

Package ‘tableExtra’

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Title Draws an awesome table
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Description Draws an awesome table.
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grid

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gtable_combine	<i>Combine gtables based on row/column names.</i>
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Description

Combine gtables based on row/column names.

Usage

```
gtable_combine(..., along = 1L, join = "outer")  
  
combine(..., along = 1L, join = "outer")
```

Arguments

...	gtables
along	dimension to align along, 1 = rows, 2 = cols.
join	when x and y have different names, how should the difference be resolved? inner keep names that appear in both, outer keep names that appear in either, left keep names from x, and right keep names from y.

gtable_rbind	<i>rbind gtables</i>
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Description

rbind gtables

cbind gtables

Usage

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

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

Arguments

...	gtables
size	how should the widths be calculated? max maximum of all widths min minimum of all widths first widths/heights of first gtable last widths/heights of last gtable
z	optional z level

pcawg_counts	<i>Mutation counts attributed to each mutational signature in each tumour.</i>
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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

SBSXXX Each SBSXXX variable represents the counts attributed to the signature SBSXXX in the corresponding tumour

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	<i>Graphical display of a table with circles of varying scales and colours. The code is inspired by the <code>gridExtra::tableGrob()</code> function.</i>
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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
rows	(optional) a character vector
cols	(optional) a character vector
theme	list of theme parameters
vp	optional viewport

Value

An R object of class grob

Author(s)

Yoann Pradat

See Also

[theme_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	<i>Define theme for awesome table plot.</i>
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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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