Package 'tableExtra'

November 23, 2020

Title Draws an awesome table

Version 0.99.1

Description Draws an awesome table.

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Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Suggests testthat,
    dplyr,
    tibble

Depends R (>= 2.10)

Imports gtable,
    grid

R topics documented:

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gtable_rbind   *rbind two or more gtables*

Description

rbind two or more gtables

cbind two or more gtables

Usage

```
gtable_rbind(..., size = "max", height = NULL, z = NULL)

gtable_cbind(..., size = "max", width = NULL, z = NULL)
```

Arguments

`...`	gtables
`size`	how should the widths be calculated?
	1. `max` maximum of all widths
	2. `min` minimum of all widths
	3. `first` widths/heights of first gtable
	4. `last` widths/heights of last gtable
`height`	padding height between grobs
`z`	optional z level
`width`	padding width between grobs

---

pcawg_counts	*Mutation counts attributed to each mutational signature in each tumour.*

Description

Data from the mutational signature analysis of Alexandrov et al. on the PCAWG data. The data is available as supplementary data to the paper "The repertoire of mutational signatures in human cancer" on the Synapse data repository syn11738669

Usage

```
data(pcawg_counts)
```

Format

A data frame with 2780 rows and 68 variables

Cancer.Types 37 different cancer types

Sample.Names Unique tumour identifiers

Accuracy Cosine similarity between the tumour's mutational profile and the reconstructed mutational profile

SBS1 Single-base-substitution signature 1. See https://cancer.sanger.ac.uk/cosmic/signatures/SBS/SBS1.tt ...

Details

pcawg_counts contains the mutation counts as attributed by the SigProfiler algorithm on the Single-Base-Substitution (SBSs) mutation catalogs of 2780 WGS tumours from the PCAWG.

Source

Synapse collaborative compute space, https://www.synapse.org/#!Synapse:syn11804065

References

Alexandrov, L.B., Kim, J., Haradhvala, N.J. et al. The repertoire of mutational signatures in human cancer. Nature 578, 94–101 (2020). https://doi.org/10.1038/s41586-020-1943-3

Examples

```
data(pcawg_counts)
```

| table_extra_grob | *Graphical display of a table with circles of varying scales and colours. The code is inspired by the* gridExtra::tableGrob() *function.* |

Description

Create a gtable containing circle grobs representing a numeric matrix.

Usage

```
table_extra_grob(
  dscale,
  dcolor = NULL,
  dscale_min = NULL,
  dscale_max = NULL,
  rows = rownames(dscale),
  cols = colnames(dscale),
  rows_more = NULL,
  cols_more = NULL,
  theme = ttheme_awesome(),
  vp = NULL
)
```

Arguments

dscale	a matrix
dcolor	(optional) a matrix
dscale_min	value for setting the minimum scale size of foreground grobs. Entries in the dscale matrix below dscale_min will have a scale of 0 (no grob).
dscale_max	value for setting the maximum scale size of foreground grobs. Entries in the dscale matrix above dscale_max will have a scale of 0 (no grob).
rows	(optional) a character vector
cols	(optional) a character vector
rows_more	(optional) a named list of additional columns (right-part) of the plot for describing the rows. The list names will be used as column headers.
cols_more	(optional) a named list of additional rows (top-part) of the plot for describing the columns The list names will be used as row headers.
theme	list of theme parameters
vp	optional viewport

Value

An R object of class `grob`

Author(s)

Yoann Pradat

See Also

ttheme_awesome()

Examples

```
library(tableExtra)
```

| tableExtra | *tableExtra: A package for awesome tables* |

Description

'tableExtra' provides a function to draw a table with grobs of varying size and colors to represent two different types of information about multiple variables in multiple samples. The package was originally developed to reproduce Figure 3 of Alexandrov, L.B., Kim, J., Haradhvala, N.J. et al. The repertoire of mutational signatures in human cancer. Nature 578, 94–101 (2020). https://doi.org/10.1038/s41586-020-1943-3

Author(s)

Yoann Pradat

| ttheme_awesome | *Define theme for awesome table plot.* |

Description

Define theme for awesome table plot.

Usage

```
ttheme_awesome(
  base_size = 8,
  base_colour = "black",
  base_family = "",
  core_size = unit(10, "mm"),
  scale_breaks = 10,
  scale_ratio = 0.25,
  color_palette = "black",
  color_breaks = NULL,
  parse = FALSE,
  padding = unit(c(0.3, 0.3), "mm"),
  ...
)
```

Arguments

`base_size`	default font size
`base_colour`	default font colour
`base_family`	default font family
`core_size`	cell size for core background grobs
`scale_breaks`	number of size categories for core foreground grobs or numeric vector of bin breaks
`scale_ratio`	ratio of minimum to maximum core foreground grobs sizes
`color_palette`	color palette for core foreground grobs
`color_breaks`	bin breaks for color palette for core foreground grobs
`parse`	logical, default behaviour for parsing text as plotmath
`padding`	length-2 unit vector specifying the horizontal and vertical padding of text within each cell
`...`	extra parameters added to the theme list

Author(s)

Yoann Pradat

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