Package ‘iheatmapr’

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Type Package

Title Interactive, Complex Heatmaps

Version 0.5.1

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 (>= 3.5.0)

Imports methods, utils, magrittr, stats, gg dendro, 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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'axis_labels.R' 'axis_titles.R' 'barplot.R' 'clustering.R'

'clusters.R' 'colorbars.R' 'colors.R' 'components.R'

'dendogram.R' 'generic_subplots.R' 'groups.R' 'main_heatmap.R'

'iheatmap.R' 'iheatmap.R' 'layout.R' 'list_utils.R' 'shiny.R'

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'utils.R'

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Description

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

Usage

```r
## 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

```r
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
```

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](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
add_col_clustering

Examples

```r
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
```

Description

add_col_clustering

Usage

```r
## 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
add_col_clusters

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

p         iheatmap object
clusters   cluster assignments, should be vector of integers, characters, or factors
name       name of colorbar indicating cluster membership
reorder    reorder rows based on clusters? default is TRUE
side       side of plot on which to add subplot
add_col_dendro

xname: name of xaxis

... 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

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,
)
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

```r
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

Description

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

Usage

```r
## 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
add_col_labels

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 add_col_labels

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
)
**add_col_plot**

**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**  
- **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**

```r
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
```

**Description**

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

Usage

```r
## 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](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

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()
)
add_col_signal

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

```r
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

Description

Adds a line plot summarizing the values across columns

Usage

```r
## 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?
add_col_title

**summary_function**

summary function to use, default is mean, options are mean, median, sd, var, mad, max, min, and sum

**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**

```r
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

**Description**

Add x axis title to plot
Usage

```r
## 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

```r
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
```
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 xaxis 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
add_iheatmap

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)),)
add_main_heatmap

```r
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
```

---

### Description

Adds an additional main heatmap to an iheatmap object

### Usage

```r
## 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,
    ...
)
```

```r
## S4 method for signature 'IheatmapVertical,matrix'
add_main_heatmap(
```

---

```r
# 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,
    ...
)
```
add_main_heatmap

```r
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
add_row_annotation

**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**

```r
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
```

**Description**

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

**Usage**

```r
## S4 method for signature 'Iheatmap'
add_row_annotation(
  p,
  annotation,
  colors = NULL,
  side = c("right", "left"),
  size = 0.05,
  buffer = 0.015,
)```

add_row_annotation

inner_buffer = buffer/2,
layout = list(),
show_colorbar = TRUE
)

Arguments

p
annotation
colors
side
size
buffer
inner_buffer
layout
show_colorbar

link[Iheatmap-class] object
data.frame or object that can be converted to data frame
list of color palettes, with one color per annotation column name
side of plot on which to add row annotation
relative size of each row annotation
relative size of buffer between previous subplot and row annotation
relative size of buffer between each annotation
layout properties for new x axis
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

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

```r
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
```

---

Description

*add_row_clustering*

Usage

```r
## 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

```r
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
```

Description

- Add row groups and order rows based on groups
add_row_clusters

Usage

```r
## 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

- `p` : iheatmap object
- `clusters` : cluster assignments, should be vector of integers, characters, or factors
- `name` : name of colorbar indicating cluster membership
- `reorder` : reorder rows based on clusters? default is TRUE
- `side` : side of plot on which to add subplot
- `yname` : name of yaxis
- `...` : 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

```r
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

## S4 method for signature 'Iheatmap,hclus'  
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**: hclus 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
add_row_groups

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

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
add_row_groups

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>title</td>
<td>name of x axis label</td>
</tr>
<tr>
<td>colors</td>
<td>palette name or vector of colors</td>
</tr>
<tr>
<td>colorbar_position</td>
<td>colorbar placement</td>
</tr>
<tr>
<td>show_colorbar</td>
<td>show the colorbar?</td>
</tr>
<tr>
<td>show_title</td>
<td>show title as axis label</td>
</tr>
<tr>
<td>side</td>
<td>side of plot on which to groups annotation</td>
</tr>
<tr>
<td>layout</td>
<td>list of layout parameters for x axis</td>
</tr>
<tr>
<td>size</td>
<td>relative size of dendrogram (relative to the main heatmap)</td>
</tr>
<tr>
<td>buffer</td>
<td>amount of space to leave empty before this plot, relative to size of first heatmap</td>
</tr>
<tr>
<td>tooltip</td>
<td>tooltip options, see setup_tooltip_options</td>
</tr>
<tr>
<td>xname</td>
<td>internal name of xaxis</td>
</tr>
<tr>
<td>yname</td>
<td>internal name of yaxis</td>
</tr>
<tr>
<td>pname</td>
<td>internal name of plot</td>
</tr>
</tbody>
</table>

**Value**

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

**Author(s)**

Alicia Schep

**See Also**

*iheatmap, add_col_groups*

**Examples**

```r
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
```
Description

Add y axis labels to plot

Usage

```r
## 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

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
add_row_signal

... 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

Description

Adds single column heatmap to iheatmap object
add_row_signal

Usage

```r
## 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
add_row_summary

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

```r
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
```

Description

Adds a line plot summarizing the values across rows

Usage

```r
## 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 argu-
  ment 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 col-
  umn groups added to the plot.

Value

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

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  add_row_title

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` on which to add subplot
Size `size` relative size of subplot relative to main heatmap
Buffer `buffer` amount of space to leave empty before this plot, relative to size of first heatmap
Xname `xname` internal name for xaxis
Yname `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

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

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

Description

Adds an arbitrary subplot to `iheatmap`

Usage

```r
## 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/](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**

```r
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
```

**Description**

Make a fairly 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

```r
## 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

- **data**: matrix of values to be plotted as heatmap
- **x**: x axis labels, by default colnames of data
- **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
- **cluster_cols**: "none", "hclust", or "k-means" for no clustering, hierarchical clustering, and k-means clustering of columns respectively
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>row_clusters</td>
<td>vector of pre-determined row cluster assignment</td>
</tr>
<tr>
<td>col_clusters</td>
<td>vector of pre-determined column cluster assignment</td>
</tr>
<tr>
<td>row_k</td>
<td>number of clusters for rows, needed if cluster_rows is kmeans or optional if hclust</td>
</tr>
<tr>
<td>col_k</td>
<td>number of clusters for columns, needed if cluster_rows is kmeans or optional if hclust</td>
</tr>
<tr>
<td>row_clust_dist</td>
<td>distance function to use for row clustering if hierarchical clustering</td>
</tr>
<tr>
<td>col_clust_dist</td>
<td>distance function to use for column clustering if hierarchical clustering</td>
</tr>
<tr>
<td>name</td>
<td>Name for colorbar</td>
</tr>
<tr>
<td>scale</td>
<td>scale matrix by rows, cols or none</td>
</tr>
<tr>
<td>scale_method</td>
<td>what method to use for scaling, either none, standardize, center, normalize</td>
</tr>
<tr>
<td>colors</td>
<td>name of RColorBrewer palette or vector of colors for main heatmap</td>
</tr>
<tr>
<td>col_clusters_colors</td>
<td>colors for col clusters annotation heatmap</td>
</tr>
<tr>
<td>col_clusters_name</td>
<td>name for col clusters colorbar</td>
</tr>
<tr>
<td>row_clusters_colors</td>
<td>colors for row clusters annotation heatmap</td>
</tr>
<tr>
<td>row_clusters_name</td>
<td>name for row clusters colorbar</td>
</tr>
<tr>
<td>show_row_clusters_colorbar</td>
<td>show the colorbar for row clusters?</td>
</tr>
<tr>
<td>show_col_clusters_colorbar</td>
<td>show the colorbar for column clusters?</td>
</tr>
<tr>
<td>row_annotation</td>
<td>row annotation data.frame</td>
</tr>
<tr>
<td>col_annotation</td>
<td>column annotation data.frame</td>
</tr>
<tr>
<td>row_annotation_colors</td>
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<tr>
<td>row_labels</td>
<td>axis labels for y axis</td>
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</tr>
<tr>
<td>row_title</td>
<td>x axis title</td>
</tr>
<tr>
<td>col_title</td>
<td>y axis title</td>
</tr>
<tr>
<td>colorbar_grid</td>
<td>colorbar grid parameters, should be result from setup_colorbar_grid</td>
</tr>
<tr>
<td>layout</td>
<td>list of layout attributes to pass to plotly, eg. list(font = list(size = 15))</td>
</tr>
<tr>
<td>source</td>
<td>source name for use with shiny</td>
</tr>
<tr>
<td>...</td>
<td>additional argument to iheatmap</td>
</tr>
</tbody>
</table>
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

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

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 iter-
atively 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
iheatmapr_event

See Also

main_heatmap, iheatmap, Iheatmap-class

iheatmapr-shiny  Shiny bindings for iheatmap

Description

Output and render functions for using iheatmapr within Shiny

Usage

iheatmaprOutput(outputId, width = "100\%", height = "400px")

renderIheatmap(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 Iheatmap 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  Access iheatmapr user input event data in shiny

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** `Iheatmap-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

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

Description

Plots initial heatmap, creates Iheatmap object

Usage

```r
## 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`
measles

Examples

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

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

measles

measles

Description

Data on measles cases for different states from 1930 to 2001

Examples

data(measles)

modify_layout

modify_layout

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

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
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

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

p link{Iheatmap-class} object
filename name of file
... additional arguments to saveWidget for saving as html or webshot 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)
**Description**

function to set parameters controlling colorbar placement in Iheatmap object

**Usage**

```r
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**

```r
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
```
Description

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

Usage

```r
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

```r
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
```
Description

test_ Heathmapr_event

Usage

test_ Heathmapr_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_ Heathmapr_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
to_widget

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

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

doxygen

Description

Function to convert `Iheatmap-class` object to widget object

Usage

```r
## 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

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

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