

Package ‘heatmaply’

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Type Package

Title Interactive Cluster Heat Maps Using 'plotly' and 'ggplot2'

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Description Create interactive cluster 'heatmaps' that can be saved as a stand-alone HTML file, embedded in 'R Markdown' documents or in a 'Shiny' app, and available in the 'RStudio' viewer pane. Hover the mouse pointer over a cell to show details or drag a rectangle to zoom. A 'heatmap' is a popular graphical method for visualizing high-dimensional data, in which a table of numbers are encoded as a grid of colored cells. The rows and columns of the matrix are ordered to highlight patterns and are often accompanied by 'dendrograms'. 'Heatmaps' are used in many fields for visualizing observations, correlations, missing values patterns, and more. Interactive 'heatmaps' allow the inspection of specific value by hovering the mouse over a cell, as well as zooming into a region of the 'heatmap' by dragging a rectangle around the relevant area. This work is based on the 'ggplot2' and 'plotly.js' engine. It produces similar 'heatmaps' to 'heatmap.2' with the advantage of speed ('plotly.js' is able to handle larger size matrix), the ability to zoom from the 'dendrogram' panes, and the placing of factor variables in the sides of the 'heatmap'.

Depends R (>= 3.0.0), plotly (>= 4.7.1), viridis

Imports ggplot2 (>= 2.2.0), dendextend (>= 1.12.0), magrittr (>= 1.0.1), reshape2, scales, seriation, utils, stats, grDevices, methods, colorspace, RColorBrewer, htmlwidgets, webshot, assertthat, egg

Suggests knitr, covr, gplots, tidyselect, rmarkdown, testthat

VignetteBuilder knitr

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URL <https://talgalili.github.io/heatmaply/>,
<https://cran.r-project.org/package=heatmaply>,
<https://github.com/talgalili/heatmaply/>,
<https://www.r-statistics.com/tag/heatmaply/>

BugReports <https://github.com/talgalili/heatmaply/issues>

LazyData true

RoxygenNote 7.1.1

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ggheatmap	<i>ggplot heatmap equivalent to heatmaply</i>
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Description

This function produces a ggplot analogue of heatmaply figures using [ggarrange](#). This function may not always support the same set of features as , and exporting the heatmaply object with, for example, [orca](#) or `heatmaply(mtcars, file = "foo.png")`.

Usage

```
ggheatmap(..., widths = NULL, heights = NULL, row_dend_left = FALSE)
```

Arguments

...	Passed to heatmaply
widths, heights	Relative widths and heights of plots.
row_dend_left	Logical argument controlling whether the row dendrogram is placed on the left of the plot.

Examples

```
ggheatmap(mtcars)
```

```
ggplot_side_color_plot
```

Side color plots for heatmaps

Description

Important for creating annotation.

Usage

```
ggplot_side_color_plot(
  df,
  palette = NULL,
  scale_title = paste(type, "side colors"),
  type = c("column", "row"),
  text_angle = if (type == "column") 0 else 90,
  is_colors = FALSE,
  fontsize = 10,
  label_name = NULL
)
```

Arguments

df	A "molten" data.frame as produced by (eg) <code>reshape2::melt</code>
palette	A function which can return colors to be used in the sidebar plot
scale_title	Title of the color scale. Not currently used.
type	Horizontal or vertical plot? Valid values are "column" and "row"
text_angle	the angle of the text of the rows/columns.
is_colors	Use if the values in df are valid colours and should not be mapped to a color scheme, and instead should be plotted directly.
fontsize	Font size (currently unused)
label_name	Name for the mouseover label, usually "row" or "column"

Value

A ggplot `geom_tile` object

heatmaply

*Cluster heatmap based on plotly***Description**

An object of class heatmapr includes all the needed information for producing a heatmap. The goal is to separate the pre-processing of the heatmap elements from the graphical rendering of the object, which could be done

(Please submit an issue on github if you have a feature that you wish to have added)

heatmaply_na is a wrapper for 'heatmaply' which comes with defaults that are better for exploring missing value (NA) patterns. Specifically, the grid_gap is set to 1, and the colors include two shades of grey. It also calculates the [is.na10](#) automatically.

heatmaply_cor is a wrapper for 'heatmaply' which comes with defaults that are better for correlation matrixes. Specifically, the limits are set from -1 to 1, and the color palette is [RdBu](#).

Usage

```
heatmaply(x, ...)
```

```
heatmaply_na(x, grid_gap = 1, colors = c("grey80", "grey20"), ...)
```

```
heatmaply_cor(x, limits = c(-1, 1), colors = cool_warm, ...)
```

```
## Default S3 method:
```

```
heatmaply(
  x,
  colors = viridis(n = 256, alpha = 1, begin = 0, end = 1, option = "viridis"),
  limits = NULL,
  na.value = "grey50",
  row_text_angle = 0,
  column_text_angle = 45,
  subplot_margin = 0,
  cellnote = NULL,
  draw_cellnote = !is.null(cellnote),
  cellnote_color = "auto",
  cellnote_textposition = "middle right",
  cellnote_size = 12,
  Rowv,
  Colv,
  distfun = dist,
  hclustfun = hclust,
  dist_method = NULL,
  hclust_method = NULL,
  distfun_row,
  hclustfun_row,
  distfun_col,
```

```
hclustfun_col,  
dendrogram = c("both", "row", "column", "none"),  
show_dendrogram = c(TRUE, TRUE),  
reorderfun = function(d, w) reorder(d, w),  
k_row = 1,  
k_col = 1,  
symm = FALSE,  
revC,  
scale = c("none", "row", "column"),  
na.rm = TRUE,  
row_dend_left = FALSE,  
margins = c(NA, NA, NA, NA),  
...,  
scale_fill_gradient_fun = NULL,  
grid_color = NA,  
grid_gap = 0,  
srtRow,  
srtCol,  
xlab = "",  
ylab = "",  
main = "",  
titleX = TRUE,  
titleY = TRUE,  
hide_colorbar = FALSE,  
key.title = NULL,  
return_ppxpy = FALSE,  
row_side_colors,  
row_side_palette = NULL,  
col_side_colors,  
col_side_palette = NULL,  
ColSideColors = NULL,  
RowSideColors = NULL,  
seriate = c("OLO", "mean", "none", "GW"),  
heatmap_layers = NULL,  
side_color_layers = NULL,  
dendrogram_layers = NULL,  
branches_lwd = 0.6,  
file,  
width = NULL,  
height = NULL,  
long_data,  
plot_method = c("ggplot", "plotly"),  
label_names = NULL,  
fontsize_row = 10,  
fontsize_col = 10,  
cexRow,  
cexCol,  
subplot_widths = NULL,
```

```

subplot_heights = NULL,
colorbar_len = 0.3,
colorbar_thickness = 30,
colorbar_xanchor = if (row_dend_left) "right" else "left",
colorbar_yanchor = "bottom",
colorbar_xpos = if (row_dend_left) -0.1 else 1.1,
colorbar_ypos = 0,
showticklabels = c(TRUE, TRUE),
dynamicTicks = FALSE,
grid_size = 0.1,
node_type = "heatmap",
point_size_mat = NULL,
point_size_name = "Point size",
label_format_fun = function(...) format(..., digits = 4),
labRow = NULL,
labCol = NULL,
custom_hovertext = NULL,
col = NULL,
dend_hoverinfo = TRUE,
side_color_colorbar_len = 0.3
)

## S3 method for class 'heatmpr'
heatmaply(
  x,
  colors = viridis(n = 256, alpha = 1, begin = 0, end = 1, option = "viridis"),
  limits = NULL,
  na.value = "grey50",
  row_text_angle = 0,
  column_text_angle = 45,
  subplot_margin = 0,
  row_dend_left = FALSE,
  margins = c(NA, NA, NA, NA),
  ...,
  scale_fill_gradient_fun = scale_fill_gradientn(colors = if (is.function(colors))
    colors(256) else colors, na.value = na.value, limits = limits),
  grid_color = NA,
  grid_gap = 0,
  srtRow,
  srtCol,
  xlab = "",
  ylab = "",
  main = "",
  titleX = TRUE,
  titleY = TRUE,
  hide_colorbar = FALSE,
  key.title = NULL,
  return_ppxpy = FALSE,

```

```

draw_cellnote = FALSE,
cellnote_color = "auto",
cellnote_textposition = "middle right",
cellnote_size = 12,
row_side_colors = x[["row_side_colors"]],
row_side_palette = NULL,
col_side_colors = x[["col_side_colors"]],
col_side_palette = NULL,
plot_method = c("ggplot", "plotly"),
ColSideColors = NULL,
RowSideColors = NULL,
heatmap_layers = NULL,
side_color_layers = NULL,
dendrogram_layers = NULL,
branches_lwd = 0.6,
label_names = c("row", "column", "value"),
fontsize_row = 10,
fontsize_col = 10,
subplot_widths = NULL,
subplot_heights = NULL,
colorbar_xanchor = if (row_dend_left) "right" else "left",
colorbar_yanchor = "bottom",
colorbar_xpos = if (row_dend_left) -0.1 else 1.1,
colorbar_ypos = 0,
colorbar_len = 0.3,
colorbar_thickness = 30,
showticklabels = c(TRUE, TRUE),
dynamicTicks = FALSE,
node_type = c("scatter", "heatmap"),
grid_size = 0.1,
point_size_mat = x[["matrix"]][["point_size_mat"]],
point_size_name = "Point size",
label_format_fun = function(...) format(..., digits = 4),
custom_hovertext = x[["matrix"]][["custom_hovertext"]],
dend_hoverinfo = TRUE,
side_color_colorbar_len = 0.3
)

```

Arguments

- | | |
|----------|---|
| x | can either be a heatmaply object, or a numeric matrix Defaults to TRUE unless x contains any NAs. |
| ... | other parameters passed to heatmaply (currently, various parameters may be ignored). |
| grid_gap | this is a fast alternative to <code>grid_color</code> . The default is 0, but if a larger value is used (for example, 1), then the resulting heatmap will have a white grid which can help identify different cells. This is implemented using style (with <code>xgap</code> and <code>ygap</code>). |

colors, col	a vector of colors to use for heatmap color. The default uses <code>viridis</code> (<code>n=256</code> , <code>alpha = 1</code> , <code>begin = 0</code> , <code>end = 1</code> , <code>option = "viridis"</code>) It is passed to <code>scale_fill_gradientn</code> . If colors is a color function (with the first argument being 'n' = the number of colors), it will be used to create 256 colors from that function. (col is there to stay compatible with <code>heatmap.2</code>)
limits	a two dimensional numeric vector specifying the data range for the scale.
na.value	color to use for missing values (default is "grey50").
row_text_angle	numeric (Default is 0), the angle of the text of the rows. (this is called <code>srtRow</code> in <code>heatmap.2</code>)
column_text_angle	numeric (Default is 45), the angle of the text of the columns. (this is called <code>srtCol</code> in <code>heatmap.2</code>)
subplot_margin	Currently not well implemented. It is passed to <code>subplot</code> . Default is 0. Either a single value or four values (all between 0 and 1). If four values are provided, the first is used as the left margin, the second is used as the right margin, the third is used as the top margin, and the fourth is used as the bottom margin. If a single value is provided, it will be used as all four margins.
cellnote	Values to be shown as annotations atop the heatmap cells.
draw_cellnote	Should the cellnote annotations be drawn? Defaults is FALSE, if cellnote is not supplied, TRUE if cellnote is supplied. If TRUE and cellnote is not supplied, x will be used for cellnote.
cellnote_color	The color of the cellnote text to be used.
cellnote_textposition	The text positioning/centering of the cellnote. Default is "middle right". Options are "top left", "top center", "top right", "middle left", "middle center", "middle right", "bottom left", "bottom center", "bottom right"
cellnote_size	The font size (HTML/CSS) of the cellnote. Default is 12.
Rowv	determines if and how the row dendrogram should be reordered. By default, it is TRUE, which implies dendrogram is computed and reordered based on row means. If NULL or FALSE, then no dendrogram is computed and no reordering is done. If a <code>dendrogram</code> (or <code>hclust</code>), then it is used "as-is", ie without any reordering. If a vector of integers, then dendrogram is computed and reordered based on the order of the vector.
Colv	determines if and how the column dendrogram should be reordered. Has the options as the Rowv argument above and additionally when x is a square matrix, Colv = "Rowv" means that columns should be treated identically to the rows.
distfun	function used to compute the distance (dissimilarity) between both rows and columns. Defaults to <code>dist</code> . The options "pearson", "spearman" and "kendall" can be used to use correlation-based clustering, which uses <code>as.dist(1 - cor(t(x)))</code> as the distance metric (using the specified correlation method).
hclustfun	function used to compute the hierarchical clustering when Rowv or Colv are not dendrograms. Defaults to <code>hclust</code> .
dist_method	default is NULL (which results in "euclidean" to be used). Can accept alternative character strings indicating the method to be passed to <code>distfun</code> . By default <code>distfun</code> is <code>dist</code> hence this can be one of "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski".

<code>hclust_method</code>	default is NULL (which results in "complete" to be used). Can accept alternative character strings indicating the method to be passed to <code>hclustfun</code> . By default <code>hclustfun</code> is <code>hclust</code> hence this can be one of "ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC). Specifying <code>hclust_method=NA</code> causes <code>heatmaply</code> to use <code>find_dend</code> to find the "optimal" dendrogram for the data.
<code>distfun_row</code>	<code>distfun</code> for row dendrogram only.
<code>hclustfun_row</code>	<code>hclustfun</code> for col dendrogram only.
<code>distfun_col</code>	<code>distfun</code> for row dendrogram only.
<code>hclustfun_col</code>	<code>hclustfun</code> for col dendrogram only.
<code>dendrogram</code>	character string indicating whether to compute 'none', 'row', 'column' or 'both' dendrograms. Defaults to 'both'. However, if <code>Rowv</code> (or <code>Colv</code>) is FALSE or NULL and <code>dendrogram</code> is 'both', then a warning is issued and <code>Rowv</code> (or <code>Colv</code>) arguments are honoured. It also accepts TRUE/FALSE as synonyms for "both"/"none".
<code>show_dendrogram</code>	Logical vector of length two, controlling whether the row and/or column dendrograms are displayed. If a logical scalar is provided, it is repeated to become a logical vector of length two.
<code>reorderfun</code>	function(d, w) of dendrogram and weights for reordering the row and column dendrograms. The default uses <code>statsreorder.dendrogram</code>
<code>k_row</code>	an integer scalar with the desired number of groups by which to color the dendrogram's branches in the rows (uses <code>color_branches</code>) If NA then <code>find_k</code> is used to deduce the optimal number of clusters.
<code>k_col</code>	an integer scalar with the desired number of groups by which to color the dendrogram's branches in the columns (uses <code>color_branches</code>) If NA then <code>find_k</code> is used to deduce the optimal number of clusters.
<code>symm</code>	logical indicating if x should be treated symmetrically; can only be true when x is a square matrix.
<code>revC</code>	logical indicating if the column order should be reversed for plotting. Default (when missing) - is FALSE, unless <code>symm</code> is TRUE. This is useful for cor matrix.
<code>scale</code>	character indicating if the values should be centered and scaled in either the row direction or the column direction, or none. The default is "none".
<code>na.rm</code>	logical (default is TRUE) indicating whether NA's should be removed when scaling (i.e.: when using <code>rowMeans/colMeans</code>). Generally it should always be kept as TRUE, and is included here mainly to stay backward compatible with <code>gplots::heatmap.2</code> . This argument does not effect the presence of NA values in the matrix itself. For removing rows/columns with NAs you should pre-process your matrix using <code>na.omit</code> (or some form of imputation).
<code>row_dend_left</code>	logical (default is FALSE). Should the row dendrogram be plotted on the left side of the heatmap. If false then it will be plotted on the right side.
<code>margins</code>	numeric vector of length 4 (default is <code>c(50,50,NA,0)</code>) containing the margins (see <code>layout</code>) for column, row and main title names, respectively. The top margin is NA by default. If <code>main==""</code> then the top margin will be set to 0, otherwise it will get 30. For a multiline title a larger default for the 3rd element should be

	set. The right margin is NA by default, meaning it will be zero if row_dend_left is FALSE, or 100 if row_dend_left is TRUE.
scale_fill_gradient_fun	A function that creates a smooth gradient for the heatmap. The default uses scale_fill_gradientn with the values of colors, limits, and na.value that are supplied by the user. The user can input a customized function, such as scale_color_gradient() in order to get other results (although the viridis default is quite recommended)
grid_color	control the color of the heatmap grid. Default is NA. Value passed to geom_tile . Do not use this parameter on larger matrix sizes, as it can dramatically prolong the build time of the heatmap. (another parameter, <code>grid_color</code> , will be added in the future - once it is implemented in plotly) In the meantime it is MUCH better to use the <code>grid_gap</code> argument.
srtRow	if supplied, this overrides <code>row_text_angle</code> (this is to stay compatible with heatmap.2)
srtCol	if supplied, this overrides <code>column_text_angle</code> (this is to stay compatible with heatmap.2)
xlab	A character title for the x axis.
ylab	A character title for the y axis.
main	A character title for the heatmap.
titleX	logical (TRUE). should x-axis titles be retained? (passed to subplot).
titleY	logical (TRUE). should y-axis titles be retained? (passed to subplot).
hide_colorbar	logical (FALSE). If TRUE, then the color bar (i.e.: the legend) is hidden.
key.title	(character) main title of the color key. If set to NULL (default) no title will be plotted.
return_ppxpy	logical (FALSE). If TRUE, then no plotting is done and the p, px and py objects are returned (before turning into plotly objects). This is a temporary option which might be removed in the future just to make it easy to create a ggplot heatmaps.
row_side_colors, col_side_colors	data.frame of factors to produce row/column side colors in the style of heatmap.2/heatmap.3 . When a data.frame is provided, the column names are used as the label names for each of the newly added <code>row_side_colors</code> . When a vector is provided it is coerced into a data.frame and the name of the side color will be just <code>row_side_colors</code> .
row_side_palette, col_side_palette	Color palette functions to be used for <code>row_side_colors</code> and <code>col_side_colors</code> respectively.
ColSideColors, RowSideColors	passed to <code>row_side_colors,col_side_colors</code> in order to keep compatibility with heatmap.2
seriate	character indicating the method of matrix sorting (default: "OLO"). Implemented options include: "OLO" (Optimal leaf ordering, optimizes the Hamiltonian path length that is restricted by the dendrogram structure - works in $O(n^4)$) "mean" (sorts the matrix based on the reorderfun using marginal means of the matrix. This is the default used by heatmap.2), "none" (the default order produced by the dendrogram), "GW" (Gruvaeus and Wainer heuristic to optimize the Hamiltonian path length that is restricted by the dendrogram structure)

heatmap_layers	ggplot object(s) (eg, list(theme_bw())) to be added to the heatmap before conversion to a plotly object.
side_color_layers	ggplot2 objects to be added to side color plots, similar to heatmap_layers.
dendrogram_layers	ggplot2 objects to be added to dendrograms, similar to heatmap_layers and side_color_layers.
branches_lwd	numeric (default is 0.6). The width of the dendrograms' branches. If NULL then it is ignored. If the "lwd" is already defined in Rowv/Colv then this parameter is ignored (it is checked using <code>has_edgePar("lwd")</code>).
file	<p>name of the file(s) into which to save the heatmaply output. Should be a character vector of strings ending with ".html" for a dynamic output, or ".png", ".jpeg", ".pdf" for a static output.</p> <p>For example: <code>heatmaply(x, file = "heatmaply_plot.html")</code> or <code>dir.create("folder"); heatmaply(x, file = "folder/heatmaply_plot.html")</code></p> <p>This is based on saveWidget, and websiteshot for the static files. For more refined control over the static file output, you should save the heatmaply object using export and pass the arguments you want based on the ones in websiteshot.</p> <p>Another example: <code>heatmaply(x, file = c("heatmaply_plot.html", "heatmaply_plot.png"))</code></p>
width, height	The width and height of the image saved. Default is which uses 800 x 500 pixels.
long_data	Data in long format. Replaces x, so both should not be used. Colnames must be c("name", "variable", "value"). If you do not have a names column you can simply use a sequence of numbers from 1 to the number of "rows" in the data.
plot_method	Use "ggplot" or "plotly" to choose which library produces heatmap and dendrogram plots
label_names	Names for labels of x, y and value/fill mouseover.
fontsize_row, fontsize_col, cexRow, cexCol	Font size for row and column labels.
subplot_widths, subplot_heights	The relative widths and heights of each subplot. The length of these vectors will vary depending on the number of plots involved.
colorbar_len	The length of the colorbar/color key relative to the total plot height. Only used if <code>plot_method = "plotly"</code>
colorbar_thickness	The thickness (width) of the colorbar/color key in pixels. Only used if <code>plot_method = "plotly"</code> .
colorbar_xanchor, colorbar_yanchor	The x and y anchoring points of the colorbar/color legend. Can be "left", "middle" or "right" for colorbar_xanchor, and "top", "middle" or "bottom" for colorbar_yanchor. See colorbar for more details.
colorbar_xpos, colorbar_ypos	The x and y co-ordinates (in proportion of the plot window) of the colorbar/color legend. See colorbar for more details.

<code>showticklabels</code>	A logical vector of length two (default is TRUE). If FALSE, then the ticks are removed from the sides of the plot. The first location refers to the x axis and the second to the y axis. If only one value is supplied (TRUE/FALSE) then it is replicated to get to length 2. When using this parameter, it might be worth also adjusting margins. This option should be used when working with medium to large matrix size as it makes the heatmap much faster (and the hover still works).
<code>dynamicTicks</code>	(default: FALSE). passed to <code>ggplotly</code> : should plotly.js dynamically generate axis tick labels? Dynamic ticks are useful for updating ticks in response to zoom/pan interactions; however, they can not always reproduce labels as they would appear in the static <code>ggplot2</code> image.
<code>grid_size</code>	When <code>node_type</code> is "scatter", this controls point size. When <code>node_type</code> is "heatmap", this controls the size of the grid between heatmap cells.
<code>node_type</code>	For <code>plot_method = "ggplot"</code> , should the heatmap be rendered as a x-y scatter plot (<code>node_type = "scatter"</code>) or a heatmap (<code>node_type = "heatmap"</code>). Default is <code>node_type = "heatmap"</code> .
<code>point_size_mat</code>	Matrix to map to point size
<code>point_size_name</code>	Name of point size mapping (for hovertext/legend)
<code>label_format_fun</code>	Function to format hovertext (eg, <code>function(...) round(...,digits=3)</code> or <code>function(...) format(...,digits=3)</code>)
<code>labRow, labCol</code>	character vectors with row and column labels to use; these default to <code>rownames(x)</code> or <code>colnames(x)</code> , respectively. if set to NA, they change the value in <code>showticklabels</code> to be FALSE. This is mainly to keep backward compatibility with <code>gplots::heatmap.2</code> .
<code>custom_hovertext</code>	Custom hovertext matrix (the same dimensions as the input). If <code>plot_method</code> is "plotly" then just this text is displayed; if <code>plot_method</code> is "ggplot" then it is appended to the existing text.
<code>dend_hoverinfo</code>	Boolean value which controls whether mouseover text is shown for the row and column dendrograms.
<code>side_color_colorbar_len</code>	As with <code>colorbar_len</code> , this controls the length of the colorbar/color key relative to the total plot height. This argument controls the <code>colorbar_len</code> of the side colour plots. Only used if <code>plot_method = "plotly"</code> .

Examples

```
## Not run:

# mtcars
# x <- heatmapr(mtcars)
library(heatmaply)
heatmaply(iris[,-5], k_row = 3, k_col = 2)
heatmaply(cor(iris[,-5]))
heatmaply(cor(iris[,-5]), limits = c(-1,1))
```

```

heatmaply(mtcars, k_row = 3, k_col = 2)
# heatmaply(mtcars, k_row = 3, k_col = 2, grid_color = "white")
heatmaply(mtcars, k_row = 3, k_col = 2, grid_gap = 1)

# make sure there is enough room for the labels:
heatmaply(mtcars, margins = c(40, 130))
# this is the same as using:
heatmaply(mtcars) %>% layout(margin = list(l = 130, b = 40))

# control text angle
heatmaply(mtcars, column_text_angle = 90, margins = c(40, 130))
# the same as using srtCol:
# heatmaply(mtcars, srtCol = 90) %>% layout(margin = list(l = 130, b = 40))

x <- mtcars
# different colors
heatmaply(x, colors = heat.colors(200))
# using special scale_fill_gradient_fun colors
heatmaply(x, scale_fill_gradient_fun = scale_color_gradient())

# We can join two heatmaps together:
library(heatmaply)
hm1 <- heatmaply(mtcars, margins = c(40, 130))
hm2 <- heatmaply(mtcars, scale = "col", margins = c(40, 130))
subplot(hm1, hm2, margin = .2)

# If we want to share the Y axis, then it is risky to keep any of the dendrograms:
library(heatmaply)
hm1 <- heatmaply(mtcars, Colv = FALSE, Rowv = FALSE, margins = c(40, 130))
hm2 <- heatmaply(mtcars, scale = "col", Colv = FALSE, Rowv = FALSE,
  margins = c(40, 130))
subplot(hm1, hm2, margin = .02, shareY = TRUE)

# We can save heatmaply as an HTML file by using:
heatmaply(iris[,-5], file = "heatmaply_iris.html")
# or a png/pdf/jpeg file using:
heatmaply(iris[,-5], file = "heatmaply_iris.png")
# or just doing it in one go:
heatmaply(iris[,-5], file = c("heatmaply_iris.html", "heatmaply_iris.png") )

# If we don't want the HTML to be selfcontained, we can use the following:
library(heatmaply)
library(htmlwidgets)
heatmaply(iris[,-5]) %>%
  saveWidget(file="heatmaply_iris.html",selfcontained = FALSE)

```

```

# Example for using RowSideColors

x <- as.matrix(datasets::mtcars)
rc <- colorspace::rainbow_hcl(nrow(x))

library(gplots)
library(viridis)
heatmap.2(x, trace = "none", col = viridis(100),
          RowSideColors=rc)

heatmaply(x, seriate = "mean",
          RowSideColors=rc)

heatmaply(x[,-c(8,9)], seriate = "mean",
          col_side_colors = c(rep(0,5), rep(1,4)),
          row_side_colors = x[,8:9])
heatmaply(x[,-c(8,9)], seriate = "mean",
          col_side_colors = data.frame(a=c(rep(0,5), rep(1,4))),
          row_side_colors = x[,8:9])

## Example of using Rowv And Colv for customized dendrograms.

x <- as.matrix(datasets::mtcars)

# now let's spice up the dendrograms a bit:
library(dendextend)

row_dend <- x %>% dist %>% hclust %>% as.dendrogram %>%
  set("branches_k_color", k = 3) %>% set("branches_lwd", 4) %>%
  ladderize
#   rotate_DendSer(ser_weight = dist(x))
col_dend <- x %>% t %>% dist %>% hclust %>% as.dendrogram %>%
  set("branches_k_color", k = 2) %>% set("branches_lwd", 4) %>%
  ladderize
#   rotate_DendSer(ser_weight = dist(t(x)))

heatmaply(x, Rowv = row_dend, Colv = col_dend)

heatmaply(is.na10(airquality))
heatmaply(is.na10(airquality), grid_gap = 1)

# grid_gap can handle quite large data matrix
heatmaply(matrix(1:10000,100,100), k_row = 3, k_col = 3, grid_gap = 1)

# Examples of playing with font size:
heatmaply(mtcars, fontsize_col = 20, fontsize_row = 5, margin = c(100,90))

```

```
# Example for using subplot_width/subplot_height

heatmaply(percentize(mtcars),
  subplot_widths=c(0.6, 0.4),
  subplot_heights=c(0.05, 0.95))

# Example of removing labels and thus making the plot faster
heatmaply(iris, showticklabels = c(T,F), margins = c(80,10))

# this is what allows for a much larger matrix to be printed:
set.seed(2017-05-18)
large_x <- matrix(rnorm(19), 1000,100)
heatmaply(large_x, dendrogram = F, showticklabels = F, margins = c(1,1))

## End(Not run)
## Not run:
heatmaply_na(airquality)

## End(Not run)
## Not run:
heatmaply_cor(cor(mtcars))

## End(Not run)
```

heatmapr

Creates a heatmapr object

Description

An object of class heatmapr includes all the needed information for producing a heatmap. The goal is to separate the pre-processing of the heatmap elements from the graphical rendering of the object, which could be done using plotly (but potentially also with other graphical devices).

Usage

```
heatmapr(
  x,
  Rowv,
  Colv,
  distfun = dist,
  hclustfun = hclust,
  dist_method = NULL,
  hclust_method = NULL,
  distfun_row,
  hclustfun_row,
```

```

distfun_col,
hclustfun_col,
dendrogram = c("both", "row", "column", "none"),
show_dendrogram = c(TRUE, TRUE),
reorderfun = function(d, w) reorder(d, w),
k_row = 1,
k_col = 1,
symm = FALSE,
revC,
scale = c("none", "row", "column"),
na.rm = TRUE,
labRow = rownames(x),
labCol = colnames(x),
cexRow,
cexCol,
digits = 3L,
cellnote = NULL,
theme = NULL,
colors = "RdYlBu",
width = NULL,
height = NULL,
xaxis_height = 80,
yaxis_width = 120,
xaxis_font_size = NULL,
yaxis_font_size = NULL,
brush_color = "#0000FF",
show_grid = TRUE,
anim_duration = 500,
row_side_colors,
col_side_colors,
seriate = c("OLO", "mean", "none", "GW"),
point_size_mat = NULL,
custom_hovertext = NULL,
...
)

```

Arguments

x	A numeric matrix Defaults to TRUE unless x contains any NAs.
Rowv	determines if and how the row dendrogram should be reordered. By default, it is TRUE, which implies dendrogram is computed and reordered based on row means. If NULL or FALSE, then no dendrogram is computed and no reordering is done. If a dendrogram (or hclust), then it is used "as-is", ie without any reordering. If a vector of integers, then dendrogram is computed and reordered based on the order of the vector.
Colv	determines if and how the column dendrogram should be reordered. Has the options as the Rowv argument above and additionally when x is a square matrix, Colv = "Rowv" means that columns should be treated identically to the rows.

<code>distfun</code>	function used to compute the distance (dissimilarity) between both rows and columns. Defaults to <code>dist</code> .
<code>hclustfun</code>	function used to compute the hierarchical clustering when <code>Rowv</code> or <code>Colv</code> are not dendrograms. Defaults to <code>hclust</code> .
<code>dist_method</code>	default is <code>NULL</code> (which results in "euclidean" to be used). Can accept alternative character strings indicating the method to be passed to <code>distfun</code> . By default <code>distfun</code> is <code>dist</code> hence this can be one of "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski".
<code>hclust_method</code>	default is <code>NULL</code> (which results in "complete" to be used). Can accept alternative character strings indicating the method to be passed to <code>hclustfun</code> By default <code>hclustfun</code> is <code>hclust</code> hence this can be one of "ward.D", "ward.D2", "single", "complete", "average" (= UPGMA), "mcquitty" (= WPGMA), "median" (= WPGMC) or "centroid" (= UPGMC).
<code>distfun_row</code>	<code>distfun</code> for row dendrogram only.
<code>hclustfun_row</code>	<code>hclustfun</code> for col dendrogram only.
<code>distfun_col</code>	<code>distfun</code> for row dendrogram only.
<code>hclustfun_col</code>	<code>hclustfun</code> for col dendrogram only.
<code>dendrogram</code>	character string indicating whether to compute 'none', 'row', 'column' or 'both' dendrograms. Defaults to 'both'. However, if <code>Rowv</code> (or <code>Colv</code>) is <code>FALSE</code> or <code>NULL</code> and <code>dendrogram</code> is 'both', then a warning is issued and <code>Rowv</code> (or <code>Colv</code>) arguments are honoured.
<code>show_dendrogram</code>	Logical vector of length controlling whether the row and column dendrograms are displayed. If a logical scalar is provided, it is repeated to become a logical vector of length two.
<code>reorderfun</code>	function(<code>d</code> , <code>w</code>) of dendrogram and weights for reordering the row and column dendrograms. The default uses <code>statsreorder.dendrogram</code>
<code>k_row</code>	an integer scalar with the desired number of groups by which to color the dendrogram's branches in the rows (uses <code>color_branches</code>) If <code>NA</code> then <code>find_k</code> is used to deduce the optimal number of clusters.
<code>k_col</code>	an integer scalar with the desired number of groups by which to color the dendrogram's branches in the columns (uses <code>color_branches</code>) If <code>NA</code> then <code>find_k</code> is used to deduce the optimal number of clusters.
<code>symm</code>	logical indicating if <code>x</code> should be treated symmetrically; can only be true when <code>x</code> is a square matrix.
<code>revC</code>	logical indicating if the column order should be reversed for plotting. Default (when missing) - is <code>FALSE</code> , unless <code>symm</code> is <code>TRUE</code> . This is useful for cor matrix.
<code>scale</code>	character indicating if the values should be centered and scaled in either the row direction or the column direction, or none. The default is "none".
<code>na.rm</code>	logical indicating whether <code>NA</code> 's should be removed.
<code>labRow</code>	character vectors with row labels to use (from top to bottom); default to <code>rownames(x)</code> .
<code>labCol</code>	character vectors with column labels to use (from left to right); default to <code>colnames(x)</code> .

<code>cexRow</code>	positive numbers. If not missing, it will override <code>xaxis_font_size</code> and will give it a value <code>cexRow*14</code>
<code>cexCol</code>	positive numbers. If not missing, it will override <code>yaxis_font_size</code> and will give it a value <code>cexCol*14</code>
<code>digits</code>	integer indicating the number of decimal places to be used by <code>round</code> for 'label'.
<code>cellnote</code>	(optional) matrix of the same dimensions as <code>x</code> that has the human-readable version of each value, for displaying on top of the heatmap cells.
<code>theme</code>	A custom CSS theme to use. Currently the only valid values are "" and "dark". "dark" is primarily intended for standalone visualizations, not R Markdown or Shiny.
<code>colors</code>	Either a colorbrewer2.org palette name (e.g. "YlOrRd" or "Blues"), or a vector of colors to interpolate in hexadecimal "#RRGGBB" format, or a color interpolation function like <code>colorRamp</code> .
<code>width</code>	Width in pixels (optional, defaults to automatic sizing).
<code>height</code>	Height in pixels (optional, defaults to automatic sizing).
<code>xaxis_height</code>	Size of axes, in pixels.
<code>yaxis_width</code>	Size of axes, in pixels.
<code>xaxis_font_size</code>	Font size of axis labels, as a CSS size (e.g. "14px" or "12pt").
<code>yaxis_font_size</code>	Font size of axis labels, as a CSS size (e.g. "14px" or "12pt").
<code>brush_color</code>	The base color to be used for the brush. The brush will be filled with a low-opacity version of this color. "#RRGGBB" format expected.
<code>show_grid</code>	TRUE to show gridlines, FALSE to hide them, or a numeric value to specify the gridline thickness in pixels (can be a non-integer).
<code>anim_duration</code>	Number of milliseconds to animate zooming in and out. For large <code>x</code> it may help performance to set this value to 0.
<code>row_side_colors, col_side_colors</code>	data.frame of factors to produce row/column side colors in the style of heatmap.2/heatmap.3. <code>col_side_colors</code> should be "wide", ie be the same dimensions as the column side colors it will produce.
<code>seriate</code>	character indicating the method of matrix sorting (default: "OLO"). Implemented options include: "OLO" (Optimal leaf ordering, optimizes the Hamiltonian path length that is restricted by the dendrogram structure - works in $O(n^4)$) "mean" (sorts the matrix based on the reorderfun using marginal means of the matrix. This is the default used by heatmap.2), "none" (the default order produced by the dendrogram), "GW" (Gruvaeus and Wainer heuristic to optimize the Hamiltonian path length that is restricted by the dendrogram structure)
<code>point_size_mat</code>	A matrix of values which can be mapped to point size
<code>custom_hovertext</code>	Custom hovertext matrix (the same dimensions as the input).
<code>...</code>	currently ignored

Source

The interface was designed based on [heatmap](#), [heatmap.2](#), and (the also d3heatmap).

See Also

[heatmap](#), [heatmap.2](#)

Examples

```
## Not run:  
library(heatmaply)  
hm <- heatmapr(mtcars, scale = "column", colors = "Blues")  
heatmaply(hm)  
  
## End(Not run)
```

is.heatmapr *Is the object of class heatmapr*

Description

Is the object of class heatmapr.

Usage

```
is.heatmapr(x)
```

Arguments

x an object.

Value

logical - is the object of class heatmapr.

is.na10	<i>Indicates which elements are missing (either 1 and 0)</i>
---------	--

Description

is.na10 is a helper function for creating heatmaps to diagnose missing value patterns. It is similar to [is.na](#) but instead of returning a logical TRUE/FALSE vector (or matrix) it returns a numeric 1/0 output. This enables the [heatmaply](#) function to be used on the data.

Usage

```
is.na10(x, ...)
```

Arguments

x	a vector, matrix or data.frame.
...	not used.

Value

Returns a numeric (instead of a logical) variable/matrix of 1 (missing) or 0 (not missing) values (hence the name is.na10) while still preserving the attributes resulted from running [is.na](#).

These are useful for funnelling into a heatmap (see the examples).

See Also

[is.na](#), the `grid_gap` parameter in [heatmaply](#).

Examples

```
## Not run:
x <- mtcars
x <- data.frame(x)
x$am <- factor(x$am)
x$vs <- factor(x$vs)
set.seed(2017-01-19)
x[sample(nrow(x))[1:6], sample(ncol(x))[1:6]] <- NA

# nice grey colors from here: https://github.com/njtierney/visdat/blob/master/R/vis_miss_ly.R
x %>% is.na10 %>% heatmaply( colors = c("grey80", "grey20"), dendrogram = "none")
x %>% is.na10 %>% heatmaply( colors = c("grey80", "grey20"), k_col = 2, k_row = 2)

heatmaply(is.na10(airquality), grid_gap = 1,
          colors = c("grey80", "grey20"), k_col = 2, k_row = 2)

## End(Not run)
```

is.plotly	<i>Checks if an object is of class plotly or not.</i>
-----------	---

Description

Helpful for the plot_method in linkheatmaply.

Usage

```
is.plotly(x)
```

Arguments

x an object to check

Value

TRUE if the object inherits "plotly" as a class.

normalize	<i>Normalization transformation (0-1)</i>
-----------	---

Description

An Empirical Normalization Transformation brings data to the 0 to 1 scale by subtracting the minimum and dividing by the maximum of all observations. This is similar to [percentize](#) in that it allows to compare variables of different scales, but it also keeps the shape of the distribution.

Usage

```
normalize(x, ...)
```

Arguments

x a vector or a data.frame.
... Currently ignored.

Value

A vector (or data.frame) after normalizing the numeric variables.

See Also

[percentize](#)

Examples

```
## Not run:
x <- mtcars
x <- data.frame(x)
x$am <- factor(x$am)
x$vs <- factor(x$vs)
heatmaply(percentize(x))
heatmaply(normalize(x))

x <- data.frame(a = 1:10, b = 11:20)
x[4:6, 1:2] <- NA
normalize(x)
normalize(x[,1])

## End(Not run)
```

percentize

Empirical Percentile Transformation

Description

An Empirical Percentile Transformation (`percentize`) is similar to taking the rank of a variable. The difference is that it is simpler to compare and interpret the transformed variables.

This is helpful for comparing several variables in a heatmap (e.g.: [heatmaply](#)).

Usage

```
percentize(x, ...)
```

Arguments

<code>x</code>	a vector or a data.frame.
<code>...</code>	Currently ignored.

Value

A vector (or data.frame) after `ecdf` was used on that vector. If `x` is a `data.frame` then only the numeric variables are transformed.

See Also

[normalize](#)

Examples

```
## Not run:
x <- mtcars
x <- data.frame(x)
x$am <- factor(x$am)
x$vs <- factor(x$vs)
heatmaply(percentize(x))

x <- data.frame(a = 1:10, b = 11:20)
x[4:6, 1:2] <- NA
percentize(x)
percentize(x[,1])

## End(Not run)
```

RColorBrewer_colors *RColorBrewer color Ramp Palette*

Description

Functions for getting the colors of RColorBrewer (i.e.: [brewer.pal](#)) without the limitation of only 9/11 color values, based on [colorRampPalette](#).

For sequential palettes this is not essential since we have [viridis](#). But for diverging palettes this is quite essential.

The sequential palettes names are Blues BuGn BuPu GnBu Greens Greys Oranges OrRd PuBu PuBuGn PuRd Purples RdPu Reds YlGn YlGnBu YlOrBr YlOrRd

The diverging palettes are BrBG PiYG PRGn PuOr RdBu RdGy RdYlBu RdYlGn Spectral And also cool_warm. The cool_warm palette is based on Kenneth Moreland's proposal (see ref). It goes from blue (cool) to red (warm), based on well thought-out design elements.

Usage

```
BrBG(n)

PiYG(n)

PRGn(n)

PuOr(n)

RdBu(n)

RdGy(n)

RdYlBu(n)
```

RdYlGn(n)
Spectral(n)
Blues(n)
BuGn(n)
BuPu(n)
GnBu(n)
Greens(n)
Greys(n)
Oranges(n)
OrRd(n)
PuBu(n)
PuBuGn(n)
PuRd(n)
Purples(n)
RdPu(n)
Reds(n)
YlGn(n)
YlGnBu(n)
YlOrBr(n)
YlOrRd(n)
cool_warm(n)

Arguments

n the number of colors (≥ 1) to be in the palette.

Value

A character vector of color names.

References

* Moreland, Kenneth. "Diverging color maps for scientific visualization." *Advances in Visual Computing* (2009): 92-103. url: <http://www.kennethmoreland.com/color-maps/> The code was provided here: <http://stackoverflow.com/a/44073011/256662> Thanks to the user YAK, who relied on the code from the Rgnuplot package (which is duplicated here, in order to save the need to import the entire package)

Examples

```
## Not run:

library(RColorBrewer)
display.brewer.all(n=11,type="div"); title(main = "Divergent color palette")
display.brewer.all(n=9,type=c("seq")); title(main = "Sequential color palette")

img <- function(obj, nam) {
  image(1:length(obj), 1, as.matrix(1:length(obj)), col=obj,
        main = nam, ylab = "", xaxt = "n", yaxt = "n", bty = "n")
}

par(mfrow = c(10,1))
img(rev(cool_warm(500)), "cool_warm, (Moreland 2009)")
img(RdBu(500), "RdBu")
img(BrBG(500), "BrBG")
img(PiYG(500), "PiYG")
img(PRGn(500), "PRGn")
img(PuOr(500), "PuOr")
img(RdGy(500), "RdGy")
img(RdYlBu(500), "RdYlBu")
img(RdYlGn(500), "RdYlGn")
img(Spectral(500), "Spectral")

library(heatmaply)
heatmaply(cor(mtcars), colors = PiYG, limits = c(-1,1))
heatmaply(cor(mtcars), colors = RdBu, limits = c(-1,1))

## End(Not run)
```

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