

# Package: tidyheatmaps (via r-universe)

September 9, 2024

**Title** Heatmaps from Tidy Data

**Version** 0.2.1.9000

**Description** The goal of 'tidyheatmaps' is to simplify the generation of publication-ready heatmaps from tidy data. By offering an interface to the powerful 'pheatmap' package, it allows for the effortless creation of intricate heatmaps with minimal code.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**Imports** dplyr, pheatmap, rlang, grDevices, tidyr, tibble, RColorBrewer

**Suggests** testthat (>= 2.1.0), knitr, rmarkdown

**URL** <https://github.com/jbengler/tidyheatmaps>,  
<https://jbengler.github.io/tidyheatmaps/>

**BugReports** <https://github.com/jbengler/tidyheatmaps/issues>

**VignetteBuilder** knitr

**Repository** <https://jbengler.r-universe.dev>

**RemoteUrl** <https://github.com/jbengler/tidyheatmaps>

**RemoteRef** HEAD

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data\_exprs

*Expression data from RNA-Seq study*

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### Description

This data was taken from a RNA-Seq study investigating the regulation of genes in response to central nervous system inflammation.

### Usage

data\_exprs

### Format

A data frame with 800 rows and 9 variables:

**ensembl\_gene\_id** Ensembl gene id

**external\_gene\_name** Gene symbol

**sample** Sample name

**expression** Normalized RNA-Seq expression value

**group** Experimental group

**sample\_type** Sample type. Either input or IP.

**condition** Condition of sampling. Either healthy or EAE.

**is\_immune\_gene** Gene is annotated as immune cell gene. Either yes or no.

**direction** Direction of regulation. Either up or down.

### Source

data\_exprs represents just a small subset of the data acquired in the study.

More details about the study can be found [here](#)

- Nature Neuroscience, [Bassoon proteinopathy drives neurodegeneration in multiple sclerosis](#)

The complete raw data can be downloaded [here](#)

- Gene Expression Omnibus, study accession [GSE104899](#)

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tidyheatmap	<i>Create heatmap from tidy data</i>
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## Description

A tidyverse-style interface to the powerful heatmap package [pheatmap](#). It enables the convenient generation of complex heatmaps from tidy data.

## Usage

```
tidyheatmap(  
  df,  
  rows,  
  columns,  
  values,  
  colors = NA,  
  color_legend_n = 15,  
  color_legend_min = NA,  
  color_legend_max = NA,  
  color_na = "#DDDDDD",  
  annotation_row = NULL,  
  annotation_col = NULL,  
  gaps_row = NULL,  
  gaps_col = NULL,  
  show_selected_row_labels = NULL,  
  show_selected_col_labels = NULL,  
  filename = NA,  
  scale = "none",  
  fontsize = 7,  
  cellwidth = NA,  
  cellheight = NA,  
  cluster_rows = FALSE,  
  cluster_cols = FALSE,  
  border_color = NA,  
  kmeans_k = NA,  
  clustering_distance_rows = "euclidean",  
  clustering_distance_cols = "euclidean",  
  clustering_method = "complete",  
  clustering_callback = function(x, ...) {  
    return(x)  
  },  
  cutree_rows = NA,  
  cutree_cols = NA,  
  treeheight_row = ifelse((class(cluster_rows) == "hclust") || cluster_rows, 50, 0),  
  treeheight_col = ifelse((class(cluster_cols) == "hclust") || cluster_cols, 50, 0),  
  legend = TRUE,  
  legend_breaks = NA,  
)
```

```

legend_labels = NA,
annotation_colors = NA,
annotation_legend = TRUE,
annotation_names_row = TRUE,
annotation_names_col = TRUE,
drop_levels = TRUE,
show_rownames = TRUE,
show_colnames = TRUE,
main = NA,
fontsize_row = fontsize,
fontsize_col = fontsize,
angle_col = c("270", "0", "45", "90", "315"),
display_numbers = FALSE,
number_format = "%.2f",
number_color = "grey30",
fontsize_number = 0.8 * fontsize,
width = NA,
height = NA,
silent = FALSE
)

```

### Arguments

<code>df</code>	A tidy dataframe in long format.
<code>rows, columns</code>	Column in the dataframe to use for heatmap rows and columns.
<code>values</code>	Column in the dataframe containing the values to be color coded in the heatmap cells.
<code>colors</code>	Vector of colors used for the color legend.
<code>color_legend_n</code>	Number of colors in the color legend.
<code>color_legend_min, color_legend_max</code>	Min and max value of the color legend. Values smaller than the <code>color_legend_min</code> will have the lowest color, values bigger than the <code>color_legend_max</code> will get the highest color.
<code>color_na</code>	Color to use for NAs in values.
<code>annotation_row, annotation_col</code>	Column(s) in the dataframe to use for row and column annotation. To use multiple columns for annotation combine them by <code>c(column1, column2)</code> .
<code>gaps_row, gaps_col</code>	Column in the dataframe to use for use for row and column gaps.
<code>show_selected_row_labels, show_selected_col_labels</code>	Only display a subset of selected labels for rows and columns. Provide selected labels as <code>c("label1", "label2")</code> .
<code>filename</code>	file path where to save the picture. Filetype is decided by the extension in the path. Currently following formats are supported: png, pdf, tiff, bmp, jpeg. Even if the plot does not fit into the plotting window, the file size is calculated so that the plot would fit there, unless specified otherwise.

scale	character indicating if the values should be centered and scaled in either the row direction or the column direction, or none. Corresponding values are "row", "column" and "none"
fontsize	base fontsize for the plot
cellwidth	individual cell width in points. If left as NA, then the values depend on the size of plotting window.
cellheight	individual cell height in points. If left as NA, then the values depend on the size of plotting window.
cluster_rows	boolean values determining if rows should be clustered or hclust object,
cluster_cols	boolean values determining if columns should be clustered or hclust object.
border_color	color of cell borders on heatmap, use NA if no border should be drawn.
kmeans_k	the number of kmeans clusters to make, if we want to aggregate the rows before drawing heatmap. If NA then the rows are not aggregated.
clustering_distance_rows	distance measure used in clustering rows. Possible values are "correlation" for Pearson correlation and all the distances supported by <code>dist</code> , such as "euclidean", etc. If the value is none of the above it is assumed that a distance matrix is provided.
clustering_distance_cols	distance measure used in clustering columns. Possible values the same as for <code>clustering_distance_rows</code> .
clustering_method	clustering method used. Accepts the same values as <code>hclust</code> .
clustering_callback	callback function to modify the clustering. Is called with two parameters: original <code>hclust</code> object and the matrix used for clustering. Must return a <code>hclust</code> object.
cutree_rows	number of clusters the rows are divided into, based on the hierarchical clustering (using <code>cutree</code> ), if rows are not clustered, the argument is ignored
cutree_cols	similar to <code>cutree_rows</code> , but for columns
treeheight_row	the height of a tree for rows, if these are clustered. Default value 50 points.
treeheight_col	the height of a tree for columns, if these are clustered. Default value 50 points.
legend	logical to determine if legend should be drawn or not.
legend_breaks	vector of breakpoints for the legend.
legend_labels	vector of labels for the legend_breaks.
annotation_colors	list for specifying <code>annotation_row</code> and <code>annotation_col</code> track colors manually. It is possible to define the colors for only some of the features. Check examples for details.
annotation_legend	boolean value showing if the legend for annotation tracks should be drawn.
annotation_names_row	boolean value showing if the names for row annotation tracks should be drawn.

annotation_names_col	boolean value showing if the names for column annotation tracks should be drawn.
drop_levels	logical to determine if unused levels are also shown in the legend
show_rownames	boolean specifying if column names are be shown.
show_colnames	boolean specifying if column names are be shown.
main	the title of the plot
fontsize_row	fontsize for rownames (Default: fontsize)
fontsize_col	fontsize for colnames (Default: fontsize)
angle_col	angle of the column labels, right now one can choose only from few predefined options (0, 45, 90, 270 and 315)
display_numbers	logical determining if the numeric values are also printed to the cells. If this is a matrix (with same dimensions as original matrix), the contents of the matrix are shown instead of original values.
number_format	format strings (C printf style) of the numbers shown in cells. For example "%.2f" shows 2 decimal places and "%.1e" shows exponential notation (see more in <a href="#">sprintf</a> ).
number_color	color of the text
fontsize_number	fontsize of the numbers displayed in cells
width	manual option for determining the output file width in inches.
height	manual option for determining the output file height in inches.
silent	do not draw the plot (useful when using the gtable output)

## Value

Invisibly a pheatmap object that is a list with components

- tree\_row the clustering of rows as hclust object
- tree\_col the clustering of columns as hclust object
- kmeans the kmeans clustering of rows if parameter kmeans\_k was specified
- gtable a gtable object containing the heatmap, can be used for combining the heatmap with other plots

## Examples

```
# Basic example
tidyheatmap(data_exprs,
             rows = external_gene_name,
             columns = sample,
             values = expression,
             scale = "row"
)
```

```
# Change number of colors in color legend
tidyheatmap(data_exprs,
             rows = external_gene_name,
             columns = sample,
             values = expression,
             scale = "row",
             color_legend_n = 5
)

# Change color in color legend
tidyheatmap(data_exprs,
             rows = external_gene_name,
             columns = sample,
             values = expression,
             scale = "row",
             colors = c("#145afc", "#ffffff", "#ee4445")
)

# Add row and column annotation
tidyheatmap(data_exprs,
             rows = external_gene_name,
             columns = sample,
             values = expression,
             scale = "row",
             annotation_col = c(sample_type, condition, group),
             annotation_row = c(is_immune_gene, direction)
)

# Add gaps between rows and columns
tidyheatmap(data_exprs,
             rows = external_gene_name,
             columns = sample,
             values = expression,
             scale = "row",
             annotation_col = c(sample_type, condition, group),
             annotation_row = c(is_immune_gene, direction),
             gaps_row = direction,
             gaps_col = group
)
```

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