g. generated with rmarkdown, these can be passed to the: `extra_dependencies` parameter of the `output_format` specific function, e.g.: `rmarkdown::render(..., output_format = rmarkdown::html_document(extra_dependencies = dep))`

Author(s)

Laure Cougnaud

getMdFromConfig	<i>Get path of the Markdown file corresponding to a specific config file.</i>
-----------------	---

Description

The name of the Markdown file is based on:

- for the general `config.yml` file: the basename of the specified `indexPath`
- for other config file (each sub-report): the name of the config file, after removal of the 'config-' part.

Usage

```
getMdFromConfig(
  configFiles,
  indexPath = "index.Rmd",
  intermediateDir = "./interim"
)
```

Arguments

configFiles	Character vector with name or path of the config file(s).
indexPath	String with path to the index file, by default 'index.Rmd' in <code>inputDir</code> .
intermediateDir	String with intermediate directory ('interim' by default), where markdown files and rds file specifying Js libraries (with <code>knit_meta</code>) for each sub report are stored.

Value

String with path to the

Author(s)

Laure Cougnaud

getMdHeader

Get Markdown header, for creation in Rmarkdown.

Description

The depth is extracted:

1. from the settings if a specified depth is provided in the 'rmd_file_depth' for the current knitted file
2. level parameter otherwise

Usage

```
getMdHeader(title, level = 1)
```

Arguments

title	String with header title.
level	Integer of length 1 with header depth/level, 1 by default

Value

String with Markdown header, to be included in R within cat.

See Also

Other clinical data reporting: [checkReportTitles\(\)](#), [convertMdToHtml\(\)](#), [forceParams\(\)](#), [getParamsFromConfig\(\)](#), [gitbook_clinDataReview_report\(\)](#), [html_clinDataReview_report\(\)](#), [knitPrintClinDataReview\(\)](#), [render_clinDataReviewReport\(\)](#)

getMetadata	<i>Read metadata file</i>
-------------	---------------------------

Description

Read the metadata file from a yaml format. This function checks for existence of the metadata file and its content. In particular, within the yaml file matches the following strings:

- `path` Path to the data. More than one path is allowed.
- `dateTime` Date and time, usually of the SDTM data creation. When printing the metadata in Rmd document, there is the possibility to add the date and time of the report generation. See [knit_print.clinDataReviewMetadata](#).
- `datasetInfo` General information about the data sets.

Usage

```
getMetadata(filePath, namesInfo)
```

Arguments

<code>filePath</code>	String of path to file. Currently only one file path is supported. If more than one paths are provided, a warning will be printed and the first path will be used.
<code>namesInfo</code>	Named vector to rename the final output when printed in Rmd. The renaming happens only if the metadata info are printed in Rmd and not in the console.

Details

Note that the input names do not necessarily have to match the exact names. For instance, the user can also write "dateTimeMySDTMData", and the function will parse for existence of the string "dateTime".

Value

A list of:

- `summaryInfo` Information extracted from the inputs path, and dateTime.
- `datasetInfo` Information extracted from datasetInfo.

Examples

```
# Create temporary yaml file
tmpdir <- tempdir()
library(yaml)

tmpYamlFile <- tempfile(
  pattern = "file", tmpdir = tempdir(), fileext = ".yaml"
)
listArgs <- list(
```

```

pathSDTMs = "path/To/SDTM",
pathSDTMReformat = "path/To/SDTMReformat",
dateTime = "20200101",
datasetInfo = list(
  list(
    column1 = "ex.xpt",
    column2 = "20200101"
  ),
  list(
    column1 = "sl.xpt",
    column2 = "20200101",
    column3 = "OK"
  )
)
)
write_yaml(
  listArgs,
  file = tmpYamlFile
)

# Run metadata
# Note: the 'datasetInfo' can also contain empty elements
getMetadata(filePath = tmpYamlFile)

```

getParamsFromConfig *Get parameters from a config file*

Description

Please note that the information from this config file and the general config file: config.yml are considered.

In case parameters are defined both in the general and specific config files, the parameter from the general config file is ignored.

Usage

```

getParamsFromConfig(
  configFile,
  configDir = file.path(inputDir, "config"),
  inputDir = "."
)

```

Arguments

configFile	String with filename of the config file of interest in YAML format.
configDir	String with directory with config files, by default a 'config' folder in inputDir. It should contain a general 'config.yml' file and dedicated 'config-[X].yml' for each chapter. The order of each chapter is specified in the 'config' slot in the general 'config.yml'.
inputDir	String with input directory, working directory by default.

Value

List with parameters from the specified configFile and the general config file: config.yml.
There are two specific handlers:

- parameters tagged with '[param] !r [value]' are evaluated in R, and their evaluated value is returned
- parameters tagged with '[param] !r-lazy [value]' are imported as character, and need to be further process with [forceParams](#) inside the report.

Parameters with YAML type 'r-lazy' are imported as character, with this additional class.

Author(s)

Laure Cougnaud

See Also

[forceParams](#)

Other clinical data reporting: [checkReportTitles\(\)](#), [convertMdToHtml\(\)](#), [forceParams\(\)](#), [getMdHeader\(\)](#), [gitbook_clinDataReview_report\(\)](#), [html_clinDataReview_report\(\)](#), [knitPrintClinDataReview\(\)](#), [render_clinDataReviewReport\(\)](#)

getParFctReferenceLines

Get parameter of function used for reference lines

Description

Get parameter of function used for reference lines

Usage

```
getParFctReferenceLines(type)
```

Arguments

type string with line type, either: 'hline', 'abline' or 'vline'.

Value

Character vector with parameter names of the functions

Author(s)

Laure Cougnaud

getPathHyperlink	<i>Get path ('href') property from hyperlink(s).</i>
------------------	--

Description

Get path ('href') property from hyperlink(s).

Usage

```
getPathHyperlink(x)
```

Arguments

x Character vector with hyperlink(s). If multiple, the hyperlinks should be separated by: ', '.

Value

Character vector of length x containing only the hyperlinks.

Author(s)

Laure Cougnaud

getPathTemplate	<i>Get path of template clinical data report</i>
-----------------	--

Description

Get path of template clinical data report

Usage

```
getPathTemplate(file, package = "clinDataReview")
```

Arguments

file String with name of the template Rmd document
package String, which package the template should be extracted from, by default the clinDataReview package.

Value

String with path to the template in the installed clinDataReview package

Author(s)

Laure Cougnaud

Examples

```
## Not run:
pathDivisionTemplate <- getPathTemplate("divisionTemplate.Rmd") # get path template in the package
file.copy(from = pathDivisionTemplate, to = ".") # copy to current directory
rmarkdown::render(pathDivisionTemplate) # run file

## End(Not run)
```

getPlotTableVars	<i>Extract variables displayed in the attached table, for each available plotting function of the clinDataReview package.</i>
------------------	---

Description

This function is used in each plotting function of the package to extract the variable(s) displayed in the table associated to the plot and their associated labels.

This can also be used in the template reports, e.g. to extract reference variable(s) for the comparison table functionality in the plot template report.

The following framework is used:

- if variables to be displayed in the table (tableVars) are not specified:
 - all variables displayed in the plot are selected, based on the plot arguments.
 - For example: the variables displayed in the x and y axis and for coloring are extracted for the [scatterplotClinData](#) plotting function.
 - Label for these variable(s) are extracted from the associated parameter (e.g. xLab for xVar and so on) or the general parameter for the variable labels (labelVars) if not specified.
- if variables to be displayed in the table (tableVars) are specified:
 - these variable(s) are returned.
 - The associated label(s) are extracted from the associated parameter (tableLab) or the general parameter for the variable labels (labelVars) if not specified.

For the functions: [plotCountClinData](#), [treemapClinData](#), [sunburstClinData](#): value to represent are included in the table and colored with a bar.

Usage

```
getPlotTableVars(plotFunction, plotArgs)
```

Arguments

plotFunction	String with name of the plotting function, be available in the clinDataReview package.
plotArgs	List with parameters passed to the plotting function.

Value

Character vector with variable to include in the table, with extra attributes (passed to `tableClinData`):

- `'tableLab'`: Named character vector with labels for the table variables
- `'tablePars'`: extra table parameters, only included if specified as input or specified internally.

labels and the table parameters .

Author(s)

Laure Cougnaud

`getSizedPlotClinData` *Get dimensions for a clinical data plot*

Description

Get dimensions for a clinical data plot

Usage

```
getSizedPlotClinData(
  width = NULL,
  height = NULL,
  gg = NULL,
  nrow = 1L,
  ncol = 1L,
  legend = TRUE,
  legendPosition = "right"
)
```

Arguments

<code>width</code>	Numeric, width of the plot in pixels, 700 by default.
<code>height</code>	Numeric, height of the plot in pixels, 700 by default.
<code>gg</code>	ggplot
<code>nrow</code>	single-length integer specifying the number of facet rows in the plot. (default = 1) Overwritten if <code>gg</code> is specified.
<code>ncol</code>	single-length integer specifying the number of facet columns in the plot. (default = 1) Overwritten if <code>gg</code> is specified.
<code>legend</code>	Logical, if TRUE (by default) a legend is available in the plot.
<code>legendPosition</code>	String with position of the legend, 'right' by default.

Value

Numeric vector with width ('width') and height ('height') of the plot in pixels.

Author(s)

Laure Cougnaud

 gitbook_clinDataReview_report

Clinical data format for bookdown report.

Description

This function is only meant to set sensitive defaults for gitbook.
[gitbook](#) can be used instead.

Usage

```
gitbook_clinDataReview_report(
  logo = NULL,
  logoHeight = "60px",
  split_by = "section+number",
  config = list(sharing = NULL, toc = list(collapse = "section")),
  extra_dependencies = NULL,
  css = NULL,
  ...
)
```

Arguments

logo	String, path to the logo. No logo is printed by default.
logoHeight	String, indicating the logo height; 60px height by default.
split_by	String, how the reports should be split, (see help of the gitbook function)
config	List with config parameters, by default: no sharing and collapsed by section. (see help of the gitbook function)
extra_dependencies	NULL by default
css	String, path to the css.
...	Extra parameters passed to the gitbook function.

Value

R Markdown output format to pass to [render_book](#).

Author(s)

Laure Cougnaud

See Also

Other clinical data reporting: [checkReportTitles\(\)](#), [convertMdToHtml\(\)](#), [forceParams\(\)](#), [getMdHeader\(\)](#), [getParamsFromConfig\(\)](#), [html_clinDataReview_report\(\)](#), [knitPrintClinDataReview\(\)](#), [render_clinDataReviewR](#)

html_clinDataReview_report

Clinical data format for rmarkdown report.

Description

This function only kept for back-compatibility, [html_document](#) can be used instead.

Usage

```
html_clinDataReview_report(extra_dependencies = NULL, ...)
```

Arguments

extra_dependencies

NULL by default.

...

Extra parameters passed to the [html_document](#) function.

Value

R Markdown output format to pass to [render](#).

Author(s)

Laure Cougnaud

See Also

Other clinical data reporting: [checkReportTitles\(\)](#), [convertMdToHtml\(\)](#), [forceParams\(\)](#), [getMdHeader\(\)](#), [getParamsFromConfig\(\)](#), [gitbook_clinDataReview_report\(\)](#), [knitPrintClinDataReview\(\)](#), [render_clinDataReviewReport\(\)](#)

JSONSchToRd

Get R Documentation from a JSON schema.

Description

Note: this function doesn't support the full JSON schema specification, currently only the functionalities required by the templates of the package are implemented.

Usage

```
JSONSchToRd(JSONSch, title = NULL)
```

Arguments

JSONSch	List with JSON schema, as returned by fromJSON .
title	(optional) String with title. This will combined with the JSON schema 'title' tag if this is specified. is not available.

Value

Character vector with R documentation for the specified JSON schema.

Supported JSON schema tags

- 'title' is used as Rd section header
- 'description' is included in the text
- parameters are extracted from the following 'properties' tag:
 - 'type': object type
 - 'doc': documentation for the parameter (custom JSON schema tag). This can contain any Roxygen tags, e.g.: `\link[package]{function}`.
 - 'pattern' (optional): required value for the parameter
 - 'items' (optional): JSON schema for the different elements of an 'object'
 - 'minItems'/'maxItems' (optional): minimum/maximum number of elements in an 'array'
 - 'enum' (optional): set of possible values
 - 'const' (optional): fixed value for the parameter (a.k.a 'constant')

If a parameter is required, it should be listed in the 'required' tag of the schema (outside of the 'properties' tag).

Author(s)

Laure Cougnaud

`knitPrintClinDataReview`

Include output from clinical data, or list of such outputs in a Rmarkdown report, with an appropriate title.

Description

Include output from clinical data, or list of such outputs in a Rmarkdown report, with an appropriate title.

Usage

```
knitPrintClinDataReview(list, sep = ".", level = 1)
```

Arguments

- | | |
|--------------------|--|
| <code>list</code> | Named list of clinical data plots, the names are used for the section header. If several section header should be created, either: <ul style="list-style-type: none">• a list of level 1 named by the different group elements, separated by <code>sep</code>, e.g. <code>list('group1.param1' = .., 'group1.param2' = ...)</code>. Such list is e.g. created with dply.• a nested list, named with the different groups, e.g. created with <code>lapply</code> |
| <code>sep</code> | String with separator used to distinguish different levels in the labels of the list. e.g. <code>'.'</code> by default. |
| <code>level</code> | Integer with base level for section, 1 by default. |

Value

No returned value, the plots are included in the report. If a element in the list are empty (NULL), these elements (and the associated sections) are not included in the report.

Author(s)

Laure Cougnaud

See Also

Other clinical data reporting: [checkReportTitles\(\)](#), [convertMdToHtml\(\)](#), [forceParams\(\)](#), [getMdHeader\(\)](#), [getParamsFromConfig\(\)](#), [gitbook_clinDataReview_report\(\)](#), [html_clinDataReview_report\(\)](#), [render_clinDataReviewReport\(\)](#)

```
knit_print.clinDataReview
```

Print clinDataReviewTable object in a knitted document (e.g. Rmarkdown document).

Description

Print clinDataReviewTable object in a knitted document (e.g. Rmarkdown document).

Usage

```
## S3 method for class 'clinDataReview'  
knit_print(x, ...)
```

Arguments

x	Object of class clinDataReview
...	Extra parameters for compatibility with knit_print , not used currently.

Author(s)

Laure Cougnaud

```
knit_print.clinDataReviewMetadata
```

Print metadata file in the clinical data report

Description

This function receives the metadata information from [getMetadata](#) and prints them in a format for an Rmd report. In general, any list could be called as long as it is composed by two elements:

- summaryInfo an R object.
- datasetInfo a data.frame or a matrix.

The first (summaryInfo) is printed as [kable](#) object and the second (datasetInfo) is printed as hide/show html button with the function [collapseHtmlContent](#).

Usage

```
## S3 method for class 'clinDataReviewMetadata'  
knit_print(x, options = list(), ...)
```

Arguments

- x List of two elements named summaryInfo and datasetInfo.
- options List of extra options to be passed as chunk options. The option dateReportRun sets to true prints the date and time of the report creation.
- ... Extra arguments to be passed.

Value

Nothing. The tables are ready to be printed in Rmd.

html code to include metadata in a report

merge.sessionInfo *Merge multiple session information*

Description

Merge multiple session information

Usage

```
## S3 method for class 'sessionInfo'  
merge(...)
```

Arguments

- ... objects of type `sessionInfo`

Value

`sessionInfo` with combined information

Author(s)

Laure Cougnaud

moveSkeletonFiles	<i>Move skeleton files from the package to a directory</i>
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Description

This function moves the files used to create the skeleton from the package to a specified directory.

Usage

```
moveSkeletonFiles(dir)
```

Arguments

dir	String, path to the directory.
-----	--------------------------------

Value

Nothing, the files are available in the specified directory.

moveXpt	<i>Move data sets from clinUtils</i>
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Description

Move SDTM data sets available in clinUtils into a specified local directory.

Usage

```
moveXpt(dir)
```

Arguments

dir	String, path to the directory.
-----	--------------------------------

Value

Nothing, the data are saved in the dedicated location.

plotCountClinData *Interactive plot of 'count' data*

Description

Note: the table and plot are not (yet) linked.

Usage

```
plotCountClinData(
  data,
  vars,
  varsLab = getLabelVar(vars, labelVars = labelVars),
  valueVar,
  valueLab = getLabelVar(valueVar, labelVars = labelVars),
  colorVar = NULL,
  colorLab = getLabelVar(valueVar, labelVars = labelVars),
  colorPalette = getOption("clinDataReview.colors"),
  colorRange = NULL,
  valueType = "total",
  titleExtra = NULL,
  title = paste(paste(valueLab, "by", paste(varsLab, collapse = " and ")), titleExtra),
  collapse = "<br>"),
  labelVars = NULL,
  width = NULL,
  height = NULL,
  pathVar = NULL,
  pathLab = getLabelVar(pathVar, labelVars = labelVars),
  hoverVars = c(vars, valueVar, colorVar),
  hoverLab = getLabelVar(hoverVars, labelVars = labelVars),
  table = FALSE,
  tableVars,
  tableLab,
  tableButton = TRUE,
  tablePars = list(),
  id = paste0("plotClinData", sample.int(n = 1000, size = 1)),
  verbose = FALSE,
  typePlot = c("sunburst", "treemap")
)
```

Arguments

data	Data.frame with data.
vars	Character vector with variables of data containing plot nodes. If multiple, they should be specified in hierarchical order (from parent to child node).
varsLab	Named character vector with labels for vars.

valueVar	String with numeric variable of data containing node value, and associated label.
valueLab	String with numeric variable of data containing node value, and associated label.
colorVar	(optional) String with coloring variable (NULL by default). By default, the treemap is colored based by section.
colorLab	(optional) String with label for colorVar.
colorPalette	(optional) Named character vector with color palette. If not specified, the viridis color palette is used. See clinColors .
colorRange	(optional) Numeric vector of length 2 with range for the color variable, in case it is a numeric variable.
valueType	String with type of values in valueVar (branchvalues of the plot_ly function), among others: 'total' (default, only if sum(child) <= to parent) or 'relative'.
titleExtra	String with extra title for the plot (appended after title).
title	String with title for the plot.
labelVars	Named character vector containing variable labels.
width	Numeric, width of the plot in pixels, 700 by default.
height	Numeric, height of the plot in pixels, 700 by default.
pathVar	String with variable of data containing hyperlinks with path to the subject-specific report, formatted as: <pre>label</pre> <p>.</p> <p>If multiple, they should be separated by: ', '.</p> <p>The report(s) will be:</p> <ul style="list-style-type: none"> • compressed to a zip file and downloaded if the user clicks on the 'p' (a.k.a 'profile') key when hovering on a point of the plot • included in a collapsible row, and clickable with hyperlinks in the table
pathLab	String with label for pathVar, included in the collapsible row in the table.
hoverVars	Character vector with variable(s) to be displayed in the hover, by default any position and aesthetic variables displayed in the plot.
hoverLab	Named character vector with labels for hoverVars.
table	Logical, if TRUE (FALSE by default) returns also a datatable containing the plot data. (The plot and the table are not linked.)
tableVars	Character vector with variables to be included in the table.
tableLab	Named character vector with labels for each tableVars.
tableButton	Logical, if TRUE (by default) the table is included within an HTML button.
tablePars	List with parameters passed to the getClinDT function.
id	String with general id for the plot:

	<ul style="list-style-type: none"> • 'id' is used as group for the SharedData • 'button:[id]' is used as button ID if table is TRUE
	If not specified, a random id, as 'plotClinData[X]' is used.
verbose	Logical, if TRUE (FALSE by default) progress messages are printed in the current console. For the visualizations, progress messages during download of subject-specific report are displayed in the browser console.
typePlot	String with plot type, 'treemap' or 'sunburst'.

Value

Either:

- if table is requested a `clinDataReview` object, a.k.a a list with the 'plot' ([plotly](#) object) and 'table' ([datatable](#) object)
- otherwise: [plotly](#) object

Author(s)

Laure Cougnaud

See Also

Other visualizations of summary statistics for clinical data: [barplotClinData\(\)](#), [boxplotClinData\(\)](#), [sunburstClinData\(\)](#), [treemapClinData\(\)](#)

processData	<i>Run specified data processing steps.</i>
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Description

This function is intended to automate all data processing steps for use in the 'clinDataReview' reports using config files.

Usage

```
processData(data, processing, labelVars = NULL, ...)
```

Arguments

data	Data.frame with data.
processing	List with details of the steps to process the data. Each element in the list should be a named list containing the parameters for the specific processing function. The name specifies which processing step, among: <ul style="list-style-type: none"> • 'annotate' for annotateData (annotations parameter) • 'filter' for filterData (filters parameter) • 'transform' for transformData (transformations parameter)

labelVars Named character vector containing variable labels.
 ... Any parameters passed to all processing functions (if this parameter is available). If specified, these parameters shouldn't be specified also in processing.

Value

Data.frame with processed data, with extra attribute: labelVars.

Author(s)

Laure Cougnaud

renamePathDateInfoMetadata
Rename variable names of metadata info

Description

Rename variable names referring to the paths and the date.

Usage

```
renamePathDateInfoMetadata(summaryInfo, namesInfo)
```

Arguments

summaryInfo A matrix, see output from [getMetadata](#).
 namesInfo Named vector to rename the final output.

Value

A matrix, same as input summaryInfo with renamed variable names.

renderInNewSession *Render a rmarkdown doc in a new session, with the possibility to save output in a log file, and saving also session information.*

Description

Note: this function is inspired from xfun::Rscript_call

Usage

```
renderInNewSession(  
  input,  
  run_pandoc = FALSE,  
  output_options = list(keep_md = TRUE),  
  encoding = "UTF-8",  
  params = NULL,  
  ...  
)
```

Arguments

input	Input file to be rendered.
run_pandoc	Logical, if TRUE (FALSE by default) convert Md to specified output with pandoc.
output_options	List of output options, by default 'keep_md = TRUE' (keep Markdown file)
encoding	String with encoding, 'UTF-8' by default.
params	List with input parameters for this document. These parameters should be accessed in the Rmd document via <code>params\$...</code> These parameters will be saved to a RDS file and imported during the report rendering.
...	Any extra parameters passed to render

Value

Output of the function executed in the new R session with additional attribute: 'sessionInfo' containing the details of the session information in the separated R session. If the report fails, an error message is returned.

Author(s)

Laure Cougnaud

render_clinDataReviewReport

Render a clinical data report.

Description

Render a clinical data report.

Usage

```
render_clinDataReviewReport(
  configFiles = NULL,
  configDir = file.path(inputDir, "config"),
  logFile = NULL,
  indexPath = file.path(inputDir, "index.Rmd"),
  inputDir = ".",
  outputDir = "./report",
  intermediateDir = "./interim",
  extraDirs = file.path(inputDir, c("figures", "tables")),
  quiet = FALSE
)
```

Arguments

configFiles	(optional) Character vector with specific config files to be converted from Rmarkdown to Markdown. If <ul style="list-style-type: none"> not specified (by default): all config files specified in the general 'config.yml' will be run (Rmd -> md) specified (expert use only): only the specified files will be run (Rmd -> md). Other config files mentioned in the general 'config.yml' file won't be rerun, so the associated 'md' file should be already available in the intermediateDir folder.
configDir	String with directory with config files, by default a 'config' folder in inputDir. It should contain a general 'config.yml' file and dedicated 'config-[X].yml' for each chapter. The order of each chapter is specified in the 'config' slot in the general 'config.yml'.
logFile	(optional) String with path to a log file, where output (also error/messages/warnings) should be stored. If specified, the entire output is re-directed to this file.
indexPath	String with path to the index file, by default 'index.Rmd' in inputDir.
inputDir	String with input directory, working directory by default.
outputDir	String with output directory, ('report' by default).
intermediateDir	String with intermediate directory ('interim' by default), where markdown files and rds file specifying Js libraries (with knit_meta) for each sub report are stored.
extraDirs	Character vector with extra directories required by the report, directory with external images . By default, the directories: 'figures', 'tables' and mentioned in the 'patientProfilePath' parameter of the general config file are included. All these folders should be available in inputDir.
quiet	Logical, if TRUE (FALSE by default) progress messages during report execution are not displayed in the console (see render).

Value

String with path to the front page of the clinical data report.

Framework

This function is based on the [render_book](#) function, enabling specification of chapter-specific input parameters, specified in YAML configuration files. This consists of:

1. importing the general config file ('config'.yml) to identify each report of interest ('config' tag)
2. for each report of interest:
 - loading the report specific parameters from the associated 'config' file (see the [getParamsFromConfig](#) function)
 - if the template should be extracted from a specified package (templatePackage tag), this template is copied to the current directory. Please note that if a file with same name is available in the working directory, this file will be overwritten.
 - executing the report ('template' tag) with the associated parameters in a **new R session for reproducibility**, to obtain the associated Markdown file
3. combining all Markdown files to a html document (see the [convertMdToHtml](#) function)

If the execution of a specific report fails with error, a warning message is triggered. A report containing only the specified title is created, to ensure output consistency (especially html file numbering) in case the report succeeds.

Available template report

see ? 'clinDataReview-templates' for list of clinical data template report available in the package.

Author(s)

Laure Cougnaud

See Also

Other clinical data reporting: [checkReportTitles\(\)](#), [convertMdToHtml\(\)](#), [forceParams\(\)](#), [getMdHeader\(\)](#), [getParamsFromConfig\(\)](#), [gitbook_clinDataReview_report\(\)](#), [html_clinDataReview_report\(\)](#), [knitPrintClinDataReview\(\)](#)

scatterplotClinData *Scatterplot of variables of interest for clinical data visualization.*

Description

Scatterplot of variables of interest for clinical data visualization.

Usage

```

scatterplotClinData(
  data,
  xVar,
  yVar,
  xLab = getLabelVar(xVar, labelVars = labelVars),
  yLab = getLabelVar(yVar, labelVars = labelVars),
  aesPointVar = list(),
  aesLineVar = list(),
  lineInclude = length(aesLineVar) > 0,
  aesLab,
  xTrans = "identity",
  yTrans = "identity",
  xPars = list(),
  yPars = list(),
  yLim = NULL,
  xLim = NULL,
  yLimExpandData = TRUE,
  xLimExpandData = TRUE,
  titleExtra = NULL,
  title = paste(paste(yLab, "vs", xLab, titleExtra), collapse = "<br>"),
  facetPars = list(),
  facetType = c("wrap", "grid"),
  scalePars = list(),
  themePars = list(legend.position = "bottom"),
  refLinePars = NULL,
  labelVars = NULL,
  width = NULL,
  height = NULL,
  hoverVars,
  hoverLab,
  idVar = "USUBJID",
  idLab = getLabelVar(idVar, labelVars = labelVars),
  pathVar = NULL,
  pathExpand = FALSE,
  table = FALSE,
  tableVars,
  tableLab,
  tableButton = TRUE,
  tablePars = list(),
  id = paste0("plotClinData", sample.int(n = 1000, size = 1)),
  verbose = FALSE
)

```

Arguments

<code>data</code>	Data.frame with input data.
<code>xVar</code>	String with column of data containing x-variable.

yVar	String with column of data containing y-variable.
xLab	String with label for xVar.
yLab	String with label for xVar.
aesPointVar	List with specification of aesthetic variable(s), for the point, passed to the mapping parameter of <code>geom_point</code> , e.g. <code>list(color = "TRTP")</code> . Please note by default symbols with fill and color are used. Color is used for the outside of the points, fill for the inside and the hover. Usually, you might want to specify both filling and coloring.
aesLineVar	List with specification of aesthetic variable(s), for the line, passed to the mapping parameter of <code>geom_point</code> , e.g. <code>list(group = "USUBJID")</code> .
lineInclude	Logical, if TRUE (by default if aesLineVar is specified) include a scatterplot.
aesLab	Named character vector with labels for each aesthetic variable.
xTrans	Transformation for the x/y- variables, passed to the trans parameter of <code>scale_x_continuous/</code> <code>scale_y_continuous</code> .
yTrans	Transformation for the x/y- variables, passed to the trans parameter of <code>scale_x_continuous/</code> <code>scale_y_continuous</code> .
xPars	List with extra parameters for x/y axis, passed to the <code>scale_x_continuous/</code> <code>scale_y_continuous</code> functions, besides trans and limits.
yPars	List with extra parameters for x/y axis, passed to the <code>scale_x_continuous/</code> <code>scale_y_continuous</code> functions, besides trans and limits.
yLim	Numeric vector of length 2 with limits for the x/y axes.
xLim	Numeric vector of length 2 with limits for the x/y axes.
yLimExpandData	Logical (TRUE by default), should the limits specified via xLim/yLim be expanded to include any data points outside of these limits? Please note that the same limits are set for all facets.
xLimExpandData	Logical (TRUE by default), should the limits specified via xLim/yLim be expanded to include any data points outside of these limits? Please note that the same limits are set for all facets.
titleExtra	String with extra title for the plot (appended after title).
title	String with title for the plot.
facetPars	List with faceting parameters, passed to the faceting function.
facetType	String with faceting type, either: <ul style="list-style-type: none"> • 'wrap': <code>facet_wrap</code> • 'grid': <code>facet_grid</code>
scalePars	List with parameters to customize scales. Each sublist should contains a set of parameters passed to the <code>scale_discrete_manual</code> function. If palette(s) are not specified, default palettes are used (see <code>getColorPalette</code> , <code>getShapePalette</code> , <code>getLinetypePalette</code>)
themePars	List with general theme parameters (see <code>theme</code>).
refLinePars	(optional) Nested list, with parameters for each reference line(s). Each sublist (a.k.a reference line) contains:

	<ul style="list-style-type: none"> • aesthetic value(s) or variable(s) for the lines (in this case column names of data) for reference lines. The line position is controlled by the aesthetics supported in geom_vline, geom_hline and geom_abline. • 'label': (optional) Logical specifying if the line should be annotated (FALSE to not annotate the line) or string with annotation label. By default, the value of the position of the horizontal/vertical line or the equation of the diagonal line is displayed.
labelVars	Named character vector containing variable labels.
width	Numeric, width of the plot in pixels, 700 by default.
height	Numeric, height of the plot in pixels, 700 by default.
hoverVars	Character vector with variables to be displayed in the hover, by default xVar, yVar and any aesthetic variables.
hoverLab	Named character vector with labels for hoverVars.
idVar	String with variable containing subject ID.
idLab	String with label for idVar.
pathVar	String with variable of data containing path to a subject-specific report. The report info should be unique for each element of idVar. The report will be: <ul style="list-style-type: none"> • opened in a different window in the browser if the user clicks on the 'p' (a.k.a 'profile') key when hovering on a point of the plot • opened in the browser via hyperlink in the table
pathExpand	Logical, if FALSE (by default) the path to subject-report is included in an hyperlink in the table, otherwise a collapsed row is created. This should be set to TRUE only if multiple paths are included for each row in pathVar (e.g. in case of summary table).
table	Logical, if TRUE (FALSE by default) returns also a datatable containing the plot data. The plot and table are linked when included in a Rmarkdown document: when clicking on an plot element, only the corresponding records are retained in the associated table; when some records are selected in the table, they are highlighted in the associated table.
tableVars	Character vector with variables to be included in the table.
tableLab	Named character vector with labels for each tableVars.
tableButton	Logical, if TRUE (by default) the table is included within an HTML button.
tablePars	List with parameters passed to the getClinDT function.
id	String with general id for the plot: <ul style="list-style-type: none"> • 'id' is used as group for the SharedData • 'button:[id]' is used as button ID if table is TRUE <p>If not specified, a random id, as 'plotClinData[X]' is used.</p>
verbose	Logical, if TRUE (FALSE by default) progress messages are printed in the current console. For the visualizations, progress messages during download of subject-specific report are displayed in the browser console.

Value

Either:

- if table is requested a clinDataReview object, a.k.a a list with the 'plot' ([plotly](#) object) and 'table' ([datatable](#) object)
- otherwise: [plotly](#) object

Author(s)

Laure Cougnaud

Examples

```
library(clinUtils)

data(dataADaMCDISCP01)
labelVars <- attr(dataADaMCDISCP01, "labelVars")

dataLB <- dataADaMCDISCP01$ADLBC
dataDM <- dataADaMCDISCP01$ADSL
dataLB <- annotateData(dataLB, annotations = list(data = dataDM))

## pairwise comparison plot of two parameters of interest:

# format data long -> wide format (one column per lab param)
dataPlot <- subset(dataLB, PARAMCD %in% c("ALT", "AST"))
library(reshape2)
dataPlotWide <- dcast(
  data = dataPlot,
  formula = USUBJID + VISIT + VISITNUM ~ PARAMCD,
  value.var = "LBSTRESN",
  fun.aggregate = mean
)

# scatterplot per visit
scatterplotClinData(
  data = dataPlotWide,
  xVar = "ALT", yVar = "AST",
  aesPointVar = list(color = "USUBJID"),
  themePars = list(legend.position = "none"),
  facetPars = list(facets = "VISIT"),
  labelVars = labelVars
)

# scatterplot with all visits, link subjects
xLab <- getLabelParamcd(paramcd = "ALT", data = dataLB,
  paramcdVar = "PARAMCD", paramVar = "PARAM")
yLab <- getLabelParamcd(paramcd = "AST", data = dataLB,
  paramcdVar = "PARAMCD", paramVar = "PARAM")
scatterplotClinData(
  data = dataPlotWide,
  xVar = "ALT", yVar = "AST",
```

```

xLab = xLab,
yLab = yLab,
aesPointVar = list(color = "VISIT", shape = "VISIT"),
aesLineVar = list(group = "USUBJID", linetype = "VISIT"),
labelVars = labelVars
)

# scatterplot of different visits versus baseline

# add baseline as extra column:
dataPlot <- subset(dataLB, PARAMCD == "ALT")
dataPlotBL <- subset(dataPlot, VISIT == "SCREENING 1")
dataPlotBL <- dataPlotBL[with(dataPlotBL, order(USUBJID, -ADY)), ]
dataPlotBL <- dataPlotBL[!duplicated(dataPlotBL$USUBJID), ]
dataPlot$LBSTRESNBL <- dataPlot[match(dataPlot$USUBJID, dataPlotBL$USUBJID), "LBSTRESN"]

# sort visits:
dataPlot$VISIT <- with(dataPlot, reorder(VISIT, VISITNUM))

xLab <- paste(labelVars["LBSTRESN"], "for last screening visit")
yLab <- paste(labelVars["LBSTRESN"], "at visit X")
paramLab <- getLabelParamcd(paramcd = "ALT", data = dataLB,
paramcdVar = "PARAMCD", paramVar = "PARAM")
scatterplotClinData(
  data = dataPlot,
  xVar = "LBSTRESNBL", xLab = xLab,
  yVar = "LBSTRESN", yLab = yLab,
  aesPointVar = list(color = "USUBJID"),
  aesLineVar = list(group = "USUBJID", color = "USUBJID"),
  hoverVars = c("USUBJID", "VISIT", "ADY", "LBSTRESN"),
  labelVars = labelVars,
  facetPars = list(facets = "VISIT"),
  themePars = list(legend.position = "none"),
  title = paste("Comparison of actual value of",
  paramLab,
  "at each visit versus baseline"
),
  refLinePars = list(
  list(slope = 1, intercept = 0, linetype = 1, color = "black",
  label = FALSE),
  list(xintercept = "A1L0", linetype = 2, color = "orange"),
  list(yintercept = "A1L0", linetype = 2, color = "orange"),
  list(xintercept = "A1HI", linetype = 2, color = "orange"),
  list(yintercept = "A1HI", linetype = 2, color = "orange",
  label = "Reference Range Upper Limit")
)
)

```

Description

By default, the number of columns is 2.

Usage

```
setFacetLayoutWrap(data, facetPars = list())
```

Arguments

data	Data.frame with data.
facetPars	List with faceting parameters, passed to the faceting function. Variables should be specified as character or formula. For 'wrap' faceting (facetType is 'wrap'), if the layout is not specified via nrow/ncol, 2 columns are used by default.

Value

Updated facetPars.

Author(s)

Laure Cougnaud

setPaletteStaticScatterplotClinData

Get standard palette for the staticScatterplotClinData function.

Description

Get standard palette for the staticScatterplotClinData function.

Usage

```
setPaletteStaticScatterplotClinData(data, var, aes, scalePars, geomAes, ...)
```

Arguments

data	Data.frame with data for the plot.
var	Character vector with variable(s) to consider. If multiple, currently only the first one is considered.
aes	String with aesthetic, either: 'color', 'shape' or 'linetype'.
scalePars	List with parameters to customize scales. Each sublist should contains a set of parameters passed to the scale_discrete_manual function. If palette(s) are not specified, default palettes are used (see getColorPalette , getShapePalette , getLinetypePalette)
geomAes	List with aesthetic for each geom.
...	Any extra parameters than x and n for the default palette fcts.

Value

List with: scalePars and geomAes, each of those potentially updated with default palette(s).

Author(s)

Laure Cougnaud

staticScatterplotClinData

Scatterplot of variables of interest for clinical data visualization

Description

Scatterplot of variables of interest for clinical data visualization

Usage

```
staticScatterplotClinData(
  data,
  xVar,
  yVar,
  xLab = getLabelVar(xVar, labelVars = labelVars),
  yLab = getLabelVar(yVar, labelVars = labelVars),
  aesPointVar = list(),
  aesLineVar = list(),
  lineInclude = length(aesLineVar) > 0,
  aesLab,
  xTrans = "identity",
  yTrans = "identity",
  xPars = list(),
  yPars = list(),
  yLim = NULL,
  xLim = NULL,
  yLimExpandData = TRUE,
  xLimExpandData = TRUE,
  titleExtra = NULL,
  title = paste(paste(yLab, "vs", xLab, titleExtra), collapse = "<br>"),
  facetPars = list(),
  facetType = c("wrap", "grid"),
  scalePars = list(),
  themePars = list(legend.position = "bottom"),
  refLinePars = NULL,
  labelVars = NULL,
  hoverVars = NULL,
  geomType = c("point", "col")
)
```

Arguments

data	Data.frame with input data.
xVar	String with column of data containing x-variable.
yVar	String with column of data containing y-variable.
xLab	String with label for xVar.
yLab	String with label for xVar.
aesPointVar	List with specification of aesthetic variable(s), for the point, passed to the mapping parameter of <code>geom_point</code> , e.g. <code>list(color = "TRTP")</code> . Please note by default symbols with fill and color are used. Color is used for the outside of the points, fill for the inside and the hover. Usually, you might want to specify both filling and coloring.
aesLineVar	List with specification of aesthetic variable(s), for the line, passed to the mapping parameter of <code>geom_point</code> , e.g. <code>list(group = "USBJID")</code> .
lineInclude	Logical, if TRUE (by default if aesLineVar is specified) include a scatterplot.
aesLab	Named character vector with labels for each aesthetic variable.
xTrans, yTrans	Transformation for the x/y- variables, passed to the trans parameter of <code>scale_x_continuous/</code> <code>scale_y_continuous</code> .
xPars, yPars	List with extra parameters for x/y axis, passed to the <code>scale_x_continuous/</code> <code>scale_y_continuous</code> functions, besides trans and limits.
yLim	Numeric vector of length 2 with limits for the x/y axes.
xLim	Numeric vector of length 2 with limits for the x/y axes.
xLimExpandData, yLimExpandData	Logical (TRUE by default), should the limits specified via xLim/yLim be expanded to include any data points outside of these limits? Please note that the same limits are set for all facets.
titleExtra	String with extra title for the plot (appended after title).
title	String with title for the plot.
facetPars	List with faceting parameters, passed to the faceting function.
facetType	String with faceting type, either: <ul style="list-style-type: none"> • 'wrap': <code>facet_wrap</code> • 'grid': <code>facet_grid</code>
scalePars	List with parameters to customize scales. Each sublist should contains a set of parameters passed to the <code>scale_discrete_manual</code> function. If palette(s) are not specified, default palettes are used (see <code>getColorPalette</code> , <code>getShapePalette</code> , <code>getLinetypePalette</code>)
themePars	List with general theme parameters (see <code>theme</code>).
refLinePars	(optional) Nested list, with parameters for each reference line(s). Each sublist (a.k.a reference line) contains: <ul style="list-style-type: none"> • aesthetic value(s) or variable(s) for the lines (in this case column names of data) for reference lines. The line position is controlled by the aesthetics supported in <code>geom_vline</code>, <code>geom_hline</code> and <code>geom_abline</code>.

	<ul style="list-style-type: none"> • 'label': (optional) Logical specifying if the line should be annotated (FALSE to not annotate the line) or string with annotation label. By default, the value of the position of the horizontal/vertical line or the equation of the diagonal line is displayed.
labelVars	Named character vector containing variable labels.
hoverVars	Character vector with variables to be displayed in the hover, by default xVar, yVar and any aesthetic variables.
geomType	String with type of the geom used, either: <ul style="list-style-type: none"> • 'point': scatterplot with <code>geom_point</code> is created • 'col': barplot with <code>geom_col</code> is created

Value

`ggplot` object

Author(s)

Laure Cougnaud

sunburstClinData *Sunburst interactive plot.*

Description

Note: the table and plot are not (yet) linked.

Usage

```
sunburstClinData(...)
```

Arguments

... Arguments passed on to `plotCountClinData`

colorVar (optional) String with coloring variable (NULL by default). By default, the treemap is colored based by section.

colorLab (optional) String with label for colorVar.

colorRange (optional) Numeric vector of length 2 with range for the color variable, in case it is a numeric variable.

vars Character vector with variables of data containing plot nodes. If multiple, they should be specified in hierarchical order (from parent to child node).

varsLab Named character vector with labels for vars.

valueVar String with numeric variable of data containing node value, and associated label.

valueLab String with numeric variable of data containing node value, and associated label.

valueType String with type of values in `valueVar` (branchvalues of the `plot_ly` function), among others: 'total' (default, only if `sum(child) <=` to parent) or 'relative'.

pathVar String with variable of data containing hyperlinks with path to the subject-specific report, formatted as:

```
<a href="./path-to-report">label</a>
```

.

If multiple, they should be separated by ', '.

The report(s) will be:

- compressed to a zip file and downloaded if the user clicks on the 'p' (a.k.a 'profile') key when hovering on a point of the plot
- included in a collapsible row, and clickable with hyperlinks in the table

pathLab String with label for `pathVar`, included in the collapsible row in the table.

table Logical, if TRUE (FALSE by default) returns also a datatable containing the plot data. (The plot and the table are not linked.)

data Data.frame with data.

colorPalette (optional) Named character vector with color palette. If not specified, the viridis color palette is used.

See [clinColors](#).

titleExtra String with extra title for the plot (appended after `title`).

title String with title for the plot.

labelVars Named character vector containing variable labels.

width Numeric, width of the plot in pixels, 700 by default.

height Numeric, height of the plot in pixels, 700 by default.

hoverVars Character vector with variable(s) to be displayed in the hover, by default any position and aesthetic variables displayed in the plot.

hoverLab Named character vector with labels for `hoverVars`.

id String with general id for the plot:

- 'id' is used as group for the [SharedData](#)
- 'button:[id]' is used as button ID if `table` is TRUE

If not specified, a random id, as 'plotClinData[X]' is used.

verbose Logical, if TRUE (FALSE by default) progress messages are printed in the current console. For the visualizations, progress messages during download of subject-specific report are displayed in the browser console.

tableVars Character vector with variables to be included in the table.

tableLab Named character vector with labels for each `tableVars`.

tableButton Logical, if TRUE (by default) the table is included within an HTML button.

tablePars List with parameters passed to the [getClinDT](#) function.

Value

Either:

- if table is requested a clinDataReview object, a.k.a a list with the 'plot' ([plotly](#) object) and 'table' ([datatable](#) object)
- otherwise: [plotly](#) object

Author(s)

Laure Cougnaud

See Also

Other visualizations of summary statistics for clinical data: [barplotClinData\(\)](#), [boxplotClinData\(\)](#), [plotCountClinData\(\)](#), [treemapClinData\(\)](#)

Examples

```
library(clinUtils)

data(dataADaMCDISCP01)
labelVars <- attr(dataADaMCDISCP01, "labelVars")

dataAE <- dataADaMCDISCP01$ADAE
dataDM <- dataADaMCDISCP01$ADSL

## example of basic sunburst:

# sunburst takes as input table with counts
library(inTextSummaryTable)

# total counts: Safety Analysis Set (patients with start date for the first treatment)
dataTotal <- subset(dataDM, RFSTDTC != "")

# compute adverse event table
tableAE <- getSummaryStatisticsTable(

  data = dataAE,
  rowVar = c("AESOC", "AEDECOD"),
  dataTotal = dataTotal,
  rowOrder = "total",
  labelVars = labelVars,
  stats = getStats("count"),

  # plotly treemap requires records (rows) for each group
  rowVarTotalInclude = "AEDECOD",
  outputType = "data.frame-base"

)

dataSunburst <- tableAE

dataSunburst$n <- as.numeric(dataSunburst$n)

# create plot
```



```

sunburstClinData(
  data = dataSunburst,
  vars = c("AESOC", "AEDECOD"),
  valueVar = "n",
  valueLab = "Number of patients with adverse events"
)

## example where sum(counts) of child = counts of parent

# counts of patients per arm/site
tableDM <- getSummaryStatisticsTable(
  data = dataDM,
  rowVar = c("ARM", "SITEID"),
  labelVars = labelVars,
  # plotly treemap requires records (rows) for each group
  rowVarTotalInclude = "SITEID",
  rowTotalInclude = TRUE,
  outputType = "data.frame-base"
)
tableDM$statN <- as.numeric(tableDM$statN)

# create the plot
sunburstClinData(
  data = tableDM,
  vars = c("ARM", "SITEID"),
  valueVar = "statN", valueLab = "Counts of patients",
  valueType = "total"
)

```

tableClinData

Create a 'clinical data table', associated to a plot.

Description

Interactive table is created, with the possibility to have clickable link to patient-specific report, and included within a button.

Usage

```

tableClinData(
  data,
  idVar = "USUBJID",
  idLab = getLabelVar(idVar, labelVars = labelVars),
  keyVar = NULL,
  keyLab = getLabelVar(keyVar, labelVars = labelVars),
  pathVar = NULL,
  pathLab = getLabelVar(pathVar, labelVars = labelVars),
  pathExpand = FALSE,
  tableVars = colnames(data),

```

```

tableLab = getLabelVar(tableVars, labelVars = labelVars),
tableButton = TRUE,
tablePars = list(),
id = paste0("plotClinData", sample.int(n = 1000, size = 1)),
labelVars = NULL,
verbose = FALSE
)

```

Arguments

data	Data.frame with data.
idVar	String with variable containing subject ID.
idLab	String with label for idVar.
keyVar	String with unique key variable, identifying unique group for which the link between the table and the plot should be done.
keyLab	String with label for keyVar.
pathVar	String with variable of data containing hyperlinks with path to the subject-specific report, formatted as: <p style="margin-left: 2em;"><code>label</code></p> <p style="margin-left: 2em;">.</p> <p style="margin-left: 2em;">If multiple, they should be separated by: ', '.</p> <p style="margin-left: 2em;">The report(s) will be:</p> <ul style="list-style-type: none"> • compressed to a zip file and downloaded if the user clicks on the 'p' (a.k.a 'profile') key when hovering on a point of the plot • included in a collapsible row, and clickable with hyperlinks in the table
pathLab	String with label for pathVar, included in the collapsible row in the table.
pathExpand	Logical, should the variable in pathExpand be included in a collapsible row or as hyperlink in the table? Should be TRUE for if multiple paths are included for each idVar, FALSE otherwise (by default).
tableVars	Character vector with variables to be included in the table.
tableLab	Named character vector with labels for each tableVars.
tableButton	Logical, if TRUE (by default) the table is included within an HTML button.
tablePars	List with parameters passed to the <code>getClinDT</code> function.
id	String with general id for the plot: <ul style="list-style-type: none"> • 'id' is used as group for the SharedData • 'button:[id]' is used as button ID if table is TRUE <p>If not specified, a random id, as 'plotClinData[X]' is used.</p>
labelVars	Named character vector containing variable labels.
verbose	Logical, if TRUE (FALSE by default) progress messages are printed in the current console.

Value

[datatable](#)

Author(s)

Laure Cougnaud

timeProfileIntervalPlot

Visualize time intervals across subjects/parameters.

Description

Visualize time intervals across subjects/parameters.

Usage

```
timeProfileIntervalPlot(  
  data,  
  paramVar,  
  paramLab = getLabelVar(paramVar, labelVars = labelVars),  
  paramVarSep = " - ",  
  paramGroupVar = NULL,  
  timeStartVar,  
  timeStartLab = getLabelVar(timeStartVar, labelVars = labelVars),  
  timeEndVar,  
  timeEndLab = getLabelVar(timeEndVar, labelVars = labelVars),  
  timeStartShapeVar = NULL,  
  timeStartShapeLab = getLabelVar(timeStartShapeVar, labelVars = labelVars),  
  timeEndShapeVar = NULL,  
  timeEndShapeLab = getLabelVar(timeEndShapeVar, labelVars = labelVars),  
  shapePalette = NULL,  
  colorVar = NULL,  
  colorLab = getLabelVar(timeStartShapeVar, labelVars = labelVars),  
  colorPalette = NULL,  
  alpha = 1,  
  yLab = NULL,  
  xLab = paste(c(timeStartLab, timeEndLab), collapse = " and " ),  
  title = NULL,  
  labelVars = NULL,  
  width = 800,  
  height = NULL,  
  hoverVars,  
  hoverLab,  
  idVar = "USUBJID",  
  idLab = getLabelVar(idVar, labelVars = labelVars),  
  pathVar = NULL,
```

```

pathLab = getLabelVar(pathVar, labelVars = labelVars),
table = FALSE,
tableVars,
tableLab,
tableButton = TRUE,
tablePars = list(),
id = paste0("plotClinData", sample.int(n = 1000, size = 1)),
verbose = FALSE
)

```

Arguments

<code>data</code>	Data.frame with data.
<code>paramVar</code>	Character vector with variable of data to represent in the y-axis.
<code>paramLab</code>	(optional) String with label for <code>paramVar</code> .
<code>paramVarSep</code>	(optional) String with separator used to combined <code>paramVar</code> if multiple.
<code>paramGroupVar</code>	(optional) Character vector with variable(s) to group/order the <code>paramVar</code> elements in the y-axis.
<code>timeStartVar</code>	String with variable with the start of the time interval.
<code>timeStartLab</code>	(optional) String with label for <code>timeStartVar</code> .
<code>timeEndVar</code>	String with variable with the end of the time interval.
<code>timeEndLab</code>	(optional) String with label for <code>timeEndVar</code> .
<code>timeStartShapeVar</code>	(optional) String with variable used for the shape of the start of the time interval.
<code>timeStartShapeLab</code>	(optional) String with label for <code>timeStartShapeVar</code> .
<code>timeEndShapeVar</code>	(optional) String with variable used for the shape of the end of the time interval.
<code>timeEndShapeLab</code>	(optional) String with label for <code>timeEndShapeVar</code> .
<code>shapePalette</code>	(optional) Character vector with shape palette for <code>timeStartShapeVar</code> and <code>timeEndShapeVar</code> .
<code>colorVar</code>	(optional) String with color variable.
<code>colorLab</code>	(optional) String with label for <code>colorVar</code> .
<code>colorPalette</code>	(optional) Named character vector with color palette. If not specified, the viridis color palette is used. See clinColors .
<code>alpha</code>	(optional) Numeric with transparency, 1 by default.
<code>xLab, yLab</code>	(optional) String with labels for the x/y-axis.
<code>title</code>	String with title for the plot.
<code>labelVars</code>	Named character vector containing variable labels.
<code>width</code>	Numeric, width of the plot in pixels, 700 by default.
<code>height</code>	Numeric, height of the plot in pixels, 700 by default.

hoverVars	Character vector with variable(s) to be displayed in the hover, by default any position and aesthetic variables displayed in the plot.
hoverLab	Named character vector with labels for hoverVars.
idVar	String with variable containing subject ID.
idLab	String with label for idVar.
pathVar	String with variable of data containing hyperlinks with path to the subject-specific report, formatted as: <pre>label</pre> <p>.</p> <p>If multiple, they should be separated by: ', '.</p> <p>The report(s) will be:</p> <ul style="list-style-type: none"> • compressed to a zip file and downloaded if the user clicks on the 'p' (a.k.a 'profile') key when hovering on a point of the plot • included in a collapsible row, and clickable with hyperlinks in the table
pathLab	String with label for pathVar, included in the collapsible row in the table.
table	Logical, if TRUE (FALSE by default) returns also a <code>datatable</code> containing the plot data. The plot and table are linked when included in a Rmarkdown document: when clicking on an plot element, only the corresponding records are retained in the associated table; when some records are selected in the table, they are highlighted in the associated table.
tableVars	Character vector with variables to be included in the table.
tableLab	Named character vector with labels for each tableVars.
tableButton	Logical, if TRUE (by default) the table is included within an HTML button.
tablePars	List with parameters passed to the <code>getClinDT</code> function.
id	String with general id for the plot: <ul style="list-style-type: none"> • 'id' is used as group for the <code>SharedData</code> • 'button:[id]' is used as button ID if table is TRUE <p>If not specified, a random id, as 'plotClinData[X]' is used.</p>
verbose	Logical, if TRUE (FALSE by default) progress messages are printed in the current console. For the visualizations, progress messages during download of subject-specific report are displayed in the browser console.

Value

Either:

- if table is requested a `clinDataReview` object, a.k.a a list with the 'plot' (`plotly` object) and 'table' (`datatable` object)
- otherwise: `plotly` object

Author(s)

Laure Cougnaud

transformData	<i>Transform data.</i>
---------------	------------------------

Description

Transform data from long to wide format. This function converts formats with the `stats::reshape` function.

Usage

```
transformData(data, transformations, verbose = FALSE, labelVars = NULL)
```

Arguments

data	Data.frame with input data to transform.
transformations	<p>Transformations (or list of those) as a list with:</p> <ul style="list-style-type: none"> • 'type': String with type of transformation. Currently, only: 'pivot_wider' is available • extra parameters for the transformation, for: <ul style="list-style-type: none"> – 'pivot_wider': <ul style="list-style-type: none"> * 'varsID': Character vector with variable(s) of data defining unique records in the wide format. Corresponds to the <code>idvar</code> parameter of the <code>reshape</code> function. * 'varPivot': String with unique variable of data containing elements to pivot in different columns in the wide format (used for column names). Corresponds to the <code>timevar</code> parameter of the <code>reshape</code> function. * 'varsValue': Character vector with variable(s) of data used to fill the columns in the wide format. Corresponds to the <code>v.names</code> parameter of the <code>reshape</code> function.
verbose	Logical, if TRUE (FALSE by default) progress messages are printed in the current console. For the visualizations, progress messages during download of subject-specific report are displayed in the browser console.
labelVars	Named character vector containing variable labels.

Value

A data.frame in wide format.

Author(s)

Laure Cougnaud

treemapClinData	<i>Treemap interactive plot.</i>
-----------------	----------------------------------

Description

Note: the table and plot are not (yet) linked.

Usage

```
treemapClinData(...)
```

Arguments

... Arguments passed on to `plotCountClinData`

`colorVar` (optional) String with coloring variable (NULL by default). By default, the treemap is colored based by section.

`colorLab` (optional) String with label for `colorVar`.

`colorRange` (optional) Numeric vector of length 2 with range for the color variable, in case it is a numeric variable.

`vars` Character vector with variables of data containing plot nodes. If multiple, they should be specified in hierarchical order (from parent to child node).

`varsLab` Named character vector with labels for `vars`.

`valueVar` String with numeric variable of data containing node value, and associated label.

`valueLab` String with numeric variable of data containing node value, and associated label.

`valueType` String with type of values in `valueVar` (branchvalues of the `plot_ly` function), among others: 'total' (default, only if `sum(child) <=` to parent) or 'relative'.

`pathVar` String with variable of data containing hyperlinks with path to the subject-specific report, formatted as:

```
<a href="./path-to-report">label</a>
```

.

If multiple, they should be separated by: ', '.

The report(s) will be:

- compressed to a zip file and downloaded if the user clicks on the 'p' (a.k.a 'profile') key when hovering on a point of the plot
- included in a collapsible row, and clickable with hyperlinks in the table

`pathLab` String with label for `pathVar`, included in the collapsible row in the table.

`table` Logical, if TRUE (FALSE by default) returns also a `datatable` containing the plot data. (The plot and the table are not linked.)

`data` `Data.frame` with data.

`colorPalette` (optional) Named character vector with color palette. If not specified, the viridis color palette is used.

See [clinColors](#).

`titleExtra` String with extra title for the plot (appended after `title`).

`title` String with title for the plot.

`labelVars` Named character vector containing variable labels.

`width` Numeric, width of the plot in pixels, 700 by default.

`height` Numeric, height of the plot in pixels, 700 by default.

`hoverVars` Character vector with variable(s) to be displayed in the hover, by default any position and aesthetic variables displayed in the plot.

`hoverLab` Named character vector with labels for `hoverVars`.

`id` String with general id for the plot:

- `'id'` is used as group for the [SharedData](#)
- `'button:[id]'` is used as button ID if `table` is TRUE

If not specified, a random id, as `'plotClinData[X]'` is used.

`verbose` Logical, if TRUE (FALSE by default) progress messages are printed in the current console. For the visualizations, progress messages during download of subject-specific report are displayed in the browser console.

`tableVars` Character vector with variables to be included in the table.

`tableLab` Named character vector with labels for each `tableVars`.

`tableButton` Logical, if TRUE (by default) the table is included within an HTML button.

`tablePars` List with parameters passed to the [getClinDT](#) function.

Value

Either:

- if `table` is requested a `clinDataReview` object, a.k.a a list with the `'plot'` ([plotly](#) object) and `'table'` ([datatable](#) object)
- otherwise: [plotly](#) object

Author(s)

Laure Cougnaud

See Also

Other visualizations of summary statistics for clinical data: [barplotClinData\(\)](#), [boxplotClinData\(\)](#), [plotCountClinData\(\)](#), [sunburstClinData\(\)](#)

Examples

```
library(clinUtils)

data(dataADaMCDISCP01)
labelVars <- attr(dataADaMCDISCP01, "labelVars")
```



```

dataDM <- dataADaMCDISCP01$ADSL
dataAE <- dataADaMCDISCP01$ADAE

library(plyr)

## basic treemap:

# treemap takes as input table with counts
library(inTextSummaryTable)

# total counts: Safety Analysis Set (patients with start date for the first treatment)
dataTotal <- subset(dataDM, RFSTDTC != "")

# compute adverse event table
tableAE <- getSummaryStatisticsTable(

data = dataAE,
rowVar = c("AESOC", "AEDECOD"),
dataTotal = dataTotal,
rowOrder = "total",
labelVars = labelVars,
stats = getStats("count"),

# plotly treemap requires records (rows) for each group
rowVarTotalInclude = "AEDECOD",
outputType = "data.frame-base"

)

dataPlot <- tableAE

dataPlot$n <- as.numeric(dataPlot$n)

# create plot
treemapClinData(
data = dataPlot,
vars = c("AESOC", "AEDECOD"),
valueVar = "n",
  valueLab = "Number of patients with adverse events"
)

## treemap with coloring

# extract worst-case scenario
dataAE$AESEVN <- as.numeric(factor(dataAE$AESEV, levels = c("MILD", "MODERATE", "SEVERE")))
if(any(is.na(dataAE$AESEVN)))
stop("Severity should be filled for all subjects.")

dataAEWC <- ddply(dataAE, c("AESOC", "AEDECOD", "USUBJID"), function(x){
x[which.max(x$AESEVN), ]
})
dataTotalRow <- list(AEDECOD =

```

```

ddply(dataAEWC, c("AESOC", "USUBJID"), function(x){
  x[which.max(x$AESEVN), ]
})
)

# compute adverse event table
tableAE <- getSummaryStatisticsTable(

data = dataAEWC,
rowVar = c("AESOC", "AEDECOD"),
var = "AESEVN",
dataTotal = dataTotal,
rowOrder = "total",
labelVars = labelVars,

# plotly treemap requires records (rows) for each group
rowVarTotalInclude = "AEDECOD",
dataTotalRow = dataTotalRow,
outputType = "data.frame-base"

)

dataPlot <- tableAE

dataPlot$statN <- as.numeric(dataPlot$statN)
dataPlot$statMean <- as.numeric(dataPlot$statMean)

# create plot
treemapClinData(
data = dataPlot,
vars = c("AESOC", "AEDECOD"),
valueVar = "statN", valueLab = "Number of patients with adverse events",
colorVar = "statMean", colorLab = "Mean severity"
)

```

varToFm	<i>Get formula for a specific variable, to be used in aesthetic specification in plot_ly.</i>
---------	---

Description

Get formula for a specific variable, to be used in aesthetic specification in [plot_ly](#).

Usage

```
varToFm(var)
```

Arguments

var Character vector with variable to combine. Otherwise with the '+' operator.

Value

`as.formula`

Author(s)

Laure Cougnaud

zipClinDataReview *Zip the clinical data report*

Description

Create a zip folder of clinical data reports with a redirect page. The clinical data report out of the `render_clinDataReviewReport` is copied into a new folder. A redirect html page is created to enable the user to navigate the report without needing to look into the new directory.

Usage

```
zipClinDataReview(  
  reportDir = "report",  
  newDir = "report_dependencies",  
  redirectPage = "report.html",  
  zipFolder = "report.zip"  
)
```

Arguments

<code>reportDir</code>	String for the path to the directory where the clinical data reports are stored
<code>newDir</code>	String for the path where the files from <code>reportDir</code> should be copied to.
<code>redirectPage</code>	String with the path of the html file that redirects to the "1-introduction.html" page of the report.
<code>zipFolder</code>	String with the path to the zipped folder.

Value

The zip folder is created in the specified location.

Index

- * **Clinical data visualization of individual profiles.**
 - scatterplotClinData, 69
- * **clinical data reporting**
 - checkReportTitles, 18
 - convertMdToHtml, 29
 - forceParams, 39
 - getMdHeader, 49
 - getParamsFromConfig, 51
 - gitbook_clinDataReview_report, 56
 - html_clinDataReview_report, 57
 - knitPrintClinDataReview, 59
 - render_clinDataReviewReport, 67
- * **visualizations of summary statistics for clinical data**
 - barplotClinData, 9
 - boxplotClinData, 13
 - plotCountClinData, 63
 - sunburstClinData, 78
 - treemapClinData, 87
- addDateOfReportRun, 3
- addFacetPanel, 4
- addReferenceLinesClinDataPlot, 5
- annotateData, 6, 65
- as.formula, 91

- barplotClinData, 9, 15, 65, 80, 88
- boxplotClinData, 11, 13, 65, 80, 88

- checkAvailabilityMetadata, 16
- checkConfigFile, 17
- checkReportTitles, 18, 30, 39, 49, 52, 57, 59, 69
- checkTemplatesName, 18
- checkValueType, 19
- clinColors, 10, 14, 21, 64, 79, 84, 88
- clinDataReview-common-args, 20
- clinDataReview-common-args-report, 21

- clinDataReview-common-args-summaryStatsVis, 22
- clinDataReview-templates, 23
- collapseHtmlContent, 28, 60
- compareTables, 25, 27, 28
- computeSummaryStatisticsTable, 27, 28
- convertMdToHtml, 18, 29, 39, 49, 52, 57, 59, 69
- createClinDataReviewReportSkeleton, 30, 31
- createExampleMetadata, 31
- createMainConfigSkeleton, 31
- createPatientProfileVar, 32
- createRedirectPage, 33
- createSubjectProfileReport, 26
- createTemplateDoc, 33

- datatable, 11, 15, 65, 73, 80, 83, 85, 88
- dlply, 59

- exportSessionInfoToMd, 34
- exportSummaryStatisticsTable, 28

- facet_grid, 71, 77
- facet_wrap, 71, 77
- filterData, 7, 35, 65
- filterDataSingle, 38
- forceParams, 18, 30, 39, 49, 52, 57, 59, 69
- formatDataForPlotClinData, 40
- formatHoverText, 41
- formatPathDateInfoMetadata, 41
- formatPlotlyClinData, 42
- formatToHierarchicalData, 43
- fromJSON, 58

- geom_abline, 5, 21, 45, 47, 72, 77
- geom_col, 78
- geom_hline, 5, 21, 45, 47, 72, 77
- geom_point, 71, 77, 78
- geom_vline, 5, 21, 45, 47, 72, 77

- getAxisLimPlot, 44
- getClinDT, 11, 15, 64, 72, 79, 82, 85, 88
- getColorPalette, 71, 75, 77
- getDataReferenceLines, 44, 45
- getDimGgplot, 46
- getFacetVars, 46
- getFctTypeReferenceLines, 47
- getJsDepClinDataReview, 47
- getLinetypePalette, 71, 75, 77
- getMdFromConfig, 48
- getMdHeader, 18, 30, 39, 49, 52, 57, 59, 69
- getMetadata, 3, 42, 50, 60, 66
- getParamsFromConfig, 18, 30, 39, 49, 51, 57, 59, 69
- getParFctReferenceLines, 52
- getPathHyperlink, 53
- getPathTemplate, 53
- getPlotTableVars, 54
- getShapePalette, 71, 75, 77
- getSizePlotClinData, 55
- ggplot, 5, 6, 20, 44, 46, 47, 55, 78
- ggplotly, 42
- gitbook, 56
- gitbook_clinDataReview_report, 18, 30, 39, 49, 52, 56, 57, 59, 69

- highlight, 43
- html_clinDataReview_report, 18, 30, 39, 49, 52, 57, 57, 59, 69
- html_document, 57
- htmlDependency, 48

- JSONSchToRd, 58

- kable, 60
- knit_print, 60
- knit_print.clinDataReview, 60
- knit_print.clinDataReviewMetadata, 50, 60
- knitPrintClinDataReview, 18, 30, 39, 49, 52, 57, 59, 69

- layout, 10
- Logic, 36

- merge.sessionInfo, 61
- moveSkeletonFiles, 62
- moveXpt, 62

- plot_ly, 19, 20, 22, 42, 64, 79, 87, 90
- plotCountClinData, 11, 15, 54, 63, 78, 80, 87, 88
- plotly, 11, 15, 43, 65, 73, 80, 85, 88
- processData, 24–28, 65

- renamePathDateInfoMetadata, 66
- render, 57, 67, 68
- render_book, 56, 69
- render_clinDataReviewReport, 18, 30, 31, 33, 39, 49, 52, 57, 59, 67, 91
- renderInNewSession, 66

- scale_discrete_manual, 71, 75, 77
- scale_x_continuous, 71, 77
- scale_y_continuous, 71, 77
- scatterplotClinData, 54, 69
- sessionInfo, 34, 61
- setFacetLayoutWrap, 74
- setPaletteStaticScatterplotClinData, 75
- SharedData, 11, 15, 21, 40, 43, 65, 72, 79, 82, 85, 88
- staticScatterplotClinData, 76
- subjectProfileEventPlot, 26
- subjectProfileIntervalPlot, 26
- subjectProfileLinePlot, 26
- subjectProfileTextPlot, 26
- sunburstClinData, 11, 15, 54, 65, 78, 88

- tableClinData, 25, 55, 81
- tag, 29
- theme, 71, 77
- timeProfileIntervalPlot, 83
- transformData, 65, 86
- treemapClinData, 11, 15, 54, 65, 80, 87

- varToFm, 90

- zipClinDataReview, 91