

Package: iheatmapr (via r-universe)

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Type Package

Title Interactive, Complex Heatmaps

Version 0.7.0

Description Make complex, interactive heatmaps. 'iheatmapr' includes a modular system for iteratively building up complex heatmaps, as well as the iheatmap() function for making relatively standard heatmaps.

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Depends R (>= 3.2.0)

Imports methods, utils, magrittr, stats, ggdendro, fastcluster, RColorBrewer, htmlwidgets, jsonlite, scales, knitr, tools

Suggests htmltools, datasets, shiny, testthat, rmarkdown, reshape2, roxygen2, covr, webshot

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VignetteBuilder knitr

URL <https://docs.ropensci.org/iheatmapr> (website)

<https://github.com/ropensci/iheatmapr>

BugReports <https://github.com/ropensci/iheatmapr/issues>

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Contents

add_col_annotation	3
add_col_barplot	4
add_col_clustering	5
add_col_clusters	7
add_col_dendro	8
add_col_groups	9
add_col_labels	11
add_col_plot	12
add_col_signal	13
add_col_summary	15
add_col_title	17
add_iheatmap	18
add_main_heatmap	21
add_row_annotation	24
add_row_barplot	25
add_row_clustering	26
add_row_clusters	28
add_row_dendro	29
add_row_groups	30
add_row_labels	32
add_row_plot	33
add_row_signal	34
add_row_summary	36
add_row_title	38
add_subplot	39
iheatmap	40
Iheatmap-class	43
iheatmapr	44
iheatmapr-shiny	45
iheatmapr_event	45
main_heatmap	46
measles	48
modify_layout	48
reorder_cols	49
reorder_rows	50
save_iheatmap	51
setup_colorbar_grid	52
setup_tooltip_options	53
test_iheatmapr_event	54
to_plotly	54

<i>add_col_annotation</i>	3
to_widget	55

Index **56**

add_col_annotation *add_col_annotation*

Description

Adds annotation heatmaps for one or more qualitative or quantitative annotations for each column of a main heatmap.

Usage

```
## S4 method for signature 'Iheatmap'
add_col_annotation(
  p,
  annotation,
  colors = NULL,
  side = c("top", "bottom"),
  size = 0.05,
  buffer = 0.015,
  inner_buffer = buffer/2,
  layout = list(),
  show_colorbar = TRUE
)
```

Arguments

- `p` link{Iheatmap-class} object
- `annotation` data.frame or object that can be converted to data frame
- `colors` list of color palettes, with one color per annotation column name
- `side` side of plot on which to add column annotation
- `size` relative size of each row annotation
- `buffer` relative size of buffer between previous subplot and column annotation
- `inner_buffer` relative size of buffer between each annotation
- `layout` layout properties for new y axis
- `show_colorbar` logical indicator to show or hide colorbar

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[iheatmap](#), [add_row_annotation](#), [add_col_signal](#), [add_col_groups](#)

Examples

```
mat <- matrix(rnorm(24), ncol = 6)
annotation <- data.frame(gender = c(rep("M", 3), rep("F", 3)),
                          age = c(20, 34, 27, 19, 23, 30))
hm <- iheatmap(mat) %>% add_col_annotation(annotation)

# Print heatmap if interactive session
if (interactive()) hm
```

add_col_barplot *add_col_barplot*

Description

Add bar plot with one bar per column above or below a main heatmap

Usage

```
## S4 method for signature 'Iheatmap'
add_col_barplot(
  p,
  y,
  ...,
  color = NULL,
  tracename = NA_character_,
  showlegend = !is.na(tracename),
  side = c("top", "bottom"),
  layout = list(),
  size = 0.2,
  buffer = 0.02,
  xname = current_xaxis(p),
  yname = NULL,
  pname = if (!is.na(tracename)) tracename else "col_barplot"
)
```

Arguments

p	iheatmap object
y	y axis values
...	additional arguments to add to plotly scatter trace, see https://plotly.com/javascript/reference/#scatter
color	color of bars

tracename	name of trace (for legend and hover)
showlegend	show in legend?
side	side of plot on which to add subplot
layout	yaxis layout list
size	relative size of subplot relative to main heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	internal name of xaxis
yname	internal name of yaxis
pname	internal name of plot

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_col_signal](#), [iheatmap](#), [add_col_plot](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm <- iheatmap(mat) %>% add_col_barplot(y = 1:5, tracename = "Strength")

# Print heatmap if interactive session
if (interactive()) hm
```

add_col_clustering *add_col_clustering*

Description

add_col_clustering

Usage

```
## S4 method for signature 'Iheatmap'
add_col_clustering(
  p,
  method = c("hclust", "kmeans", "groups"),
  name = "Col<br>Clusters",
  k = NULL,
  groups = NULL,
```

```

    clust_dist = stats::dist,
    colors = NULL,
    show_colorbar = TRUE,
    side = c("top", "bottom"),
    yname = NULL,
    xname = current_xaxis(p)
  )

```

Arguments

p	iheatmap object
method	"hclust" or "kmeans" for hierarchical or k-means clustering, respectively
name	name of colorbar indicating cluster membership
k	number of clusters for rows, needed if order is kmeans or optional if hclust
groups	vector of group assignments
clust_dist	distance function to use for clustering if hierarchical clustering
colors	colors to use for annotation of grouping, can be RColorBrewer palette name or vector of colors
show_colorbar	show the colorbar for the heatmap indicating cluster membership
side	side of plot on which to add subplot
yname	name of yaxis
xname	name of xaxis

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_row_clustering](#), [iheatmap](#)

Examples

```

mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm <- iheatmap(mat) %>% add_col_clustering(method = "hclust", k = 2)

# Print heatmap if interactive session
if (interactive()) hm

```

add_col_clusters *add_col_clusters*

Description

Add column groups and order columns based on groups

Usage

```
## S4 method for signature 'Iheatmap'  
add_col_clusters(  
  p,  
  clusters,  
  name = "Col<br>Clusters",  
  reorder = TRUE,  
  side = c("top", "bottom"),  
  xname = current_xaxis(p),  
  ...  
)
```

Arguments

<code>p</code>	iheatmap object
<code>clusters</code>	cluster assignments, should be vector of integers, characters, or factors
<code>name</code>	name of colorbar indicating cluster membership
<code>reorder</code>	reorder rows based on clusters? default is TRUE
<code>side</code>	side of plot on which to add subplot
<code>xname</code>	name of xaxis
<code>...</code>	additional arguments to pass to add_col_groups for creation of annotation heatmap indicating cluster membership

Details

This function is very similar to [add_col_groups](#); the main difference is that with this function column will get reordered based on the groups.

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_row_clusters](#), [add_col_clustering](#), [iheatmap](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
clusters <- c("A", "B", "A", "B", "A")

hm <- iheatmap(mat) %>% add_col_clusters(clusters)

# Print heatmap if interactive session
if (interactive()) hm
```

```
add_col_dendro      add_col_dendro
```

Description

Adds column dendrogram to iheatmap object

Usage

```
## S4 method for signature 'Iheatmap,hclust'
add_col_dendro(
  p,
  dendro,
  reorder = TRUE,
  side = c("top", "bottom"),
  size = 0.15,
  buffer = 0.005,
  xname = current_xaxis(p),
  yname = NULL,
  sname = "col_dendro"
)
```

Arguments

p	iheatmap object
dendro	hclust object
reorder	reorder rows based on dendrogram order?
side	side of plot on which to add dendro
size	relative size of dendrogram (relative to the main heatmap)
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	internal name of xaxis
yname	internal name of yaxis
sname	internal name of shape

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also[add_col_clustering](#), [iheatmap](#), [add_row_dendro](#)**Examples**

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
dend <- hclust(dist(t(mat)))
hm <- iheatmap(mat) %>% add_col_dendro(dend)

# Print heatmap if interactive session
if (interactive()) hm
```

add_col_groups	<i>add_col_groups</i>
----------------	-----------------------

Description

Adds annotation to heatmap indicating what group every column of main heatmap belongs to

Usage

```
## S4 method for signature 'Iheatmap'
add_col_groups(
  p,
  groups,
  name = "Column<br>Groups",
  title = "Groups",
  colors = pick_discrete_colors(groups, p),
  colorbar_position = get_colorbar_position(p),
  show_colorbar = TRUE,
  show_title = TRUE,
  side = c("top", "bottom"),
  layout = list(),
  size = 0.05,
  buffer = 0.015,
  tooltip = setup_tooltip_options(),
  xname = current_xaxis(p),
  yname = NULL,
  pname = name
)
```

Arguments

p	Iheatmap-class object
groups	vector of group names
name	name of colorbar
title	name of x axis label
colors	palette name or vector of colors
colorbar_position	colorbar placement
show_colorbar	show the colorbar?
show_title	show title as axis label
side	side of plot on which to groups annotation
layout	list of layout parameters for x axis
size	relative size of dendrogram (relative to the main heatmap)
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
tooltip	tooltip options, see setup_tooltip_options
xname	internal name of xaxis
yname	internal name of yaxis
pname	internal name of plot

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[iheatmap](#), [add_row_groups](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
col_groups <- c("A","A","B","D","B")
hm <- iheatmap(mat) %>% add_col_groups(col_groups, name = "My Groups")

# Print heatmap if interactive session
if (interactive()) hm
```

add_col_labels	<i>add_col_labels</i>
----------------	-----------------------

Description

Add x axis labels to plot

Usage

```
## S4 method for signature 'Iheatmap'  
add_col_labels(  
  p,  
  tickvals = NULL,  
  ticktext = NULL,  
  textangle = -90,  
  font = get_layout(p)$font,  
  side = c("bottom", "top"),  
  size = 0.1,  
  buffer = 0.005,  
  xname = current_xaxis(p),  
  yname = NULL  
)
```

Arguments

p	link{Iheatmap-class} object
tickvals	column indices at which to place axis tick labels
ticktext	text for axis tick labels
textangle	angle for ticktext
font	list of plotly font attributes, see https://plotly.com/javascript/reference/#layout-font
side	side of plot on which to add subplot
size	relative size of subplot relative to main heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	name for xaxis
yname	name for yaxis

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_row_title](#), [iheatmap](#), [add_col_labels](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm1 <- iheatmap(mat) %>% add_col_labels()
hm2 <- iheatmap(mat) %>% add_col_labels(ticktext = letters[22:26])

# Print heatmap if interactive session
if (interactive()) hm1
if (interactive()) hm2
```

add_col_plot

add_col_plot

Description

Add a scatter or line plot with one point per column of the main heatmap

Usage

```
## S4 method for signature 'Iheatmap'
add_col_plot(
  p,
  y,
  ...,
  mode = c("lines+markers", "lines", "markers"),
  color = NULL,
  tracename = NA_character_,
  showlegend = !is.na(tracename),
  side = c("top", "bottom"),
  layout = list(),
  size = 0.2,
  buffer = 0.02,
  xname = current_xaxis(p),
  yname = NULL,
  pname = if (!is.na(tracename)) tracename else "col_plot"
)
```

Arguments

p	iheatmap object
y	y axis values
...	additional arguments to add to plotly scatter trace, see https://plotly.com/javascript/reference/#scatter
mode	mode of plot – one of "lines+markers", "lines", or "markers"

color	color of bars
tracename	name of trace (for legend and hover)
showlegend	show in legend?
side	side of plot on which to add subplot
layout	yaxis layout list
size	relative size of subplot relative to main heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	internal name of xaxis
yname	internal name of yaxis
pname	internal name of plot

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_col_signal](#), [iheatmap](#), [add_col_barplot](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm <- iheatmap(mat) %>% add_col_plot(y = 1:5, tracename = "Strength")

# Print heatmap if interactive session
if (interactive()) hm
```

add_col_signal	<i>add_col_signal</i>
----------------	-----------------------

Description

Adds column signal to iheatmap object

Usage

```
## S4 method for signature 'Iheatmap'
add_col_signal(
  p,
  signal,
  name,
  title = name,
  yname = NULL,
  xname = current_xaxis(p),
  pname = name,
  colorbar_position = get_colorbar_position(p),
  colors = pick_continuous_colors(zmid, zmin, zmax, p = p),
  zmin = min(signal, na.rm = TRUE),
  zmax = max(signal, na.rm = TRUE),
  zmid = 0,
  side = c("top", "bottom"),
  size = 0.05,
  buffer = 0.015,
  text = signif(signal, digits = 3),
  tooltip = setup_tooltip_options(),
  show_colorbar = TRUE,
  show_title = TRUE,
  layout = list()
)
```

Arguments

p	iheatmap object
signal	vector of signal
name	name of colorbar
title	label for y axis
yname	internal name of yaxis
xname	internal name of xaxis
pname	internal name of plot
colorbar_position	colorbar placement
colors	palette or vector of colors to use
zmin	minimum for colorscale
zmax	maximum for colorscale
zmid	midpoint for colorscale
side	side of plot on which to add groups
size	relative size of dendrogram (relative to the main heatmap)
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
text	text of value to display for data

tooltip tooltip options, see [setup_tooltip_options](#)
 show_colorbar show the colorbar?
 show_title show title as axis label
 layout y axis layout parameters to use

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[iheatmap](#), [add_row_groups](#)
[add_row_signal](#), [iheatmap](#), [add_col_annotation](#)

Examples

```

mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm <- iheatmap(mat) %>% add_col_signal(signal = 1:5, name = "Strength")

# Print heatmap if interactive session
if (interactive()) hm

```

add_col_summary *add_col_summary*

Description

Adds a line plot summarizing the values across columns

Usage

```

## S4 method for signature 'Iheatmap'
add_col_summary(
  p,
  groups = NULL,
  heatmap_name = NULL,
  colors = NULL,
  tracename = "Col Summary",
  showlegend = FALSE,
  side = c("top", "bottom"),
  layout = list(),
  size = 0.3,
  buffer = 0.02,

```

```

xname = current_xaxis(p),
yname = NULL,
type = c("scatter", "bar"),
summary_function = c("mean", "median", "sd", "var", "mad", "max", "min", "sum"),
...
)

```

Arguments

p	Iheatmap-class object
groups	vector of group labels, name of groups colorbar, or TRUE – see Details
heatmap_name	name of a heatmap within the plot
colors	vector of colors or RColorBrewer palette name
tracename	name of trace
showlegend	show legend?
side	side of plot on which to add subplot
layout	xaxis layout list
size	relative size of subplot relative to main heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	internal name of xaxis
yname	internal name of yaxis
type	scatter or bar?
summary_function	summary function to use, default is mean, options are mean, median, sd, var, mad, max, min, and sum
...	additional arguments to add_col_plot or add_col_barplot

Details

If adding the column summary to a vertically oriented heatmap, the summary will be based on the topmost heatmap if side is "top" and based on the bottom heatmap if side is "bottom" unless a "heatmap_name" is specified. The heatmap_name should match the "pname" argument given to a previously added heatmap.

The column summary is based on specific rows if a "groups" argument is given. The groups argument can either be a vector of group assignments for each row, the "pname" for an existing set of groups incorporated into the plot using [add_row_groups](#), [add_row_annotation](#), [add_row_clusters](#), or [add_row_clustering](#). If groups is set to TRUE, then the function will use an existing set of row groups added to the plot.

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_row_summary](#), [iheatmap](#), [add_col_plot](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm1 <- iheatmap(mat) %>% add_col_summary()
hm2 <- iheatmap(mat) %>% add_col_summary(groups = c("A", "A", "B", "B"))

# Print heatmap if interactive session
if (interactive()) hm1
if (interactive()) hm2
```

add_col_title	<i>add_col_title</i>
---------------	----------------------

Description

Add x axis title to plot

Usage

```
## S4 method for signature 'Iheatmap'
add_col_title(
  p,
  title,
  textangle = 0,
  font = get_layout(p)$font,
  side = c("bottom", "top"),
  size = 0.1,
  buffer = 0.01,
  xname = current_xaxis(p),
  yname = NULL
)
```

Arguments

p	iheatmap object
title	title of axis
textangle	angle of text
font	list of plotly font attributes, see https://plotly.com/javascript/reference/#layout-font
side	side of plot on which to add subplot
size	relative size of subplot relative to main heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	name for xaxis
yname	name for yaxis

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_col_labels](#), [iheatmap](#), [add_row_title](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm <- iheatmap(mat) %>% add_col_title("My x-axis")

# Print heatmap if interactive session
if (interactive()) hm
```

add_iheatmap

add_iheatmap

Description

add_iheatmap

Usage

```
## S4 method for signature 'IheatmapHorizontal,matrix'
add_iheatmap(
  p,
  data,
  x = default_x(data),
  cluster_cols = c("none", "hclust", "kmeans", "groups"),
  col_clusters = NULL,
  col_k = NULL,
  col_clust_dist = stats::dist,
  name = "Signal",
  scale = c("none", "rows", "cols"),
  scale_method = c("standardize", "center", "normalize"),
  colors = NULL,
  col_clusters_colors = NULL,
  col_clusters_name = "Col<br>Clusters",
  show_col_clusters_colorbar = TRUE,
  row_annotation = NULL,
  col_annotation = NULL,
  row_annotation_colors = NULL,
```

```

    col_annotation_colors = NULL,
    row_labels = NULL,
    col_labels = NULL,
    row_title = NULL,
    col_title = NULL,
    buffer = 0.2,
    ...
)

## S4 method for signature 'IheatmapVertical,matrix'
add_iheatmap(
  p,
  data,
  y = default_y(data),
  cluster_rows = c("none", "hclust", "kmeans", "groups"),
  row_clusters = NULL,
  row_k = NULL,
  row_clust_dist = stats::dist,
  name = "Signal",
  scale = c("none", "rows", "cols"),
  scale_method = c("standardize", "center", "normalize"),
  colors = NULL,
  row_clusters_colors = NULL,
  row_clusters_name = "Col<br>Clusters",
  show_row_clusters_colorbar = TRUE,
  row_annotation = NULL,
  col_annotation = NULL,
  row_annotation_colors = NULL,
  col_annotation_colors = NULL,
  row_labels = NULL,
  col_labels = NULL,
  row_title = NULL,
  col_title = NULL,
  buffer = 0.2,
  ...
)

```

Arguments

p	iheatmap object
data	matrix of values to be plotted as heatmap
x	x axis labels, by default colnames of data
cluster_cols	"none", "hclust", or "k-means" for no clustering, hierarchical clustering, and k-means clustering of columns respectively
col_clusters	vector of pre-determined column cluster assignment
col_k	number of clusters for columns, needed if cluster_rows is kmeans or optional if hclust

```

col_clust_dist distance function to use for column clustering if hierarchical clustering
name          Name for colorbar
scale         scale matrix by rows, cols or none
scale_method  what method to use for scaling, either standardize, center, normalize
colors        name of RColorBrewer palette or vector of colors for main heatmap
col_clusters_colors
                colors for col clusters annotation heatmap
col_clusters_name
                name for col clusters colorbar
show_col_clusters_colorbar
                show the colorbar for column clusters?

row_annotation row annotation data.frame
col_annotation column annotation data.frame
row_annotation_colors
                list of colors for row annotations heatmap
col_annotation_colors
                list of colors for col annotations heatmap

row_labels    axis labels for y axis
col_labels    axis labels for x axis
row_title     x axis title
col_title     y axis title
buffer        amount of space to leave empty before this plot, relative to size of first heatmap
...           additional argument to add_iheatmap
y             y axis labels, by default rownames of data
cluster_rows  "none","hclust", or "k-means" for no clustering, hierarchical clustering, and k-
                means clustering of rows respectively

row_clusters  vector of pre-determined row cluster assignment
row_k         number of clusters for rows, needed if cluster_rows is kmeans or optional if
                hclust

row_clust_dist distance function to use for row clustering if hierarchical clustering
row_clusters_colors
                colors for row clusters annotation heatmap
row_clusters_name
                name for row clusters colorbar
show_row_clusters_colorbar
                show the colorbar for row clusters?

```

Details

By default, no scaling is done of rows or columns. This can be changed by specifying the 'scale' argument. There are three options for scaling methods. "standardize" subtracts the mean and divides by standard deviation, "center" just subtracts the mean, and "normalize" divides by the sum of the values. "normalize" should only be used for data that is all positive! If alternative scaling is desired, the scaling should be done prior to calling the iheatmap function.

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[iheatmap](#), [main_heatmap](#)

Examples

```
mat <- matrix(rnorm(24), nrow = 6)
mat2 <- matrix(rnorm(24), nrow = 6)
annotation = data.frame(gender = c(rep("M", 3),rep("F",3)),
                        age = c(20,34,27,19,23,30))

hm <- iheatmap(mat,
  cluster_rows = "hclust",
  cluster_cols = "hclust",
  col_k = 3) %>%
add_iheatmap(mat2,
  cluster_cols = "hclust",
  col_k = 3,
  row_annotation = annotation)

# Print heatmap if interactive session
if (interactive()) hm
```

add_main_heatmap *add_main_heatmap*

Description

Adds an additional main heatmap to an iheatmap object

Usage

```
## S4 method for signature 'IheatmapHorizontal,matrix'
add_main_heatmap(
  p,
  data,
  name = "Signal",
  x = default_x(data),
  colors = pick_continuous_colors(zmid, zmin, zmax, p),
  colorbar_position = get_colorbar_position(p),
  show_colorbar = TRUE,
  zmin = min(data, na.rm = TRUE),
```

```

    zmax = max(data, na.rm = TRUE),
    zmid = 0,
    col_order = NULL,
    x_categorical = NULL,
    side = c("right", "left"),
    size = 1,
    buffer = 0.04,
    text = signif(data, digits = 3),
    tooltip = setup_tooltip_options(),
    xname = NULL,
    pname = name,
    ...
)

## S4 method for signature 'IheatmapVertical,matrix'
add_main_heatmap(
  p,
  data,
  name = "Signal",
  y = default_y(data),
  colors = pick_continuous_colors(zmid, zmin, zmax, p),
  colorbar_position = get_colorbar_position(p),
  show_colorbar = TRUE,
  zmin = min(data, na.rm = TRUE),
  zmax = max(data, na.rm = TRUE),
  zmid = 0,
  row_order = NULL,
  y_categorical = NULL,
  side = c("bottom", "top"),
  size = 1,
  buffer = 0.04,
  text = signif(data, digits = 3),
  tooltip = setup_tooltip_options(),
  yname = NULL,
  pname = name,
  ...
)

```

Arguments

p	Iheatmap-class object
data	matrix
name	name of colorbar, will determine if colorbar is shared with existing plot
x	x axis labels (by default rownames of data); only used if orientation is horizontal
colors	color palette name or vector of colors
colorbar_position	colorbar placement

show_colorbar	display the colorbar?
zmin	minimum for colorscale
zmax	maximum for colorscale
zmid	midpoint for scale
col_order	column ordering for this heatmap; only used if orientation is horizontal
x_categorical	is x categorical? will guess if not provided
side	which side of the current plot to add this heatmap?
size	relative size of plot. size relative to first heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
text	text of value to display for data
tooltip	tooltip options, see setup_tooltip_options
xname	internal name for x axis
pname	internal name for plot
...	additional arguments (ignored)
y	y axis labels (by default colnames of data); only used if orientation is vertical
row_order	row ordering for this heatmap; only used if orientation is vertical
y_categorical	is y categorical? will guess if not provided
yname	internal name for y axis

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[iheatmap](#), [main_heatmap](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
mat2 <- matrix(rnorm(24), ncol = 6, nrow = 4)
hm <- iheatmap(mat) %>% add_main_heatmap(mat2)

# Print heatmap if interactive session
if (interactive()) hm
```

add_row_annotation *add_row_annotation*

Description

Adds annotation heatmaps for one or more qualitative or quantitative annotations for each row of a main heatmap.

Usage

```
## S4 method for signature 'Iheatmap'
add_row_annotation(
  p,
  annotation,
  colors = NULL,
  side = c("right", "left"),
  size = 0.05,
  buffer = 0.015,
  inner_buffer = buffer/2,
  layout = list(),
  show_colorbar = TRUE
)
```

Arguments

p	link{Iheatmap-class} object
annotation	data.frame or object that can be converted to data frame
colors	list of color palettes, with one color per annotation column name
side	side of plot on which to add row annotation
size	relative size of each row annotation
buffer	relative size of buffer between previous subplot and row annotation
inner_buffer	relative size of buffer between each annotation
layout	layout properties for new x axis
show_colorbar	logical indicator to show or hide colorbar

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[iheatmap](#), [add_row_annotation](#), [add_col_signal](#), [add_col_groups](#)

Examples

```

mat <- matrix(rnorm(24), nrow = 6)
annotation <- data.frame(gender = c(rep("M", 3), rep("F", 3)),
                          age = c(20, 34, 27, 19, 23, 30))
hm <- iheatmap(mat) %>% add_row_annotation(annotation)

# Print heatmap if interactive session
if (interactive()) hm

```

add_row_barplot *add_row_barplot*

Description

add_row_barplot

Usage

```

## S4 method for signature 'Iheatmap'
add_row_barplot(
  p,
  x,
  ...,
  color = NULL,
  tracename = NA_character_,
  showlegend = !is.na(tracename),
  side = c("right", "left"),
  layout = list(),
  size = 0.2,
  buffer = 0.02,
  xname = NULL,
  yname = current_yaxis(p),
  pname = if (!is.na(tracename)) tracename else "row_barplot"
)

```

Arguments

p	iheatmap object
x	x axis values
...	additional arguments to add to plotly scatter trace, see https://plotly.com/javascript/reference/#scatter
color	color of bars
tracename	name of trace (for legend and hover)
showlegend	show in legend?
side	side of plot on which to add subplot

layout	yaxis layout list
size	relative size of subplot relative to main heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	internal name of xaxis
yname	internal name of yaxis
pname	internal name of plot

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_row_signal](#), [iheatmap](#), [add_row_plot](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm <- iheatmap(mat) %>% add_row_barplot(x = 1:4, tracename = "Strength")

# Print heatmap if interactive session
if (interactive()) hm
```

add_row_clustering *add_row_clustering*

Description

add_row_clustering

Usage

```
## S4 method for signature 'Iheatmap'
add_row_clustering(
  p,
  method = c("hclust", "kmeans", "groups"),
  name = "Row<br>Clusters",
  k = NULL,
  groups = NULL,
  clust_dist = stats::dist,
  colors = NULL,
  show_colorbar = TRUE,
  side = c("left", "right"),
```

```
xname = NULL,  
yname = current_yaxis(p)  
)
```

Arguments

p	iheatmap object
method	"hclust" or "kmeans" for hierarchical or k-means clustering, respectively
name	name of colorbar indicating cluster membership
k	number of clusters for rows, needed if order is kmeans or optional if hclust
groups	vector of group assignments
clust_dist	distance function to use for clustering if hierarchical clustering
colors	colors to use for annotation of grouping, can be RColorBrewer palette name or vector of colors
show_colorbar	show the colorbar for the heatmap indicating cluster membership
side	side of plot on which to add subplot
xname	name of xaxis
yname	name of yaxis

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_col_clustering](#), [iheatmap](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)  
hm <- iheatmap(mat) %>% add_row_clustering(method = "hclust", k = 2)  
  
# Print heatmap if interactive session  
if (interactive()) hm
```

add_row_clusters *add_row_clusters*

Description

Add row groups and order rows based on groups

Usage

```
## S4 method for signature 'Iheatmap'  
add_row_clusters(  
  p,  
  clusters,  
  name = "Row<br>Clusters",  
  reorder = TRUE,  
  side = c("left", "right"),  
  yname = current_yaxis(p),  
  ...  
)
```

Arguments

<code>p</code>	iheatmap object
<code>clusters</code>	cluster assignments, should be vector of integers, characters, or factors
<code>name</code>	name of colorbar indicating cluster membership
<code>reorder</code>	reorder rows based on clusters? default is TRUE
<code>side</code>	side of plot on which to add subplot
<code>yname</code>	name of yaxis
<code>...</code>	additional arguments to pass to add_row_groups for creation of annotation heatmap indicating cluster membership

Details

This function is very similar to [add_row_groups](#); the main difference is that with this function rows will get reordered based on the groups.

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_row_clustering](#), [add_col_clusters](#), [iheatmap](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
clusters <- c("A", "B", "A", "B")

hm <- iheatmap(mat) %>% add_row_clusters(clusters)

# Print heatmap if interactive session
if (interactive()) hm
```

```
add_row_dendro      add_row_dendro
```

Description

Adds row dendrogram to iheatmap object

Usage

```
## S4 method for signature 'Iheatmap,hclust'
add_row_dendro(
  p,
  dendro,
  reorder = TRUE,
  side = c("left", "right"),
  size = 0.15,
  buffer = 0.005,
  xname = NULL,
  yname = current_yaxis(p),
  sname = "row_dendro"
)
```

Arguments

p	iheatmap object
dendro	hclust object
reorder	reorder rows based on dendrogram order?
side	side of plot on which to add dendrogram
size	relative size of dendrogram (relative to the main heatmap)
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	internal name of xaxis
yname	internal name of yaxis
sname	internal name of shapes

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also[add_row_clustering](#), [iheatmap](#), [add_col_dendro](#)**Examples**

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
dend <- hclust(dist(mat))
hm <- iheatmap(mat) %>% add_row_dendro(dend)

# Print heatmap if interactive session
if (interactive()) hm
```

add_row_groups	<i>add_row_groups</i>
----------------	-----------------------

Description

Adds annotation to heatmap indicating what group every row of main heatmap belongs to

Usage

```
## S4 method for signature 'Iheatmap'
add_row_groups(
  p,
  groups,
  name = "Row<br>Groups",
  title = "Groups",
  colors = pick_discrete_colors(groups, p),
  colorbar_position = get_colorbar_position(p),
  show_colorbar = TRUE,
  show_title = TRUE,
  side = c("right", "left"),
  layout = list(),
  size = 0.05,
  buffer = 0.005,
  tooltip = setup_tooltip_options(),
  xname = NULL,
  yname = current_yaxis(p),
  pname = name
)
```

Arguments

p	Iheatmap-class object
groups	vector of group names
name	name of colorbar
title	name of x axis label
colors	palette name or vector of colors
colorbar_position	colorbar placement
show_colorbar	show the colorbar?
show_title	show title as axis label
side	side of plot on which to groups annotation
layout	list of layout parameters for x axis
size	relative size of dendrogram (relative to the main heatmap)
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
tooltip	tooltip options, see setup_tooltip_options
xname	internal name of xaxis
yname	internal name of yaxis
pname	internal name of plot

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[iheatmap](#), [add_col_groups](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
row_groups <- c("A","A","B","D")
hm <- iheatmap(mat) %>% add_row_groups(row_groups, name = "My Groups")

# Print heatmap if interactive session
if (interactive()) hm
```

add_row_labels	<i>add_row_labels</i>
----------------	-----------------------

Description

Add y axis labels to plot

Usage

```
## S4 method for signature 'Iheatmap'  
add_row_labels(  
  p,  
  tickvals = NULL,  
  ticktext = NULL,  
  textangle = 0,  
  font = get_layout(p)$font,  
  side = c("left", "right"),  
  size = 0.1,  
  buffer = 0.005,  
  xname = NULL,  
  yname = current_yaxis(p)  
)
```

Arguments

p	Iheatmap-class object
tickvals	row indices at which to place axis tick labels
ticktext	text for axis tick labels
textangle	angle for ticktext
font	list of plotly font attributes, see https://plotly.com/javascript/reference/#layout-font
side	side of plot on which to add subplot
size	relative size of subplot relative to main heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	internal name for xaxis
yname	internal name for yaxis

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_row_title](#), [iheatmap](#), [add_col_labels](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm1 <- iheatmap(mat) %>% add_row_labels()
hm2 <- iheatmap(mat) %>% add_row_labels(ticktext = letters[23:26])

# Print heatmaps if interactive session
if (interactive()) hm1
if (interactive()) hm2
```

add_row_plot

add_row_plot

Description

Add a scatter or line plot with one point per row of the main heatmap

Usage

```
## S4 method for signature 'Iheatmap'
add_row_plot(
  p,
  x,
  ...,
  mode = c("lines+markers", "lines", "markers"),
  color = NULL,
  tracename = NA_character_,
  showlegend = !is.na(tracename),
  side = c("right", "left"),
  layout = list(),
  size = 0.2,
  buffer = 0.02,
  xname = NULL,
  yname = current_yaxis(p),
  pname = if (!is.na(tracename)) tracename else "row_plot"
)
```

Arguments

p	iheatmap object
x	x axis values
...	additional arguments to add to plotly scatter trace, see https://plotly.com/javascript/reference/#scatter

mode	mode of plot – one of "lines+markers", "lines", or "markers"
color	color of bars
tracename	name of trace (for legend and hover)
showlegend	show in legend?
side	side of plot on which to add subplot
layout	yaxis layout list
size	relative size of subplot relative to main heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	internal name of xaxis
yname	internal name of yaxis
pname	internal name of plot

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_row_signal](#), [iheatmap](#), [add_row_barplot](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm <- iheatmap(mat) %>% add_row_plot(x = 1:4, tracename = "Strength")

# Print heatmap if interactive session
if (interactive()) hm
```

add_row_signal

add_row_signal

Description

Adds single column heatmap to iheatmap object

Usage

```
## S4 method for signature 'Iheatmap'
add_row_signal(
  p,
  signal,
  name,
  title = name,
  xname = NULL,
  yname = current_yaxis(p),
  pname = name,
  colorbar_position = get_colorbar_position(p),
  colors = pick_continuous_colors(zmid, zmin, zmax, p = p),
  zmin = min(signal, na.rm = TRUE),
  zmax = max(signal, na.rm = TRUE),
  zmid = 0,
  side = c("right", "left"),
  size = 0.05,
  buffer = 0.015,
  text = signif(signal, digits = 3),
  tooltip = setup_tooltip_options(),
  show_colorbar = TRUE,
  show_title = TRUE,
  layout = list()
)
```

Arguments

p	iheatmap object
signal	vector of signal
name	name of colorbar
title	label for x axis
xname	internal name of xaxis
yname	internal name of yaxis
pname	internal name of plot
colorbar_position	colorbar placement
colors	color palette or vector of colors
zmin	minimum for colorscale
zmax	maximum for colorscale
zmid	midpoint for colorscale
side	side of plot on which to add dendro
size	relative size of dendrogram (relative to the main heatmap)
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
text	text of value to display for data

tooltip tooltip options, see [setup_tooltip_options](#)
 show_colorbar show the colorbar?
 show_title show title as axis label
 layout list of x axis layout parameters

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[iheatmap](#), [add_col_groups](#)
[add_col_signal](#), [iheatmap](#), [add_row_annotation](#)

Examples

```

mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm <- iheatmap(mat) %>% add_row_signal(signal = 1:4, name = "Strength")

# Print heatmap if interactive session
if (interactive()) hm

```

add_row_summary *add_row_summary*

Description

Adds a line plot summarizing the values across rows

Usage

```

## S4 method for signature 'Iheatmap'
add_row_summary(
  p,
  groups = NULL,
  heatmap_name = NULL,
  colors = NULL,
  tracename = "Row Summary",
  showlegend = FALSE,
  side = c("right", "left"),
  layout = list(),
  size = 0.3,
  buffer = 0.02,

```

```

    xname = NULL,
    yname = current_yaxis(p),
    type = c("scatter", "bar"),
    summary_function = c("mean", "median", "sd", "var", "mad", "max", "min", "sum"),
    ...
)

```

Arguments

p	Iheatmap-class object
groups	vector of group labels, name of groups colorbar, or TRUE – see Details
heatmap_name	name of a heatmap within the Iheatmap-class object
colors	vector of colors or RColorBrewer palette name
tracename	name of trace
showlegend	show legend?
side	side of plot on which to add subplot
layout	xaxis layout list
size	relative size of subplot relative to main heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	internal name of xaxis
yname	internal name of yaxis
type	scatter or bar?
summary_function	summary function to use, default is mean, options are mean, median, sd, var, mad, max, min, and sum
...	additional arguments to add_row_plot or add_row_barplot

Details

If adding the row summary to a horizontally oriented heatmap, the summary will be based on the right-most heatmap if side is "right" and based on the left heatmap if side is "left" unless a "heatmap_name" is specified. The heatmap_name should match the "pname" argument given to a previously added heatmap.

The row summary is based on specific columns if a "groups" argument is given. The groups argument can either be a vector of group assignments for each row, the "pname" for an existing set of groups incorporated into the plot using [add_col_groups](#), [add_col_annotation](#), [add_col_clusters](#), or [add_col_clustering](#). If groups is set to TRUE, then the function will use an existing set of column groups added to the plot.

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_col_summary](#), [iheatmap](#), [add_row_plot](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm1 <- iheatmap(mat) %>% add_row_summary()
hm2 <- iheatmap(mat) %>% add_row_summary(groups = c("A","A","B","B","B"))

# Print heatmap if interactive session
if (interactive()) hm1
if (interactive()) hm2
```

add_row_title	<i>add_row_title</i>
---------------	----------------------

Description

Add y axis title to plot

Usage

```
## S4 method for signature 'Iheatmap'
add_row_title(
  p,
  title,
  textangle = ifelse(side == "left", -90, 90),
  font = get_layout(p)$font,
  side = c("left", "right"),
  size = 0.1,
  buffer = 0.01,
  xname = NULL,
  yname = current_yaxis(p)
)
```

Arguments

p	iheatmap object
title	title of axis
textangle	angle of text
font	list of plotly font attributes, see https://plotly.com/javascript/reference/#layout-font
side	side of plot on which to add subplot
size	relative size of subplot relative to main heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	internal name for xaxis
yname	internal name for yaxis

Value

`Iheatmap-class` object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

`add_col_title`, `iheatmap`, `add_row_labels`

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm <- iheatmap(mat) %>% add_row_title("Samples")

# Print heatmap if interactive session
if (interactive()) hm
```

add_subplot

add_subplot

Description

Adds an arbitrary subplot to iheatmap

Usage

```
## S4 method for signature 'Iheatmap'
add_subplot(
  p,
  ...,
  side = c("top", "bottom", "right", "left"),
  layout = list(),
  size = 1,
  buffer = 0.1,
  xname = if (side %in% c("top", "bottom")) current_xaxis(p) else NULL,
  yname = if (side %in% c("left", "right")) current_yaxis(p) else NULL,
  pname = "subplot"
)
```

Arguments

`p` iheatmap object

... arguments to pass to plotly trace, see plotly.js documentation at <https://plotly.com/javascript/reference/>

side	which side of the current plot to add this heatmap? "right", "left", "top", or "bottom"
layout	axis layout parameters (list)
size	relative size of plot. size relative to first heatmap
buffer	amount of space to leave empty before this plot, relative to size of first heatmap
xname	internal name of xaxis
yname	internal name of yaxis
pname	internal name of plot

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[iheatmap](#)

Examples

```
mat <- matrix(rnorm(24), ncol = 6)
hm <- iheatmap(mat) %>% add_subplot(x = 1:5, y=1:5, side = "top")

# Print heatmap if interactive session
if (interactive()) hm
```

iheatmap

iheatmap

Description

Make a family standard interactive heatmap with optional clustering and row and column annotations. For more flexibility and options, see the [main_heatmap](#) function and other modular functions as described in vignette.

Usage

```
## S4 method for signature 'matrix'
iheatmap(
  data,
  x = default_x(data),
  y = default_y(data),
  cluster_rows = c("none", "hclust", "kmeans"),
```



```

cluster_cols = c("none", "hclust", "kmeans"),
row_clusters = NULL,
col_clusters = NULL,
row_k = NULL,
col_k = NULL,
row_clust_dist = stats::dist,
col_clust_dist = stats::dist,
name = "Signal",
scale = c("none", "rows", "cols"),
scale_method = c("standardize", "center", "normalize"),
colors = NULL,
col_clusters_colors = NULL,
col_clusters_name = "Col<br>Clusters",
row_clusters_colors = NULL,
row_clusters_name = "Row<br>Clusters",
show_row_clusters_colorbar = TRUE,
show_col_clusters_colorbar = TRUE,
row_annotation = NULL,
col_annotation = NULL,
row_annotation_colors = NULL,
col_annotation_colors = NULL,
row_labels = NULL,
col_labels = NULL,
row_title = NULL,
col_title = NULL,
colorbar_grid = setup_colorbar_grid(),
layout = list(),
source = "iheatmapr",
...
)

```

Arguments

<code>data</code>	matrix of values to be plotted as heatmap
<code>x</code>	x axis labels, by default colnames of data
<code>y</code>	y axis labels, by default rownames of data
<code>cluster_rows</code>	"none", "hclust", or "k-means" for no clustering, hierarchical clustering, and k-means clustering of rows respectively
<code>cluster_cols</code>	"none", "hclust", or "k-means" for no clustering, hierarchical clustering, and k-means clustering of columns respectively
<code>row_clusters</code>	vector of pre-determined row cluster assignment
<code>col_clusters</code>	vector of pre-determined column cluster assignment
<code>row_k</code>	number of clusters for rows, needed if <code>cluster_rows</code> is <code>kmeans</code> or optional if <code>hclust</code>
<code>col_k</code>	number of clusters for columns, needed if <code>cluster_cols</code> is <code>kmeans</code> or optional if <code>hclust</code>

<code>row_clust_dist</code>	distance function to use for row clustering if hierarchical clustering
<code>col_clust_dist</code>	distance function to use for column clustering if hierarchical clustering
<code>name</code>	Name for colorbar
<code>scale</code>	scale matrix by rows, cols or none
<code>scale_method</code>	what method to use for scaling, either none, standardize, center, normalize
<code>colors</code>	name of RColorBrewer palette or vector of colors for main heatmap
<code>col_clusters_colors</code>	colors for col clusters annotation heatmap
<code>col_clusters_name</code>	name for col clusters colorbar
<code>row_clusters_colors</code>	colors for row clusters annotation heatmap
<code>row_clusters_name</code>	name for row clusters colorbar
<code>show_row_clusters_colorbar</code>	show the colorbar for row clusters?
<code>show_col_clusters_colorbar</code>	show the colorbar for column clusters?
<code>row_annotation</code>	row annotation data.frame
<code>col_annotation</code>	column annotation data.frame
<code>row_annotation_colors</code>	list of colors for row annotations heatmap
<code>col_annotation_colors</code>	list of colors for col annotations heatmap
<code>row_labels</code>	axis labels for y axis
<code>col_labels</code>	axis labels for x axis
<code>row_title</code>	x axis title
<code>col_title</code>	y axis title
<code>colorbar_grid</code>	colorbar grid parameters, should be result from setup_colorbar_grid
<code>layout</code>	list of layout attributes to pass to plotly, eg. <code>list(font = list(size = 15))</code>
<code>source</code>	source name for use with shiny
<code>...</code>	additional argument to iheatmap

Details

By default, no scaling is done of rows or columns. This can be changed by specifying the 'scale' argument. There are three options for scaling methods. "standardize" subtracts the mean and divides by standard deviation, "center" just subtracts the mean, and "normalize" divides by the sum of the values. "normalize" should only be used for data that is all positive! If alternative scaling is desired, the scaling should be done prior to calling the iheatmap function.

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also[iheatmap](#), [add_iheatmap](#), [to_widget](#)**Examples**

```
mat <- matrix(rnorm(24), nrow = 6)
annotation = data.frame(gender = c(rep("M", 3),rep("F",3)),
  age = c(20,34,27,19,23,30))
hm <- iheatmap(mat,
  cluster_rows = "hclust",
  cluster_cols = "kmeans",
  col_k = 3,
  row_annotation = annotation)

# Print heatmap if interactive session
if (interactive()) hm
```

Iheatmap-class

*Iheatmap-class***Description**

Class to store complex interactive heatmap objects from `iheatmapr` package

Details

This is a virtual class with two children classes, `IheatmapHorizontal` and `IheatmapVertical`. For `IheatmapHorizontal` additional main heatmaps are added horizontally, and for `IheatmapVertical` additional main heatmaps are added vertically. For details on accessing certain slots of this class, see [access_component](#) documentation.

Slots

`plots` list of plot element in [IheatmapPlots](#) format
`shapes` list of shape element in [IheatmapShapes](#) format
`annotations` list of annotation elements in [IheatmapAnnotations](#) format
`xaxes` list of x axes in [IheatmapAxes](#) format
`yaxes` list of y axes in [IheatmapAxes](#) format
`colorbars` list of colorbars in [IheatmapColorbars](#) format
`colorbar_grid` colorbar grid parameters in [IheatmapColorbarGrid](#) format
`current_xaxis` name of current x axis
`current_yaxis` name of current y axis
`layout` list of plotly layout parameters
`source` source name, for use with shiny

Author(s)

Alicia Schep

See Also

[iheatmap](#), [main_heatmap](#), [access_component](#)

iheatmapr

iheatmapr

Description

Interactive complex heatmaps in R

Details

iheatmapr is a package for building complex, interactive heatmaps in R that can be explored in interactive R sessions or incorporated into rmarkdown documents, shiny applications, or standalone html files.

The package includes a modular system for building up complex heatmaps, where subplots get iteratively added to the top/left/right/bottom of the main heatmap(s). The [iheatmap](#) function provides a wrapper around many of the common modular subcomponents to build fairly standard, moderately complex heatmap.

See the vignette for detailed instructions for how to use the package.

iheatmapr uses the plotly javascript library (<https://plotly.com/>) for making the interactive figures and htmlwidgets (<http://www.htmlwidgets.org/>) for rendering them in R.

Author(s)

Alicia Schep

See Also

[main_heatmap](#), [iheatmap](#), [Iheatmap-class](#)

iheatmapr-shiny	<i>Shiny bindings for iheatmapr</i>
-----------------	-------------------------------------

Description

Output and render functions for using iheatmapr within Shiny

Usage

```
iheatmaprOutput(outputId, width = "100%", height = "400px")
renderIheatmapr(expr, env = parent.frame(), quoted = FALSE)
```

Arguments

outputId	output variable to read from
width, height	Must be a valid CSS unit (like "100%", "400px", "auto") or a number, which will be coerced to a string and have "px" appended.
expr	An expression that generates an Iheatmapr object
env	The environment in which to evaluate expr.
quoted	Is expr a quoted expression (with quote())? This is useful if you want to save an expression in a variable.

iheatmapr_event	<i>Access iheatmapr user input event data in shiny</i>
-----------------	--

Description

This function must be called within a reactive shiny context.

Usage

```
iheatmapr_event(
  object,
  event = c("hover", "click", "relayout"),
  session = shiny::getDefaultReactiveDomain()
)
```

Arguments

object	Iheatmapr-class object
event	The type of plotly event. Currently 'plotly_hover', 'plotly_click', 'plotly_selected', and 'plotly_relayout' are supported.
session	a shiny session object (the default should almost always be used).

Examples

```
## Not run:
shiny::runApp(system.file("examples", "shiny_example", package = "iheatmapr"))

## End(Not run)
```

main_heatmap

main_heatmap

Description

Plots initial heatmap, creates Iheatmap object

Usage

```
## S4 method for signature 'matrix'
main_heatmap(
  data,
  name = "Signal",
  x = default_x(data),
  y = default_y(data),
  colors = pick_continuous_colors(zmid, zmin, zmax),
  colorbar_grid = setup_colorbar_grid(),
  colorbar_position = 1,
  zmid = 0,
  zmin = min(data, na.rm = TRUE),
  zmax = max(data, na.rm = TRUE),
  orientation = c("horizontal", "vertical"),
  x_categorical = NULL,
  y_categorical = NULL,
  row_order = seq_len(nrow(data)),
  col_order = seq_len(ncol(data)),
  text = signif(data, digits = 3),
  tooltip = setup_tooltip_options(),
  xname = "x",
  yname = "y",
  pname = name,
  source = "iheatmapr",
  show_colorbar = TRUE,
  layout = list()
)
```

Arguments

data	matrix
name	name of colorbar

x	x axis labels (by default rownames of data)
y	y axis labels (by default colnames of data)
colors	color palette or vector of colors
colorbar_grid	colorbar grid parameters, should be result from setup_colorbar_grid
colorbar_position	colorbar placement, should be positive integer
zmid	midpoint for colorscale
zmin	minimum for colorscale
zmax	maximum for colorscale
orientation	should new main plots be added horizontally or vertically?
x_categorical	is x categorical? will guess if not provided
y_categorical	is y categorical? will guess if not provided
row_order	row ordering for this heatmap– will be used for all subsequent elements sharing y axis
col_order	column ordering for this heatmap– will be used for all subsequent elements sharing x axis
text	text of value to display for data
tooltip	tooltip options, see setup_tooltip_options
xname	internal name for xaxis
yname	internal name for yaxis
pname	internal plot name
source	source name for use with shiny
show_colorbar	logical to indicate whether to show colorbar
layout	list of layout attributes to pass to plotly, eg. list(font = list(size = 15))

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_iheatmap](#), [to_widget](#), [iheatmap](#), [Iheatmap-class](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm <- main_heatmap(mat)

# Print heatmap if interactive session
if (interactive()) hm
```

measles	<i>measles</i>
---------	----------------

Description

Data on measles cases for different states from 1930 to 2001

Examples

```
data(measles)
```

modify_layout	<i>modify_layout</i>
---------------	----------------------

Description

modify_layout

Usage

```
## S4 method for signature 'Iheatmap'  
modify_layout(x, new_layout)
```

Arguments

x	Iheatmap
new_layout	list of new layout parameter

Value

modified Iheatmap object

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)  
hm <- main_heatmap(mat) %>% modify_layout(list(margin = list(b = 120)))  
  
# Print heatmap if interactive session  
if (interactive()) hm
```

reorder_cols	<i>reorder_cols</i>
--------------	---------------------

Description

Reorder the columns of an [Iheatmap-class](#) object

Usage

```
## S4 method for signature 'IheatmapHorizontal,integer'  
reorder_cols(p, col_order, xname = current_xaxis(p))
```

```
## S4 method for signature 'IheatmapVertical,integer'  
reorder_cols(p, col_order)
```

Arguments

p	Iheatmap-class object
col_order	integer vector
xname	name of xaxis to reorder, only applicable if object is oriented horizontally

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_row_clustering](#), [reorder_cols](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)  
dend <- hclust(dist(t(mat)))  
hm <- iheatmap(mat) %>% reorder_cols(dend$order)  
  
# Print heatmap if interactive session  
if (interactive()) hm
```

reorder_rows	<i>reorder_rows</i>
--------------	---------------------

Description

Reorder the rows of an [Iheatmap-class](#) object

Usage

```
## S4 method for signature 'IheatmapHorizontal,integer'  
reorder_rows(p, row_order)
```

```
## S4 method for signature 'IheatmapVertical,integer'  
reorder_rows(p, row_order, yname = current_yaxis(p))
```

Arguments

p	Iheatmap-class object
row_order	integer vector
yname	name of yaxis to reorder, only applicable if object is oriented vertically

Value

[Iheatmap-class](#) object, which can be printed to generate an interactive graphic

Author(s)

Alicia Schep

See Also

[add_row_clustering](#), [reorder_cols](#)

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)  
dend <- hclust(dist(mat))  
hm <- iheatmap(mat) %>% reorder_rows(dend$order)  
  
# Print heatmap if interactive session  
if (interactive()) hm
```

save_iheatmap	<i>save_iheatmap</i>
---------------	----------------------

Description

save an `link{Iheatmap-class}` object, either as standalone HTML or as static pdf/png/jpeg

Usage

```
## S4 method for signature 'Iheatmap,character'  
save_iheatmap(p, filename, ...)
```

Arguments

<code>p</code>	<code>link{Iheatmap-class}</code> object
<code>filename</code>	name of file
<code>...</code>	additional arguments to <code>saveWidget</code> for saving as html or <code>webshot</code> for saving as pdf/png/jpeg

Details

Note that this function requires the `webshot` package. If deploying a shiny app that calls this function in `shinyapps.io`, loading the `webshot` library and calling `webshot::install_phantomjs()` is needed for the the save functionality to work.

Author(s)

Alicia Schep

Examples

```
mat <- matrix(rnorm(24), nrow = 6)  
hm <- iheatmap(mat)  
## Not run:  
save_iheatmap(hm, "example_iheatmap.png")  
  
## End(Not run)
```

setup_colorbar_grid *setup_colorbar_grid*

Description

function to set parameters controlling colorbar placement in Iheatmap object

Usage

```
setup_colorbar_grid(  
  nrows = 3,  
  y_length = y_spacing * 0.9,  
  x_spacing = 0.16,  
  y_spacing = y_start/nrows,  
  x_start = 1.05,  
  y_start = 0.9  
)
```

Arguments

nrows	number of rows in colorbar grid
y_length	length of colorbar
x_spacing	spacing along horizontal axis between colorbars
y_spacing	spacing along vertical axis between colorbars
x_start	left most position of colorbar grid
y_start	top most position of colorbar grid

Value

[IheatmapColorbarGrid-class](#) object

Examples

```
cb_grid <- setup_colorbar_grid(nrows = 2, x_spacing = 0.2)  
mat <- matrix(rnorm(24), nrow = 6)  
hm <- iheatmap(mat, colorbar_grid = cb_grid, cluster_rows = "kmeans",  
               cluster_cols = "kmeans", row_k = 3, col_k = 2)  
  
# Print heatmap if interactive session  
if (interactive()) hm
```

setup_tooltip_options *Tooltip Options*

Description

This function setups tooltip options for heatmap components of iheatmapr complex heatmaps.

Usage

```
setup_tooltip_options(  
  row = TRUE,  
  col = TRUE,  
  value = TRUE,  
  prepend_row = "Row: ",  
  prepend_col = "Col: ",  
  prepend_value = "Value: "  
)
```

Arguments

row	logical, include row name in tooltip?
col	logical, include column name in tooltip?
value	logical, include value in tooltip?
prepend_row	text to prepend to row name
prepend_col	text to prepend to column name
prepend_value	text to prepend to value

Value

a HeatmapTooltipOptions object which stores these options and can be passed to 'tooltip' argument to main_heatmap and other functions.

Examples

```
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)  
hm1 <- main_heatmap(mat,  
  tooltip = setup_tooltip_options(row = FALSE, col = FALSE,  
    prepend_value = "Value is "))  
  
# Print heatmap if interactive session  
if (interactive()) hm1
```

test_iheatmapr_event *test_iheatmapr_event*

Description

test_iheatmapr_event

Usage

```
test_iheatmapr_event(ihm, event = c("click", "hover", "relayout"))
```

Arguments

ihm	Iheatmap object
event	name of event, either "click", "hover", or "relayout"

Value

shiny app

Examples

```
## Not run:
mat <- matrix(rnorm(20), ncol = 5, nrow = 4)
hm <- main_heatmap(mat)
test_iheatmapr_event(hm, "click")

## End(Not run)
```

to_plotly *Convert Iheatmap to plotly spec*

Description

Function to convert link{Iheatmap-class} object to a plotly spec either as a list or json

Usage

```
to_plotly_list(p)
```

```
to_plotly_json(p)
```

Arguments

p	Iheatmap-class object to convert
---	--

Value

Returns a JSON for a plotly spec for `to_plotly_spec` and as a list of same plotly object for `to_plotly_list`.

Examples

```
mat <- matrix(rnorm(24), nrow = 6)
hm_json <- iheatmap(mat) %>% to_plotly_json()
hm_list <- iheatmap(mat) %>% to_plotly_list()
```

`to_widget``to_widget`

Description

Function to convert `link{Iheatmap-class}` object to widget object

Usage

```
## S4 method for signature 'Iheatmap'
to_widget(p)
```

Arguments

`p` [Iheatmap-class](#) object to convert

Value

htmlwidgets object

Author(s)

Alicia Schep

See Also

[iheatmap](#), [main_heatmap](#)

Examples

```
mat <- matrix(rnorm(24), nrow = 6)
hm <- iheatmap(mat) %>% to_widget()
class(hm)

# Print heatmap if interactive session
if (interactive()) hm
```

Index

access_component, [43](#), [44](#)
add_col_annotation, [3](#), [15](#), [37](#)
add_col_annotation, Iheatmap-method
 (add_col_annotation), [3](#)
add_col_barplot, [4](#), [13](#), [16](#)
add_col_barplot, Iheatmap-method
 (add_col_barplot), [4](#)
add_col_clustering, [5](#), [7](#), [9](#), [27](#), [37](#)
add_col_clustering, Iheatmap-method
 (add_col_clustering), [5](#)
add_col_clusters, [7](#), [28](#), [37](#)
add_col_clusters, Iheatmap-method
 (add_col_clusters), [7](#)
add_col_dendro, [8](#), [30](#)
add_col_dendro, Iheatmap, hclust-method
 (add_col_dendro), [8](#)
add_col_groups, [4](#), [7](#), [9](#), [24](#), [31](#), [36](#), [37](#)
add_col_groups, Iheatmap-method
 (add_col_groups), [9](#)
add_col_labels, [11](#), [12](#), [18](#), [33](#)
add_col_labels, Iheatmap-method
 (add_col_labels), [11](#)
add_col_plot, [5](#), [12](#), [16](#), [17](#)
add_col_plot, Iheatmap-method
 (add_col_plot), [12](#)
add_col_signal, [4](#), [5](#), [13](#), [13](#), [24](#), [36](#)
add_col_signal, Iheatmap-method
 (add_col_signal), [13](#)
add_col_summary, [15](#), [38](#)
add_col_summary, Iheatmap-method
 (add_col_summary), [15](#)
add_col_title, [17](#), [39](#)
add_col_title, Iheatmap-method
 (add_col_title), [17](#)
add_iheatmap, [18](#), [43](#), [47](#)
add_iheatmap, IheatmapHorizontal, matrix-method
 (add_iheatmap), [18](#)
add_iheatmap, IheatmapVertical, matrix-method
 (add_iheatmap), [18](#)
add_main_heatmap, [21](#)
add_main_heatmap, IheatmapHorizontal, matrix-method
 (add_main_heatmap), [21](#)
add_main_heatmap, IheatmapVertical, matrix-method
 (add_main_heatmap), [21](#)
add_row_annotation, [4](#), [16](#), [24](#), [24](#), [36](#)
add_row_annotation, Iheatmap-method
 (add_row_annotation), [24](#)
add_row_barplot, [25](#), [34](#), [37](#)
add_row_barplot, Iheatmap-method
 (add_row_barplot), [25](#)
add_row_clustering, [6](#), [16](#), [26](#), [28](#), [30](#), [49](#), [50](#)
add_row_clustering, Iheatmap-method
 (add_row_clustering), [26](#)
add_row_clusters, [7](#), [16](#), [28](#)
add_row_clusters, Iheatmap-method
 (add_row_clusters), [28](#)
add_row_dendro, [9](#), [29](#)
add_row_dendro, Iheatmap, hclust-method
 (add_row_dendro), [29](#)
add_row_groups, [10](#), [15](#), [16](#), [28](#), [30](#)
add_row_groups, Iheatmap-method
 (add_row_groups), [30](#)
add_row_labels, [32](#), [39](#)
add_row_labels, Iheatmap-method
 (add_row_labels), [32](#)
add_row_plot, [26](#), [33](#), [37](#), [38](#)
add_row_plot, Iheatmap-method
 (add_row_plot), [33](#)
add_row_signal, [15](#), [26](#), [34](#), [34](#)
add_row_signal, Iheatmap-method
 (add_row_signal), [34](#)
add_row_summary, [17](#), [36](#)
add_row_summary, Iheatmap-method
 (add_row_summary), [36](#)
add_row_title, [12](#), [18](#), [33](#), [38](#)
add_row_title, Iheatmap-method
 (add_row_title), [38](#)
add_subplot, [39](#)

- add_subplot, Iheatmap-method
 - (add_subplot), 39
- iheatmap, 4–7, 9, 10, 12, 13, 15, 17, 18, 21,
 - 23, 24, 26–28, 30, 31, 33, 34, 36,
 - 38–40, 40, 43, 44, 47, 55
- iheatmap, matrix-method (iheatmap), 40
- Iheatmap-class, 43
- IheatmapAnnotations, 43
- IheatmapAxes, 43
- IheatmapColorbarGrid, 43
- IheatmapColorbars, 43
- IheatmapHorizontal (Iheatmap-class), 43
- IheatmapHorizontal-class
 - (Iheatmap-class), 43
- IheatmapPlots, 43
- iheatmapr, 44
- iheatmapr-shiny, 45
- iheatmapr_event, 45
- iheatmaprOutput (iheatmapr-shiny), 45
- IheatmapShapes, 43
- IheatmapVertical (Iheatmap-class), 43
- IheatmapVertical-class
 - (Iheatmap-class), 43
- main_heatmap, 21, 23, 40, 44, 46, 55
- main_heatmap, matrix-method
 - (main_heatmap), 46
- measles, 48
- modify_layout, 48
- modify_layout, Iheatmap-method
 - (modify_layout), 48
- renderIheatmap (iheatmapr-shiny), 45
- reorder_cols, 49, 49, 50
- reorder_cols, IheatmapHorizontal, integer-method
 - (reorder_cols), 49
- reorder_cols, IheatmapVertical, integer-method
 - (reorder_cols), 49
- reorder_rows, 50
- reorder_rows, IheatmapHorizontal, integer-method
 - (reorder_rows), 50
- reorder_rows, IheatmapVertical, integer-method
 - (reorder_rows), 50
- save_iheatmap, 51
- save_iheatmap, Iheatmap, character-method
 - (save_iheatmap), 51
- saveWidget, 51
- setup_colorbar_grid, 42, 47, 52
- setup_tooltip_options, 10, 15, 23, 31, 36,
 - 47, 53
- test_iheatmapr_event, 54
- to_plotly, 54
- to_plotly_json (to_plotly), 54
- to_plotly_list (to_plotly), 54
- to_widget, 43, 47, 55
- to_widget, Iheatmap-method (to_widget),
 - 55
- webshot, 51