Package ‘ComplexHeatmap’

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Type Package

Title Make Complex Heatmaps

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VignetteBuilder knitr

Description Complex heatmaps are efficient to visualize associations
    between different sources of data sets and reveal potential patterns.
    Here the ComplexHeatmap package provides a highly flexible way to arrange
    multiple heatmaps and supports various annotation graphics.

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### Description

Make complex heatmaps

### Details

This package aims to provide a simple and flexible way to arrange multiple heatmaps as well as flexible annotation graphics.

The package is implemented in an object-oriented way. The heatmap lists are abstracted into several classes.

- **Heatmap-class**: a single heatmap containing heatmap body, row/column names, titles, dendrograms and annotations.
- **HeatmapList-class**: a list of heatmaps and annotations.
- **HeatmapAnnotation-class**: a list of row/column annotations.

There are also several internal classes:

- **SingleAnnotation-class**: a single row annotation or column annotation.
- **ColorMapping-class**: mapping from values to colors.
- **AnnotationFunction-class**: construct an annotation function which allows subsetting.

Following two high-level functions take use of functionality of complex heatmaps:

- **oncoPrint**: oncoPrint plot which visualize genomic alterations in a set of genes.
• `densityHeatmap`: use heatmaps to visualize density distributions.


Examples

```r
# There is no example
NULL
```

---

`+.AdditiveUnit`  
*Horizontally Add Heatmaps or Annotations to a Heatmap List*

Description

Horizontally Add Heatmaps or Annotations to a Heatmap List

Usage

```r
## S3 method for class 'AdditiveUnit'

x + y
```

Arguments

- `x`: A `Heatmap-class` object, a `HeatmapAnnotation-class` object or a `HeatmapList-class` object.
- `y`: A `Heatmap-class` object, a `HeatmapAnnotation-class` object or a `HeatmapList-class` object.

Details

It is only a helper function. It actually calls `add_heatmap,Heatmap-method`, `add_heatmap,HeatmapList-method` or `add_heatmap,HeatmapAnnotation-method` depending on the class of the input objects.

The `HeatmapAnnotation-class` object to be added should only be row annotations. Column annotations should be added to the heatmap list by `%v%`.

`x` and `y` can also be `NULL`.

Value

A `HeatmapList-class` object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>
AdditiveUnit

See Also

%v% operator is used for vertical heatmap list.

Examples

# There is no example
NULL

AdditiveUnit

Constructor Method for AdditiveUnit Class

Description

Constructor Method for AdditiveUnit Class

Usage

AdditiveUnit(...)  

Arguments

...  

Black hole arguments.

Details

This method is not used in the package.

Value

No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL
AdditiveUnit-class  
Class for Concatenating Heatmaps and Annotations

Description
Class for Concatenating Heatmaps and Annotations

Details
This class is a super class for Heatmap-class, HeatmapList-class and HeatmapAnnotation-class classes. It is only designed for + generic method and the %v%v method so that above three classes can be appended to each other.

Examples
# There is no example
NULL

add_heatmap-dispatch  Method dispatch page for add_heatmap

Description
Method dispatch page for add_heatmap.

Dispatch
add_heatmap can be dispatched on following classes:

- add_heatmap,HeatmapAnnotation-method,HeatmapAnnotation-class class method
- add_heatmap,Heatmap-method,Heatmap-class class method
- add_heatmap,HeatmapList-method,HeatmapList-class class method

Examples
# no example
NULL
Add Heatmap to the Heatmap List

Description

Add Heatmap to the Heatmap List

Usage

## S4 method for signature 'Heatmap'
add_heatmap(object, x, direction = c("horizontal", "vertical"))

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>A Heatmap-class object.</td>
</tr>
<tr>
<td>x</td>
<td>a Heatmap-class object, a HeatmapAnnotation-class object or a HeatmapList-class object.</td>
</tr>
<tr>
<td>direction</td>
<td>Whether the heatmap is added horizontal or vertically?</td>
</tr>
</tbody>
</table>

Details

Normally we directly use + for horizontal concatenation and %v% for vertical concatenation.

Value

A HeatmapList-class object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL
**Description**

Add Annotations or Heatmaps as a Heatmap List

**Usage**

```r
## S4 method for signature 'HeatmapAnnotation'
add_heatmap(object, x, direction = c("horizontal", "vertical"))
```

**Arguments**

- `object`: A `HeatmapAnnotation-class` object.
- `x`: A `Heatmap-class` object, a `HeatmapAnnotation-class` object or a `HeatmapList-class` object.
- `direction`: Whether it is horizontal list or a vertical list?

**Details**

Normally we directly use `+` for horizontal concatenation and `%v%` for vertical concatenation.

**Value**

A `HeatmapList-class` object.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```
add_heatmap-HeatmapList-method

Add heatmaps and row annotations to the heatmap list

Description

Add heatmaps and row annotations to the heatmap list

Usage

## S4 method for signature 'HeatmapList'
add_heatmap(object, x, direction = c("horizontal", "vertical"))

Arguments

- **object**: a HeatmapList-class object.
- **x**: a Heatmap-class object or a HeatmapAnnotation-class object or a HeatmapList-class object.
- **direction**: direction of the concatenation.

Details

There is a shortcut function +.AdditiveUnit.

Value

A HeatmapList-class object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL
adjust_dend_by_x  Adjust the Positions of nodes/leaves in the Dendrogram

Description

Adjust the Positions of nodes/leaves in the Dendrogram

Usage

```r
adjust_dend_by_x(dend, leaf_pos = 1:nobs(dend)-0.5)
```

Arguments

- `dend`: A `dendrogram` object.
- `leaf_pos`: A vector of positions of leaves. The value can also be a `unit` object.

Details

The positions of nodes stored as `x` attribute are recalculated based on the new positions of leaves. By default, the position of leaves are at 0.5, 1.5, ..., n-0.5.

Examples

```r
m = matrix(rnorm(100), 10)
dend = as.dendrogram(hclust(dist(m)))
dend = adjust_dend_by_x(dend, sort(runif(10)))
str(dend)
dend = adjust_dend_by_x(dend, unit(1:10, "cm"))
str(dend)
```

adjust_heatmap_list-HeatmapList-method

Adjust Heatmap List

Description

Adjust Heatmap List

Usage

```r
## S4 method for signature 'HeatmapList'
adjust_heatmap_list(object)
```

Arguments

- `object`: A `HeatmapList-class` object.
**Details**

This function adjusts settings in all other heatmaps according to the main heatmap. It also adjusts the size of heatmap annotations to make them aligned nicely. This function is only for internal use.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```

---

**alter_graphic**  
*Automatically generate alter_fun*

**Description**

Automatically generate alter_fun

**Usage**

```r
alter_graphic(graphic = c("rect", "point"),
              width = 1, height = 1,
              horiz_margin = unit(1, "pt"),
              vertical_margin = unit(1, "pt"),
              fill = "red", col = NA, pch = 16, ...)
```

**Arguments**

- **graphic**: Graphic to draw.
- **width**: Relative width of the rectangle.
- **height**: Relative height of the rectangle.
- **horiz_margin**: Horizontal margin. E.g. if you want 1mm margin on top and 1mm margin at bottom of the rectangle, set this value to `unit(1, 'mm')`.
- **vertical_margin**: Vertical margin.
- **fill**: Filled color.
- **col**: Border color.
- **pch**: Pch for points
- **...**: Pass to `gpar`
AnnotationFunction

Details
This function aims to simplify the definition of functions in alter_fun. Now it only supports rectangles and points.

Examples

```r
mat = read.table(textConnection("s1,s2,s3
g1,snv;indel,snv,indel
g2,,snv;indel,snv
g3,snv,,indel;snv"), row.names = 1, header = TRUE, sep = ",", stringsAsFactors = FALSE)
mat = as.matrix(mat)
col = c(snv = "red", indel = "blue")
oncoPrint(mat,
alter_fun = list(
  snv = alter_graphic("rect", width = 0.9, height = 0.9, fill = col["snv"]),
  indel = alter_graphic("rect", width = 0.9, height = 0.9, fill = col["indel"])
), col = col)
```

---

AnnotationFunction Constructor of AnnotationFunction Class

Description
Constructor of AnnotationFunction Class

Usage
```
AnnotationFunction(fun, fun_name = "", which = c("column", "row"), cell_fun = NULL, var_import = list(), n = NA, data_scale = c(0, 1), subset_rule = list(), subsettable = length(subset_rule) > 0, show_name = TRUE, width = NULL, height = NULL)
```

Arguments

- **fun**  
  A function which defines how to draw the annotation. See **Details** section.

- **fun_name**  
  The name of the function. It is only used for printing the object.

- **which**  
  Whether it is drawn as a column annotation or a row annotation?

- **cell_fun**  
  A simplified version of fun. cell_fun only accepts one single index and it draws repeatedly in each annotation cell.

- **var_import**  
  The names of the variables or the variable themselves that the annotation function depends on. See **Details** section.

- **n**  
  Number of observations in the annotation. It is not mandatory, but it is better to provide this information so that the higher order HeatmapAnnotation knows it and it can perform check on the consistency of annotations and heatmaps.
data_scale The data scale on the data axis (y-axis for column annotation and x-axis for row annotation). It is only used when `decorate_annotation` is used with "native" unit coordinates.

subset_rule The rule of subsetting variables in `var_import`. It should be set when users want the final object to be subsettable. See **Details** section.

subsettable Whether the object is subsettable?

show_name It is used to turn off the drawing of annotation names in `HeatmapAnnotation`. Annotations always have names associated and normally they will be drawn beside the annotation graphics to tell what the annotation is about. e.g. the annotation names put beside the points annotation graphics. However, for some of the annotations, the names are not necessarily to be drawn, such as text annotations drawn by `anno_text` or an empty annotation drawn by `anno_empty`. In this case, when `show_names` is set to FALSE, there will be no annotation names drawn for the annotation.

width The width of the plotting region (the viewport) that the annotation is drawn. If it is a row annotation, the width must be an absolute unit. Since the `AnnotationFunction` object is always contained by the `SingleAnnotation-class` object, you can only set the width of row annotations or height of column annotations, while e.g. the height of the row annotation is always `unit(1, "npc")` which means it always fully filled in the parent `SingleAnnotation` and only in `HeatmapAnnotation` can adjust the height of the row annotations.

height The height of the plotting region (the viewport) that the annotation is drawn. If it is a column annotation, the width must be an absolute unit.

Details

In the package, we have implemented quite a lot annotation functions by `AnnotationFunction` constructor: `anno_empty`, `anno_image`, `anno_points`, `anno_lines`, `anno_barplot`, `anno_boxplot`, `anno_histogram`, `anno_density`, `anno_joyplot`, `anno_horizon`, `anno_text` and `anno_mark`. These built-in annotation functions support as both row annotations and column annotations and they are all subsettable.

The built-in annotation functions are already enough for most of the analysis, nevertheless, if users want to know more about how to construct the `AnnotationFunction` class manually, they can refer to https://jokergoo.github.io/ComplexHeatmap-reference/book/heatmap-annotations.html#implement-new-annotation-functions.

Value

A `AnnotationFunction-class` object which can be used in `HeatmapAnnotation`.

Examples

```R
x = 1:10
anno1 = AnnotationFunction(
  fun = function(index, k, n) {
    n = length(index)
    pushViewport(viewport(xscale = c(0.5, n + 0.5), yscale = c(0, 10)))
    grid.rect()
  }
)```
The AnnotationFunction Class

Description
The AnnotationFunction Class

Details
The heatmap annotation is basically graphics aligned to the heatmap columns or rows. There is no restriction for the graphic types, e.g., it can be heatmap-like annotation or points. Here the AnnotationFunction class is designed for creating complex and flexible annotation graphics. As the main part of the class, it uses a user-defined function to define the graphics. It also keeps information of the size of the plotting regions of the annotation. And most importantly, it allows subsetting to the annotation to draw a subset of the graphics, which is the base for the splitting of the annotations. See AnnotationFunction constructor for details.

Examples
# There is no example
NULL

Grob for Annotation Axis

Description
Grob for Annotation Axis

Usage
annotation_axis_grob(at = NULL, labels = at, labels_rot = 0, gp = gpar(),
side = "left", facing = "outside", direction = "normal", scale = NULL)
**Arguments**

- **at**: Break values. If it is not specified, it is inferred from data scale in current viewport.
- **labels**: Corresponding labels.
- **labels_rot**: Rotations of labels.
- **gp**: Graphic parameters.
- **side**: side of the axis of the annotation viewport.
- **facing**: Facing of the axis.
- **direction**: Direction of the axis. Value should be "normal" or "reverse".
- **scale**: The data scale. If it is NULL, it is inferred from current viewport.

**Value**

A grob object.

**Examples**

```r
gb = annotation_axis_grob(at = 1:5, labels = month.name[1:5], labels_rot = 0,
    side = "left", facing = "outside")
grid.newpage()
pushViewport(viewport(xscale = c(0, 4), yscale = c(0, 6), width = 0.6, height = 0.6))
grid.rect()
grid.text('side = "left", facing = "outside"')
grid.draw(gb)
popViewport()

gb = annotation_axis_grob(at = 1:5, labels = month.name[1:5], labels_rot = 0,
    side = "left", facing = "inside")
grid.newpage()
pushViewport(viewport(xscale = c(0, 4), yscale = c(0, 6), width = 0.6, height = 0.6))
grid.rect()
grid.text('side = "left", facing = "inside"')
grid.draw(gb)
popViewport()

gb = annotation_axis_grob(at = 1:5, labels = month.name[1:5], labels_rot = 0,
    side = "right", facing = "outside")
grid.newpage()
pushViewport(viewport(xscale = c(0, 4), yscale = c(0, 6), width = 0.6, height = 0.6))
grid.rect()
grid.text('side = "right", facing = "outside"')
grid.draw(gb)
popViewport()

gb = annotation_axis_grob(at = 1:5, labels = month.name[1:5], labels_rot = 0,
    side = "right", facing = "inside")
grid.newpage()
pushViewport(viewport(xscale = c(0, 4), yscale = c(0, 6), width = 0.6, height = 0.6))
grid.rect()
```
```R
grid.text('side = "right", facing = "inside"')
grid.draw(gb)
popViewport()

gb = annotation_axis_grob(at = 1:3, labels = month.name[1:3], labels_rot = 0, side = "top", facing = "outside")
grid.newpage()
pushViewport(viewport(xscale = c(0, 4), yscale = c(0, 6), width = 0.6, height = 0.6))
grid.rect()
grid.text('side = "top", facing = "outside"')
grid.draw(gb)
popViewport()

gb = annotation_axis_grob(at = 1:3, labels = month.name[1:3], labels_rot = 90, side = "top", facing = "outside")
grid.newpage()
pushViewport(viewport(xscale = c(0, 4), yscale = c(0, 6), width = 0.6, height = 0.6))
grid.rect()
grid.text('side = "top", facing = "outside"')
grid.draw(gb)
popViewport()

gb = annotation_axis_grob(at = 1:3, labels = month.name[1:3], labels_rot = 45, side = "top", facing = "outside")
grid.newpage()
pushViewport(viewport(xscale = c(0, 4), yscale = c(0, 6), width = 0.6, height = 0.6))
grid.rect()
grid.text('side = "top", facing = "outside"')
grid.draw(gb)
popViewport()

gb = annotation_axis_grob(at = 1:3, labels = month.name[1:3], labels_rot = 0, side = "top", facing = "inside")
grid.newpage()
pushViewport(viewport(xscale = c(0, 4), yscale = c(0, 6), width = 0.6, height = 0.6))
grid.rect()
grid.text('side = "top", facing = "inside"')
grid.draw(gb)
popViewport()

gb = annotation_axis_grob(at = 1:3, labels = month.name[1:3], labels_rot = 0, side = "bottom", facing = "outside")
grid.newpage()
pushViewport(viewport(xscale = c(0, 4), yscale = c(0, 6), width = 0.6, height = 0.6))
grid.rect()
grid.text('side = "bottom", facing = "outside"')
grid.draw(gb)
popViewport()

gb = annotation_axis_grob(at = 1:3, labels = month.name[1:3], labels_rot = 0, side = "bottom", facing = "inside")
grid.newpage()
pushViewport(viewport(xscale = c(0, 4), yscale = c(0, 6), width = 0.6, height = 0.6))
grid.rect()
grid.text('side = "bottom", facing = "inside"')
grid.draw(gb)
popViewport()
```
annotation_legend_size-HeatmapList-method

Size of the Annotation Legends

Description
Size of the Annotation Legends

Usage
## S4 method for signature 'HeatmapList'
annotation_legend_size(object, legend_list = list(), ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>a HeatmapList-class object.</td>
</tr>
<tr>
<td>legend_list</td>
<td>A list of self-defined legend, should be wrapped into grob objects. It is normally constructed by Legend.</td>
</tr>
<tr>
<td>...</td>
<td>Other arguments.</td>
</tr>
</tbody>
</table>
Details

Internally, all annotation legends are packed by `packLegend` as a single `grob` object. This function is only for internal use.

Value

A `unit` object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

anno_barplot Barplot Annotation

Description

Barplot Annotation

Usage

`anno_barplot(x, baseline = 0, which = c("column", "row"), border = TRUE, bar_width = 0.6, beside = FALSE, attach = FALSE, gp = gpar(fill = "#CCCCCC"), ylim = NULL, extend = 0.05, axis = TRUE, axis_param = default_axis_param(which), add_numbers = FALSE, numbers_gp = gpar(fontsize = 8), numbers_rot = ifelse(which == "column", 45, 0), numbers_offset = unit(2, "mm"), width = NULL, height = NULL, ...)`

Arguments

- **x** The value vector. The value can be a vector or a matrix. The length of the vector or the number of rows of the matrix is taken as the number of the observations of the annotation. If `x` is a vector, the barplots will be represented as stacked barplots.
- **baseline** baseline of bars. The value should be "min" or "max", or a numeric value. It is enforced to be zero for stacked barplots.
- **which** Whether it is a column annotation or a row annotation?
- **border** Wether draw borders of the annotation region?
- **bar_width** Relative width of the bars. The value should be smaller than one.
When \( x \) is a matrix, will bars be positioned beside each other or as stacked bars?

When \( \text{beside} \) is \( \text{TRUE} \), it controls whether bars should be attached.

Graphical parameters for bars. The length of each graphic parameter can be 1, length of \( x \) if \( x \) is a vector, or number of columns of \( x \) if \( x \) is a matrix.

Data ranges. By default it is \( \text{range}(x) \) if \( x \) is a vector, or \( \text{range}(\text{rowSums}(x)) \) if \( x \) is a matrix.

The extension to both side of \( \text{ylim} \). The value is a percent value corresponding to \( \text{ylim}[2] - \text{ylim}[1] \).

Whether to add axis?

Parameters for controlling axis. See \( \text{default_axis_param} \) for all possible settings and default parameters.

Whether to add numbers to the bars. It only works when \( x \) is a simple vector.

Graphics parameters for the numbers.

Rotation of numbers.

Offset to the default positions (1mm away the top of the bars).

Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.

Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.

Other arguments.

An annotation function which can be used in \( \text{HeatmapAnnotation} \).

See Also


Examples

\[
\begin{align*}
\text{anno} & = \text{anno_barplot}(1:10) \\
\text{draw(anno, test = "a vector")}
\end{align*}
\]

\[
\begin{align*}
\text{m} & = \text{matrix(runif(4*10), nc = 4)} \\
\text{m} & = \text{t(apply(m, 1, function(x) x/sum(x)))} \\
\text{anno} & = \text{anno_barplot(m, gp = gpar(fill = 2:5), bar_width = 1, height = unit(6, "cm"))} \\
\text{draw(anno, test = "proportion matrix")}
\end{align*}
\]
anno_block

<table>
<thead>
<tr>
<th><strong>anno_block</strong></th>
<th><strong>Block annotation</strong></th>
</tr>
</thead>
</table>

**Description**

Block annotation

**Usage**

```r
anno_block(align_to = NULL, gp = gpar(), labels = NULL, labels_gp = gpar(),
labels_rot = ifelse(which == "row", 90, 0),
labels_offset = unit(0.5, "npc"), labels_just = "center",
which = c("column", "row"), width = NULL, height = NULL, show_name = FALSE,
panel_fun = NULL)
```

**Arguments**

- **align_to**
  If you don’t want to create block annotation for all slices, you can specify a list of indices that cover continuously adjacent rows or columns.

- **gp**
  Graphic parameters.

- **labels**
  Labels put on blocks.

- **labels_gp**
  Graphic parameters for labels.

- **labels_rot**
  Rotation for labels.

- **labels_offset**
  Positions of the labels. It controls offset on y-directions for column annotation and on x-direction for row annotation.

- **labels_just**
  Justification of the labels.

- **which**
  Is it a row annotation or a column annotation?

- **width**
  Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.

- **height**
  Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.

- **show_name**
  Whether show annotation name.

- **panel_fun**
  A self-defined function that draws graphics in each slice. It must have two arguments: 1. row/column indices for the current slice and 2. a vector of levels from the split variable that correspond to current slice. When graphics is set, all other graphics parameters in `anno_block` are ignored.

**Details**

The block annotation is used for representing slices. The length of all arguments should be 1 or the number of slices.

**Value**

An annotation function which can be used in `HeatmapAnnotation`.

See Also


Examples

Heatmap(matrix(rnorm(100), 10),
    top_annotation = HeatmapAnnotation(foo = anno_block(gp = gpar(fill = 2:4),
        labels = c("group1", "group2", "group3"), labels_gp = gpar(col = "white"))),
    column_km = 3,
    left_annotation = rowAnnotation(foo = anno_block(gp = gpar(fill = 2:4),
        labels = c("group1", "group2", "group3"), labels_gp = gpar(col = "white"))),
    row_km = 3)
#
# ============= set the panel_fun argument ==============
#
# col = c("1" = "red", "2" = "blue", "A" = "green", "B" = "orange")
Heatmap(matrix(rnorm(100), 10), row_km = 2, row_split = sample(c("A", "B"), 10, replace = TRUE)) +
rowAnnotation(foo = anno_block(
    panel_fun = function(index, levels) {
        grid.rect(gp = gpar(fill = col[levels[2]], col = "black"))
        grid.text(paste(levels, collapse = ","), 0.5, 0.5, rot = 90,
        gp = gpar(col = col[levels[1]]))
    })
)

labels = c("1" = "one", "2" = "two", "A" = "Group_A", "B" = "Group_B")
Heatmap(matrix(rnorm(100), 10), row_km = 2, row_split = sample(c("A", "B"), 10, replace = TRUE)) +
rowAnnotation(foo = anno_block(panel_fun = function(index, levels) {
    grid.rect(gp = gpar(fill = col[levels[2]], col = "black"))
    grid.text(paste(levels, collapse = ","), 0.5, 0.5, rot = 90,
    gp = gpar(col = col[levels[1]]))
}))

Heatmap(matrix(rnorm(100), 10), row_km = 2, row_split = sample(c("A", "B"), 10, replace = TRUE)) +
rowAnnotation(foo = anno_block(
    panel_fun = function(index, levels) {
        grid.rect(gp = gpar(fill = col[levels[2]], col = "black"))
        txt = paste(levels, collapse = ",")
        txt = paste0(txt, 
            "\n", length(index), " rows")
        grid.text(txt, 0.5, 0.5, rot = 0,
        gp = gpar(col = col[levels[1]]))
    },
    width = unit(3, "cm")
))
#
# =========== set align_to =============
# col = c("foo" = "red", "bar" = "blue")
Heatmap(matrix(rnorm(100), 10), cluster_rows = FALSE) +
rowAnnotation(foo = anno_block(
    align_to = list(foo = 1:4, bar = 6:10),
    panel_fun = function(index, nm) {
        grid.rect(gp = gpar(fill = col[nm]))
    })
)
anno_boxplot

Boxplot Annotation

Description

Boxplot Annotation

Usage

anno_boxplot(x, which = c("column", "row"), border = TRUE, gp = gpar(fill = "#CCCCCC"), ylim = NULL, extend = 0.05, outline = TRUE, box_width = 0.6, add_points = FALSE, pch = 16, size = unit(4, "pt"), pt_gp = gpar(), axis = TRUE, axis_param = default_axis_param(which), width = NULL, height = NULL, ...)

Arguments

x A matrix or a list. If x is a matrix and if which is column, statistics for boxplots are calculated by columns, if which is row, the calculation is done by rows.
which Whether it is a column annotation or a row annotation?
border Whether draw borders of the annotation region?
gp Graphic parameters for the boxes. The length of the graphic parameters should be one or the number of observations.
ylim Data ranges.
extend The extension to both side of ylim. The value is a percent value corresponding to ylim[2] - ylim[1].
outline Whether draw outline of boxplots?
box_width Relative width of boxes. The value should be smaller than one.
add_points Whether add points on top of the boxes?
pch Point style.
size Point size.
pt_gp Graphics parameters for points.
axis Whether to add axis?
axis_param parameters for controlling axis. See default_axis_param for all possible settings and default parameters.
width Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.
height Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.
... Other arguments.
Value

An annotation function which can be used in HeatmapAnnotation.

See Also

box-annotation

Examples

```r
set.seed(123)
m = matrix(rnorm(100), 10)
anno = anno_boxplot(m, height = unit(4, "cm"))
draw(anno, test = "anno_boxplot")
anno = anno_boxplot(m, height = unit(4, "cm"), gp = gpar(fill = 1:10))
draw(anno, test = "anno_boxplot with gp")
```

anno_customize

Customized annotation

Description

Customized annotation

Usage

```r
anno_customize(x, graphics = list(), which = c("column", "row"), border = TRUE, width = NULL, height = NULL, verbose = TRUE)
```

Arguments

- `x`: A categorical variable.
- `graphics`: A list of functions that define graphics for each level in `x`.
- `which`: Is it a row annotation or a column annotation?
- `width`: Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.
- `height`: Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.
- `border`: Whether to draw border.
- `verbose`: Whether to print messages.

Details

Functions in `graphics` define simple graphics drawn in each annotation cell. The function takes four arguments:

- `x,y`: Center of the annotation cell.
- `w,h`: Width and height of the annotation cell.
Value

An annotation function which can be used in `HeatmapAnnotation`.

Examples

```r
x = sort(sample(letters[1:3], 10, replace = TRUE))
graphics = list(
  "a" = function(x, y, w, h) grid.points(x, y, pch = 16),
  "b" = function(x, y, w, h) grid.rect(x, y, w*0.8, h*0.8, gp = gpar(fill = "red")),
  "c" = function(x, y, w, h) grid.segments(x - 0.5*w, y - 0.5*h, x + 0.5*w, y + 0.5*h, gp = gpar(lty = 2))
)
anno = anno_customize(x, graphics = graphics)

m = matrix(rnorm(100), 10)
Heatmap(m, top_annotation = HeatmapAnnotation(bar = x, foo = anno))

# Add legends for "foo"
ht = Heatmap(m, top_annotation = HeatmapAnnotation(bar = x, foo = anno))
lgd = Legend(title = "foo", at = names(graphics), graphics = graphics)
draw(ht, annotation_legend_list = list(lgd))
```
max_density  Maximal density values in the plot. Normally you don’t need to manually set it, but when you have multiple density annotations and you want to compare between them, you should manually set this argument to make density distributions are in a same scale.

heatmap_colors  A vector of colors for interpolating density values.

joyplot_scale  Relative height of density distribution. A value higher than 1 increases the height of the density distribution and the plot will represented as so-called "joyplot".

border  Whether draw borders of the annotation region?

gp  Graphic parameters for the boxes. The length of the graphic parameters should be one or the number of observations.

axis  Whether to add axis?

axis_param  parameters for controlling axis. See default_axis_param for all possible settings and default parameters.

width  Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.

height  Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.

Value

An annotation function which can be used in HeatmapAnnotation.

See Also


Examples

m = matrix(rnorm(100), 10)
anno = anno_density(m, which = "row")
draw(anno, test = "normal density")
anno = anno_density(m, which = "row", type = "violin")
draw(anno, test = "violin")
anno = anno_density(m, which = "row", type = "heatmap")
draw(anno, test = "heatmap")
anno = anno_density(m, which = "row", type = "heatmap",
   heatmap_colors = c("white", "orange"))
draw(anno, test = "heatmap, colors")
anno_empty

Empty Annotation

Usage

anno_empty(which = c("column", "row"), border = TRUE, zoom = FALSE, width = NULL, height = NULL, show_name = FALSE)

Arguments

which Whether it is a column annotation or a row annotation?
border Whether draw borders of the annotation region?
zoom If it is true and when the heatmap is split, the empty annotation slices will have equal height or width, and you can see the correspondence between the annotation slices and the original heatmap slices.
width Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.
height Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.
show_name Whether to show annotation name.

Details

It creates an empty annotation and holds space, later users can add graphics by `decorate_annotation`. This function is useful when users have difficulty to implement `AnnotationFunction` object.

In following example, an empty annotation is first created and later points are added:

```r
m = matrix(rnorm(100), 10)
ht = Heatmap(m, top_annotation = HeatmapAnnotation(pt = anno_empty()))
ht = draw(ht)
cr = column_order(ht)[[1]]
pt_value = 1:10
decorate_annotation("pt", {
  pushViewport(viewport(xscale = c(0.5, ncol(mat)+0.5), yscale = range(pt_value))),
  grid.points(seq_len(ncol(mat)), pt_value[cr], pch = 16, default.units = "native"),
  grid.yaxis()
  popViewport()
})

And it is similar as using `anno_points`:

Heatmap(m, top_annotation = HeatmapAnnotation(pt = anno_points(pt_value)))
```
**anno_histogram** 31

**Value**

An annotation function which can be used in `HeatmapAnnotation`.

**See Also**


**Examples**

```r
anno = anno_empty()
draw(anno, test = "anno_empty")
anno = anno_empty(border = FALSE)
draw(anno, test = "anno_empty without border")
```

---

**anno_histogram**  Histogram Annotation

**Description**

Histogram Annotation

**Usage**

```r
anno_histogram(x, which = c("column", "row"), n_breaks = 11,
border = FALSE, gp = gpar(fill = "#CCCCCC"),
axis = TRUE, axis_param = default_axis_param(which),
width = NULL, height = NULL)
```

**Arguments**

- `x` A matrix or a list. If `x` is a matrix and if `which` is `column`, statistics for boxplots are calculated by columns, if `which` is `row`, the calculation is done by rows.
- `which` Whether it is a column annotation or a row annotation?
- `n_breaks` Number of breaks for calculating histogram.
- `border` Whether draw borders of the annotation region?
- `gp` Graphic parameters for the boxes. The length of the graphic parameters should be one or the number of observations.
- `axis` Whether to add axis?
- `axis_param` parameters for controlling axis. See `default_axis_param` for all possible settings and default parameters.
- `width` Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.
- `height` Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.
anno_horizon

Value
An annotation function which can be used in HeatmapAnnotation.

See Also

Examples

```r
m = matrix(rnorm(1000), nc = 10)
anno = anno_histogram(t(m), which = "row")
draw(anno, test = "row histogram")
anno = anno_histogram(t(m), which = "row", gp = gpar(fill = 1:10))
draw(anno, test = "row histogram with color")
anno = anno_histogram(t(m), which = "row", n_breaks = 20)
draw(anno, test = "row histogram with color")
```

anno_horizon

Horizon chart Annotation

Description
Horizon chart Annotation

Usage

```r
anno_horizon(x, which = c("column", "row"),
gp = gpar(pos_fill = "#D73027", neg_fill = "#313695"),
n_slice = 4, slice_size = NULL, negative_from_top = FALSE,
normalize = TRUE, gap = unit(0, "mm"),
axis = TRUE, axis_param = default_axis_param(which),
width = NULL, height = NULL)
```

Arguments

- `x` A matrix or a list. If `x` is a matrix or a data frame, columns correspond to observations.
- `which` Whether it is a column annotation or a row annotation?
- `gp` Graphic parameters for the boxes. The length of the graphic parameters should be one or the number of observations. There are two unstandard parameters specifically for horizon chart: `pos_fill` and `neg_fill` controls the filled color for positive values and negative values.
- `n_slice` Number of slices on y-axis.
- `slice_size` Height of the slice. If the value is not NULL, `n_slice` will be recalculated.
anno_horizon

negative_from_top
Whether the areas for negative values start from the top or the bottom of the plotting region?

normalize
Whether normalize x by max(abs(x)).

gap
Gap size of neighbouring horizon chart.

axis
Whether to add axis?

axis_param
parameters for controlling axis. See default_axis_param for all possible settings and default parameters.

width
Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.

height
Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.

Details
Horizon chart as row annotation is only supported.

Value
An annotation function which can be used in HeatmapAnnotation.

See Also

Examples

lt = lapply(1:20, function(x) cumprod(1 + runif(1000, -x/100, x/100)) - 1)
anno = anno_horizon(lt, which = "row")
draw(anno, test = "horizon chart")
anno = anno_horizon(lt, which = "row",
  gp = gpar(pos_fill = "orange", neg_fill = "darkgreen"))
draw(anno, test = "horizon chart, col")
anno = anno_horizon(lt, which = "row", negative_from_top = TRUE)
draw(anno, test = "horizon chart + negative_from_top")
anno = anno_horizon(lt, which = "row", gap = unit(1, "mm"))
draw(anno, test = "horizon chart + gap")
anno = anno_horizon(lt, which = "row",
  gp = gpar(pos_fill = rep(c("orange", "red"), each = 10),
    neg_fill = rep(c("darkgreen", "blue"), each = 10)))
draw(anno, test = "horizon chart, col")
anno_image  

Image Annotation

Description

Image Annotation

Usage

anno_image(image, which = c("column", "row"), border = TRUE, 
  gp = gpar(fill = NA, col = NA), space = unit(1, "mm"), 
  width = NULL, height = NULL)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>image</td>
<td>A vector of file paths of images. The format of the image is inferred from the suffix name of the image file. NA values or empty strings in the vector means no image to drawn.</td>
</tr>
<tr>
<td>which</td>
<td>Whether it is a column annotation or a row annotation?</td>
</tr>
<tr>
<td>border</td>
<td>Wether draw borders of the annotation region?</td>
</tr>
<tr>
<td>gp</td>
<td>Graphic parameters for annotation grids. If the image has transparent background, the fill parameter can be used to control the background color in the annotation grids.</td>
</tr>
<tr>
<td>space</td>
<td>The space around the image to the annotation grid borders. The value should be a unit object.</td>
</tr>
<tr>
<td>width</td>
<td>Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.</td>
</tr>
<tr>
<td>height</td>
<td>Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.</td>
</tr>
</tbody>
</table>

Details

This function supports image formats in png, svg, pdf, eps, jpeg/jpg, tiff. png, jpeg/jpg and tiff images are imported by readPNG, readJPEG and readTIFF, and drawn by grid.raster. svg images are firstly reformatted by rsvg::rsvg_svg and then imported by readPicture and drawn by grid.picture. pdf and eps images are imported by PostScriptTrace and readPicture, later drawn by grid.picture.

Different image formats can be mixed in the image vector.

Value

An annotation function which can be used in HeatmapAnnotation.
See Also


Examples

# download the free icons from https://github.com/Keyamoon/IcoMoon-Free
## Not run:
image = sample(dir("~/Downloads/IcoMoon-Free-master/PNG/64px", full.names = TRUE), 10)
anno = anno_image(image)
draw(anno, test = "png")
image[1:5] = ""
anno = anno_image(image)
draw(anno, test = "some of png")

## End(Not run)

anno_joyplot

Joyplot Annotation

Description

Joyplot Annotation

Usage

anno_joyplot(x, which = c("column", "row"), gp = gpar(fill = "#000000"),
              scale = 2, transparency = 0.6,
              axis = TRUE, axis_param = default_axis_param(which),
              width = NULL, height = NULL)

Arguments

x A matrix or a list. If x is a matrix or a data frame, columns correspond to observations.
which Whether it is a column annotation or a row annotation?
gp Graphic parameters for the boxes. The length of the graphic parameters should be one or the number of observations.
scale Relative height of the curve. A value higher than 1 increases the height of the curve.
transparency Transparency of the filled colors. Value should be between 0 and 1.
axis Whether to add axis?
axis_param parameters for controlling axis. See default_axis_param for all possible settings and default parameters.
width Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.
height Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.
Value

An annotation function which can be used in HeatmapAnnotation.

See Also


Examples

```r
m = matrix(rnorm(1000), nc = 10)
lm = apply(m, 2, function(x) data.frame(density(x)[c("x", "y")]))
anno = anno_joyplot(lm, width = unit(4, "cm"), which = "row")
draw(anno, test = "joyplot")
anno = anno_joyplot(lm, width = unit(4, "cm"), which = "row", gp = gpar(fill = 1:10))
draw(anno, test = "joyplot + col")
anno = anno_joyplot(lm, width = unit(4, "cm"), which = "row", scale = 1)
draw(anno, test = "joyplot + scale")

m = matrix(rnorm(5000), nc = 50)
lm = apply(m, 2, function(x) data.frame(density(x)[c("x", "y")]))
anno = anno_joyplot(lm, width = unit(4, "cm"), which = "row", gp = gpar(fill = NA), scale = 4)
draw(anno, test = "joyplot")
```

anno_lines

Lines Annotation

Description

Lines Annotation

Usage

```r
anno_lines(x, which = c("column", "row"), border = TRUE, gp = gpar(),
  add_points = smooth, smooth = FALSE, pch = 16, size = unit(2, "mm"), pt_gp = gpar(), ylim = NULL,
  extend = 0.05, axis = TRUE, axis_param = default_axis_param(which),
  width = NULL, height = NULL)
```

Arguments

- **x**: The value vector. The value can be a vector or a matrix. The length of the vector or the number of rows of the matrix is taken as the number of the observations of the annotation.
- **which**: Whether it is a column annotation or a row annotation?
- **border**: Wether draw borders of the annotation region?
- **gp**: Graphic parameters for lines. The length of each graphic parameter can be 1, or number of columns of x is x is a matrix.
### add_points
Whether to add points on the lines?

### smooth
If it is TRUE, smoothing by `loess` is performed. If it is TRUE, add_points is set to TRUE by default.

### pch
Point type. The length setting is the same as gp.

### size
Point size, the value should be a `unit` object. The length setting is the same as gp.

### pt_gp
Graphic parameters for points. The length setting is the same as gp.

### ylim
Data ranges. By default it is `range(x)`.

### extend
The extension to both side of ylim. The value is a percent value corresponding to `ylim[2] - ylim[1]`.

### axis
Whether to add axis?

### axis_param
parameters for controlling axis. See `default_axis_param` for all possible settings and default parameters.

### width
Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.

### height
Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.

### Value
An annotation function which can be used in `HeatmapAnnotation`.

### See Also


### Examples

```r
anno = anno_lines(runif(10))
draw(anno, test = "anno_lines")
anno = anno_lines(cbind(c(1:5, 1:5), c(5:1, 5:1)), gp = gpar(col = 2:3))
draw(anno, test = "matrix")
anno = anno_lines(cbind(c(1:5, 1:5), c(5:1, 5:1)), gp = gpar(col = 2:3),
add_points = TRUE, pt_gp = gpar(col = 5:6), pch = c(1, 16))
draw(anno, test = "matrix")
```
Usage

anno_link(…)

Arguments

… Pass to anno_zoom.

Details

This function is the same as anno_zoom. It links subsets of rows or columns to a list of graphic regions.

Examples

# There is no example
NULL

anno_mark Link annotation with labels

Description

Link annotation with labels

Usage

anno_mark(at, labels, which = c("column", "row"),
  side = ifelse(which == "column", "top", "right"),
  lines_gp = gpar(), labels_gp = gpar(),
  labels_rot = ifelse(which == "column", 90L, 0L), padding = unit(1, "mm"),
  link_width = unit(5, "mm"), link_height = link_width,
  link_gp = lines_gp,
  extend = unit(0, "mm"))

Arguments

at Numeric index from the original matrix.
labels Corresponding labels.
which Whether it is a column annotation or a row annotation?
side Side of the labels. If it is a column annotation, valid values are "top" and "bottom"; If it is a row annotation, valid values are "left" and "right".
lines_gp Please use link_gp instead.
link_gp Graphic settings for the segments.
labels_gp Graphic settings for the labels.
anno_numeric

<table>
<thead>
<tr>
<th>labels_rot</th>
<th>Rotations of labels, scalar.</th>
</tr>
</thead>
<tbody>
<tr>
<td>padding</td>
<td>Padding between neighbouring labels in the plot.</td>
</tr>
<tr>
<td>link_width</td>
<td>Width of the segments.</td>
</tr>
<tr>
<td>link_height</td>
<td>Similar as link_width, used for column annotation.</td>
</tr>
<tr>
<td>extend</td>
<td>By default, the region for the labels has the same width (if it is a column annotation) or same height (if it is a row annotation) as the heatmap. The size can be extended by this options. The value can be a proportion number or a unit object. The length can be either one or two.</td>
</tr>
</tbody>
</table>

Details

Sometimes there are many rows or columns in the heatmap and we want to mark some of the rows. This annotation function is used to mark these rows and connect labels and corresponding rows with links.

Value

An annotation function which can be used in HeatmapAnnotation.

See Also


Examples

anno = anno_mark(at = c(1:4, 20, 60, 97:100), labels = month.name[1:10], which = "row")
draw(anno, index = 1:100, test = "anno_mark")

m = matrix(1:1000, byrow = TRUE, nr = 100)
anno = anno_mark(at = c(1:4, 20, 60, 97:100), labels = month.name[1:10], which = "row")
Heatmap(m, cluster_rows = FALSE, cluster_columns = FALSE) + rowAnnotation(mark = anno)
Heatmap(m) + rowAnnotation(mark = anno)

anno_numeric

Numeric labels annotation

Description

Numeric labels annotation

Usage

anno_numeric(x, rg = range(x), labels_gp = gpar(), x_convert = NULL, labels_format = NULL, labels_offset = unit(4, "pt"), bg_gp = gpar(fill = "#8080FF", col = "#8080FF"), bar_width = unit(1, "npc") - unit(4, "pt"), round_corners = TRUE, r = unit(0.05, "snpc"), which = c("row", "column"), align_to = "left", width = NULL)
Arguments

- **x**: A vector of numeric values.
- **rg**: Range. A numeric vector of length two.
- **labels_gp**: Graphics parameters for labels.
- **x_convert**: A function applied on x. E.g., when x contains p-values, to map x to the heights of bars, a transformation of \(-\log_{10}(x)\) is normally applied.
- **labels_format**: A function applied on x. E.g., when x is a numeric, `labels_format` can be set to `function(x) sprintf("%.2f", x)`.
- **labels_offset**: Offset of labels to the left or right of bars.
- **bg_gp**: Graphics parameters for the background bars.
- **bar_width**: Width of bars. Note it corresponds to the vertical direction.
- **round_corners**: Whether to draw bars with round corners?
- **r**: Radius of the round corners.
- **which**: Row or column. Currently it only supports row annotation.
- **align_to**: Which side bars as well as the labels are aligned to. Values can be "left" or "right". If x contains both positive and negative values, align_to can also be set to 0 so that bars are aligned to pos = 0.
- **width**: Width of the annotation.

Examples

```r
m = matrix(rnorm(100), 10)
x = rnorm(10)
Heatmap(m, right_annotation = rowAnnotation(numeric = anno_numeric(x)))
```

anno_oncoprint_barplot

*Barplot Annotation for oncoPrint*

Description

Barplot Annotation for oncoPrint

Usage

```r
anno_oncoprint_barplot(type = NULL, which = c("column", "row"),
bar_width = 0.6, beside = FALSE, ylim = NULL, show_fraction = FALSE, axis = TRUE,
axis_param = if(which == "column") default_axis_param("column") else list(side = "top", labels_rot =
width = NULL, height = NULL, border = FALSE)
```
Arguments

- **type**: A vector of the alteration types in the data. It can be a subset of all alteration types if you don’t want to show them all.
- **which**: Is it a row annotation or a column annotation?
- **bar_width**: Width of the bars.
- **beside**: Will bars be stacked or be positioned beside each other?
- **ylim**: Data range.
- **show_fraction**: Whether to show the numbers or the fractions?
- **axis**: Whether draw axis?
- **axis_param**: Parameters for controlling axis.
- **width**: Width of the annotation.
- **height**: Height of the annotation.
- **border**: Whether draw the border?

Details

This annotation function should always be used with `oncoPrint`.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```
# There is no example
NULL
```

Usage

```
anno_points(x, which = c("column", "row"), border = TRUE, gp = gpar(), pch = 16,
            size = unit(2, "mm"), ylim = NULL, extend = 0.05, axis = TRUE,
            axis_param = default_axis_param(which), width = NULL, height = NULL, ...)
```
Arguments

x  The value vector. The value can be a vector or a matrix. The length of the vector or the number of rows of the matrix is taken as the number of the observations of the annotation.

which  Whether it is a column annotation or a row annotation?

border  Whether draw borders of the annotation region?

gp  Graphic parameters for points. The length of each graphic parameter can be 1, length of x if x is a vector, or number of columns of x is x is a matrix.

pch  Point type. The length setting is the same as gp.

size  Point size, the value should be a unit object. The length setting is the same as gp.

ylim  Data ranges. By default it is range(x).

extend  The extension to both side of ylim. The value is a percent value corresponding to ylim[2] - ylim[1].

axis  Whether to add axis?

axis_param  parameters for controlling axis. See default_axis_param for all possible settings and default parameters.

width  Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.

height  Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.

...  Other arguments.

Value

An annotation function which can be used in HeatmapAnnotation.

See Also


Examples

anno = anno_points(runif(10))
draw(anno, test = "anno_points")
anno = anno_points(matrix(runif(20), nc = 2), pch = 1:2)
draw(anno, test = "matrix")
anno_simple

Simple Annotation

Description

Simple Annotation

Usage

anno_simple(x, col, na_col = "grey",
which = c("column", "row"), border = FALSE, gp = gpar(),
pch = NULL, pt_size = unit(1, "snpc")*0.8, pt_gp = gpar(),
simple_anno_size = ht_opt$simple_anno_size,
width = NULL, height = NULL)

Arguments

x The value vector. The value can be a vector or a matrix. The length of the vector or the number of the matrix is taken as the number of the observations of the annotation. The value can be numeric or character and NA value is allowed.

col Color that maps to x. If x is numeric and needs a continuous mapping, col should be a color mapping function which accepts a vector of values and returns a vector of colors. Normally it is generated by colorRamp2. If x is discrete (numeric or character) and needs a discrete color mapping, col should be a vector of colors with levels in x as vector names. If col is not specified, the color mapping is randomly generated by ComplexHeatmap:::default_col.

na_col Color for NA value.

which Whether it is a column annotation or a row annotation?

border Wether draw borders of the annotation region?

gp Graphic parameters for grid borders. The fill parameter is disabled.

pch Points/symbols that are added on top of the annotation grids. The value can be numeric or single letters. It can be a vector if x is a vector and a matrix if x is a matrix. No points are drawn if the corresponding values are NA.

pt_size Size of the points/symbols. It should be a unit object. If x is a vector, the value of pt_size can be a vector, while if x is a matrix, pt_size can only be a single value.

pt_gp Graphic parameters for points/symbols. The length setting is same as pt_size. If pch is set as letters, the fontsize should be set as pt_gp = gpar(fontsize = ...).

simple_anno_size size of the simple annotation.

width Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.

height Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.
Details

The "simple annotation" is the most widely used annotation type which is heatmap-like, where the grid colors correspond to the values. `anno_simple` also supports to add points/symbols on top of the grids where the it can be normal point (when `pch` is set as numbers) or letters (when `pch` is set as single letters).

Value

An annotation function which can be used in `HeatmapAnnotation`.

See Also


Examples

```r
anno = anno_simple(1:10)
draw(anno, test = "a numeric vector")

anno = anno_simple(cbind(1:10, 10:1))
draw(anno, test = "a matrix")

anno = anno_simple(1:10, pch = c(1:4, NA, 6:8, NA, 10))
draw(anno, test = "pch has NA values")

anno = anno_simple(1:10, pch = c(rep("A", 5), rep(NA, 5)))
draw(anno, test = "pch has NA values")

pch = matrix(1:20, nc = 2)
pch[sample(length(pch), 10)] = NA
anno = anno_simple(cbind(1:10, 10:1), pch = pch)
draw(anno, test = "matrix, pch is a matrix with NA values")
```
## Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>which</code></td>
<td>Whether it is a column annotation or a row annotation?</td>
</tr>
<tr>
<td><code>border</code></td>
<td>Whether draw borders of the annotation region?</td>
</tr>
<tr>
<td><code>bar_width</code></td>
<td>Relative width of the bars. The value should be smaller than one.</td>
</tr>
<tr>
<td><code>axis</code></td>
<td>Whether to add axis?</td>
</tr>
<tr>
<td><code>axis_param</code></td>
<td>Parameters for controlling axis. See <code>default_axis_param</code> for all possible settings and default parameters.</td>
</tr>
<tr>
<td><code>ylim</code></td>
<td>Data ranges. <code>ylim</code> for barplot is enforced to be <code>c(0, 1)</code>.</td>
</tr>
<tr>
<td><code>extend</code></td>
<td>The extension to both side of <code>ylim</code>. The value is a percent value corresponding to <code>ylim[2] - ylim[1]</code>. This argument is only for boxplot.</td>
</tr>
<tr>
<td><code>outline</code></td>
<td>Whether draw outline of boxplots?</td>
</tr>
<tr>
<td><code>box_width</code></td>
<td>Relative width of boxes. The value should be smaller than one.</td>
</tr>
<tr>
<td><code>pch</code></td>
<td>Point style.</td>
</tr>
<tr>
<td><code>size</code></td>
<td>Point size.</td>
</tr>
<tr>
<td><code>gp</code></td>
<td>Graphic parameters.</td>
</tr>
<tr>
<td><code>width</code></td>
<td>Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.</td>
</tr>
<tr>
<td><code>height</code></td>
<td>Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.</td>
</tr>
</tbody>
</table>

## Details

`anno_summary` is a special annotation function that it only works for one-column or one-row heatmap. It shows the summary of the values in the heatmap. If the values in the heatmap is discrete, the proportion of each level (the sum is normalized to 1) is visualized as stacked barplot. If the heatmap is split into multiple slices, multiple bars are put in the annotation. If the value is continuous, boxplot is used.

In the barplot, the color schema is used as the same as the heatmap, while for the boxplot, the color needs to be controlled by `gp`.

## Value

An annotation function which can be used in `HeatmapAnnotation`.

## See Also


## Examples

```r
ha = HeatmapAnnotation(summary = anno_summary(height = unit(4, "cm")))
v = sample(letters[1:2], 50, replace = TRUE)
split = sample(letters[1:2], 50, replace = TRUE)
Heatmap(v, top_annotation = ha, width = unit(1, "cm"), split = split)
```
ha = HeatmapAnnotation(summary = anno_summary(gp = gpar(fill = 2:3), height = unit(4, "cm")))
v = rnorm(50)
Heatmap(v, top_annotation = ha, width = unit(1, "cm"), split = split)

---

### anno_text

**Text Annotation**

**Description**

Text Annotation

**Usage**

```r
anno_text(x, which = c("column", "row"), gp = gpar(),
        rot = guess_rot(), just = guess_just(),
        offset = guess_location(), location = guess_location(),
        width = NULL, height = NULL, show_name = FALSE)
```

**Arguments**

- `x` A vector of text.
- `which` Whether it is a column annotation or a row annotation?
- `gp` Graphic parameters.
- `rot` Rotation of the text, pass to `grid.text`.
- `just` Justification of text, pass to `grid.text`.
- `offset` Deprecated, use `location` instead.
- `location` Position of the text. By default `rot`, `just` and `location` are automatically inferred according to whether it is a row annotation or column annotation. The value of `location` should be a `unit` object, normally in `npc` unit. E.g. `unit(0, 'npc')` means the most left of the annotation region and `unit(1, 'npc')` means the most right of the annotation region.
- `width` Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.
- `height` Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.
- `show_name` Whether to show the annotation name.

**Value**

An annotation function which can be used in `HeatmapAnnotation`.

**See Also**

Examples

anno = anno_text(month.name)
draw(anno, test = "month names")
anno = anno_text(month.name, gp = gpar(fontsize = 16))
draw(anno, test = "month names with fontsize")
anno = anno_text(month.name, gp = gpar(fontsize = 1:12+4))
draw(anno, test = "month names with changing fontsize")
anno = anno_text(month.name, which = "row")
draw(anno, test = "month names on rows")
anno = anno_text(month.name, location = 0, rot = 45,
    just = "left", gp = gpar(col = 1:12))
draw(anno, test = "with rotations")
anno = anno_text(month.name, location = 1,
    rot = 45, just = "right", gp = gpar(fontsize = 1:12+4))
draw(anno, test = "with rotations")

Description

Text box annotations

Usage

anno_textbox(align_to, text, background_gp = gpar(fill = "#DDDDDD", col = "#AAAAAA"),
    which = c("row", "column"), by = "anno_link", side = c("right", "left"), ...)

Arguments

align_to It controls how the text boxes are aligned to the heatmap rows. The value can
be a categorical vector which have the same length as heatmap rows, or a list of
row indices. It does not necessarily include all row indices.

text The corresponding texts. The value should be a list of texts. To control graphics
parameters of texts in the boxes, The value of text can also be set as a list of
data frames where the first column contains the text, from the second column
contains graphics parameters for each text. The column names should be "col",
"fontsize", "fontfamily" and "fontface".

background_gp Graphics for the background.

which Only "row" is allowed.

by Are text boxed arranged by anno_link or by anno_block?

side Side of the annotation to the heatmap.

... Pass to textbox_grob.
Examples

```r
require(circlize)
mat = matrix(rnorm(100*10), nrow = 100)

split = sample(letters[1:10], 100, replace = TRUE)
text = lapply(unique(split), function(x) {
data.frame(month.name, col = rand_color(12, friendly = TRUE), fontsize = runif(12, 6, 14))
})
names(text) = unique(split)

Heatmap(mat, cluster_rows = FALSE, row_split = split,
         right_annotation = rowAnnotation(wc = anno_textbox(split, text)))
```

anno_zoom

---

Zoom annotation

Description

`anno_zoom` is a function for adding zoom annotations to a heatmap. It is used to highlight specific parts of the heatmap by drawing boxes around them.

Usage

```r
anno_zoom(align_to, panel_fun = function(index, nm = NULL) { grid.rect() },
          which = c("column", "row"), side = ifelse(which == "column", "top", "right"),
          size = NULL, gap = unit(1, "mm"),
          link_width = unit(5, "mm"), link_height = link_width, link_gp = gpar(),
          extend = unit(0, "mm"), width = NULL, height = NULL, internal_line = TRUE)
```

Arguments

- `align_to`: It defines how the boxes correspond to the rows or the columns in the heatmap. If the value is a list of indices, each box corresponds to the rows or columns with indices in one vector in the list. If the value is a categorical variable (e.g. a factor or a character vector) that has the same length as the rows or columns in the heatmap, each box corresponds to the rows/columns in each level in the categorical variable.

- `panel_fun`: A self-defined function that defines how to draw graphics in the box. The function must have an `index` argument which is the indices for the rows/columns that the box corresponds to. It can have second argument `nm` which is the "name" of the selected part in the heatmap. The corresponding value for `nm` comes from `align_to` if it is specified as a categorical variable or a list with names.

- `which`: Whether it is a column annotation or a row annotation?

- `side`: Side of the boxes. If it is a column annotation, valid values are "top" and "bottom"; if it is a row annotation, valid values are "left" and "right".
anno_zoom

size
The size of boxes. It can be pure numeric that they are treated as relative fractions of the total height/width of the heatmap. The value of size can also be absolute units.

gap
Gaps between boxes.

link_gp
Graphic settings for the segments.

link_width
Width of the segments.

link_height
Similar as link_width, used for column annotation.

extend
By default, the region for the labels has the same width (if it is a column annotation) or same height (if it is a row annotation) as the heatmap. The size can be extended by this options. The value can be a proportion number or a unit object. The length can be either one or two.

width
Width of the annotation. The value should be an absolute unit. Width is not allowed to be set for column annotation.

height
Height of the annotation. The value should be an absolute unit. Height is not allowed to be set for row annotation.

internal_line
Internally used.

Details
anno_zoom creates several plotting regions (boxes) which can be corresponded to subsets of rows/columns in the heatmap.

Value
An annotation function which can be used in HeatmapAnnotation.

See Also

Examples
set.seed(123)
m = matrix(rnorm(100*10), nrow = 100)
subgroup = sample(letters[1:3], 100, replace = TRUE, prob = c(1, 5, 10))
rg = range(m)
panel_fun = function(index, nm) {
pushViewport(viewport(xscale = rg, yscale = c(0, 2)))
grid.rect()
grid.xaxis(gp = gpar(fontsize = 8))
grid.boxplot(m[index, ], pos = 1, direction = "horizontal")
grid.text(paste("distribution of group", nm), mean(rg), y = 1.9,
just = "top", default.units = "native", gp = gpar(fontsize = 10))
popViewport()
}
anno = anno_zoom(align_to = subgroup, which = "row", panel_fun = panel_fun,
size = unit(2, "cm"), gap = unit(1, "cm"), width = unit(4, "cm"))
Heatmap(m, right_annotation = rowAnnotation(foo = anno), row_split = subgroup)
## Description

Attach heatmap annotations to the heatmap

## Usage

```r
## S4 method for signature 'Heatmap'
attach_annotation(object, ha, side = c("top", "bottom", "left", "right"),
gap = unit(1, "points"))
```

### Arguments

- **object**: A `Heatmap-class` object.
- **ha**: A `HeatmapAnnotation-class` object.
- **side**: Which side of the heatmap. Value should be in "top", "bottom", "left", "right".
- **gap**: Space between the two heatmap annotations.

### Examples

```r
m = matrix(rnorm(100), 10)
ht = Heatmap(m)
ha = HeatmapAnnotation(foo = 1:10)
ht = attach_annotation(ht, ha)
ht
ha2 = HeatmapAnnotation(bar = letters[1:10])
ht = attach_annotation(ht, ha2)
ht
```

## bar3D

### Description

Draw 3D bars

### Usage

```r
bar3D(x, y, w, h, l, theta = 60, default.units = "npc", fill = "white", col = "black")
```
Arguments

- `x`: x coordinate of the center point in the bottom face.
- `y`: y coordinate of the center point in the bottom face.
- `w`: Width of the bottom face.
- `h`: Height of the bottom face.
- `l`: Length of the bars (in the z-direction).
- `theta`: The angle for the projection.
- `default.units`: Units.
- `fill`: Filled colors for the bars.
- `col`: Border colors.

Examples

```r
grid.newpage()
bar3D(c(0.3, 0.7), 0.5, 0.2, 0.2, 0.2, fill = 2:3)
```

---

bin_genome

Bin the genome

Description

Bin the genome

Usage

```r
bin_genome(species = "hg19", bins = 2000, bin_size = NULL, ...)
```

Arguments

- `species`: Abbreviation of the genome, pass to `read.chromInfo`.
- `bins`: Number of bins. The final number of bins is approximately equal to it.
- `bin_size`: Size of the bins. If `bin_size` is set, `bins` is ignored.
- `...`: All pass to `read.chromInfo`. E.g. you can set a subset of chromosomes there.

Value

A GRanges object of the genomic bins.

Examples

```r
# There is no example
NULL
```
c.ColorMapping

Concatenate A List of ColorMapping objects

Description

Concatenate A List of ColorMapping objects

Usage

```r
## S3 method for class 'ColorMapping'
c(..., name = NULL)
```

Arguments

- `...` A list of `ColorMapping-class` objects.
- `name` Name of the new merged color mapping.

Details

Only discrete color mappings can be concatenated.

Examples

```r
cm1 = ColorMapping(colors = c("A" = "red", "B" = "black"))
cm2 = ColorMapping(colors = c("B" = "blue", "C" = "green"))
c(cm1, cm2)
```

c.HeatmapAnnotation

Concatenate Heatmap Annotations

Description

Concatenate Heatmap Annotations

Usage

```r
## S3 method for class 'HeatmapAnnotation'
c(..., gap = unit(1, "points"))
```

Arguments

- `...` `HeatmapAnnotation-class` objects.
- `gap` Gap between the groups of annotations.
Details

The heatmap annotations should have same number of observations.

Examples

```r
ha1 = HeatmapAnnotation(foo = 1:10)
ha2 = HeatmapAnnotation(bar = anno_points(10:1))
ha = c(ha1, ha2)
ha
ha3 = HeatmapAnnotation(sth = cbind(1:10, 10:1))
ha = c(ha1, ha2, ha3, gap = unit(c(1, 4), "mm"))
ha
```

cluster_between_groups

Cluster only between Groups

Description

Cluster only between Groups

Usage

```r
cluster_between_groups(mat, factor)
```

Arguments

- `mat` A matrix where clustering is applied on columns.
- `factor` A categorical vector.

Details

The clustering is only applied between groups and inside a group, the order is unchanged.

Value

A `dendrogram` object.

Examples

```r
m = matrix(rnorm(120), nc = 12)
colnames(m) = letters[1:12]
fa = rep(c("a", "b", "c"), times = c(2, 4, 6))
dend = cluster_between_groups(m, fa)
grid.dendrogram(dend, test = TRUE)
```
**cluster_within_group**  
*Cluster within and between Groups*

**Description**
Cluster within and between Groups

**Usage**
```r
cluster_within_group(mat, factor)
```

**Arguments**
- `mat`  
  A matrix where clustering is applied on columns.
- `factor`  
  A categorical vector.

**Details**
The clustering is firstly applied in each group, then clustering is applied to group means. The within-group dendrograms and between-group dendrogram are finally connected by `merge_dendrogram`. In the final dendrogram, the within group dendrograms are enforced to be flat lines to emphasize that the within group dendrograms have no sense to compare to between-group dendrogram.

**Value**
A `dendrogram` object. The order of columns can be retrieved by `order.dendrogram`.

**Examples**
```r
m = matrix(rnorm(120), nc = 12)
colnames(m) = letters[1:12]
fa = rep(c("a", "b", "c"), times = c(2, 4, 6))
dend = cluster_within_group(m, fa)
grid.dendrogram(dend, test = TRUE)
```

---

**ColorMapping**  
*Constructor Method for ColorMapping Class*

**Description**
Constructor Method for ColorMapping Class

**Usage**
```r
ColorMapping(name, colors = NULL, levels = NULL, 
             col_fun = NULL, breaks = NULL, na_col = "#FFFFFF", full_col = NULL)
```
Arguments

- **name**: Name for this color mapping. The name is automatically generated if it is not specified.
- **colors**: Discrete colors.
- **levels**: Levels that correspond to colors. If colors is name indexed, levels can be ignored.
- **col_fun**: Color mapping function that maps continuous values to colors.
- **breaks**: Breaks for the continuous color mapping. If col_fun is generated by `colorRamp2`, breaks is automatically inferred from the color mapping function.
- **na_col**: Colors for NA values.
- **full_col**: A super set of colors, used internally.

Details

colors and levels are used for discrete color mapping. col_fun and breaks are used for continuous color mapping.

Value

A **ColorMapping-class** object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
cm = ColorMapping(colors = c("A" = "red", "B" = "black"))
cm
require(circlize)
col_fun = colorRamp2(c(0, 1), c("white", "red"))
cm = ColorMapping(col_fun = col_fun)
```

Description

Class for Color Mapping

Details

The **ColorMapping-class** handles color mapping for discrete values and continuous values. Discrete values are mapped by setting a vector of colors and continuous values are mapped by setting a color mapping function.
Methods

The ColorMapping-class provides following methods:

- **ColorMapping**: constructor methods.
- **map_to_colors**: mapping values to colors.
- **color_mapping_legend**: draw legend or get legend as an object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
# There is no example
NULL
```

---

**color_mapping_legend-ColorMapping-method**

*Draw Legend Based on Color Mapping*

Description

Draw Legend Based on Color Mapping

Usage

```r
## S4 method for signature 'ColorMapping'
color_mapping_legend(object,
  plot = TRUE, ...,
  color_bar = object@type,
  title = object@name,
  title_gp = gpar(fontsize = 10, fontface = "bold"),
  title_position = "topleft",
  grid_height = unit(4, "mm"),
  grid_width = unit(4, "mm"),
  tick_length = unit(0.8, "mm"),
  border = NULL,
  at = object@levels,
  labels = at,
  labels_gp = gpar(fontsize = 10),
  labels_rot = 0,
  nrow = NULL,
  ncol = 1,
  by_row = FALSE,
```
```
legend_gp = gpar(),
legend_height = NULL,
legend_width = NULL,
legend_direction = c("vertical", "horizontal"),
break_dist = NULL,

graphics = NULL,
param = NULL)
```

Arguments

- `object` A `ColorMapping-class` object.
- `plot` Whether to plot or just return the legend object?
- `...` Pass to `draw,Legends-method`.
- `color_bar` "continuous" or "discrete". It controls whether to show the discrete legend for the continuous color mapping.
- `title` Title of the legend, by default it is the name of the legend.
- `title_gp` Graphical parameters for legend title.
- `title_position` Position of the title. See `Legend` for all possible values.
- `grid_height` Height of each legend grid. Pass to `Legend`.
- `grid_width` Width of each legend grid. Pass to `Legend`.
- `tick_length` Length of the ticks on the continuous legends. Value should be a `unit` object.
- `border` Color for legend grid borders. Pass to `Legend`.
- `at` Break values of the legend. By default it is the levels in the `ColorMapping-class` object.
- `labels` Labels corresponding to break values.
- `labels_gp` Graphical parameters for legend labels.
- `labels_rot` Rotation of labels.
- `nrow` Pass to `Legend`. It controls the layout of legend grids if they are arranged in multiple rows or columns.
- `ncol` Pass to `Legend`. It controls the layout of legend grids if they are arranged in multiple rows or columns.
- `by_row` Pass to `Legend`. It controls the order of legend grids if they are arranged in multiple rows or columns.
- `legend_gp` Graphic parameters for legend.
- `legend_height` Height of the legend body. It only works when `color_bar` is continuous and direction is vertical. Pass to `Legend`.
- `legend_width` Width of the legend body. It only works when `color_bar` is continuous and direction is horizontal. Pass to `Legend`.
- `legend_direction` When `color_bar` is continuous, whether the legend is vertical or horizontal? Pass to `Legend`.

columnAnnotation

break_dist  A zooming factor to control relative distance of two neighbouring break values. The length of it should be length(at) - 1 or a scalar.

graphics  Internally used.

param  All the legend-related parameters can be specified as a single list.

Details
The legend is constructed by Legend.

Value
A Legends-class object.

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples
# There is no example
NULL

---
columnAnnotation  Construct Column Annotations

Description
Construct Column Annotations

Usage
columnAnnotation(...)

Arguments
...  Pass to HeatmapAnnotation.

Details
The function is identical to

HeatmapAnnotation(..., which = "column")

Value
A HeatmapAnnotation-class object.
Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

column_dend-dispatch  Method dispatch page for column_dend

Description

Method dispatch page for column_dend.

Dispatch

column_dend can be dispatched on following classes:

• column_dend,Heatmap-method, Heatmap-class class method
• column_dend,HeatmapList-method, HeatmapList-class class method

Examples

# no example
NULL

column_dend-Heatmap-method

Get Column Dendrograms from a Heatmap

Description

Get Column Dendrograms from a Heatmap

Usage

```r
## S4 method for signature 'Heatmap'
column_dend(object, on_slice = FALSE)
```

Arguments

- object: A `Heatmap-class` object.
- on_slice: If the value is TRUE, it returns the dendrogram on the slice level.
The format of the returned object depends on whether rows/columns of the heatmaps are split.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
mat = matrix(rnorm(100), 10)
ht = Heatmap(mat)
ht = draw(ht)
column_dend(ht)
ht = Heatmap(mat, column_km = 2)
ht = draw(ht)
column_dend(ht)
```

Description

Get Column Dendrograms from a `Heatmap` List

Usage

```r
## S4 method for signature 'HeatmapList'
column_dend(object, name = NULL, on_slice = FALSE)
```

Arguments

- `object`: A `HeatmapList-class` object.
- `name`: Name of a specific heatmap.
- `on_slice`: If the value is TRUE, it returns the dendrogram on the slice level.

Value

The format of the returned object depends on whether rows/columns of the heatmaps are split.

Author(s)

Zuguang Gu <z.gu@dkfz.de>
Examples

mat = matrix(rnorm(100), 10)
ht_list = Heatmap(mat) + Heatmap(mat)
ht_list = draw(ht_list)
column_dend(ht_list)
ht_list = Heatmap(mat, column_km = 2) + Heatmap(mat, column_km = 2)
ht_list = draw(ht_list)
column_dend(ht_list)
column_dend(ht_list, on_slice = TRUE)
ht_list = Heatmap(mat) %v% Heatmap(mat)
ht_list = draw(ht_list)
column_dend(ht_list)
ht_list = Heatmap(mat, column_km = 2) %v% Heatmap(mat)
ht_list = draw(ht_list)
column_dend(ht_list)

---

column_order-dispatch  Method dispatch page for column_order

Description

Method dispatch page for column_order.

Dispatch

column_order can be dispatched on following classes:

- column_order,Heatmap-method,Heatmap-class class method
- column_order,HeatmapList-method,HeatmapList-class class method

Examples

# no example
NULL

---

column_order-Heatmap-method

Get Column Order from a Heatmap List

Description

Get Column Order from a Heatmap List
## S4 method for signature 'Heatmap'
column_order(object)

### Arguments

- **object**: A *Heatmap-class* object.

### Value

The format of the returned object depends on whether rows/columns of the heatmaps are split.

### Author(s)

Zuguang Gu <z.gu@dkfz.de>

### Examples

```r
cmat <- matrix(rnorm(100), 10)
ht <- Heatmap(cmat)
ht <- draw(ht)
column_order(ht)
ht <- Heatmap(cmat, column_km = 2)
ht <- draw(ht)
column_order(ht)
```

---

## S4 method for signature 'HeatmapList'
column_order(object, name = NULL)

### Arguments

- **object**: A *HeatmapList-class* object.
- **name**: Name of a specific heatmap.

### Value

The format of the returned object depends on whether rows/columns of the heatmaps are split.
Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
mat = matrix(rnorm(100), 10)
ht_list = Heatmap(mat) + Heatmap(mat)
ht_list = draw(ht_list)
column_order(ht_list)
ht_list = Heatmap(mat, column_km = 2) + Heatmap(mat, column_km = 2)
ht_list = draw(ht_list)
column_order(ht_list)
ht_list = Heatmap(mat) %v% Heatmap(mat)
ht_list = draw(ht_list)
column_order(ht_list)
ht_list = Heatmap(mat, column_km = 2) %v% Heatmap(mat)
ht_list = draw(ht_list)
column_order(ht_list)
```

deg = comb_degree(m)

### comb_degree

**Degrees of the Combination sets**

**Description**

Degrees of the Combination sets

**Usage**

```r
comb_degree(m)
```

**Arguments**

- `m` A combination matrix returned by `make_comb_mat`.

**Details**

The degree for a combination set is the number of sets that are selected.

**Value**

A vector of degrees of the combination sets.

**Examples**

```r
set.seed(123)
l = list(a = sample(letters, 10),
    b = sample(letters, 15),
    c = sample(letters, 20))
m = make_comb_mat(l)
comb_degree(m)
```
### comb_name

**Names of the Combination sets**

**Description**

Names of the Combination sets

**Usage**

```r
comb_name(m, readable = FALSE)
```

**Arguments**

- `m` A combination matrix returned by `make_comb_mat`.
- `readable` Whether the combination represents as e.g. "A&B&C".

**Details**

The name of the combination sets are formatted as a string of binary bits. E.g. for three sets of "a", "b", "c", the combination set with name "101" corresponds to select set a, not select set b and select set c. The definition of "select" depends on the value of `mode` from `make_comb_mat`.

**Value**

A vector of names of the combination sets.

**Examples**

```r
set.seed(123)
l_t = list(a = sample(letters, 10),
         b = sample(letters, 15),
         c = sample(letters, 20))
m = make_comb_mat(l_t)
comb_name(m)
comb_name(m, readable = TRUE)
```

### comb_size

**Sizes of the Combination sets**

**Description**

Sizes of the Combination sets

**Usage**

```r
comb_size(m, degree = NULL)
```
Arguments

\( m \)  
A combination matrix returned by \texttt{make_comb_mat}.

\( \text{degree} \)  
degree of the intersection. The value can be a vector.

Value

A vector of sizes of the combination sets.

Examples

```r
set.seed(123)
lt = list(a = sample(letters, 10),
          b = sample(letters, 15),
          c = sample(letters, 20))
m = make_comb_mat(lt)
comb_size(m)
```

```
compare_heatmap(mat)
```

**Description**

Compare heatmaps between \texttt{stats::heatmap()} and \texttt{ComplexHeatmap::heatmap()}.

**Usage**

```r
compare_heatmap(...)```

**Arguments**

...  
The same set of arguments passed to \texttt{stats::heatmap} and \texttt{ComplexHeatmap::heatmap}.

**Details**

The function plots two heatmaps, one by \texttt{stats::heatmap()} and one by \texttt{ComplexHeatmap::heatmap()}. Users can see the difference between the two implementations.

**Examples**

```r
mat = matrix(rnorm(100), 10)
compare_heatmap(mat)
```
**compare_heatmap.2**  
*Compare heatmaps between gplots::heatmap.2() and ComplexHeatmap::heatmap()*

---

**Description**

Compare heatmaps between gplots::heatmap.2() and ComplexHeatmap::heatmap()

**Usage**

```r
compare_heatmap.2(...) 
```

**Arguments**

...  

The same set of arguments passed to gplots::heatmap.2 and ComplexHeatmap::heatmap.2.

**Details**

The function plots two heatmaps, one by gplots::heatmap.2 and one by ComplexHeatmap::heatmap.2. Users can see the difference between the two implementations.

**Examples**

```r
mat = matrix(rnorm(100), 10)
compare_heatmap.2(mat)
```

---

**compare_pheatmap**  
*Compare heatmaps between pheatmap::pheatmap() and ComplexHeatmap::pheatmap()*

---

**Description**

Compare heatmaps between pheatmap::pheatmap() and ComplexHeatmap::pheatmap()

**Usage**

```r
compare_pheatmap(...) 
```

**Arguments**

...  

The same set of arguments passed to pheatmap::pheatmap and ComplexHeatmap::pheatmap.

**Details**

The function plots two heatmaps, one by pheatmap::pheatmap and one by ComplexHeatmap::pheatmap. Users can see the difference between the two implementations.
complement_size

Examples

```r
mat = matrix(rnorm(100), 10)
compare_pheatmap(mat)
```

complement_size | Complement Set Size

Description

Complement Set Size

Usage

```r
complement_size(m)
```

Arguments

- `m` A combination matrix returned by `make_comb_mat`.

Value

If there is no complement set, it returns zero.

Examples

```r
# There is no example
NULL
```

component_height-dispatch

\textit{Method dispatch page for component\_height}

Description

Method dispatch page for component\_height.

Dispatch

component\_height can be dispatched on following classes:

- `component\_height,HeatmapList\_method,HeatmapList\_class` class method
- `component\_height,Heatmap\_method,Heatmap\_class` class method
Examples

# no example
NULL

---

**component_height-Heatmap-method**

*Heights of Heatmap Components*

**Description**

Heights of Heatmap Components

**Usage**

```r
## S4 method for signature 'Heatmap'
component_height(object, k = HEATMAP_LAYOUT_COLUMN_COMPONENT)
```

**Arguments**

- `object` A `Heatmap-class` object.
- `k` Which components in the heatmap. The value should numeric indices or the names of the corresponding column component. See **Details**.

**Details**

All column components are: `column_title_top, column_dend_top, column_names_top, column_anno_top, heatmap_body, column_anno_bottom, column_names_bottom, column_dend_bottom, column_title_bottom`.

This function is only for internal use.

**Value**

A `unit` object.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

# There is no example
NULL
## component_height-HeatmapList-method

### Height of Heatmap List Components

**Description**

Height of Heatmap List Components

**Usage**

```r
## S4 method for signature 'HeatmapList'
component_height(object, k = HEATMAP_LIST_LAYOUT_COLUMN_COMPONENT)
```

**Arguments**

- `object`: A `HeatmapList-class` object.
- `k`: Which component in the heatmap list. Values are in `ComplexHeatmap:::HEATMAP_LIST_LAYOUT_COLUMN_COMPONENT`.

**Value**

A unit object.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```

---

## component_width-dispatch

**Method dispatch page for component_width**

**Description**

Method dispatch page for component_width.

**Dispatch**

component_width can be dispatched on following classes:

- `component_width,HeatmapList-method,HeatmapList-class` class method
- `component_width,Heatmap-method,Heatmap-class` class method
Examples

# no example
NULL

## S4 method for signature 'Heatmap'
component_width(object, k = HEATMAP_LAYOUT_ROW_COMPONENT)

Arguments

object       A Heatmap-class object.
k           Which components in the heatmap. The value should numeric indices or the names of the corresponding row component. See **Details**.

Details

All row components are: row_title_left, row_dend_left, row_names_left, row_anno_left, heatmap_body, row_anno_right, row_names_right, row_dend_right, row_title_right.

This function is only for internal use.

Value

A unit object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL
Width of Heatmap List Components

Usage

## S4 method for signature 'HeatmapList'
component_width(object, k = HEATMAP_LIST_LAYOUT_ROW_COMPONENT)

Arguments

- object: A `HeatmapList-class` object.
- k: Which component in the heatmap list. Values are in `ComplexHeatmap:::HEATMAP_LIST_LAYOUT_ROW_COMPONENT`.

Details

This function is only for internal use.

Value

A `unit` object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL
Copy the AnnotationFunction Object

Description
Copy the AnnotationFunction Object

Usage
## S4 method for signature 'AnnotationFunction'
copy_all(object)

Arguments
object The AnnotationFunction-class object.

Details
In AnnotationFunction-class, there is an environment which stores some external variables for
the annotation function (specified by the var_import argument when constructing the AnnotationFunction-class
object. This copy_all,AnnotationFunction-method hard copies all the variables into a new isolated environment.
The environment is at object@var_env.

Examples
# There is no example
NULL

Description
Method dispatch page for copy_all.

Dispatch
copy_all can be dispatched on following classes:

- copy_all,AnnotationFunction-method, AnnotationFunction-class class method
- copy_all,SingleAnnotation-method, SingleAnnotation-class class method
copy_all-SingleAnnotation-method

Examples

```r
# no example
NULL
```

---

copy_all-SingleAnnotation-method

*Copy the SingleAnnotation object*

---

Description

Copy the SingleAnnotation object

Usage

```r
## S4 method for signature 'SingleAnnotation'

copy_all(object)
```

Arguments

- `object` The `SingleAnnotation-class` object.

Details

Since the SingleAnnotation object always contains an `AnnotationFunction-class` object, it calls `copy_all,AnnotationFunction-method` to hard copy the variable environment.

Examples

```r
# There is no example
NULL
```

decorate_annotation    *Decorate Heatmap Annotation*

Description

Decorate Heatmap Annotation

Usage

```r
decorate_annotation(annotation, code, slice = 1, envir = new.env(parent = parent.frame()))
```
Arguments

- **annotation**: Name of the annotation.
- **code**: Code that adds graphics in the selected heatmap annotation.
- **slice**: Index of the row slices or the column slice in the heatmap.
- **envir**: Where to look for variables inside code.

Details

There is a viewport for every column annotation and row annotation. This function constructs the name of the viewport, goes to the viewport by `seekViewport`, runs code to that viewport, and finally goes back to the original viewport.

Value

The function returns no value.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also


Examples

```r
set.seed(123)
ha1 = HeatmapAnnotation(df = data.frame(type = rep(letters[1:2], 5)))
ha2 = rowAnnotation(point = anno_points(runif(10), which = "row"))
Heatmap(matrix(rnorm(100), 10), name = "mat", km = 2,
  top_annotation = ha1) + ha2
decorate_annotation("type", {
  grid.circle(x = unit(c(0.2, 0.4, 0.6, 0.8), "npc"),
    gp = gpar(fill = "#FF000080"))
})
decorate_annotation("point", {
  grid.rect(gp = gpar(fill = "#FF000080"))
}, slice = 2)
```
Usage

decorate_column_dend(..., envir = new.env(parent = parent.frame()))

Arguments

... Pass to decorate_dend.

envir Where to look for variables inside code.

Details

This is a wrapper function which pre-defined which argument in decorate_dend.

Value

The function returns no value.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL
decorate_column_title

Description
Decorate Heatmap Column Titles

Usage
decorate_column_title(..., envir = new.env(parent = parent.frame()))

Arguments
... Pass to decorate_title.
envir Where to look for variables inside code.

Details
This is a helper function which pre-defined which argument in decorate_title.

Value
The function returns no value.

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples
# There is no example
NULL
**decorate_dend**

**Decorate Heatmap Dendrograms**

**Description**

Decorate Heatmap Dendrograms

**Usage**

```r
decorate_dend(heatmap, code, slice = 1, which = c("column", "row"),
  envir = new.env(parent = parent.frame()))
```

**Arguments**

- `heatmap` Name of the heatmap.
- `code` Code that adds graphics in the selected heatmap dendrogram.
- `slice` Index of the row slice or column slice in the heatmap.
- `which` Is the dendrogram on rows or on columns?
- `envir` Where to look for variables inside `code`.

**Details**

If you know the number of leaves in the dendrogram, it is simple to calculate the position of every leave in the dendrogram. E.g., for the column dendrogram, the i\textsuperscript{th} leave is located at:

```r
# assume nc is the number of columns in the column slice
unit((i-0.5)/nc, "npc")
```

**Value**

This function returns no value.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**See Also**


**Examples**

```r
set.seed(123)
Heatmap(matrix(rnorm(100), 10), name = "mat", km = 2)
decorate_dend("mat", {
  grid.rect(gp = gpar(fill = "#FF000080"))
}, which = "row", slice = 2)
```
**decorate_dimnames**  
*Decorate Heatmap Dimension Names*

**Description**
Decorate Heatmap Dimension Names

**Usage**

```r
decorate_dimnames(heatmap, code, slice = 1, which = c("column", "row"), 
                 envir = new.env(parent = parent.frame()))
```

**Arguments**
- `heatmap` Name of the heatmap.  
- `code` Code that adds graphics in the selected viewport.  
- `slice` Index of the row slice or column slice in the heatmap.  
- `which` on rows or on columns?  
- `envir` where to look for variables inside `code`.

**Details**
If you know the dimensions of the matrix, it is simple to calculate the position of every row name or column name in the heatmap. E.g., for the column column, the \(i\)-th name is located at:

```r
# assume nc is the number of columns in the column slice 
unit((i-0.5)/nc, "npc")
```

**Value**
The function returns no value.

**Author(s)**
Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
set.seed(123)  
mat = matrix(rnorm(100), 10)  
rownames(mat) = letters[1:10]  
colnames(mat) = LETTERS[1:10]  
Heatmap(mat, name = "mat", km = 2)  

decorate_dimnames("mat", {  
    grid.rect(gp = gpar(fill = "#FF000080"))  
}, which = "row", slice = 2)
```
**decorate_heatmap_body**  
Decorate Heatmap Bodies

### Description

Decorate Heatmap Bodies

### Usage

```r
decorate_heatmap_body(heatmap, code,  
  slice = 1, row_slice = slice, column_slice = 1,  
  envir = new.env(parent = parent.frame()))
```

### Arguments

- **heatmap**: Name of the heatmap which is set as `name` argument in `Heatmap` function.
- **code**: Code that adds graphics in the selected heatmap body.
- **slice**: Index of the row slice in the heatmap.
- **row_slice**: Index of the row slice in the heatmap.
- **column_slice**: Index of the column slice in the heatmap.
- **envir**: Where to look for variables inside `code`.

### Details

There is a viewport for each slice in each heatmap. This function constructs the name of the viewport, goes to the viewport by `seekViewport`, runs the code to that viewport and finally goes back to the original viewport.

### Value

This function returns no value.

### Author(s)

Zuguang Gu <z.gu@dkfz.de>

### See Also


### Examples

```r
set.seed(123)
Heatmap(matrix(rnorm(100), 10), name = "mat")
decorate_heatmap_body("mat", {  
  grid.circle(gp = gpar(fill = "#FF000080"))  
})
```
### `decorate_row_dend`  
**Decorate Heatmap Row Dendrograms**

#### Description
Decorate Heatmap Row Dendrograms

#### Usage
```r
decorate_row_dend(..., envir = new.env(parent = parent.frame()))
```

#### Arguments
- `...` Pass to `decorate_dend`.
- `envir` Where to look for variables inside code?

#### Details
This is a helper function which pre-defined which argument in `decorate_dend`.

#### Value
The function returns no value.

#### Author(s)
Zuguang Gu <z.gu@dkfz.de>

#### Examples
```r
# There is no example
NULL
```

### `decorate_row_names`  
**Decorate Heatmap Row Names**

#### Description
Decorate Heatmap Row Names

#### Usage
```r
decorate_row_names(..., envir = new.env(parent = parent.frame()))
```
**describe_row_title**

**Arguments**

... Pass to **decorate_dimnames**.

**envir** Where to look for variables inside code.

**Details**

This is a helper function which pre-defined which argument in **decorate_dimnames**.

**Value**

The function returns no value.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```
Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

---

**decorate_title**  
*Decorate Heatmap Titles*

Description

Decorate Heatmap Titles

Usage

```r
decorate_title(heatmap, code, slice = 1, which = c("column", "row"),
               envir = new.env(parent = parent.frame()))
```

Arguments

- `heatmap`  
  Name of the heatmap.
- `code`  
  Code that adds graphics in the selected viewport.
- `slice`  
  Index of the row slice or column slice in the heatmap.
- `which`  
  Is it a row title or a column title?
- `envir`  
  Where to look for variables inside `code`.

Details

There is a viewport for row titles and column title in the heatmap. This function constructs the name of the viewport, goes to the viewport by `seekViewport`, runs code to that viewport and finally goes back to the original viewport.

Value

The function returns no value.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

The Default Parameters for Annotation Axis

The Default Parameters for Annotation Axis

Usage

default_axis_param(which)

Arguments

which Whether it is for column annotation or row annotation?

Details

There are following parameters for the annotation axis:

at The breaks of axis. By default it is automatically inferred.
labels The corresponding axis labels.
labels_rot The rotation of the axis labels.
gp Graphic parameters of axis labels. The value should be a unit object.
side If it is for column annotation, the value should only be one of left and right. If it is for row annotation, the value should only be one of top and bottom.
facing Whether the axis faces to the outside of the annotation region or inside. Sometimes when appending more than one heatmaps, the axes of column annotations of one heatmap might overlap to the neighbouring heatmap, setting facing to inside may invold it.
direction The direction of the axis. Value should be "normal" or "reverse".

All the parameters are passed to annotation_axis_grob to construct an axis grob.

Examples

default_axis_param("column")
default_axis_param("row")
default_get_type

Default get_type for oncoPrint()

Description

Default get_type for oncoPrint()

Usage

default_get_type(x)

Arguments

x

A strings which encode multiple alterations.

Details

It recognizes following separators: ;:, |.

Examples

# There is no example
NULL

dendrogramGrob

Grob for Dendrogram

Description

Grob for Dendrogram

Usage

dendrogramGrob(dend, facing = c("bottom", "top", "left", "right"),
    order = c("normal", "reverse"), gp = gpar())

Arguments

dend A dendrogram object.
facing Facing of the dendrogram.
order If it is set to reverse, the first leaf is put on the right if the dendrogram is horizontal and it is put on the top if the dendrogram is vertical.
gp Graphic parameters for the dendrogram segments. If any of col, lwd or lty is set in the edgePar attribute of a node, the corresponding value defined in gp will be overwritten for this node, so gp is like global graphic parameters for dendrogram segments.
**dend_heights**

Details

If `dend` has not been processed by `adjust_dend_by_x`, internally `adjust_dend_by_x` is called to add `x` attributes to each node/leaf.

Value

A `grob` object which is constructed by `segmentsGrob`.

Examples

```r
# There is no example
NULL
```

---

<table>
<thead>
<tr>
<th><strong>dend_heights</strong></th>
<th><strong>Height of the Dendrograms</strong></th>
</tr>
</thead>
</table>

Description

Height of the Dendrograms

Usage

```
dend_heights(x)
```

Arguments

- `x` (a `dendrogram` object or a list of `dendrogram` objects.

Examples

```r
# There is no example
NULL
```

---

<table>
<thead>
<tr>
<th><strong>dend_xy</strong></th>
<th><strong>Coordinates of the Dendrogram</strong></th>
</tr>
</thead>
</table>

Description

Coordinates of the Dendrogram

Usage

```
dend_xy(dend)
```
**Arguments**

- `dend`: a `dendrogram` object.

**Details**

`dend` will be processed by `adjust_dend_by_x` if it is processed yet.

**Value**

A list of leave positions \(x\) and dendrogram height \(y\).

**Examples**

```r
m = matrix(rnorm(100), 10)
dend1 = as.dendrogram(hclust(dist(m)))
dend_xy(dend1)

dend1 = adjust_dend_by_x(dend1, sort(runif(10)))
dend_xy(dend1)

dend1 = adjust_dend_by_x(dend1, unit(1:10, "cm"))
dend_xy(dend1)
```

**densityHeatmap**

*Visualize Density Distribution by Heatmap*

**Description**

Visualize Density Distribution by Heatmap

**Usage**

```r
densityHeatmap(data,
   density_param = list(na.rm = TRUE),
   col = rev(brewer.pal(11, "Spectral")),
   color_space = "LAB",
   ylab = deparse(substitute(data)),
   column_title = paste0("Density heatmap of ", deparse(substitute(data))),
   title = column_title,
   ylim = NULL,
   range = ylim,

title_gp = gpar(fontsize = 14),
ylab_gp = gpar(fontsize = 12),
tick_label_gp = gpar(fontsize = 10),
quantile_gp = gpar(fontsize = 10),
show_quantiles = TRUE,
```

```
densityHeatmap

column_order = NULL,
column_names_side = "bottom",
show_column_names = TRUE,
column_names_max_height = unit(6, "cm"),
column_names_gp = gpar(fontsize = 12),
column_names_rot = 90,

cluster_columns = FALSE,
clustering_distance_columns = "ks",
clustering_method_columns = "complete",
mc.cores = 1, cores = mc.cores,
...

Arguments

data
A matrix or a list. If it is a matrix, density is calculated by columns.
density_param
Parameters send to density, na.rm is enforced to be TRUE.
col
A vector of colors that density values are mapped to.
color_space
The color space in which colors are interpolated. Pass to colorRamp2.
ylab
Label on y-axis.
column_title
Title of the heatmap.
title
Same as column_title.
ylim
Ranges on the y-axis.
range
Same as ylim.
title_gp
Graphic parameters for title.
ylab_gp
Graphic parameters for y-labels.
tick_label_gp
Graphic parameters for y-ticks.
quantile_gp
Graphic parameters for the quantiles.
show_quantiles
Whether show quantile lines.
column_order
Order of columns.
column_names_side
Pass to Heatmap.
show_column_names
Pass to Heatmap.
column_names_max_height
Pass to Heatmap.
column_names_gp
Pass to Heatmap.
column_names_rot
Pass to Heatmap.
cluster_columns
Whether cluster columns?
clustering_distance_columns

There is a specific distance method ks which is the Kolmogorov-Smirnov statistic between two distributions. For other methods, the distance is calculated on the density matrix.

clustering_method_columns

Pass to Heatmap.

mc.cores

Multiple cores for calculating ks distance. This argument will be removed in future versions.

cores

Multiple cores for calculating ks distance.

... Pass to Heatmap.

Details

To visualize data distribution in a matrix or in a list, we normally use boxplot or violinplot. We can also use colors to map the density values and visualize distribution of values through a heatmap. It is useful if you have huge number of columns in data to visualize.

The density matrix is generated with 500 rows ranging between the maximum and minimal values in all densities.

Value

A Heatmap-class object. It can only add other heatmaps/annotations vertically.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also


Examples

```r
matrix = matrix(rnorm(100), 10); colnames(matrix) = letters[1:10]
densityHeatmap(matrix)

lt = list(rnorm(10), rnorm(10))
densityHeatmap(lt)

ha = HeatmapAnnotation(points = anno_points(runif(10)),
    anno = rep(c("A", "B"), each = 5), col = list(anno = c("A" = "red", "B" = "blue")))
densityHeatmap(matrix, top_annotation = ha)
densityHeatmap(matrix, top_annotation = ha) %v% Heatmap(matrix, height = unit(6, "cm"))
```
**dim.Heatmap**

*Dimension of the Heatmap*

**Description**

Dimension of the Heatmap

**Usage**

```r
## S3 method for class 'Heatmap'
dim(x)
```

**Arguments**

- `x` A `Heatmap-class` object.

**Examples**

```r
# There is no example
NULL
```

---

**dist2**

*Calculate Pairwise Distance from a Matrix*

**Description**

Calculate Pairwise Distance from a Matrix

**Usage**

```r
dist2(x, pairwise_fun = function(x, y) sqrt(sum((x - y)^2)), ...)
```

**Arguments**

- `x` A matrix or a list. If it is a matrix, the distance is calculated by rows.
- `pairwise_fun` A function which calculates distance between two vectors.
- `...` Pass to `as.dist`.

**Details**

You can construct any type of distance measurements by defining a pair-wise distance function. The function is implemented by two nested for loops, so the efficiency may not be so good.
Value

A `dist` object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
lt = lapply(1:10, function(i) {
    sample(letters, sample(6:10, 1))
})
dist2(lt, function(x, y) {
    length(intersect(x, y))/length(union(x, y))
})
```

---

`draw-AnnotationFunction-method`

*Draw the AnnotationFunction Object*

Description

Draw the AnnotationFunction Object

Usage

```r
## S4 method for signature 'AnnotationFunction'
draw(object, index, k = 1, n = 1, test = FALSE, ...)
```

Arguments

- `object`: The `AnnotationFunction-class` object.
- `index`: Index of observations.
- `k`: Current slice index.
- `n`: Total number of slices.
- `test`: Is it in test mode? The value can be logical or a text which is plotted as the title of plot.
- `...`: Pass to `viewport`.

Details

Normally it is called internally by the `SingleAnnotation-class`.

When `test` is set to `TRUE`, the annotation graphic is directly drawn, which is generally for testing purpose.
Examples

# There is no example
NULL

draw-dispatch  
Method dispatch page for draw

Description

Method dispatch page for draw.

Dispatch

draw can be dispatched on following classes:

- draw,HeatmapAnnotation-method, HeatmapAnnotation-class class method
- draw,Legends-method, Legends-class class method
- draw,SingleAnnotation-method, SingleAnnotation-class class method
- draw,AnnotationFunction-method, AnnotationFunction-class class method
- draw,Heatmap-method, Heatmap-class class method
- draw,HeatmapList-method, HeatmapList-class class method

Examples

# no example
NULL

draw-Heatmap-method  
Draw a Single Heatmap

Description

Draw a Single Heatmap

Usage

## S4 method for signature 'Heatmap'
draw(object, internal = FALSE, test = FALSE, ...)
Arguments

object A Heatmap-class object.
internal If TRUE, it is only used inside the calling of draw,HeatmapList-method. It only draws the heatmap without legends where the legend will be drawn by draw,HeatmapList-method.
test Only for testing. If it is TRUE, the heatmap body is directly drawn.
... Pass to draw,HeatmapList-method.

Details

The function creates a HeatmapList-class object which only contains a single heatmap and call draw,HeatmapList-method to make the final heatmap.

There are some arguments which control the some settings of the heatmap such as legends. Please go to draw,HeatmapList-method for these arguments.

Value

A HeatmapList-class object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL
Arguments

object
index
k
n
...

test

anno_mark_param

No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example

NULL

draw-HeatmapList-method

Description

Draw a list of heatmaps

Usage

## S4 method for signature 'HeatmapList'
draw(object,
      newpage = TRUE,
      background = "white",
      row_title = character(0),
      row_title_side = c("left", "right"),
      row_title_gp = gpar(fontsize = 13),
      column_title = character(0),
      column_title_side = c("top", "bottom"),
column_title_gp = gpar(fontsize = 13),

heatmap_legend_side = c("right", "left", "bottom", "top"),
merge_legends = ht_opt$merge_legends,
show_heatmap_legend = TRUE,
heatmap_legend_list = list(),
annotation_legend_side = c("right", "left", "bottom", "top"),
show_annotation_legend = TRUE,
annotation_legend_list = list(),
align_heatmap_legend = NULL,
align_annotation_legend = NULL,
legend_grouping = c("adjusted", "original"),
gap = unit(2, "mm"),
ht_gap = gap,

main_heatmap = which(sapply(object@ht_list, inherits, "Heatmap"))[1],
padding = GLOBAL_PADDING,
adjust_annotation_extension = NULL,

auto_adjust = TRUE,
row_dend_side = c("original", "left", "right"),
row_sub_title_side = c("original", "left", "right"),
column_dend_side = c("original", "top", "bottom"),
column_sub_title_side = c("original", "top", "bottom"),

row_gap = NULL,
cluster_rows = NULL,
cluster_row_slices = NULL,
clustering_distance_rows = NULL,
clustering_method_rows = NULL,
row_dend_width = NULL,
show_row_dend = NULL,
row_dend_reorder = NULL,
row_dend_gp = NULL,
row_order = NULL,
km = NULL,
split = NULL,
row_km = km,
row_km_repeats = NULL,
row_split = split,
height = NULL,
heatmap_height = NULL,

column_gap = NULL,
cluster_columns = NULL,
cluster_column_slices = NULL,
clustering_distance_columns = NULL,
Arguments

object         a HeatmapList-class object.
newpage        whether create a new page for the graphics. If you want to arrange multiple plots in one page, I suggest to use grid.grabExpr.
background     Background color of the whole plot.
row_title      title on the row.
row_title_side will the title be put on the left or right of the heatmap.
row_title_gp  graphic parameters for drawing text.
column_title  title on the column.
column_title_side will the title be put on the top or bottom of the heatmap.
column_title_gp  graphic parameters for drawing text.
heatmap_legend_side  side to put heatmap legend
merge_legends  merge heatmap legends and annotation legends to put into one column.
show_heatmap_legend  whether show heatmap legends
heatmap_legend_list  use-defined legends which are put after the heatmap legends
annotation_legend_side  side of the annotation legends
show_annotation_legend  whether show annotation legends
annotation_legend_list  user-defined legends which are put after the annotation legends
align_heatmap_legend How to align the legends to heatmap. Possible values are "heatmap_center", "heatmap_top" and "global_center". If the value is NULL, it automatically picks the proper value from the three options.
align_annotation_legend  How to align the legends to heatmap. Possible values are "heatmap_center", "heatmap_top" and "global_center".
legend_grouping  How the legends are grouped. Values should be "adjusted" or "original". If it is set as "original", all annotation legends are grouped together.
gap  gap between heatmaps/annotations
ht_gap  same as gap.
main_heatmap  index of main heatmap. The value can be a numeric index or the heatmap name
padding  padding of the whole plot. The value is a unit vector of length 4, which corresponds to bottom, left, top and right.
adjust_annotation_extension whether take annotation name into account when calculating positions of graphic elements.
auto_adjust  whether apply automatic adjustment? The auto-adjustment includes turning off dendrograms, titles and row/columns for non-main heatmaps.
row_dend_side  side of the dendrogram from the main heatmap
row_sub_title_side  side of the row title from the main heatmap
column_dend_side  side of the dendrogram from the main heatmap
column_sub_title_side
    side of the column title from the main heatmap
row_gap
    this modifies row_gap of the main heatmap
cluster_rows
    this modifies cluster_rows of the main heatmap
cluster_row_slices
    this modifies cluster_row_slices of the main heatmap
clustering_distance_rows
    this modifies clustering_distance_rows of the main heatmap
clustering_method_rows
    this modifies clustering_method_rows of the main heatmap
row_dend_width
    this modifies row_dend_width of the main heatmap
show_row_dend
    this modifies show_row_dend of the main heatmap
row_dend_reorder
    this modifies row_dend_reorder of the main heatmap
row_dend_gp
    this modifies row_dend_gp of the main heatmap
row_order
    this modifies row_order of the main heatmap
km
    = this modifies km of the main heatmap
split
    this modifies split of the main heatmap
row_km
    this modifies row_km of the main heatmap
row_km_repeats
    this modifies row_km_repeats of the main heatmap
row_split
    this modifies row_split of the main heatmap
height
    this modifies height of the main heatmap
heatmap_height
    this modifies heatmap_height of the main heatmap
column_gap
    this modifies column_gap of the main heatmap
cluster_columns
    this modifies cluster_columns of the main heatmap
cluster_column_slices
    this modifies cluster_column_slices of the main heatmap
clustering_distance_columns
    this modifies clustering_distance_columns of the main heatmap
clustering_method_columns
    this modifies clustering_method_columns of the main heatmap
column_dend_width
    this modifies column_dend_width of the main heatmap
show_column_dend
    this modifies show_column_dend of the main heatmap
column_dend_reorder
    this modifies column_dend_reorder of the main heatmap
column_dend_gp
    this modifies column_dend_gp of the main heatmap
column_order
    this modifies column_order of the main heatmap
column_km
    this modifies column_km of the main heatmap
draw-HeatmapList-method

column_km_repeats
this modifies column_km_repeats of the main heatmap

column_split
this modifies column_split of the main heatmap

width
this modifies width of the main heatmap

heatmap_width
this modifies heatmap_width of the main heatmap

use_raster
this modifies use_raster of every heatmap.

raster_device
this modifies raster_device of every heatmap.

raster_quality
this modifies raster_quality of every heatmap.

raster_device_param
this modifies raster_device_param of every heatmap.

raster_resize
this modifies raster_resize of every heatmap.

post_fun
A self-defined function will be executed after all the heatmaps are drawn.

save_last
Whether to save the last plot?

heatmap_row_names_gp
this set the value in ht_opt and reset back after the plot is done

heatmap_column_names_gp
this set the value in ht_opt and reset back after the plot is done

heatmap_row_title_gp
this set the value in ht_opt and reset back after the plot is done

heatmap_column_title_gp
this set the value in ht_opt and reset back after the plot is done

legend_title_gp
this set the value in ht_opt and reset back after the plot is done

legend_title_position
this set the value in ht_opt and reset back after the plot is done

legend_labels_gp
this set the value in ht_opt and reset back after the plot is done

legend_grid_height
this set the value in ht_opt and reset back after the plot is done

legend_grid_width
this set the value in ht_opt and reset back after the plot is done

legend_border
this set the value in ht_opt and reset back after the plot is done

legend_gap
Gap between legends. The value should be a vector of two units. One for gaps between vertical legends and one for the horizontal legends. If only one single unit is specified, the same gap set for the vertical and horizontal legends.

heatmap_border
this set the value in ht_opt and reset back after the plot is done

annotation_border
this set the value in ht_opt and reset back after the plot is done

fastcluster
this set the value in ht_opt and reset back after the plot is done

simple_anno_size
this set the value in ht_opt and reset back after the plot is done

show_parent_dend_line
this set the value in ht_opt and reset back after the plot is done
**draw-Legends-method**

*Details*

The function first calls `make_layout,HeatmapList-method` to calculate the layout of the heatmap list and the layout of every single heatmap, then makes the plot by re-calling the graphic functions which are already recorded in the layout.

*Value*

This function returns a `HeatmapList-class` object for which the layout has been created.

*Author(s)*

Zuguang Gu <z.gu@dkfz.de>

*See Also*


*Examples*

```r
# There is no example
NULL
```

**draw-Legends-method  Draw the Legends**

**Description**

Draw the Legends

**Usage**

```r
## S4 method for signature 'Legends'
draw(object, x = unit(0.5, "npc"), y = unit(0.5, "npc"), just = "centre", test = FALSE)
```

**Arguments**

- `object` The grob object returned by `Legend` or `packLegend`.
- `x` The x position of the legends, measured in current viewport.
- `y` The y position of the legends, measured in current viewport.
- `just` Justification of the legends.
- `test` Only used for testing.
Details

In the legend grob, there should always be a viewport attached which is like a wrapper of all the graphic elements in a legend. If in the object, there is already a viewport attached, it will modify the x, y and valid.just of the viewport. If there is not viewport attached, a viewport with specified x, y and valid.just is created and attached.

You can also directly use grid.draw to draw the legend object, but you can only control the position of the legends by first creating a parent viewport and adjusting the position of the parent viewport.

Examples

```r
lgd = Legend(at = 1:4, title = "foo")
draw(lgd, x = unit(0, "npc"), y = unit(0, "npc"), just = c("left", "bottom"))

# and a similar version of grid.draw
pushViewport(viewport(x = unit(0, "npc"), y = unit(0, "npc"), just = c("left", "bottom")))
grid.draw(lgd)
popViewport()
```

Description

Draw the Single Annotation

Usage

```r
## S4 method for signature 'SingleAnnotation'
draw(object, index, k = 1, n = 1, test = FALSE,
     anno_mark_param = list())
```

Arguments

- `object` A `SingleAnnotation-class` object.
- `index` A vector of indices.
- `k` The index of the slice.
- `n` Total number of slices. k and n are used to adjust annotation names. E.g. if k is 2 and n is 3, the annotation names are not drawn.
- `test` Is it in test mode? The value can be logical or a text which is plotted as the title of plot.
- `anno_mark_param` It contains specific parameters for drawing `anno_mark`.

Value

No value is returned.
**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```

---

**draw_annotation-Heatmap-method**

*Draw Heatmap Annotations on the Heatmap*

**Description**

Draw Heatmap Annotations on the Heatmap

**Usage**

```r
## S4 method for signature 'Heatmap'
draw_annotation(object, which = c("top", "bottom", "left", "right"), k = 1, ...)
```

**Arguments**

- `object` A `Heatmap-class` object.
- `which` The position of the heatmap annotation.
- `k` Slice index.
- `...` Pass to `viewport` which includes the complete heatmap annotation.

**Details**

A viewport is created which contains column/top annotations.

The function calls `draw,HeatmapAnnotation-method` to draw the annotations.

This function is only for internal use.

**Value**

This function returns no value.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```
draw_annotation_legend-HeatmapList-method

Draw legends for All Annotations

Description

Draw legends for All Annotations

Usage

## S4 method for signature 'HeatmapList'
draw_annotation_legend(object, legend_list = list(), ...)

Arguments

- **object**: A HeatmapList-class object.
- **legend_list**: A list of self-defined legends, should be wrapped into grob objects. It is normally constructed by Legend.
- **...**: Other arguments.

Details

We call the "annotation legends" as the secondary legends. For horizontal heatmap list, the legends are those from all top/bottom annotations, and for vertical heatmap list, the legends are those from all left/right annotations.

A viewport is created which contains annotation legends.

This function is only for internal use.

Value

This function returns no value.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL
Draw Heatmap Dendrograms

Usage

## S4 method for signature 'Heatmap'
draw_dend(object,  
  which = c("row", "column"), k = 1, max_height = NULL, ...)

Arguments

object  A Heatmap-class object.
which  Are the dendrograms put on the row or on the column of the heatmap?
k  Slice index.
max_height  maximal height of dendrogram.
...  Pass to viewport which includes the complete heatmap dendrograms.

Details

A viewport is created which contains dendrograms.
This function is only for internal use.

Value

This function returns no value.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

grid.dendrogram

Examples

# There is no example
NULL
draw_dimnames-Heatmap-method

*Draw row names or column names*

Description

Draw row names or column names

Usage

```r
## S4 method for signature 'Heatmap'
draw_dimnames(object,
    which = c("row", "column"), k = 1, ...)
```

Arguments

- `object`: A `Heatmap-class` object.
- `which`: Are the names put on the row or on the column of the heatmap?
- `k`: Slice index.
- `...`: Pass to `viewport` which includes the complete heatmap row/column names.

Details

A viewport is created which contains row names or column names.

This function is only for internal use.

Value

This function returns no value.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
# There is no example
NULL
```
**Draw Heatmap Body**

**Description**

Draw Heatmap Body

**Usage**

```r
## S4 method for signature 'Heatmap'
draw_heatmap_body(object, kr = 1, kc = 1, ...)
```

**Arguments**

- `object`: A `Heatmap-class` object.
- `kr`: Row slice index.
- `kc`: Column slice index.
- `...`: Pass to `viewport` which includes the slice of heatmap body.

**Details**

A viewport is created which contains subset rows and columns of the heatmap.

This function is only for internal use.

**Value**

This function returns no value.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```
draw_heatmap_legend-HeatmapList-method

*Draw legends for All Heatmaps*

**Description**

Draw legends for All Heatmaps

**Usage**

```r
## S4 method for signature 'HeatmapList'
draw_heatmap_legend(object, legend_list = list(), ...)
```

**Arguments**

- `object` A `HeatmapList-class` object.
- `legend_list` A list of self-defined legends, should be wrapped into `grob` objects. It is normally constructed by `Legend`.
- `...` Other arguments.

**Details**

Actually we call the "heatmap legends" as the main legends. For horizontal heatmap list, the legends are those from heatmap/row annotation/left/right annotation. For vertical heatmap list, the legends are those from heatmap/column annotation/top/bottom annotation. If `merge_legends` is true in `draw,HeatmapList-method`, then it contains all legends shown on the plot.

A viewport is created which contains heatmap legends.

This function is only for internal use.

**Value**

This function returns no value.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```
**Description**

Draw the List of Heatmaps

**Usage**

```r
## S4 method for signature 'HeatmapList'
draw_heatmap_list(object)
```

**Arguments**

- `object` A `HeatmapList-class` object.

**Details**

It only draws the list of heatmaps without legends and titles.

This function is only for internal use.

**Value**

This function returns no value.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```
draw_title-method

Method dispatch page for draw_title.

Dispatch
draw_title can be dispatched on following classes:

- draw_title,HeatmapList-method,HeatmapList-class class method
- draw_title,Heatmap-method,Heatmap-class class method

Examples

# no example
NULL

draw_title-Heatmap-method

Draw Heatmap Title

Description

Draw Heatmap Title

Usage

## S4 method for signature 'Heatmap'
draw_title(object,
    which = c("row", "column"), k = 1, ...)

Arguments

object A Heatmap-class object.
which Is title put on the row or on the column of the heatmap?
k Slice index.
... Pass to viewport which includes the complete heatmap title.

Details

A viewport is created which contains heatmap title.
This function is only for internal use.
Value

This function returns no value.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

Draw Heatmap List Title

Description

Draw Heatmap List Title

Usage

## S4 method for signature 'HeatmapList'
draw_title(object,
    which = c("column", "row"))

Arguments

object A HeatmapList-class object.
which Is it a row title or a column title.

Details

A viewport is created which contains heatmap list title.
This function is only for internal use.

Value

This function returns no value.

Author(s)

Zuguang Gu <z.gu@dkfz.de>
Examples

# There is no example
NULL

---

**extract_comb**  
*Extract Elements in a Combination set*

**Description**

Extract Elements in a Combination set

**Usage**

```r
extract_comb(m, comb_name)
```

**Arguments**

- `m` A combination matrix returned by `make_comb_mat`
- `comb_name` The valid combination set name should be from `comb_name`

**Details**

It returns the combination set.

**Examples**

```r
set.seed(123)
lt = list(a = sample(letters, 10),
         b = sample(letters, 15),
         c = sample(letters, 20))
m = make_comb_mat(lt)
extract_comb(m, "110")
```

---

**frequencyHeatmap**  
*Visualize Frequency Distribution by Heatmap*

**Description**

Visualize Frequency Distribution by Heatmap
Usage

```r
frequencyHeatmap(data,
  breaks = "Sturges",
  stat = c("count", "density", "proportion"),

  col = brewer.pal(9, "Blues"),
  color_space = "LAB",
  ylab = deparse(substitute(data)),
  column_title = paste0("Frequency heatmap of ", deparse(substitute(data))),
  title = column_title,
  ylim = NULL,
  range = ylim,

  title_gp = gpar(fontsize = 14),
  ylab_gp = gpar(fontsize = 12),
  tick_label_gp = gpar(fontsize = 10),

  column_order = NULL,
  column_names_side = "bottom",
  show_column_names = TRUE,
  column_names_max_height = unit(6, "cm"),
  column_names_gp = gpar(fontsize = 12),
  column_names_rot = 90,
  cluster_columns = FALSE,

  use_3d = FALSE,
  ...
)
```

Arguments

- **data** A matrix or a list. If it is a matrix, density is calculated by columns.
- **breaks** Pass to `hist`. Please only set equal bin size.
- **stat** Statistic to use.
- **col** A vector of colors that density values are mapped to.
- **color_space** The color space in which colors are interpolated. Pass to `colorRamp2`.
- **ylab** Label on y-axis.
- **column_title** Title of the heatmap.
- **title** Same as `column_title`.
- **ylim** Ranges on the y-axis.
- **range** Same as `ylim`.
- **title_gp** Graphic parameters for title.
- **ylab_gp** Graphic parameters for y-labels.
- **tick_label_gp** Graphic parameters for y-ticks.
- **column_order** Order of columns.
full_comb_code

column_names_side
   Pass to Heatmap.
show_column_names
   Pass to Heatmap.
column_names_max_height
   Pass to Heatmap.
column_names_gp
   Pass to Heatmap.
column_names_rot
   Pass to Heatmap.
cluster_columns
   Whether cluster columns?
use_3d
   Whether to visualize the frequencies as a 3D heatmap with Heatmap3D?
...
   Pass to Heatmap or Heatmap3D (if use_3d = TRUE).

Value

A Heatmap-class object. It can only add other heatmaps/annotations vertically.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
matrix = matrix(rnorm(100), 10); colnames(matrix) = letters[1:10]
frequencyHeatmap(matrix)
frequencyHeatmap(matrix, use_3d = TRUE)
```
**getXY_in_parent_vp**

### Examples

```r
full_comb_code(2)
full_comb_code(3)
full_comb_code(4)
full_comb_code(4, TRUE)
```

---

**getXY_in_parent_vp**  *Convert XY in a Parent Viewport*

### Description

Convert XY in a Parent Viewport

### Usage

```r
getXY_in_parent_vp(u, vp_name = "ROOT")
```

### Arguments

- **u**: A list of two units which correspond to x and y.
- **vp_name**: The name of the parent viewport.

### Details

It converts a coordinate measured in current viewport to the coordinate in a parent viewport.

In the conversion, all units are recalculated as absolute units, so if you change the size of the interactive graphic window, you need to rerun the function.

### Value

A list of two units.

### Examples

```r
grid.newpage()
pushViewport(viewport(x = 0.5, y = 0.5, width = 0.5, height = 0.5, just = c("left", "bottom")))
grid.rect()
grid.points(x = unit(2, "cm"), y = unit(2, "cm"), pch = 1)
u = list(x = unit(2, "cm"), y = unit(2, "cm"))
u2 = getXY_in_parent_vp(u)
popViewport()
grid.rect(gp = gpar(col = "red"))
grid.points(x = u2$x, u2$y, pch = 2)
```
Description

Get a List of ColorMapping objects

Usage

```r
## S4 method for signature 'HeatmapAnnotation'
get_color_mapping_list(object)
```

Arguments

- `object`: A `HeatmapAnnotation-class` object.

Details

Color mappings for visible simple annotations are only returned. This function is only for internal use.

Value

A list of `ColorMapping-class` objects or an empty list.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
# There is no example
NULL
```
get_legend_param_list-HeatmapAnnotation-method

Get a List of Annotation Legend Parameters

Description
Get a List of Annotation Legend Parameters

Usage
## S4 method for signature 'HeatmapAnnotation'
get_legend_param_list(object)

Arguments
object  A HeatmapAnnotation-class object.

Details
The annotation legend parameters for visible simple annotations are only returned.
This function is only for internal use.

Value
A list.

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples
# There is no example
NULL

grid.annotation_axis  Draw Annotation Axis

Description
Draw Annotation Axis

Usage
grid.annotation_axis(at = NULL, labels = at, labels_rot = 0, gp = gpar(),
side = "left", facing = "outside", direction = "normal")
Arguments

- **at**: Break values. If it is not specified, it is inferred from data scale in current viewport.
- **labels**: Corresponding labels.
- **labels_rot**: Rotations of labels.
- **gp**: Graphic parameters.
- **side**: side of the axis of the annotation viewport.
- **facing**: Facing of the axis.
- **direction**: direction of the axis. Value should be "normal" or "reverse".

Details

It uses `annotation_axis_grob` to construct the grob object, then use `grid.draw` to draw the axis.

Examples

```r
# See examples in `annotation_axis_grob`
NULL
```

---

**grid.boxplot**

*Draw a Single Boxplot*

**Description**

Draw a Single Boxplot

**Usage**

```r
grid.boxplot(value, pos, outline = TRUE, box_width = 0.6, pch = 1, size = unit(2, "mm"), gp = gpar(fill = "#CCCCCC"), direction = c("vertical", "horizontal"))
```

**Arguments**

- **value**: A vector of numeric values.
- **pos**: Position of the boxplot.
- **outline**: Whether draw outlines?
- **box_width**: width of the box.
- **pch**: Point type.
- **size**: Point size.
- **gp**: Graphic parameters.
- **direction**: Whether the box is vertical or horizontal.
grid.dendrogram

Details

All the values are measured with native coordinate.

Examples

```r
tl = list(rnorm(100), rnorm(100))
grid.newpage()
pushViewport(viewport(xscale = c(0.5, 2.5), yscale = range(lt)))
grid.boxplot(lt[[1]], pos = 1, gp = gpar(fill = "red"))
grid.boxplot(lt[[2]], pos = 2, gp = gpar(fill = "green"))
popViewport()
```

---

**grid.dendrogram**  
*Draw the Dendrogram*

Description

Draw the Dendrogram

Usage

```r
grid.dendrogram(dend, ..., test = FALSE)
```

Arguments

- **dend**: A `dendrogram` object.
- **...**: Pass to `dendrogramGrob`.
- **test**: Is it in test mode? If it is in test mode, a viewport is created by calculating proper xlim and ylim.

Details

`grid.dendrogram` supports drawing dendrograms with self-defined leaf positions. The positions of leaves can be defined by `adjust_dend_by_x`. Also the dendrogram can be customized by setting the `edgePar` attribute for each node (basically for controlling the style of segments), e.g. by `color_branches`.

To draw the dendrogram, a viewport should be firstly created. `dend_xy` can be used to get the positions of leaves and height of the dendrogram.

Examples

```r
m = matrix(rnorm(100), 10)
dend = as.dendrogram(hclust(dist(m)))
grid.newpage()
pushViewport(viewport(xscale = c(0, 10.5), yscale = c(0, dend_heights(dend)),
        width = 0.9, height = 0.9))
grid.dendrogram(dend)
```
grid.draw.Legends

Draw the Legends

Description

Draw the Legends

Usage

## S3 method for class 'Legends'
grid.draw(x, recording = TRUE)

Arguments

x The grob object returned by Legend or packLegend.
recording Pass to grid.draw.

Details

This function is actually an S3 method of the Legends class for the grid.draw general method. It applies grid.draw on the grob slot of the object.

Examples

lgd = Legend(at = 1:4, title = "foo")
pushViewport(viewport(x = unit(0, "npc"), y = unit(0, "npc"), just = c("left", "bottom")))
grid.draw(lgd)
popViewport()
grid.textbox

Draw multiple texts in a box

Description

Draw multiple texts in a box

Usage

grid.textbox(text, x = unit(0.5, "npc"), y = unit(0.5, "npc"), gp = gpar(), ...)

Arguments

- **text**: A vector of texts. The value can be single words or phrases/sentences.
- **x**: X position.
- **y**: Y position.
- **gp**: Graphics parameters of texts.
- **...**: Pass to textbox_grob.

Details

All details can be found in the help page of textbox_grob.

Examples

# There is no example
NULL

---

gt_render

Mark the text for the rendering by gridtext package

Description

Mark the text for the rendering by gridtext package

Usage

gt_render(x, ...)

Arguments

- **x**: Text labels. The value can be a vector.
- **...**: Other parameters passed to richtext_grob.
Details

Text marked by `gt_render` will be rendered by `richtext_grob` function.

Examples

```r
if(requireNamespace("gridtext")) {
  mat = matrix(rnorm(100), 10)
  rownames(mat) = letters[1:10]
  ht = Heatmap(mat,
               column_title = gt_render("Some <span style='color:blue'>blue text **in bold.**</span><br>And *italics text.*
                              And some <span style='font-size:18pt; color:black'>large</span> text.", r = unit(2, "pt"), padding = unit(c(2, 2, 2, 2), "pt"),
               column_title_gp = gpar(box_fill = "orange"),
               row_labels = gt_render(letters[1:10], padding = unit(c(2, 10, 2, 10), "pt")),
               row_names_gp = gpar(box_col = "red"),
               row_km = 2,
               row_title = gt_render(c("title1", "title2")),
               row_title_gp = gpar(box_fill = "yellow"),
               heatmap_legend_param = list(
                             title = gt_render("<span style='color:orange'>**Legend title**</span>"),
                             title_gp = gpar(box_fill = "grey"),
                             at = c(-3, 0, 3),
                             labels = gt_render(c("*negative* three", "zero", "*positive* three"))
               ))
  ht = rowAnnotation(
    foo = anno_text(gt_render(sapply(LETTERS[1:10], strrep, 10), align_widths = TRUE),
                    gp = gpar(box_col = "blue", box_lwd = 2),
                    just = "right",
                    location = unit(1, "npc"))
  ) + ht
  draw(ht)
}
```

Heatmap

Constructor method for Heatmap class

Description

Constructor method for Heatmap class

Usage

```r
Heatmap(matrix, col, name,
         na_col = "grey",
         color_space = "LAB",
         rect_gp = gpar(col = NA),
         border = NA,
         border_gp = gpar(col = "black"),
         cell_fun = NULL,
         layer_fun = NULL,
         ```
jitter = FALSE,
row_title = character(0),
row_title_side = c("left", "right"),
row_title_gp = gpar(fontsize = 13.2),
row_title_rot = switch(row_title_side[1], "left" = 90, "right" = 270),
column_title = character(0),
column_title_side = c("top", "bottom"),
column_title_gp = gpar(fontsize = 13.2),
column_title_rot = 0,

cluster_rows = TRUE,
cluster_row_slices = TRUE,
clustering_distance_rows = "euclidean",
clustering_method_rows = "complete",
row_dend_side = c("left", "right"),
row_dend_width = unit(10, "mm"),
show_row_dend = TRUE,
row_dend_reorder = is.logical(cluster_rows) || is.function(cluster_rows),
row_dend_gp = gpar(),
cluster_columns = TRUE,
cluster_column_slices = TRUE,
clustering_distance_columns = "euclidean",
clustering_method_columns = "complete",
column_dend_side = c("top", "bottom"),
column_dend_height = unit(10, "mm"),
show_column_dend = TRUE,
column_dend_gp = gpar(),
column_dend_reorder = is.logical(cluster_columns) || is.function(cluster_columns),

row_order = NULL,
column_order = NULL,

row_labels = rownames(matrix),
row_names_side = c("right", "left"),
show_row_names = TRUE,
row_names_max_width = unit(6, "cm"),
row_names_gp = gpar(fontsize = 12),
row_names_rot = 0,
row_names_centered = FALSE,
column_labels = colnames(matrix),
column_names_side = c("bottom", "top"),
show_column_names = TRUE,
column_names_max_height = unit(6, "cm"),
column_names_gp = gpar(fontsize = 12),
column_names_rot = 90,
column_names_centered = FALSE,
top_annotation = NULL,
bottom_annotation = NULL,
left_annotation = NULL,
right_annotation = NULL,

km = 1,
split = NULL,
row_km = km,
row_km_repeats = 1,
row_split = split,
column_km = 1,
column_km_repeats = 1,
column_split = NULL,
gap = unit(1, "mm"),
row_gap = unit(1, "mm"),
column_gap = unit(1, "mm"),
show_parent_dend_line = ht_opt$show_parent_dend_line,

heatmap_width = unit(1, "npc"),
width = NULL,
heatmap_height = unit(1, "npc"),
height = NULL,

show_heatmap_legend = TRUE,
heatmap_legend_param = list(title = name),

use_raster = NULL,
raster_device = c("png", "jpeg", "tiff", "CairoPNG", "CairoJPEG", "CairoTIFF", "agg_png"),
raster_quality = 1,
raster_device_param = list(),
raster_resize_mat = FALSE,
raster_by_magick = requireNamespace("magick", quietly = TRUE),
raster_magick_filter = NULL,
post_fun = NULL)

Arguments

matrix        A matrix. Either numeric or character. If it is a simple vector, it will be converted
to a one-column matrix.

col           A vector of colors if the color mapping is discrete or a color mapping function if
the matrix is continuous numbers (should be generated by colorRamp2). If the
matrix is continuous, the value can also be a vector of colors so that colors can
be interpolated. Pass to ColorMapping. For more details and examples, please
a-single-heatmap.html#colors.

name          Name of the heatmap. By default the heatmap name is used as the title of the
heatmap legend.
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>na_col</td>
<td>Color for NA values.</td>
</tr>
<tr>
<td>rect_gp</td>
<td>Graphic parameters for drawing rectangles (for heatmap body). The value should be specified by <code>gpar</code> and <code>fill</code> parameter is ignored.</td>
</tr>
<tr>
<td>color_space</td>
<td>The color space in which colors are interpolated. Only used if <code>matrix</code> is numeric and <code>col</code> is a vector of colors. Pass to <code>colorRamp2</code>.</td>
</tr>
<tr>
<td>border</td>
<td>Whether draw border. The value can be logical or a string of color.</td>
</tr>
<tr>
<td>border_gp</td>
<td>Graphic parameters for the borders. If you want to set different parameters for different heatmap slices, please consider to use <code>decorate_heatmap_body</code>.</td>
</tr>
<tr>
<td>cell_fun</td>
<td>Self-defined function to add graphics on each cell. Seven parameters will be passed into this function: <code>j</code>, <code>i</code>, <code>x</code>, <code>y</code>, <code>width</code>, <code>height</code>, <code>fill</code> which are column index, row index in matrix, coordinate of the cell, the width and height of the cell and the filled color. <code>x</code>, <code>y</code>, <code>width</code> and <code>height</code> are all <code>unit</code> objects.</td>
</tr>
<tr>
<td>jitter</td>
<td>Random shifts added to the matrix. The value can be logical or a single numeric value. It it is <code>TRUE</code>, random values from uniform distribution between 0 and 1e-10 are generated. If it is a numeric value, the range for the uniform distribution is <code>(0, jitter)</code>. It is mainly to solve the problem of &quot;Error: node stack overflow&quot; when there are too many identical rows/columns for plotting the dendrograms. ADD: From version 2.5.6, the error of node stack overflow has been fixed, now this argument is ignored.</td>
</tr>
<tr>
<td>row_title</td>
<td>Title on the row.</td>
</tr>
<tr>
<td>row_title_side</td>
<td>Will the title be put on the left or right of the heatmap?</td>
</tr>
<tr>
<td>row_title_gp</td>
<td>Graphic parameters for row title.</td>
</tr>
<tr>
<td>row_title_rot</td>
<td>Rotation of row title.</td>
</tr>
<tr>
<td>column_title</td>
<td>Title on the column.</td>
</tr>
<tr>
<td>column_title_side</td>
<td>Will the title be put on the top or bottom of the heatmap?</td>
</tr>
<tr>
<td>column_title_gp</td>
<td>Graphic parameters for column title.</td>
</tr>
<tr>
<td>column_title_rot</td>
<td>Rotation of column titles.</td>
</tr>
<tr>
<td>cluster_rows</td>
<td>If the value is a logical, it controls whether to make cluster on rows. The value can also be a <code>hclust</code> or a <code>dendrogram</code> which already contains clustering. Check <a href="https://jokergoo.github.io/ComplexHeatmap-reference/book/a-single-heatmap.html#clustering">https://jokergoo.github.io/ComplexHeatmap-reference/book/a-single-heatmap.html#clustering</a>.</td>
</tr>
<tr>
<td>cluster_row_slices</td>
<td>If rows are split into slices, whether perform clustering on the slice means?</td>
</tr>
</tbody>
</table>
| clustering_distance_rows | It can be a pre-defined character which is in ("euclidean", "maximum", "man-
|                                          | hattan", "canberra", "binary", "minkowski", "pearson", "spearman", "kendall"). It can also be a function. If the function has one argument, the input argument |
should be a matrix and the returned value should be a \texttt{dist} object. If the function has two arguments, the input arguments are two vectors and the function calculates distance between these two vectors.

\texttt{clustering\_method\_rows}

Method to perform hierarchical clustering, pass to \texttt{hclust}.

\texttt{row\_dend\_side}

Should the row dendrogram be put on the left or right of the heatmap?

\texttt{row\_dend\_width}

Width of the row dendrogram, should be a \texttt{unit} object.

\texttt{show\_row\_dend}

Whether show row dendrogram?

\texttt{row\_dend\_gp}

Graphic parameters for the dendrogram segments. If users already provide a \texttt{dendrogram} object with edges rendered, this argument will be ignored.

\texttt{row\_dend\_reorder}

Apply reordering on row dendrograms. The value can be a logical value or a vector which contains weight which is used to reorder rows. The reordering is applied by \texttt{reorder.dendrogram}.

\texttt{cluster\_columns}

Whether make cluster on columns? Same settings as \texttt{cluster\_rows}.

\texttt{cluster\_column\_slices}

If columns are split into slices, whether perform clustering on the slice means?

\texttt{clustering\_distance\_columns}

Same setting as \texttt{clustering\_distance\_rows}.

\texttt{clustering\_method\_columns}

Method to perform hierarchical clustering, pass to \texttt{hclust}.

\texttt{column\_dend\_side}

Should the column dendrogram be put on the top or bottom of the heatmap?

\texttt{column\_dend\_height}

Height of the column cluster, should be a \texttt{unit} object.

\texttt{show\_column\_dend}

Whether show column dendrogram?

\texttt{column\_dend\_gp}

Graphic parameters for dendrogram segments. Same settings as \texttt{row\_dend\_gp}.

\texttt{column\_dend\_reorder}

Apply reordering on column dendrograms. Same settings as \texttt{row\_dend\_reorder}.

\texttt{row\_order}

Order of rows. Manually setting row order turns off clustering.

\texttt{column\_order}

Order of column.

\texttt{row\_labels}

Optional row labels which are put as row names in the heatmap.

\texttt{row\_names\_side}

Should the row names be put on the left or right of the heatmap?

\texttt{show\_row\_names}

Whether show row names.

\texttt{row\_names\_max\_width}

Maximum width of row names viewport.

\texttt{row\_names\_gp}

Graphic parameters for row names.

\texttt{row\_names\_rot}

Rotation of row names.

\texttt{row\_names\_centered}

Should row names put centered?
column_labels  Optional column labels which are put as column names in the heatmap.
column_names_side  Should the column names be put on the top or bottom of the heatmap?
column_names_max_height  Maximum height of column names viewport.
show_column_names  Whether show column names.
column_names_gp  Graphic parameters for drawing text.
column_names_rot  Rotation of column names.
column_names_centered  Should column names put centered?
top_annotation  A HeatmapAnnotation object.
bbox_annotation  A HeatmapAnnotation object.
left_annotation  It should be specified by rowAnnotation.
right_annotation  It should be specified by rowAnnotation.
kmean  Apply k-means clustering on rows. If the value is larger than 1, the heatmap will be split by rows according to the k-means clustering. For each row slice, hierarchical clustering is still applied with parameters above.
split  A vector or a data frame by which the rows are split. But if cluster_rows is a clustering object, split can be a single number indicating to split the dendrogram by cutree.
row_kmean  Same as km.
row_kmean_repeats  Number of k-means runs to get a consensus k-means clustering. Note if row_kmean_repeats is set to more than one, the final number of groups might be smaller than row_kmean, but this might means the original row_kmean is not a good choice.
row_split  Same as split.
column_kmean  K-means clustering on columns.
column_kmean_repeats  Number of k-means runs to get a consensus k-means clustering. Similar as row_kmean_repeats.
gap  Gap between row slices if the heatmap is split by rows. The value should be a unit object.
row_gap  Same as gap.
column_gap  Gap between column slices.
show_parent_dend_line
When heatmap is split, whether to add a dashed line to mark parent dendrogram
and children dendrograms?

width
Width of the heatmap body.

height
Height of the heatmap body.

heatmap_width
Width of the whole heatmap (including heatmap components)

heatmap_height
Height of the whole heatmap (including heatmap components). Check

show_heatmap_legend
Whether show heatmap legend?

heatmap_legend_param
A list contains parameters for the heatmap legends. See color_mapping_legend,ColorMapping-method
for all available parameters.

use_raster
Whether render the heatmap body as a raster image. It helps to reduce file size
when the matrix is huge. If number of rows or columns is more than 2000, it
is by default turned on. Note if cell_fun is set, use_raster is enforced to be
FALSE.

raster_device
Graphic device which is used to generate the raster image.

raster_quality
A value larger than 1.

raster_device_param
A list of further parameters for the selected graphic device. For raster image sup-

raster_resize_mat
Whether resize the matrix to let the dimension of the matrix the same as the
dimension of the raster image? The value can be logical. If it is TRUE, mean
is used to summarize the sub matrix which corresponds to a single pixel. The
value can also be a summary function, e.g. max.

raster_by_magick
Whether to use image_resize to scale the image.

raster_magick_filter
Pass to filter argument of image_resize. A character scalar and all possible
values are in filter_types. The default is "Lanczos".

post_fun
A function which will be executed after the heatmap list is drawn.

Details
The initialization function only applies parameter checking and fill values to the slots with some
validation.

Following methods can be applied to the Heatmap-class object:

• show,Heatmap-method: draw a single heatmap with default parameters
• draw,Heatmap-method: draw a single heatmap.
• + or %v% append heatmaps and annotations to a list of heatmaps.
Heatmap-class

The constructor function pretends to be a high-level graphic function because the show method of the Heatmap-class object actually plots the graphics.

Value

A Heatmap-class object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also


Examples

# There is no example
NULL

Heatmap-class  

Class for a Single Heatmap

Description

Class for a Single Heatmap

Details

The Heatmap-class is not responsible for heatmap legend and annotation legends. The draw,Heatmap-method method constructs a HeatmapList-class object which only contains one single heatmap and call draw,HeatmapList-method to make the complete heatmap.

Methods

The Heatmap-class provides following methods:

- Heatmap: constructor method.
- draw,Heatmap-method: draw a single heatmap.
- add_heatmap,Heatmap-method append heatmaps and annotations to a list of heatmaps.
- row_order,HeatmapList-method: get order of rows
- column_order,HeatmapList-method: get order of columns
- row_dend,HeatmapList-method: get row dendrograms
- column_dend,HeatmapList-method: get column dendrograms
Heatmap3D

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

Heatmap3D

3D Heatmap

Description

3D Heatmap

Usage

Heatmap3D(matrix,
..., 
bar_rel_width = 0.6,
bar_rel_height = 0.6,
bar_max_length = unit(1, "cm"),
bar_angle = 60,
row_names_side = "left",
show_row_dend = FALSE,
show_column_dend = FALSE)

Arguments

matrix The input matrix. Values should be non-negative.
... All pass to Heatmap.
bar_rel_width A factor between 0 and 1.
bar_rel_height A factor between 0 and 1.
bar_max_length Maximal length of bars. Value should be in absolute unit.
bar_angle Angle for the projection.
row_names_side Row names are by default put on the left side of the heatmap.
show_row_dend By default the dendrogram is not drawn.
show_column_dend By default the dendrogram is not drawn.

Details

For large matrices, the plotting might be slow.
Examples

```r
m = matrix(sample(100, 36), 6)
Heatmap3D(m)
```

Description

Constructor Method for HeatmapAnnotation class

Usage

```r
HeatmapAnnotation(...,
df = NULL, name, col, na_col = "grey",
annotation_legend_param = list(),
show_legend = TRUE,
which = c("column", "row"),
gp = gpar(col = NA),
border = FALSE,
gap = unit(1, "points"),
show_annotation_name = TRUE,
annotation_label = NULL,
annotation_name_gp = gpar(),
annotation_name_offset = NULL,
annotation_name_side = ifelse(which == "column", "right", "bottom"),
annotation_name_rot = NULL,
annotation_name_align = FALSE,
annotation_height = NULL,
annotation_width = NULL,
height = NULL,
width = NULL,
simple_anno_size = ht_opt$simple_anno_size,
simple_anno_size_adjust = FALSE)
```

Arguments

- `...` Name-value pairs where the names correspond to annotation names and values can be a vector, a matrix and an annotation function. Each pair is sent to `SingleAnnotation` to construct a single annotation.
- `df` A data frame. Each column will be treated as a simple annotation. The data frame must have column names.
- `name` Name of the heatmap annotation, optional.
col A list of colors which contain color mapping to df or simple annotations defined in .... See SingleAnnotation for how to set colors.

na_col Color for NA values in simple annotations.

annotation_legend_param A list which contains parameters for annotation legends. See color_mapping_legend,ColorMapping-method for all possible options.

show_legend Whether show annotation legends. The value can be one single value or a vector.

which Are these row annotations or column annotations?

gp Graphic parameters for simple annotations (with fill parameter ignored).

border border of single annotations.

gap Gap between annotations. It can be a single value or a vector of unit objects.

show_annotation_name Whether show annotation names? For column annotation, annotation names are drawn either on the left or the right, and for row annotations, names are draw either on top or at the bottom. The value can be a vector.

annotation_label Labels for the annotations. By default it is the same as individual annotation names.

annotation_name_gp Graphic parameters for annotation names. Graphic parameters can be vectors.

annotation_name_offset Offset to the annotation names, a unit object. The value can be a vector.

annotation_name_side Side of the annotation names.

annotation_name_rot Rotation of the annotation names. The value can be a vector.

annotation_name_align Whether to align the annotation names.

annotation_height Height of each annotation if annotations are column annotations.

annotation_width Width of each annotation if annotations are row annotations.

height Height of the whole column annotations.

width Width of the whole heatmap annotations.

simple_anno_size Size of the simple annotation.

simple_anno_size_adjust Whether also adjust the size of simple annotations when adjusting the whole heatmap annotation.

Details

For arguments show_legend, border, annotation_name_offset, annotation_name_side, annotation_name_rot, show_annotation_name, they can be set as named vectors to modify values for some of the annotations, e.g. assuming you have an annotation with name foo, you can specify border = c(foo = TRUE) in HeatmapAnnotation.
There are three ways to specify heatmap annotations:
1. If the annotation is simply a vector or a matrix, it can be specified like `HeatmapAnnotation(foo = 1:10)`. 2. If the annotations are already stored as a data frame, it can be specified like `HeatmapAnnotation(df = df)`. 3. For complex annotations, users can use the pre-defined annotation functions such as `anno_points`: `HeatmapAnnotation(foo = anno_points(1:10))`.


Value

A `HeatmapAnnotation-class` object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

There are two helper functions: `rowAnnotation` and `columnAnnotation`.

Examples

```r
# There is no example
NULL
```

---

**HeatmapAnnotation-class**

*Class for Heatmap Annotations*

**Description**

Class for Heatmap Annotations

**Details**

A complex heatmap contains a list of annotations which are represented as graphics placed on rows and columns. The `HeatmapAnnotation-class` contains a list of single annotations which are represented as a list of `SingleAnnotation-class` objects.

**Methods**

The `HeatmapAnnotation-class` provides following methods:

- `HeatmapAnnotation`: constructor method.
- `draw,HeatmapAnnotation-method`: draw the annotations.
HeatmapList

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

HeatmapList

Constructor method for HeatmapList class

Description
Constructor method for HeatmapList class

Usage

HeatmapList(...)

Arguments

... arguments

Details
There is no public constructor method for the HeatmapList-class.

Value
No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL
HeatmapList-class

Class for a list of heatmaps

Description

Class for a list of heatmaps

Details

A heatmap list is defined as a list of heatmaps and annotations.

Methods

The HeatmapList-class provides following methods:

- **draw,HeatmapList-method**: draw the list of heatmaps and row annotations.
- **add_heatmap,HeatmapList-method**: add heatmaps to the list of heatmaps.
- **row_order,HeatmapList-method**: get order of rows
- **column_order,HeatmapList-method**: get order of columns
- **row_dend,HeatmapList-method**: get row dendrograms
- **column_dend,HeatmapList-method**: get column dendrograms

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
# There is no example
NULL
```

heatmap_legend_size-HeatmapList-method

Size of the Heatmap Legends

Description

Size of the Heatmap Legends

Usage

```r
## S4 method for signature 'HeatmapList'
heatmap_legend_size(object, legend_list = list(), ...)
```
Arguments

- **object** A `HeatmapList-class` object.
- **legend_list** A list of self-defined legend, should be wrapped into `grob` objects. It is normally constructed by `Legend`.
- ... Other arguments.

Details

Internally, all heatmap legends are packed by `packLegend` as a single `grob` object.

This function is only for internal use.

Value

A `unit` object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
# There is no example
NULL
```

---

**height.AnnotationFunction**

*Height of the AnnotationFunction Object*

Description

Height of the AnnotationFunction Object

Usage

```r
## S3 method for class 'AnnotationFunction'
height(x, ...)
```

Arguments

- **x** The `AnnotationFunction-class` object.
- ... Other arguments.

Details

Internally used.
height.Heatmap

**Examples**

```r
anno = anno_points(1:10)
ComplexHeatmap:::height(anno)
anno = anno_points(1:10, which = "row")
ComplexHeatmap:::height(anno)
```

---

**Description**

Height of the Heatmap

**Usage**

```r
## S3 method for class 'Heatmap'
height(x, ...)
```

**Arguments**

- `x` The `HeatmapList-class` object returned by `draw.Heatmap-method`.
- `...` Other arguments.

**Examples**

```r
# There is no example
NULL
```

---

height.HeatmapAnnotation

**Height of the HeatmapAnnotation Object**

**Description**

Height of the HeatmapAnnotation Object

**Usage**

```r
## S3 method for class 'HeatmapAnnotation'
height(x, ...)
```

**Arguments**

- `x` The `HeatmapAnnotation-class` object.
- `...` Other arguments.
Details
Internally used.

Examples
# There is no example
NULL

height.HeatmapList  Height of the Heatmap List

Description
Height of the Heatmap List

Usage
## S3 method for class 'HeatmapList'
height(x, ...)

Arguments
x  The HeatmapList-class object returned by draw.HeatmapList-method.
...  Other arguments.

Examples
# There is no example
NULL

height.Legends  Height of the Legends

Description
Height of the Legends

Usage
## S3 method for class 'Legends'
height(x, ...)

Arguments
x  The Legends-class object returned by draw.Legends-method.
...  Other arguments.

Examples
# There is no example
NULL
Arguments

- **x**: The `grob` object returned by `Legend` or `packLegend`.
- **...**: Other arguments.

Value

The returned unit x is always in mm.

Examples

```r
lgd = Legend(labels = 1:10, title = "foo", legend_gp = gpar(fill = "red"))
ComplexHeatmap:::height(lgd)
```

Description

Height of the `SingleAnnotation` object

Usage

```r
# S3 method for class 'SingleAnnotation'
height(x, ...)
```

Arguments

- **x**: The `SingleAnnotation-class` object.
- **...**: Other arguments.

Details

Internally used.

Examples

```r
# There is no example
NULL
```
heightAssign.AnnotationFunction

Assign the Height to the AnnotationFunction Object

Description
Assign the Height to the AnnotationFunction Object

Usage
## S3 replacement method for class 'AnnotationFunction'
height(x, ...) <- value

Arguments
- x: The AnnotationFunction-class object.
- value: A unit object.
- ...: Other arguments.

Details
Internally used.

Examples
# There is no example
NULL

heightAssign.HeatmapAnnotation

Assign the Height to the HeatmapAnnotation Object

Description
Assign the Height to the HeatmapAnnotation Object

Usage
## S3 replacement method for class 'HeatmapAnnotation'
height(x, ...) <- value
**Arguments**

- **x**  The **HeatmapAnnotation-class** object.
- **value**  A **unit** object.
- ...  Other arguments.

**Details**

Internally used.

**Examples**

```r
# There is no example
NULL
```

---

**heightAssign.SingleAnnotation**

Assign the Height to the SingleAnnotation Object

**Description**

Assign the Height to the SingleAnnotation Object

**Usage**

```r
## S3 replacement method for class 'SingleAnnotation'
height(x, ...) <- value
```

**Arguments**

- **x**  The **SingleAnnotation-class** object.
- **value**  A **unit** object.
- ...  Other arguments.

**Details**

Internally used.

**Examples**

```r
# There is no example
NULL
```
### heightDetails.annotation_axis

**Height for annotation_axis Grob**

**Description**

Height for annotation_axis Grob

**Usage**

```r
## S3 method for class 'annotation_axis'
heightDetails(x)
```

**Arguments**

- `x` The annotation_axis grob returned by `annotation_axis_grob`.

**Details**

The physical height of the grob can be get by `convertWidth(grobHeight(axis_grob), "mm")`.

**Examples**

```r
# There is no example
NULL
```

### heightDetails.legend

**Grob height for packed_legends**

**Description**

Grob height for packed_legends

**Usage**

```r
## S3 method for class 'legend'
heightDetails(x)
```

**Arguments**

- `x` A legend object.

**Examples**

```r
# There is no example
NULL
```
## heightDetails.legend_body

### Description

Grob height for legend_body

### Usage

```r
## S3 method for class 'legend_body'
heightDetails(x)
```

### Arguments

- `x` A legend_body object.

### Examples

```r
# There is no example
NULL
```

## heightDetails.packed_legends

### Description

Grob height for packed_legends

### Usage

```r
## S3 method for class 'packed_legends'
heightDetails(x)
```

### Arguments

- `x` A packed_legends object.

### Examples

```r
# There is no example
NULL
```
### heightDetails.textbox

*Height for textbox grob*

#### Description

Height for textbox grob

#### Usage

```r
## S3 method for class 'textbox'
heightDetails(x)
```

#### Arguments

- `x` The text box grob returned by `textbox_grob`.

#### Value

A `unit` object.

#### Examples

```r
# There is no example
NULL
```

---

### ht_global_opt

*Global Options for Heatmaps*

#### Description

Global Options for Heatmaps

#### Usage

```r
ht_global_opt(..., RESET = FALSE, READ.ONLY = NULL, LOCAL = FALSE, ADD = FALSE)
```

#### Arguments

- `...` Options.
- `RESET` Reset all the option values.
- `READ.ONLY` TRUE means only to return read-only values, FALSE means only to return non-read-only values, NULL means to return both.
- `LOCAL` Wswitch to local mode.
- `ADD` Add new options.
**ht_opt**

**Details**

This function is deprecated. Please use `ht_opt` instead. However, changes by this function will also be synchronized in `ht_opt`.

**Examples**

```r
# There is no example
NULL
```

### Description

Global Options for Heatmaps

### Usage

```r
ht_opt(..., RESET = FALSE, READ.ONLY = NULL, LOCAL = FALSE, ADD = FALSE)
```

### Arguments

- `...` Options, see 'Details' section.
- `RESET` Reset all the option values.
- `READ.ONLY` Please ignore this argument.
- `LOCAL` Please ignore this argument.
- `ADD` Please ignore this argument.

### Details

You can set some parameters for all heatmaps/annotations simultaneously by this global function. Please note you should put it before your heatmap code and reset all option values after drawing the heatmaps to get rid of affecting next heatmap.

There are following parameters to control all heatmaps:

- `heatmap_row_names_gp` set row_names_gp in all Heatmap.
- `heatmap_column_names_gp` set column_names_gp in all Heatmap.
- `heatmap_row_title_gp` set row_title_gp in all Heatmap.
- `heatmap_column_title_gp` set column_title_gp in all Heatmap.
- `heatmap_border` set border in all Heatmap.

Following parameters control the legends:

- `legend_title_gp` set title_gp in all heatmap legends and annotation legends.
legend_title_position set title_position in all heatmap legends and annotation legends.

legend_labels_gp set labels_gp in all heatmap legends and annotation legends.

legend_grid_width set grid_width in all heatmap legends and annotation legends.

legend_grid_height set grid_height in all heatmap legends and annotation legends.

legend_border set border in all heatmap legends and annotation legends.

legend_gap Gap between legends. The value should be a vector of two units. One for gaps between vertical legends and one for the horizontal legends. If only one single unit is specified, the same gap set for the vertical and horizontal legends.

merge_legend wether merge heatmap and annotation legends.

Following parameters control heatmap annotations:

annotation_border border in all HeatmapAnnotation.

simple_anno_size size for the simple annotation.

Following parameters control the space between heatmap components:

DENDROGRAM_PADDING space between dendrograms and heatmap body.

DIMNAME_PADDING space between row/column names and heatmap body.

TITLE_PADDING space between row/column titles and heatmap body. The value can have length of two which corresponds to the botton and top padding.

COLUMN_ANNO_PADDING space between column annotations and heatmap body.

ROW_ANNO_PADDING space between row annotations and heatmap body.

HEATMAP_LEGEND_PADDING space between heatmap legends and heatmaps

ANNOTATION_LEGEND_PADDING space between annotation legends and heatmaps

Other parameters:

fast_hclust whether use hclust to speed up clustering?

show_parent_dend_line when heatmap is split, whether to add a dashed line to mark parent dendrogram and children dendrograms?

COLOR default colors for continuous color mapping.

You can get or set option values by the traditional way (like options) or by $ operator:

```r
# to get option values
ht_opt("heatmap_row_names_gp")
ht_opt$heatmap_row_names_gp

# to set option values
ht_opt("heatmap_row_names_gp" = gpar(fontsize = 8))
ht_opt$heatmap_row_names_gp = gpar(fontsize = 8)
```

Reset to the default values by ht_opt(RESET = TRUE).
ht_size

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples
ht_opt

ht_size                  Calculate the width and height of the heatmaps

Description
Calculate the width and height of the heatmaps

Usage
ht_size(ht)

Arguments
ht                  A Heatmap-class or HeatmapList-class object.

Value
A list of two elements: width and height.

Examples
# There is no example
NULL

is_abs_unit               Test Whether it is an Absolute Unit

Description
Test Whether it is an Absolute Unit

Usage
is_abs_unit(u)

Arguments
u               A unit object.
Details

Besides the normal absolute units (e.g. "mm", "inches"), this function simply assumes grob objects as absolute units.

For a complex unit which is combination of different units, it is absolute only if all units included are absolute units.

Value

A logical value.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

is_abs_unit(unit(1, "mm"))
is_abs_unit(unit(1, "npc"))
is_abs_unit(grobWidth(textGrob("foo")))
is_abs_unit(unit(1, "mm") + unit(1, "npc"))
Arguments

at
Breaks of the legend. The values can be either numeric or character. If it is not specified, the values of labels are taken as labels.

labels
Labels corresponding to at. If it is not specified, the values of at are taken as labels.

col_fun
A color mapping function which is used to make a continuous legend. Use colorRamp2 to generate the color mapping function. If at is missing, the breaks recorded in the color mapping function are used for at.

name
Name of the legend, internally used.

grob
The legend body can be specified by a pre-constructed grob object.

break_dist
A zooming factor to control relative distance of two neighbouring break values. The length of it should be length(at) - 1 or a scalar.

nrow
For legend which is represented as grids, nrow controls number of rows of the grids if the grids are arranged into multiple rows.

ncol
Similar as nrow, ncol controls number of columns of the grids if the grids are arranged into multiple columns. Note at a same time only one of nrow and ncol can be specified.

by_row
Are the legend grids arranged by rows or by columns?

grid_height
The height of legend grid. It can also control the height of the continuous legend if it is horizontal.

grid_width
The width of legend grid. It can also control the width of the continuous legend if it is vertical.

tick_length
Length of the ticks on the continuous legends. Value should be a unit object.

gap
If legend grids are put into multiple rows or columns, this controls the gap between neighbouring rows or columns, measured as a unit object.

column_gap
The same as gap.

row_gap
Space between legend rows.

labels_gp
Graphic parameters for labels.

labels_rot
Text rotation for labels. It should only be used for horizontal continuous legend.

border
Color of legend grid borders. It also works for the ticks in the continuous legend.

background
Background colors for the grids. It is used when points and lines are the legend graphics.

type
Type of legends. The value can be one of grid, points, lines and boxplot.

graphics
Self-defined graphics for legends. The value should be a list of functions. Each function should accept four arguments: x and y: positions of the legend grid (center point), w and h: width and height of the legend grid.

legend_gp
Graphic parameters for the legend grids. You should control the filled color of the legend grids by gpar(fill = ...).

pch
Type of points if points are used as legend. Note you can use single-letter as pch, e.g. pch = 'A'. There are three additional integers that are valid for pch: 26 and 27 for single diagonal lines and 28 for double diagonal lines.
size         Size of points.
legend_height Height of the whole legend body. It is only used for vertical continous legend.
legend_width Width of the whole legend body. It is only used for horizontal continous legend.
direction    Direction of the legend, vertical or horizontal?
title        Title of the legend.
title_gp     Graphic parameters of the title.
title_position Position of title relative to the legend. topleft, topcenter, leftcenter-rot and lefttop-rot are only for vertical legend and leftcenter, lefttop are only for horizontal legend.
title_gap    Gap between title and the legend body.

Details

Most of the argument can also be set in heatmap_legend_param argument in Heatmap or annotation_legend_param argument in HeatmapAnnotation to configure legend styles for heatmap and annotations.

Value

A Legends-class object.

See Also

packLegend packs multiple legends into one Legends-class object.


Examples

lgd = Legend(labels = month.name[1:6], title = "foo", legend_gp = gpar(fill = 1:6))
draw(lgd, test = "add labels and title")

require(circlize)
col_fun = colorRamp2(c(0, 0.5, 1), c("blue", "white", "red"))
lgd = Legend(col_fun = col_fun, title = "foo")
draw(lgd, test = "only col_fun")

col_fun = colorRamp2(c(0, 0.5, 1), c("blue", "white", "red"))
lgd = Legend(col_fun = col_fun, title = "foo", at = c(0, 0.1, 0.15, 0.5, 0.9, 0.95, 1))
draw(lgd, test = "unequal interval breaks")
Legends

Constructor method for Legends class

Description

Constructor method for Legends class

Usage

Legends(...)

Arguments

... arguments.

Details

There is no public constructor method for the Legends-class.

Value

No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

Legends-class

The Class for Legends

Description

The Class for Legends

Details

This is a very simple class for legends that it only has one slot which is the real grob of the legends. Construct a single legend by Legend and a group of legends by packLegend.
Examples

```r
glg = Legend(at = 1:4)
glg
lgd@grob
```

---

length.HeatmapAnnotation

*Number of Annotations*

---

Description

Number of Annotations

Usage

```r
## S3 method for class 'HeatmapAnnotation'
length(x)
```

Arguments

- `x` A `HeatmapAnnotation-class` object.

Examples

```r
# There is no example
NULL
```

---

length.HeatmapList

*Length of the HeatmapList object*

---

Description

Length of the HeatmapList object

Usage

```r
## S3 method for class 'HeatmapList'
length(x)
```

Arguments

- `x` A `HeatmapList-class` object

Examples

```r
# There is no example
NULL
```


### list_components

*List All Heatmap Components*

**Description**

List All Heatmap Components

**Usage**

```r
list_components(pattern = NULL)
```

**Arguments**

- `pattern` A regular expression.

**Value**

A vector of viewport names.

**Examples**

```r
# There is no example
NULL
```

### list_to_matrix

*Convert a List of Sets to a Binary Matrix*

**Description**

Convert a List of Sets to a Binary Matrix

**Usage**

```r
list_to_matrix(lt, universal_set = NULL)
```

**Arguments**

- `lt` A list of vectors.
- `universal_set` The universal set.

**Details**

It converts the list which have `m` sets to a binary matrix with `n` rows and `m` columns where `n` is the size of universal set.
Examples

```r
set.seed(123)
lt = list(a = sample(letters, 5),
        b = sample(letters, 10),
        c = sample(letters, 15))
list_to_matrix(lt)
list_to_matrix(lt, universal_set = letters)
```

---

**Description**

Make Cluster on Columns

**Usage**

```r
## S4 method for signature 'Heatmap'
make_column_cluster(object)
```

**Arguments**

- `object` A `Heatmap-class` object.

**Details**

The function will fill or adjust `column_dend_list`, `column_order_list`, `column_title` and `matrix_param` slots.

If `order` is defined, no clustering will be applied.

This function is only for internal use.

**Value**

A `Heatmap-class` object.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```
**make_comb_mat**  

*Make a Combination Matrix for UpSet Plot*

**Description**

Make a Combination Matrix for UpSet Plot

**Usage**

```r
make_comb_mat(..., mode = c("distinct", "intersect", "union"),
  top_n_sets = Inf, min_set_size = -Inf,
  universal_set = NULL, complement_size = NULL,
  value_fun = NULL, set_on_rows = TRUE)
```

**Arguments**

- `...`: The input sets. If it is represented as a single variable, it should be a matrix/data frame or a list. If it is multiple variables, it should be name-value pairs, see Input section for explanation.
- `mode`: The mode for forming the combination set, see Mode section.
- `top_n_sets`: Number of sets with largest size.
- `min_set_size`: The minimal set size that is used for generating the combination matrix.
- `universal_set`: The universal set. If it is set, the size of the complement set of all sets is also calculated. It if is specified, complement_size is ignored.
- `complement_size`: The size for the complement of all sets. If it is specified, the combination set name will be like "00...".
- `value_fun`: For each combination set, how to calculate the size? If it is a scalar set, the length of the vector is the size of the set, while if it is a region-based set, (i.e. GRanges or IRanges object), the sum of widths of regions in the set is calculated as the size of the set.
- `set_on_rows`: Used internally.

**Value**

A matrix also in a class of `comb_mat`.

Following functions can be applied to it: `set_name, comb_name, set_size, comb_size, comb_degree, extract_comb` and `t.comb_mat`.

**Input**

To represent multiple sets, the variable can be represented as:

1. A list of sets where each set is a vector, e.g.:
list(set1 = c("a", "b", "c"),
     set2 = c("b", "c", "d", "e"),
     ...)

2. A binary matrix/data frame where rows are elements and columns are sets, e.g.:

    a b c
    h 1 1 1
    t 1 0 1
    j 1 0 0
    u 1 0 1
    w 1 0 0
    ...

If the variable is a data frame, the binary columns (only contain 0 and 1) and the logical columns are only kept.

The set can be genomic regions, then it can only be represented as a list of GRanges objects.

Mode

E.g. for three sets (A, B, C), the UpSet approach splits the combination of selecting elements in the set or not in the set and calculates the sizes of the combination sets. For three sets, all possible combinations are:

    A B C
    1 1 1
    1 1 0
    1 0 1
    0 1 1
    1 0 0
    0 1 0
    0 0 1

A value of 1 means to select that set and 0 means not to select that set. E.g., "1 1 0" means to select set A, B while not set C. Note there is no "0 0 0", because the background size is not of interest here. With the code of selecting and not selecting the sets, next we need to define how to calculate the size of that combination set. There are three modes:

1. distinct mode: 1 means in that set and 0 means not in that set, then "1 1 0" means a set of elements also in set A and B, while not in C (i.e. setdiff(intersect(A, B), C)). Under this mode, the seven combination sets are the seven partitions in the Venn diagram and they are mutually exclusive.

2. intersect mode: 1 means in that set and 0 is not taken into account, then, "1 1 0" means a set of elements in set A and B, and they can also in C or not in C (i.e. intersect(A, B)). Under this mode, the seven combination sets can overlap.

3. union mode: 1 means in that set and 0 is not taken into account. When there are multiple 1, the relationship is OR. Then, "1 1 0" means a set of elements in set A or B, and they can also in C or not in C (i.e. union(A, B)). Under this mode, the seven combination sets can overlap.
Examples

```r
set.seed(123)
l = list(a = sample(letters, 10),
       b = sample(letters, 15),
       c = sample(letters, 20))
m = make_comb_mat(l)

mat = list_to_matrix(l)
m = make_comb_mat(mat)
```

```r
## Not run:
require(circlize)
require(GenomicRanges)
l = lapply(1:4, function(i) generateRandomBed())
l = lapply(l, function(df) GRanges(seqnames = df[, 1],
                           ranges = IRanges(df[, 2], df[, 3])))
names(l) = letters[1:4]
m = make_comb_mat(l)
```

```r
## End(Not run)
```

Description

Method dispatch page for `make_layout`.

Dispatch

`make_layout` can be dispatched on following classes:

- `make_layout,Heatmap-method`, `Heatmap-class` class method
- `make_layout,HeatmapList-method`, `HeatmapList-class` class method

Examples

```
# no example
NULL
```
**Description**

Make the Layout of a Single Heatmap

**Usage**

```r
## S4 method for signature 'Heatmap'
make_layout(object)
```

**Arguments**

- `object`: A `Heatmap-class` object.

**Details**

The layout of the single heatmap will be established by setting the size of each heatmap component. Also how to make graphics for heatmap components will be recorded by saving as functions.

Whether to apply row clustering or column clustering affects the layout, so clustering should be applied first by `prepare,Heatmap-method` before making the layout.

This function is only for internal use.

**Value**

A `Heatmap-class` object.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```
Description

Make Layout for the Heatmap List

Usage

```r
## S4 method for signature 'HeatmapList'
make_layout(object,
row_title = character(0),
row_title_side = c("left", "right"),
row_title_gp = gpar(fontsize = 14),
column_title = character(0),
column_title_side = c("top", "bottom"),
column_title_gp = gpar(fontsize = 14),
heatmap_legend_side = c("right", "left", "bottom", "top"),
merge_legends = FALSE,
show_heatmap_legend = TRUE,
heatmap_legend_list = list(),
annotation_legend_side = c("right", "left", "bottom", "top"),
show_annotation_legend = TRUE,
annotation_legend_list = list(),
align_heatmap_legend = NULL,
align_annotation_legend = NULL,
legend_grouping = c("adjusted", "original"),
ht_gap = unit(2, "mm"),
main_heatmap = which(sapply(object@ht_list, inherits, "Heatmap"))[1],
padding = GLOBAL_PADDING,

auto_adjust = TRUE,
row_dend_side = c("original", "left", "right"),
row_sub_title_side = c("original", "left", "right"),
column_dend_side = c("original", "top", "bottom"),
column_sub_title_side = c("original", "top", "bottom"),

row_gap = NULL,
cluster_rows = NULL,
cluster_row_slices = NULL,
clustering_distance_rows = NULL,
clustering_method_rows = NULL,
```
Arguments

object A HeatmapList-class object.
row_title Title on the row.
row_title_side Will the title be put on the left or right of the heatmap list?
row_title_gp Graphic parameters for the row title.
column_title Title on the column.
column_title_side Will the title be put on the top or bottom of the heatmap?
column_title_gp Graphic parameters for the column title.
heatmap_legend_side Side of the heatmap legends.
merge_legends Whether to put heatmap legends and annotation legends together. By default they are put in different viewports.

show_heatmap_legend Whether show heatmap legends.

heatmap_legend_list A list of self-defined legends, should be wrapped into a list of grob objects. Normally they are constructed by Legend.

annotation_legend_side Side of annotation legends.

show_annotation_legend Whether show annotation legends.

annotation_legend_list A list of self-defined legends, should be wrapped into a list of grob objects. Normally they are constructed by Legend.

align_heatmap_legend How to align the legends to heatmap. Possible values are "heatmap_center", "heatmap_top" and "global_center". If the value is NULL, it automatically picks the proper value from the three options.

align_annotation_legend How to align the legends to heatmap. Possible values are "heatmap_center", "heatmap_top" and "global_center".

legend_grouping How the legends are grouped. Values should be "adjusted" or "original".

ht_gap Gap between heatmaps, should be a unit object. It can be a vector of length 1 or the number of heatmaps/annotations.

main_heatmap Name or index for the main heatmap.

padding Padding of the whole plot. The four values correspond to the bottom, left, top and right paddings.

auto_adjust whether apply automatic adjustment? The auto-adjustment includes turning off dendrograms, titles and row/columns for non-main heatmaps.

row_dend_side If auto-adjustment is on, to put the row dendrograms of the main heatmap to the most left side of the heatmap list or the most right side?

row_sub_title_side There can be sub titles generated by the splitting of heatmaps. Similar setting as row_dend_side.

column_dend_side Similar setting as row_dend_side.

column_sub_title_side Similar setting as row_sub_title_side.

row_gap Overwrite the corresponding setting in the main heatmap.

cluster_rows Overwrite the corresponding setting in the main heatmap.

cluster_row_slices Overwrite the corresponding setting in the main heatmap.
clustering_distance_rows
  Overwrite the corresponding setting in the main heatmap.
clustering_method_rows
  Overwrite the corresponding setting in the main heatmap. Same setting as in Heatmap, if it is specified, clustering_method_rows in main heatmap is ignored.
row_dend_width
  Overwrite the corresponding setting in the main heatmap.
show_row_dend
  Same Overwrite the corresponding setting in the main heatmap.
row_dend_reorder
  Overwrite the corresponding setting in the main heatmap.
row_dend_gp
  Overwrite the corresponding setting in the main heatmap.
row_km
  Overwrite the corresponding setting in the main heatmap.
row_km_repeats
  Overwrite the corresponding setting in the main heatmap.
row_split
  Overwrite the corresponding setting in the main heatmap.
height
  Overwrite the corresponding setting in the main heatmap.
heatmap_height
  Overwrite the corresponding setting in the main heatmap.
column_gap
  Overwrite the corresponding setting in the main heatmap.
cluster_columns
  Overwrite the corresponding setting in the main heatmap.
cluster_column_slices
  Overwrite the corresponding setting in the main heatmap.
clustering_distance_columns
  Overwrite the corresponding setting in the main heatmap.
clustering_method_columns
  Overwrite the corresponding setting in the main heatmap.
column_dend_width
  Column Overwrite the corresponding setting in the main heatmap.
show_column_dend
  Overwrite the corresponding setting in the main heatmap.
column_dend_reorder
  Overwrite the corresponding setting in the main heatmap.
column_dend_gp
  Overwrite the corresponding setting in the main heatmap.
column_order
  Overwrite the corresponding setting in the main heatmap.
column_km
  Overwrite the corresponding setting in the main heatmap.
column_km_repeats
  Overwrite the corresponding setting in the main heatmap.
column_split
  Overwrite the corresponding setting in the main heatmap.
width
  Overwrite the corresponding setting in the main heatmap.
heatmap_width
  Overwrite the corresponding setting in the main heatmap.
use_raster
  Overwrite the corresponding setting in every heatmap.
raster_device Overwrite the corresponding setting in every heatmap.
raster_quality Overwrite the corresponding setting in every heatmap.
raster_device_param Overwrite the corresponding setting in every heatmap.
raster_resize Overwrite the corresponding setting in every heatmap.

Details
It sets the size of each component of the heatmap list and adjusts graphic parameters for each heatmap if necessary.
This function is only for internal use.

Value
A HeatmapList-class object in which settings for all heatmap are adjusted.

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples
# There is no example
NULL

make_row_cluster-Heatmap-method
Make Cluster on Rows

Description
Make Cluster on Rows

Usage
## S4 method for signature 'Heatmap'
make_row_cluster(object)

Arguments
object A Heatmap-class object.

Details
The function will fill or adjust row_dend_list, row_order_list, row_title and matrix_param slots.
If order is defined, no clustering will be applied.
This function is only for internal use.
Value

A Heatmap-class object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

Description

Map Values to Colors

Usage

## S4 method for signature 'ColorMapping'
map_to_colors(object, x)

Arguments

object A ColorMapping-class object.

x Input values.

Details

It maps a vector of values to a vector of colors.

This function provides a uniform way for discrete and continuous color mapping.

Value

A vector of colors.

Author(s)

Zuguang Gu <z.gu@dkfz.de>
Examples

```r
cm = ColorMapping(colors = c("A" = "red", "B" = "black"))
map_to_colors(cm, sample(c("A", "B"), 10, replace = TRUE))
require(circlize)
col_fun = colorRamp2(c(0, 1), c("white", "red"))
cm = ColorMapping(col_fun = col_fun)
map_to_colors(cm, runif(10))
```

---

### `max_text_height`

**Maximum Height of Text**

**Description**

Maximum Height of Text

**Usage**

```r
max_text_height(text, gp = gpar(), rot = 0)
```

**Arguments**

- `text` A vector of text.
- `gp` Graphic parameters for text.
- `rot` Rotation of the text, scalar.

**Details**

It simply calculates maximum height of a list of `textGrob` objects.

Note it ignores the text rotation.

**Value**

A `unit` object.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**See Also**

- `max_text_width` calculates the maximum width of a text vector.

**Examples**

```r
x = c("a", "b\nb", "c\nc\nc")
max_text_height(x, gp = gpar(fontsize = 10))
```
max_text_width

Maximum Width of Text

Description

Maximum Width of Text

Usage

max_text_width(text, gp = gpar(), rot = 0)

Arguments

text A vector of text.
gp Graphic parameters for text.
rot Rotation of the text, scalar.

Details

It simply calculates maximum width of a list of textGrob objects.
Note it ignores the text rotation.

Value

A unit object which is in "mm".

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

max_text_height calculates the maximum height of a text vector.

Examples

x = c("a", "bb", "ccc")
max_text_width(x, gp = gpar(fontsize = 10))
merge_dendrogram

Merge Dendrograms

Description

Merge Dendrograms

Usage

merge_dendrogram(x, y, only_parent = FALSE, ...)

Arguments

x

The parent dendrogram.

y

The children dendrograms. They are connected to the leaves of the parent dendrogram. So the length of y should be as same as the number of leaves of the parent dendrogram.

only_parent

Whether only returns the parent dendrogram where the height and node positions have been adjusted by children dendrograms.

...

Other arguments.

Details

Do not retrieve the order of the merged dendrogram. It is not reliable.

Examples

m1 = matrix(rnorm(100), nr = 10)
m2 = matrix(rnorm(80), nr = 8)
m3 = matrix(rnorm(50), nr = 5)
dend1 = as.dendrogram(hclust(dist(m1)))
dend2 = as.dendrogram(hclust(dist(m2)))
dend3 = as.dendrogram(hclust(dist(m3)))
dend_p = as.dendrogram(hclust(dist(rbind(colMeans(m1), colMeans(m2), colMeans(m3)))))
dend_m = merge_dendrogram(dend_p, list(dend1, dend2, dend3))
grid.dendrogram(dend_m, test = TRUE)

dend_m = merge_dendrogram(dend_p, list(dend1, dend2, dend3), only_parent = TRUE)
grid.dendrogram(dend_m, test = TRUE)

require(dendextend)
dend1 = color_branches(dend1, k = 1, col = "red")
dend2 = color_branches(dend2, k = 1, col = "blue")
dend3 = color_branches(dend3, k = 1, col = "green")
dend_p = color_branches(dend_p, k = 1, col = "orange")
dend_m = merge_dendrogram(dend_p, list(dend1, dend2, dend3))
grid.dendrogram(dend_m, test = TRUE)
names.HeatmapAnnotation

Annotation Names

Description
Annotation Names

Usage
## S3 method for class 'HeatmapAnnotation'
names(x)

Arguments
x A HeatmapAnnotation-class object.

Examples
ha = HeatmapAnnotation(foo = 1:10, bar = anno_points(10:1))
names(ha)

names.HeatmapList

Names of the heatmaps/annotations

Description
Names of the heatmaps/annotations

Usage
## S3 method for class 'HeatmapList'
names(x)

Arguments
x A HeatmapList-class object

Examples
# There is no example
NULL
namesAssign.HeatmapAnnotation

Assign Annotation Names

Description
Assign Annotation Names

Usage
## S3 replacement method for class 'HeatmapAnnotation'
names(x) <- value

Arguments
x                     A HeatmapAnnotation-class object.
value                 A vector of new names.

Examples
ha = HeatmapAnnotation(foo = 1:10, bar = anno_points(10:1))
names(ha) = c("A", "B")
names(ha)

ncol.Heatmap

Number of Columns in the Heatmap

Description
Number of Columns in the Heatmap

Usage
## S3 method for class 'Heatmap'
ncol(x)

Arguments
x                     A Heatmap-class object.

Examples
# There is no example
NULL
### nobs.AnnotationFunction

**Description**

Number of Observations

**Usage**

```r
## S3 method for class 'AnnotationFunction'
nobs(object, ...)
```

**Arguments**

- `object` The `AnnotationFunction-class` object.
- `...` Other arguments.

**Details**

returns NA.

**Examples**

```r
anno = anno_points(1:10)
nobs(anno)
```

### nobs.HeatmapAnnotation

**Description**

Number of Observations

**Usage**

```r
## S3 method for class 'HeatmapAnnotation'
nobs(object, ...)
```

**Arguments**

- `object` The `HeatmapAnnotation-class` object.
- `...` Other arguments.
Value

If there is no nobs information for any of its SingleAnnotation-class object, it returns NA.

Examples

# There is no example
NULL

nobs.SingleAnnotation  Number of Observations

Description

Number of Observations

Usage

## S3 method for class 'SingleAnnotation'
nobs(object, ...)

Arguments

object                 The SingleAnnotation-class object.
...                    Other arguments.

Details

It returns the n slot of the annotation function. If it does not exist, it returns NA.

Examples

# There is no example
NULL
normalize_comb_mat Normalize a list of combination matrice

Description
Normalize a list of combination matrices

Usage
normalize_comb_mat(..., full_comb_sets = FALSE, complement_set = FALSE)

Arguments
...
Combination matrices.
full_comb_sets Whether the combination matrices contain the full sets of combination sets?
complement_set Whether the combination matrices also contain the complement set?

Details
It normalizes a list of combination matrices to make them have the same number and order of sets and combination sets.
The sets (by set_name) from all combination matrices should be the same.

Examples
# There is no example
NULL

normalize_genomic_signals_to_bins
Overlap genomic signals to the genomic bins

Description
Overlap genomic signals to the genomic bins

Usage
normalize_genomic_signals_to_bins(gr, value, value_column = NULL, method = "weighted",
empty_value = NA, window = GHEATMAP_ENV$chr_window)
normalize_genomic_signals_to_bins

Arguments

- **gr**: A GRanges object.
- **value**: The corresponding signals corresponding to gr.
- **value_column**: If value is not set and the values are in the meta-columns in gr, you can specify the column indices for these value columns, better to use name indices.
- **method**: One of "weighted", "w0" and "absolute". For the three different methods, please refer to [https://bioconductor.org/packages/release/bioc/vignettes/EnrichedHeatmap/inst/doc/EnrichedHeatmap.html#toc_7](https://bioconductor.org/packages/release/bioc/vignettes/EnrichedHeatmap/inst/doc/EnrichedHeatmap.html#toc_7).
- **empty_value**: The value for the bins where no signal is overlapped.
- **window**: The genomic bins generated from bin_genome.

Details

The genomic bins should be generated by bin_genome in advance. The genomic bins are saved internally, so that multiple uses of bin_genome ensure they all return the matrices with the same rows.

It supports following values.

- When neither value nor value_column is set, it simply overlap gr to the genomic bins and returns a one-column logical matrix which represents whether the current genomic bin overlaps to any signal.
- When the signals are numeric, value can be a numeric vector or a matrix, or value_column can contain multiple columns. The function returns a numeric matrix where the values are properly averaged depending on what method was used.
- When the signals are character, value can only be a vector or value_column can only contain one single column. The function returns a one-column character matrix.

Value

A matrix with the same row as the genomic bins.

Examples

```r
## Not run:
require(circlize)
require(GenomicRanges)

chr_window = bin_genome("hg19")

#### the first is a numeric matrix #######
bed1 = generateRandomBed(nr = 1000, nc = 10)
gr1 = GRanges(seqnames = bed1[, 1], ranges = IRanges(bed1[, 2], bed1[, 3]))

num_mat = normalize_genomic_signals_to_bins(gr1, bed1[, -(1:3)])

#### the second is a character matrix ######
bed_list = lapply(1:10, function(i) {
```
```r
normalize_genomic_signals_to_bins

generateRandomBed(nr = 1000, nc = 1,
fun = function(n) sample(c("gain", "loss"), n, replace = TRUE))

char_mat = NULL
for(i in 1:10) {
  bed = bed_list[[i]]
  bed = bed[sample(nrow(bed), 20), , drop = FALSE]
  gr_cv = GRanges(seqnames = bed[, 1], ranges = IRanges(bed[, 2], bed[, 3]))
  char_mat = cbind(char_mat, normalize_genomic_signals_to_bins(gr_cv, bed[, 4]))
}

#### two numeric columns ########
bed2 = generateRandomBed(nr = 100, nc = 2)
gr2 = GRanges(seqnames = bed2[, 1], ranges = IRanges(bed2[, 2], bed2[, 3]))
v = normalize_genomic_signals_to_bins(gr2, bed2[, 4:5])

##### a list of genes need to be highlighted
bed3 = generateRandomBed(nr = 40, nc = 0)
gr3 = GRanges(seqnames = bed3[, 1], ranges = IRanges(bed3[, 2], bed3[, 3]))
gr3$gene = paste0("gene_", 1:length(gr3))
mtch = as.matrix(findOverlaps(chr_window, gr3))
at = mtch[, 1]
labels = mcols(gr3)[mtch[, 2], 1]

##### order of the chromosomes ######
chr = as.vector(seqnames(chr_window))
chr_level = paste0("chr", c(1:22, "X", "Y"))
chr = factor(chr, levels = chr_level)

#### make the heatmap #######
subgroup = rep(c("A", "B"), each = 5)
ht_opt$TITLE_PADDING = unit(c(4, 4), "points")
ht_list = Heatmap(num_mat, name = "mat", col = colorRamp2(c(-1, 0, 1), c("green", "white", "red")),
row_split = chr, cluster_rows = FALSE, show_column_dend = FALSE,
column_split = subgroup, cluster_column_slices = FALSE,
column_title = "numeric matrix",
top_annotation = HeatmapAnnotation(subgroup = subgroup, annotation_name_side = "left"),
row_title_rot = 0, row_title_gp = gpar(fontsize = 10), border = TRUE,
row_gap = unit(0, "points") +
Heatmap(char_mat, name = "CNV", col = c("gain" = "red", "loss" = "blue"),
border = TRUE, column_title = "character matrix") +
rowAnnotation(label = anno_mark(at = at, labels = labels)) +
rowAnnotation(pt = anno_points(v, gp = gpar(col = 4:5), pch = c(1, 16)),
width = unit(2, "cm") +
rowAnnotation(bar = anno_barplot(v[, 1], gp = gpar(col = ifelse(v[, 1] > 0, 2, 3))),
width = unit(2, "cm"))
draw(ht_list, merge_legend = TRUE)

##### or horizontally ###
```
nrow.Heatmap

Number of Rows in the Heatmap

Description

Number of Rows in the Heatmap

Usage

```r
## S3 method for class 'Heatmap'
nrow(x)
```

Arguments

- `x` A `Heatmap-class` object.

Examples

```r
# There is no example
NULL
```
oncoPrint  

Make oncoPrint

Description

Make oncoPrint

Usage

oncoPrint(mat, name,
    get_type = default_get_type,
    alter_fun,
    alter_fun_is_vectorized = NULL,
    col = NULL,
    top_annotation = HeatmapAnnotation(cbar = anno_oncoprint_barplot()),
    right_annotation = rowAnnotation(rbar = anno_oncoprint_barplot()),
    left_annotation = NULL,
    bottom_annotation = NULL,
    show_pct = TRUE,
    pct_gp = gpar(fontsize = 10),
    pct_digits = 0,
    pct_side = "left",
    pct_include = NULL,
    row_labels = NULL,
    show_row_names = TRUE,
    row_names_side = "right",
    row_names_gp = pct_gp,
    row_split = NULL,
    column_labels = NULL,
    column_names_gp = gpar(fontsize = 10),
    column_split = NULL,
    row_order = NULL,
    column_order = NULL,
    cluster_rows = FALSE,
    cluster_columns = FALSE,
    remove_empty_columns = FALSE,
    remove_empty_rows = FALSE,
    show_column_names = FALSE,
    heatmap_legend_param = NULL,
    ...)
Arguments

- **mat**: The value should be a character matrix which encodes multiple alterations or a list of matrices for which every matrix contains binary value representing whether the alteration is present or absent. When the value is a list, the names of the list represent alteration types. You can use `unify_mat_list` to make all matrix having same row names and column names.

- **name**: Name of the oncoPrint. Not necessary to specify.

- **get_type**: If different alterations are encoded in the matrix as complex strings, this self-defined function determines how to extract them. It only works when `mat` is a matrix. The default value is `default_get_type`.

- **alter_fun**: A single function or a list of functions which defines how to add graphics for different alterations. You can use `alter_graphic` to automatically generate for rectangles and points.

- **alter_fun_is_vectorized**: Whether `alter_fun` is implemented vectorized. Internally the function will guess.

- **col**: A vector of color for which names correspond to alteration types.

- **top_annotation**: Annotation put on top of the oncoPrint. By default it is barplot which shows the number of genes with a certain alteration in each sample.

- **right_annotation**: Annotation put on the right of the oncoPrint. By default it is barplot which shows the number of samples with a certain alteration in each gene.

- **left_annotation**: Annotation put on the left of the oncoPrint.

- **bottom_annotation**: Annotation put at the bottom of the oncoPrint.

- **show_pct**: Whether show percent values on the left of the oncoprint?

- **pct_gp**: Graphic paramters for percent values

- **pct_digits**: Digits for the percent values.

- **pct_side**: Side of the percent values to the oncoPrint. This argument is currently disabled.

- **pct_include**: Alteration types that are included for the calculation of percent values.

- **row_labels**: Labels as the row names of the oncoPrint.

- **show_row_names**: Whether show row names?

- **row_names_side**: Side of the row names to the oncoPrint. This argument is currently disabled.

- **row_names_gp**: Graphic parameters for the row names.

- **row_split**: Pass to `Heatmap`.

- **column_labels**: Pass to `Heatmap`.

- **column_names_gp**: Pass to `Heatmap`.

- **column_split**: Pass to `Heatmap`.

- **row_order**: Order of rows. By default rows are sorted by the number of occurrence of the alterations.
order.comb_mat

cluster_rows  If it is set, it must be a dendrogram/hclust object.
cluster_columns  If it is set, it must be a dendrogram/hclust object.
column_order  Order of columns. By default the columns are sorted to show the mutual exclusivity of alterations.
remove_empty_columns  If there is no alteration in some samples, whether remove them on the oncoPrint?
remove_empty_rows  If there is no alteration in some samples, whether remove them on the oncoPrint?
show_column_names  Whether show column names?
heatmap_legend_param  pass to `Heatmap`.
...  Pass to `Heatmap`.

Details

The 'memo sort' method is from https://gist.github.com/armish/564a65ab874a770e2c26. Thanks to B. Arman Aksoy for contributing the code.

Value

A `Heatmap-class` object which means you can add other heatmaps or annotations to it.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

order.comb_mat  

Order of the Combination Sets

Description

Order of the Combination Sets

Usage

order.comb_mat(m, decreasing = TRUE, on = "comb_set")
packLegend

Arguments

- **on**
  - A combination matrix returned by `make_comb_mat`.
- **decreasing**
  - Whether the ordering is applied decreasingly.

Details

It first sorts by the degree of the combination sets then by the combination matrix.

Examples

```r
# There is no example
NULL
```

Description

Pack Legends

Usage

```r
packLegend(..., gap = unit(4, "mm"), row_gap = unit(4, "mm"), column_gap = unit(4, "mm"),
          direction = c("vertical", "horizontal"),
          max_width = NULL, max_height = NULL, list = NULL)
```

Arguments

- **...**
  - A list of objects returned by `Legend`.
- **gap**
  - Gap between two neighbouring legends. The value is a `unit` object with length of one. It is the same as `row_gap` if the direction if vertical and the same as `column_gap` if the direction is horizontal.
- **row_gap**
  - Horizontal gaps between legends.
- **column_gap**
  - Vertical gaps between legends.
- **direction**
  - The direction to arrange legends.
- **max_width**
  - The maximal width of the total packed legends. It only works for horizontal arrangement. If the total width of the legends exceeds it, the legends will be arranged into multiple rows.
- **max_height**
  - Similar as `max_width`, but for the vertical arrangement of legends.
- **list**
  - The list of legends can be specified as a list.
pheatmap

Value

A Legends-class object.

See Also


Examples

require(circlize)
col_fun = colorRamp2(c(0, 0.5, 1), c("blue", "white", "red"))
lgd1 = Legend(at = 1:6, legend_gp = gpar(fill = 1:6), title = "legend1")
lgd2 = Legend(col_fun = col_fun, title = "legend2", at = c(0, 0.25, 0.5, 0.75, 1))
pd = packLegend(lgd1, lgd2)
draw(pd, test = "two legends")
pd = packLegend(lgd1, lgd2, direction = "horizontal")
draw(pd, test = "two legends packed horizontally")

pheatmap

Translate pheatmap::pheatmap to ComplexHeatmap::Heatmap

Description

Translate pheatmap::pheatmap to ComplexHeatmap::Heatmap

Usage

pheatmap(mat,
color = colorRampPalette(rev(brewer.pal(n = 7, name = "RdYlBu")))(100),
kmeans_k = NA,
breaks = NA,
border_color = ifelse(nrow(mat) < 100 & ncol(mat) < 100, "grey60", NA),
cellwidth = NA,
cellheight = NA,
scale = "none",
cluster_rows = TRUE,
cluster_cols = TRUE,
clustering_distance_rows = "euclidean",
clustering_distance_cols = "euclidean",
clustering_method = "complete",
clustering_callback = NA,
cutree_rows = NA,
cutree_cols = NA,
treeheight_row = ifelse(class(cluster_rows) == "hclust" || cluster_rows, 50, 0),
treeheight_col = ifelse(class(cluster_cols) == "hclust" || cluster_cols, 50, 0),
legend = TRUE,
legend_breaks = NA,
Arguments

mat

The input matrix.

color

The same as in `pheatmap`. Here you don’t necessarily need to generate a long
color vector. The discrete colors sent to \texttt{colorRampPalette} are also OK here. E.g. \texttt{colorRampPalette(rev(brewer.pal(n = 7, name = "RdYlBu")))(100)} can be simply replaced as \texttt{rev(brewer.pal(n = 7, name = "RdYlBu"))}.

\begin{verbatim}
# kmeans_k
breaks
border_color
cellwidth
cellheight
scale
cluster_rows
cluster_cols
clustering_distance_rows
clustering_distance_cols
clustering_method
clustering_callback
cutree_rows
cutree_cols
treeheight_row
treeheight_col
legend
legend_breaks
legend_labels
annotation_row
annotation_col
annotation
annotation_colors
annotation_legend
annotation_names_row
annotation_names_col
drop_levels
show_rownames
show_colnames
\end{verbatim}
main   The same as in `pheatmap`.

fontsize  The same as in `pheatmap`.

fontsize_row  The same as in `pheatmap`.

fontsize_col  The same as in `pheatmap`.

angle_col  The same as in `pheatmap`.

display_numbers  The same as in `pheatmap`.

number_format  The same as in `pheatmap`.

number_color  The same as in `pheatmap`.

fontsize_number  The same as in `pheatmap`.

gaps_row  The same as in `pheatmap`.

gaps_col  The same as in `pheatmap`.

labels_row  The same as in `pheatmap`.

labels_col  The same as in `pheatmap`.

filename  Not supported.

width  Not supported.

height  Not supported.

silent  Not supported.

na_col  The same as in `pheatmap`.

name  Name of the heatmap. This argument is passed to `Heatmap`.

ttfamily  Font family for row and column names.

fontfamily_row  Font family for row names.

fontfamily_col  Font family for column names.

ttface  Font face for row and column names.

ttface_row  Font face for row names.

ttface_col  Font face for column names.

heatmap_legend_param  Pass to `Heatmap`.

...  Other arguments passed to `Heatmap`.

ttfamily_draw  Whether to run `draw()` function to the heatmap object.

**Details**

This function aims to execute `pheatmap::pheatmap` code purely with `ComplexHeatmap`.

**Value**

A `Heatmap-class` object.
See Also

See https://jokergoo.github.io/2020/05/06/translate-from-pheatmap-to-complexheatmap/
compare_pheatmap that compares heatmaps between pheatmap::pheatmap() and ComplexHeatmap::pheatmap().

Examples

# There is no example
NULL

---

**pindex**  
*Get Values in a Matrix by Pair-wise Indices*

**Description**

Get Values in a Matrix by Pair-wise Indices

**Usage**

```
pindex(m, i, j)
```

**Arguments**

- `m`  
  A matrix or a 3-dimension array.

- `i`  
  Row indices or the indices in the first dimension.

- `j`  
  Column indices or the indices in the second dimension.

**Value**

If `m` is a matrix, the value returned is a vector `c(m[i1, j1], m[i2, j2], ...)'`.

If `m` is an array, the value returned is a matrix `rbind(m[i1, j1, ], m[i2, j2, ], ...)'`.

**Examples**

```r
m = matrix(rnorm(100), 10)
m2 = m[m > 0]
ind = do.call("rbind", lapply(1:10, function(ci) {
  i = which(m[, ci] > 0)
  cbind(i = i, j = rep(ci, length(i)))
}))
pindex(m, ind[, 1], ind[, 2])
identical(pindex(m, ind[, 1], ind[, 2]), m[m > 0])

# 3d array
arr = array(1:27, dim = c(3, 3, 3))
pindex(arr, 1:2, 2:3)
identical(pindex(arr, 1:2, 2:3),
  rbind(arr[1, 2, ], arr[2, 3, ]))
```
plot.Heatmap

Draw heatmap

Description
Draw heatmap

Usage
## S3 method for class 'Heatmap'
plot(x, ...)

Arguments
x A Heatmap-class object.
... All pass to draw,Heatmap-method.

Examples
# There is no example
NULL

plot.HeatmapAnnotation

Draw heatmap annotations

Description
Draw heatmap annotations

Usage
## S3 method for class 'HeatmapAnnotation'
plot(x, ...)

Arguments
x A HeatmapAnnotation-class object.
... All pass to draw,HeatmapList-method.

Examples
# There is no example
NULL
plot.HeatmapList

Description
Draw heatmap

Usage
## S3 method for class 'HeatmapList'
plot(x, ...)

Arguments
x An HeatmapList-class object.
...
All pass to draw.HeatmapList-method.

Examples
# There is no example
NULL

prepare-Heatmap-method

Description
Prepare the Heatmap

Usage
## S4 method for signature 'Heatmap'
prepare(object, process_rows = TRUE, process_columns = TRUE)

Arguments
object A Heatmap-class object.
process_rows Whether to process rows of the heatmap.
process_columns Whether to process columns of the heatmap.
The preparation of the heatmap includes following steps:

- making clustering on rows (by calling `make_row_cluster`, `Heatmap-method`)
- making clustering on columns (by calling `make_column_cluster`, `Heatmap-method`)
- making the layout of the heatmap (by calling `make_layout`, `Heatmap-method`)

This function is only for internal use.

**Value**

The `Heatmap-class` object.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

```r
# There is no example
NULL
```

---

**Description**

Print the `comb_mat` Object

**Usage**

```r
## S3 method for class 'comb_mat'
print(x, ...)
```

**Arguments**

- `x` A combination matrix returned by `make_comb_mat`.
- `...` Other arguments

**Examples**

```r
# There is no example
NULL
```
Description

Restore the index vector to index matrix in layer_fun

Usage

restore_matrix(j, i, x, y)

Arguments

j Column indices directly from layer_fun.
i Row indices directly from layer_fun.
x Position on x-direction directly from layer_fun.
y Position on y-direction directly from layer_fun.

Details

The values that are sent to layer_fun are all vectors (for the vectorization of the grid graphic functions), however, the heatmap slice where layer_fun is applied to, is still represented by a matrix, thus, it would be very convinient if all the arguments in layer_fun can be converted to the sub-matrix for the current slice. Here, as shown in above example, restore_matrix does the job. restore_matrix directly accepts the first four argument in layer_fun and returns an index matrix, where rows and columns correspond to the rows and columns in the current slice, from top to bottom and from left to right. The values in the matrix are the natural order of e.g. vector j in current slice.

For following code:

```r
Heatmap(small_mat, name = "mat", col = col_fun,
row_km = 2, column_km = 2,
layer_fun = function(j, i, x, y, w, h, fill) {
  ind_mat = restore_matrix(j, i, x, y)
  print(ind_mat)
}
)
```

The first output which is for the top-left slice:

```
[1,] 1 4 7 10 13
[2,] 2 5 8 11 14
[3,] 3 6 9 12 15
```
As you see, this is a three-row and five-column index matrix where the first row corresponds to the top row in the slice. The values in the matrix correspond to the natural index (i.e. 1, 2, ...) in j, i, x, y, ... in layer_fun. Now, if we want to add values on the second column in the top-left slice, the code which is put inside layer_fun would look like:

```r
for(ind in ind_mat[, 2]) {
    grid.text(small_mat[i[ind], j[ind]], x[ind], y[ind], ...)
}
```

**Examples**

```r
set.seed(123)
mat = matrix(rnorm(81), nr = 9)
Heatmap(mat, row_km = 2, column_km = 2,
        layer_fun = function(j, i, x, y, width, height, fill) {
           ind_mat = restore_matrix(j, i, x, y)
           print(ind_mat)
        })
```

```r
set.seed(123)
mat = matrix(round(rnorm(81), 2), nr = 9)
Heatmap(mat, row_km = 2, column_km = 2,
        layer_fun = function(j, i, x, y, width, height, fill) {
           ind_mat = restore_matrix(j, i, x, y)
           ind = unique(c(ind_mat[2, ], ind_mat[, 3]))
           grid.text(pindex(mat, i[ind], j[ind]), x[ind], y[ind])
        })
```

---

**Description**

Resize the Width or Height of Heatmap Annotations

**Usage**

```r
## S4 method for signature 'HeatmapAnnotation'
re_size(object,
        annotation_height = NULL,
        annotation_width = NULL,
        height = NULL,
        width = NULL,
        simple_anno_size = object@param$simple_anno_size,
        simple_anno_size_adjust = object@param$simple_anno_size_adjust)
```
Arguments

- **object**: A `HeatmapAnnotation-class` object.
- **annotation_height**: A vector of annotation heights in `unit` class.
- **annotation_width**: A vector of annotation widths in `unit` class.
- **height**: The height of the complete heatmap annotation.
- **width**: The width of the complete heatmap annotation.
- **simple_anno_size**: The size of one line of the simple annotation.
- **simple_anno_size_adjust**: Whether adjust the size of the simple annotation?

Details

The function only adjust height for column annotations and width for row annotations.

The basic rules are (take `height` and `annotation_height` for example):
1. If `annotation_height` is set and all `annotation_height` are absolute units, `height` is ignored.
2. If `annotation_height` contains non-absolute units, `height` also need to be set and the non-absolute units should be set in a simple form such as `1:10` or `unit(1, "null").
3. `simple_anno_size` is only used when `annotation_height` is NULL.
4. If only `height` is set, non-simple annotation is adjusted while keeps simple annotation unchanged.
5. If only `height` is set and all annotations are simple annotations, all annotations are adjusted, and `simple_anno_size` is disabled.
6. If `simple_anno_size_adjust` is FALSE, the size of the simple annotations will not change.

Examples

```r
# There is no example
NULL
```

---

**rowAnnotation**

*Construct Row Annotations*

Description

Construct Row Annotations

Usage

```r
rowAnnotation(...)  # Pass to HeatmapAnnotation.
```
Details

The function is identical to

HeatmapAnnotation(..., which = "row")

Value

A HeatmapAnnotation-class object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

---

row_anno_barplot  Barplots as Row Annotation

Description

Barplots as Row Annotation

Usage

row_anno_barplot(...)

Arguments

... pass to anno_barplot.

Details

A wrapper of anno_barplot with pre-defined which to row.
You can directly use anno_barplot for row annotation if you call it in rowAnnotation.

Value

See help page of anno_barplot.

Examples

# There is no example
NULL
row_anno_boxplot  

Boxplots as Row Annotation

Description
Boxplots as Row Annotation

Usage
row_anno_boxplot(...)

Arguments
... pass to anno_boxplot.

Details
A wrapper of anno_boxplot with pre-defined which to row.
You can directly use anno_boxplot for row annotation if you call it in rowAnnotation.

Value
See help page of anno_boxplot.

Examples
# There is no example
NULL

---

row_anno_density  

Density as Row Annotation

Description
Density as Row Annotation

Usage
row_anno_density(...)  

Arguments
... pass to anno_density.
Details

A wrapper of `anno_density` with pre-defined `which` to `row`.
You can directly use `anno_density` for row annotation if you call it in `rowAnnotation`.

Value

See help page of `anno_density`.

Examples

```r
# There is no example
NULL
```

**row_anno_points**

*Points as Row Annotation*

**Description**

Points as Row Annotation

**Usage**

`row_anno_points(...)`

**Arguments**

... pass to `anno_points`.

**Details**

A wrapper of `anno_points` with pre-defined `which` to `row`.

You can directly use `anno_points` for row annotation if you call it in `rowAnnotation`.

**Value**

See help page of `anno_points`.

**Examples**

```r
# There is no example
NULL
```

**row_anno_text**

*Text as Row Annotation*

**Description**

Text as Row Annotation

**Usage**

`row_anno_text(...)`

**Arguments**

... pass to `anno_text`.
Details

A wrapper of \texttt{anno\_text} with pre-defined which to row.

You can directly use \texttt{anno\_text} for row annotation if you call it in \texttt{row\_Annotation}.

Value

See help page of \texttt{anno\_text}.

Examples

\begin{verbatim}
# There is no example
NULL
\end{verbatim}

\begin{verbatim}

\end{verbatim}
Description

Get Row Dendrograms from a Heatmap

Usage

## S4 method for signature 'Heatmap'
row_dend(object, on_slice = FALSE)

Arguments

- object: A Heatmap-class object.
- on_slice: If the value is TRUE, it returns the dendrogram on the slice level.

Value

The format of the returned object depends on whether rows/columns of the heatmaps are split.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
mat = matrix(rnorm(100), 10)
ht = Heatmap(mat)
ht = draw(ht)
row_dend(ht)
ht = Heatmap(mat, row_km = 2)
ht = draw(ht)
row_dend(ht)
```

Description

Get Row Dendrograms from a Heatmap List
Usage

```#
S4 method for signature 'HeatmapList'
row_dend(object, name = NULL, on_slice = FALSE)
```

Arguments

- `object` A `HeatmapList-class` object.
- `name` Name of a specific heatmap.
- `on_slice` If the value is TRUE, it returns the dendrogram on the slice level.

Value

The format of the returned object depends on whether rows/columns of the heatmaps are split.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
mat = matrix(rnorm(100), 10)
ht_list = Heatmap(mat) + Heatmap(mat)
ht_list = draw(ht_list)
row_dend(ht_list)
ht_list = Heatmap(mat, row_km = 2) + Heatmap(mat)
ht_list = draw(ht_list)
row_dend(ht_list)
row_dend(ht_list, on_slice = TRUE)
ht_list = Heatmap(mat, row_km = 2) %+% Heatmap(mat)
ht_list = draw(ht_list)
row_dend(ht_list)
```

Description

Method dispatch page for `row_order`.

Dispatch

`row_order` can be dispatched on following classes:

- `row_order,HeatmapList-method,HeatmapList-class` class method
- `row_order,Heatmap-method,Heatmap-class` class method
Get Row Order from a Heatmap

Description

Get Row Order from a Heatmap

Usage

## S4 method for signature 'Heatmap'
row_order(object)

Arguments

object A Heatmap-class object.

Value

The format of the returned object depends on whether rows/columns of the heatmaps are split.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

mat = matrix(rnorm(100), 10)
ht = Heatmap(mat)
ht = draw(ht)
row_order(ht)
ht = Heatmap(mat, row_km = 2)
ht = draw(ht)
row_order(ht)
Get Row Order from a Heatmap List

Description

Get Row Order from a Heatmap List

Usage

```r
## S4 method for signature 'HeatmapList'
row_order(object, name = NULL)
```

Arguments

- `object`: A `HeatmapList-class` object.
- `name`: Name of a specific heatmap.

Value

The format of the returned object depends on whether rows/columns of the heatmaps are split.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
mat = matrix(rnorm(100), 10)
ht_list = Heatmap(mat) + Heatmap(mat)
ht_list = draw(ht_list)
row_order(ht_list)
ht_list = Heatmap(mat, row_km = 2) + Heatmap(mat)
ht_list = draw(ht_list)
row_order(ht_list)
ht_list = Heatmap(mat, row_km = 2) %v% Heatmap(mat)
ht_list = draw(ht_list)
row_order(ht_list)
```
set_component_height-Heatmap-method

Set Height of Heatmap Component

Description

Set Height of Heatmap Component

Usage

```r
## S4 method for signature 'Heatmap'
set_component_height(object, k, v)
```

Arguments

- `object`: A `Heatmap-class` object.
- `k`: Which column component? The value should a numeric index or the name of the corresponding column component. See **Details**.
- `v`: Height of the component, a unit object.

Details

All column components are: `column_title_top, column_dend_top, column_names_top, column_anno_top, heatmap_body, column_anno_bottom, column_names_bottom, column_dend_bottom, column_title_bottom`.

This function is only for internal use.

Value

The `Heatmap-class` object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
# There is no example
NULL
```
Description

Set Width of Heatmap Component

Usage

```r
## S4 method for signature 'Heatmap'
set_component_width(object, k, v)
```

Arguments

- `object`: A `Heatmap-class` object.
- `k`: Which row component? The value should a numeric index or the name of the corresponding row component. See **Details**.
- `v`: width of the component, a `unit` object.

Details

All row components are: `row_title_left, row_dend_left, row_names_left, row_anno_left, heatmap_body, row_anno_right, row_names_right, row_dend_right, row_title_right`.

This function is only for internal use.

Value

The `Heatmap-class` object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
# There is no example
NULL
```
### set_name

**Description**
Set Names

**Usage**
```r
set_name(m)
```

**Arguments**
- `m`: A combination matrix returned by `make_comb_mat`.

**Value**
A vector of set names.

**Examples**
```r
set.seed(123)
l = list(a = sample(letters, 10),
        b = sample(letters, 15),
        c = sample(letters, 20))
m = make_comb_mat(l)
set_name(m)
```

### set_nameAssign

**Description**
Modify Set Names

**Usage**
```r
set_name(x, ...) <- value
```

**Arguments**
- `x`: A combination matrix returned by `make_comb_mat`.
- `value`: New set names.
- `...`: Other arguments.
Examples

```r
set.seed(123)
l = list(a = sample(letters, 10),
       b = sample(letters, 15),
       c = sample(letters, 20))
m = make_comb_mat(l)
set_name(m) = c("A", "B", "C")
m
```

Description

Set Sizes

Usage

```r
set_size(m)
```

Arguments

- **m** A combination matrix returned by `make_comb_mat`.

Value

A vector of set sizes.

Examples

```r
set.seed(123)
l = list(a = sample(letters, 10),
       b = sample(letters, 15),
       c = sample(letters, 20))
m = make_comb_mat(l)
set_size(m)
```
show-AnnotationFunction-method

Print the AnnotationFunction Object

Description
Print the AnnotationFunction Object

Usage
## S4 method for signature 'AnnotationFunction'
show(object)

Arguments
object The AnnotationFunction-class object.

Examples
# There is no example
NULL

show-ColorMapping-method

Print the ColorMapping Object

Description
Print the ColorMapping Object

Usage
## S4 method for signature 'ColorMapping'
show(object)

Arguments
object A ColorMapping-class object.

Value
This function returns no value.

Author(s)
Zuguang Gu <z.gu@dkfz.de>
**Examples**

```r
# There is no example
NULL
```

**show-dispatch**  
*Method dispatch page for show*

**Description**

Method dispatch page for show.

**Dispatch**

show can be dispatched on following classes:

- `show,AnnotationFunction-method, AnnotationFunction-class` class method
- `show,Heatmap-method, Heatmap-class` class method
- `show,HeatmapList-method, HeatmapList-class` class method
- `show,ColorMapping-method, ColorMapping-class` class method
- `show,HeatmapAnnotation-method, HeatmapAnnotation-class` class method
- `show,SingleAnnotation-method, SingleAnnotation-class` class method

**Examples**

```r
# no example
NULL
```

**show-Heatmap-method**  
*Draw the Single Heatmap with Defaults*

**Description**

Draw the Single Heatmap with Defaults

**Usage**

```r
## S4 method for signature 'Heatmap'
show(object)
```

**Arguments**

- `object` A `Heatmap-class` object.
Details
It actually calls \texttt{drawHeatmap-method}, but only with default parameters. If users want to customize the heatmap, they can pass parameters directly to \texttt{drawHeatmap-method}.

Value
The \texttt{HeatmapList-class} object.

Author(s)
Zuguang Gu <z.gu@dkfz.de>

Examples
# There is no example
NULL
show-HeatmapList-method

Draw a list of heatmaps with default parameters

Description

Draw a list of heatmaps with default parameters

Usage

## S4 method for signature 'HeatmapList'

show(object)

Arguments

object a HeatmapList-class object.

Details

Actually it calls draw,HeatmapList-method, but only with default parameters. If users want to customize the heatmap, they can pass parameters directly to draw,HeatmapList-method.

Value

This function returns no value.

Examples

# There is no example
NULL

show-SingleAnnotation-method

Print the SingleAnnotation object

Description

Print the SingleAnnotation object

Usage

## S4 method for signature 'SingleAnnotation'

show(object)
Arguments

object A SingleAnnotation-class object.

Value

No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

---

SingleAnnotation Constructor Method for SingleAnnotation Class

Description

Constructor Method for SingleAnnotation Class

Usage

SingleAnnotation(name, value, col, fun, 
    label = NULL, 
    na_col = "grey", 
    which = c("column", "row"), 
    show_legend = TRUE, 
    gp = gpar(col = NA), 
    border = FALSE, 
    legend_param = list(), 
    show_name = TRUE, 
    name_gp = gpar(fontsize = 12), 
    name_offset = NULL, 
    name_side = ifelse(which == "column", "right", "bottom"), 
    name_rot = NULL, 
    simple_anno_size = ht_opt$simple_anno_size, 
    width = NULL, height = NULL)
Arguments

- **name**: Name for the annotation. If it is not specified, an internal name is assigned.
- **value**: A vector or a matrix of discrete or continuous values.
- **col**: Colors corresponding to value. If the mapping is discrete, the value of col should be a named vector; If the mapping is continuous, the value of col should be a color mapping function.
- **fun**: A user-defined function to add annotation graphics. The argument of this function should be at least a vector of index that corresponds to rows or columns. Normally the function should be constructed by `AnnotationFunction` if you want the annotation supports splitting. See **Details** for more explanation.
- **label**: Label for the annotation. By default is the annotation name.
- **na_col**: Color for NA values in the simple annotations.
- **which**: Whether the annotation is a row annotation or a column annotation?
- **show_legend**: If it is a simple annotation, whether show legend in the final heatmap?
- **gp**: Since simple annotation is represented as rows of grids. This argument controls graphic parameters for the simple annotation. The fill parameter is ignored here.
- **border**: border, only work for simple annotation
- **legend_param**: Parameters for the legend. See `color_mapping_legend,ColorMapping-method` for all possible options.
- **show_name**: Whether show annotation name?
- **name_gp**: Graphic parameters for annotation name.
- **name_offset**: Offset to the annotation, a unit object.
- **name_side**: 'right' and 'left' for column annotations and 'top' and 'bottom' for row annotations.
- **name_rot**: Rotation of the annotation name.
- **simple_anno_size**: size of the simple annotation.
- **width**: The width of the plotting region (the viewport) that the annotation is drawn. If it is a row annotation, the width must be an absolute unit.
- **height**: The height of the plotting region (the viewport) that the annotation is drawn. If it is a column annotation, the width must be an absolute unit.

Details

A single annotation is a basic unit of complex heatmap annotations where the heatmap annotations are always a list of single annotations. An annotation can be simply heatmap-like (here we call it simple annotation) or more complex like points, lines, boxes (for which we call it complex annotation).

In the `SingleAnnotation` constructor, value, col, na_col are used to construct a `anno_simple` annotation function which is generated internally by `AnnotationFunction`. The legend of the simple annotation can be automatically generated.
For constructing a complex annotation, users need to use `fun` which is a user-defined function. Normally it is constructed by `AnnotationFunction`. One big advantage for using `AnnotationFunction` is the annotation function or the graphics drawn by the annotation function can be split according to row splitting or column splitting of the heatmap. Users can also provide a "pure" function which is a normal R function for the `fun` argument. The function only needs one argument which is a vector of index for rows or columns depending whether it is a row annotation or column annotation. The other two optional arguments are the current slice index and total number of slices. See **Examples** section for an example. If it is a normal R function, it will be constructed into the `AnnotationFunction-class` object internally.

The `SingleAnnotation-class` is a simple wrapper on top of `AnnotationFunction-class` only with annotation name added. The class also store the "extended area" relative to the area for the annotation graphics. The extended areas are those created by annotation names and axes.

Value

A `SingleAnnotation-class` object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

There are following built-in annotation functions that can be directly used to generate complex annotations: `anno_simple`, `anno_points`, `anno_lines`, `anno_barplot`, `anno_histogram`, `anno_boxplot`, `anno_density`, `anno_text`, `anno_joyplot`, `anno_horizon`, `anno_image`, `anno_block`, `anno_summary` and `anno_mark`.

Examples

```r
ha = SingleAnnotation(value = 1:10)
draw(ha, test = "single column annotation")

m = cbind(1:10, 10:1)
colnames(m) = c("a", "b")
ha = SingleAnnotation(value = m)
draw(ha, test = "matrix as column annotation")

anno = anno_barplot(matrix(nc = 2, c(1:10, 10:1)))
ha = SingleAnnotation(fun = anno)
draw(ha, test = "anno_barplot as input")

fun = function(index, k = 1, n = 1) {
  # because there variables outside the function for use, we put it a local environment
  value = 1:10
  pushViewport(viewport(xscale = c(0.5, length(index) + 0.5), yscale = range(value)))
  grid.points(seq_along(index), value[index])
  grid.rect()
}
```

if(k == 1) grid.yaxis()
  popViewport()
}
})

ha = SingleAnnotation(fun = fun, height = unit(4, "cm"))
draw(ha, index = 1:10, test = "self-defined function")

SingleAnnotation-class

Class for a Single Annotation

Description

Class for a Single Annotation

Details

The SingleAnnotation-class is used for storing data for a single annotation and provides methods for drawing annotation graphics.

Methods

The SingleAnnotation-class provides following methods:

- SingleAnnotation: constructor method
- draw,SingleAnnotation-method: draw the single annotation.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

See Also

The SingleAnnotation-class is always used internally. The public HeatmapAnnotation-class contains a list of SingleAnnotation-class objects and is used to add annotation graphics on heatmaps.

Examples

# There is no example
NULL
### size.AnnotationFunction

*Size of the AnnotationFunction Object*

**Description**

Size of the AnnotationFunction Object

**Usage**

```r
## S3 method for class 'AnnotationFunction'
size(x, ...)
```

**Arguments**

- `x`: The `AnnotationFunction-class` object.
- `...`: Other arguments.

**Details**

It returns the width if it is a row annotation and the height if it is a column annotation. Internally used.

**Examples**

```r
anno = anno_points(1:10)
ComplexHeatmap:::size(anno)
anno = anno_points(1:10, which = "row")
ComplexHeatmap:::size(anno)
```

### size.HeatmapAnnotation

*Size of the HeatmapAnnotation Object*

**Description**

Size of the HeatmapAnnotation Object

**Usage**

```r
## S3 method for class 'HeatmapAnnotation'
size(x, ...)
```
Arguments

  x  
       The HeatmapAnnotation-class object.

  ...  
       Other arguments.

Details

It returns the width if it is a row annotation and the height if it is a column annotation.
Internally used.

Examples

# There is no example
NULL

---

**Description**

Size of the SingleAnnotation Object

**Usage**

```r
## S3 method for class 'SingleAnnotation'
size(x, ...)
```

Arguments

  x  
       The SingleAnnotation-class object.

  ...  
       Other arguments.

Details

It returns the width if it is a row annotation and the height if it is a column annotation.
Internally used.

Examples

# There is no example
NULL

---
sizeAssign.AnnotationFunction

Assign the Size to the AnnotationFunction Object

Description

Assign the Size to the AnnotationFunction Object

Usage

## S3 replacement method for class 'AnnotationFunction'

size(x, ...) <- value

Arguments

x The AnnotationFunction-class object.
value A unit object.
...
Other arguments.

Details

It assigns to the width if it is a row annotation and the height if it is a column annotation. Internally used.

Examples

anno = anno_points(1:10)
ComplexHeatmap:::size(anno) = unit(4, "cm")
ComplexHeatmap:::size(anno)

sizeAssign.HeatmapAnnotation

Assign the Size to the HeatmapAnnotation Object

Description

Assign the Size to the HeatmapAnnotation Object

Usage

## S3 replacement method for class 'HeatmapAnnotation'

size(x, ...) <- value
Assign the Size to the SingleAnnotation Object

Description

Assign the Size to the SingleAnnotation Object

Usage

```r
## S3 replacement method for class 'SingleAnnotation'
size(x, ...) <- value
```

Arguments

- `x` The `HeatmapAnnotation-class` object.
- `value` A `unit` object.
- `...` Other arguments.

Details

It assigns the width if it is a row annotation and the height if it is a column annotation. Internally used.

Examples

```r
# There is no example
NULL
```
smartAlign2

Adjust positions of rectangular shapes

Description

Adjust positions of rectangular shapes

Usage

smartAlign2(start, end, range, plot = FALSE)

Arguments

- `start`: position which corresponds to the start (bottom or left) of the rectangle-shapes.
- `end`: position which corresponds to the end (top or right) of the rectangular shapes.
- `range`: data ranges (the minimal and maximal values)
- `plot`: Whether plot the correspondence between the original positions and the adjusted positions. Only for testing.

Details

This is an improved version of the `smartAlign`.

It adjusts the positions of the rectangular shapes to make them do not overlap

Examples

```r
range = c(0, 10)
pos1 = rbind(c(1, 2), c(5, 7))
smartAlign2(pos1, range = range, plot = TRUE)

range = c(0, 10)
pos1 = rbind(c(-0.5, 2), c(5, 7))
smartAlign2(pos1, range = range, plot = TRUE)

pos1 = rbind(c(-1, 2), c(3, 4), c(5, 6), c(7, 11))
pos1 = pos1 + runif(length(pos1), max = 0.3, min = -0.3)
par(mfrow = c(3, 3))
for(i in 1:9) {
  ind = sample(4, 4)
  smartAlign2(pos1[ind, ], range = range, plot = TRUE)
}
par(mfrow = omfrow)

pos1 = rbind(c(3, 6), c(4, 7))
smartAlign2(pos1, range = range, plot = TRUE)

pos1 = rbind(c(1, 8), c(3, 10))
smartAlign2(pos1, range = range, plot = TRUE)
```
str.comb_mat

Description
str method

Usage
## S3 method for class 'comb_mat'
str(object, ...)

Arguments
object A combination matrix returned by make_comb_mat.
... Other arguments.

Examples
# There is no example
NULL

subset_gp

Subset a gpar Object

Description
Subset a gpar Object

Usage
subset_gp(gp, i)

Arguments
gp A gpar object.
i A vector of indices.

Value
A gpar object.

Examples
gp = gpar(col = 1:10, fill = 1)
subset_gp(gp, 1:5)
**subset_matrix_by_row**  Subset the Matrix by Rows

**Description**
Subset the Matrix by Rows

**Usage**
subset_matrix_by_row(x, i)

**Arguments**
- **x**  A matrix.
- **i**  The row indices.

**Details**
Mainly used for constructing the `AnnotationFunction-class` object.

**Examples**
# There is no example
NULL

**subset_no**  Do not do subsetting

**Description**
Do not do subsetting

**Usage**
subset_no(x, i)

**Arguments**
- **x**  A vector.
- **i**  The indices.

**Details**
Mainly used for constructing the `AnnotationFunction-class` object.
**subset_vector**

**Examples**

```r
# There is no example
NULL
```

**Description**

Subset the vector

**Usage**

```r
subset_vector(x, i)
```

**Arguments**

- `x` A vector.
- `i` The indices.

**Details**

Mainly used for constructing the `AnnotationFunction-class` object.

**Examples**

```r
# There is no example
NULL
```

**summary.Heatmap**

**Print the Summary of a Heatmap**

**Description**

Print the Summary of a Heatmap

**Usage**

```r
## S3 method for class 'Heatmap'
summary(object, ...)  
```

**Arguments**

- `object` A `Heatmap-class` object.
- `...` Other arguments.
summary.HeatmapList

Summary of a Heatmap List

Description
Summary of a Heatmap List

Usage
## S3 method for class 'HeatmapList'
summary(object, ...)

Arguments
object       A HeatmapList-class object.
...          Other arguments.

Examples
# There is no example
NULL

---

t.comb_mat

Transpost the Combination Matrix

Description
Transpost the Combination Matrix

Usage
## S3 method for class 'comb_mat'
t(x)

Arguments
x       A combination matrix returned by make_comb_mat.
Examples

```r
c <- sample(letters, 20)
l <- list(a = sample(letters, 10),
         b = sample(letters, 15),
         c = sample(letters, 20))
m <- make_comb_mat(lt)
t(m)
```

Test alter_fun for oncoPrint()

Description

Test alter_fun for oncoPrint()

Usage

test_alter_fun(fun, type, asp_ratio = 1)

Arguments

- `type`: A vector of alteration types. It is only used when `fun` is a single function.
- `asp_ratio`: The aspect ratio (width/height) for the small rectangles.

Details

This function helps you to have a quick view of how the graphics for each alteration type and combinations look like.

Examples

```r
alter_fun = list(
  mut1 = function(x, y, w, h) grid.rect(x, y, w, h, gp = gpar(fill = "red", col = NA)),
  mut2 = function(x, y, w, h) grid.rect(x, y, w, h, gp = gpar(fill = "blue", col = NA)),
  mut3 = function(x, y, w, h) grid.rect(x, y, w, h, gp = gpar(fill = "yellow", col = NA)),
  mut4 = function(x, y, w, h) grid.rect(x, y, w, h, gp = gpar(fill = "purple", col = NA)),
  mut5 = function(x, y, w, h) grid.points(x, y, pch = 16),
  mut6 = function(x, y, w, h) grid.points(x, y, pch = 16),
  mut7 = function(x, y, w, h) grid.segments(x - w*0.5, y - h*0.5, x + w*0.5, y + h*0.5, gp = gpar(lwd = 2))
)
test_alter_fun(alter_fun)
```
textbox_grob

A simple grob for the word cloud

Description

A simple grob for the word cloud

Usage

textbox_grob(text, x = unit(0.5, "npc"), y = unit(0.5, "npc"), just = "centre",
gp = gpar(), background_gp = gpar(col = "black", fill = "transparent"), round_corners = FALSE, r = unit(0.1, "snpc"),
line_space = unit(4, "pt"), text_space = unit(4, "pt"), max_width = unit(100, "mm"),
padding = unit(4, "pt"), first_text_from = "top", add_new_line = FALSE, word_wrap = FALSE)

Arguments

text  A vector of texts. The value can be single words or phrases/sentences.
x    X position.
y    Y position.
just Justification of the box in the viewport.
gp Graphics parameters of texts.
background_gp Graphics parameters for the box.
round_corners Whether to draw round corners for the box.
r Radius of the round corners.
line_space Space between lines. The value can be a unit object or a numeric scalar which is measured in mm.
text_space Space between texts The value can be a unit object or a numeric scalar which is measured in mm.
max_width The maximal width of the viewport to put the word cloud. The value can be a unit object or a numeric scalar which is measured in mm. Note this might be larger than the final width of the returned grob object.
padding Padding of the box, i.e. space between text and the four box borders. The value should be a unit object with length 1, 2 or 4. If length of the input unit is 2, the first value is the padding both to the top and to the bottom, and the second value is the padding to the left and right. If length of the input unit is 4, the four values correspond to paddings to the bottom, left, top and right of the box.
first_text_from Should the texts be added from the top of the box or from the bottom? Value should be either "top" or "bottom".
add_new_line Whether to add new line after every text? If TRUE, each text will be in a separated line.
word_wrap Whether to apply word wrap for phrases/sentences.
Value

A grob object. The width and height of the grob can be get by `grobWidth` and `grobHeight`.

Examples

```r
words = sapply(1:30, function(x) strrep(sample(letters, 1), sample(3:10, 1)))
grid.newpage()
grid.textbox(words, gp = gpar(fontsize = runif(30, min = 5, max = 30)))

sentences = c("This is sentence 1", "This is a long long long long long long sentence.")
grid.newpage()
grid.textbox(sentences)
grid.textbox(sentences, word_wrap = TRUE)
grid.textbox(sentences, word_wrap = TRUE, add_new_line = TRUE)
```

`unify_mat_list`  

Unify a List of Matrix

Description

Unify a List of Matrix

Usage

```r
unify_mat_list(mat_list, default = 0)
```

Arguments

- `mat_list`: A list of matrix. All of them should have dimension names.
- `default`: Default values for the newly added rows and columns.

Details

All matrix will be unified to have same row names and column names.

Value

A list of matrix

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
# There is no example
NULL
```
Make the UpSet plot

Usage

UpSet(m,
  comb_col = "black",
  pt_size = unit(3, "mm"), lwd = 2,
  bg_col = "#F0F0F0", bg_pt_col = "#CCCCCC",
  set_order = order(set_size(m), decreasing = TRUE),
  comb_order = if(attr(m, "param")$set_on_rows) {
    order.comb_mat(m[, set_order], decreasing = TRUE)
  } else {
    order.comb_mat(m[ set_order, ], decreasing = TRUE)
  },
  top_annotation = upset_top_annotation(m),
  right_annotation = upset_right_annotation(m),
  left_annotation = NULL,
  row_names_side = "left",
  ...)

Arguments

m A combination matrix returned by `make_comb_mat`. The matrix can be transposed to switch the position of sets and combination sets.

comb_col The color for the dots representing combination sets.

pt_size The point size for the dots representing combination sets.

lwd The line width for the combination sets.

bg_col Color for the background rectangles.

bg_pt_col Color for the dots representing the set is not selected.

set_order The order of sets.

comb_order The order of combination sets.

top_annotation A `HeatmapAnnotation` object on top of the combination matrix.

left_annotation A `HeatmapAnnotation` object on top of the combination matrix.

right_annotation A `HeatmapAnnotation` object on the right of the combination matrix.

row_names_side The side of row names.

... Other arguments passed to `Heatmap`. 
Details

By default, the sets are on rows and combination sets are on columns. The positions of the two types of sets can be switched by transposing the matrix.

When sets are on rows, the default top annotation is the barplot showing the size of each combination sets and the default right annotation is the barplot showing the size of the sets. The annotations are simply constructed by `HeatmapAnnotation` and `anno_barplot` with some parameters pre-set.

Users can check the source code of `upset_top_annotation` and `upset_right_annotation` to find out how the annotations are defined.

To change or to add annotations, users just need to define a new `HeatmapAnnotation` object. E.g. if we want to change the side of the axis and name on top annotation:

```r
Upset(..., top_annotation =
  HeatmapAnnotation(
    "Intersection size" = anno_barplot(
      comb_size(m),
      border = FALSE,
      gp = gpar(fill = "black"),
      height = unit(2, "cm"),
      axis_param = list(side = "right")
    ),
    annotation_name_side = "right",
    annotation_name_rot = 0)
)
```

To add more annotations on top, users just add it in `HeatmapAnnotation`:

```r
Upset(..., top_annotation =
  HeatmapAnnotation(
    "Intersection size" = anno_barplot(
      comb_size(m),
      border = FALSE,
      gp = gpar(fill = "black"),
      height = unit(2, "cm"),
      axis_param = list(side = "right")
    ),
    "anno1" = anno_points(...),
    "anno2" = some_vector,
    annotation_name_side = "right",
    annotation_name_rot = 0)
)
```

And so is for the right annotations.

`UpSet` returns a `Heatmap-class` object, which means, you can add it with other heatmaps and annotations by `+` or `%v%`. 
Examples

```r
set.seed(123)
l t = list(a = sample(letters, 10),
          b = sample(letters, 15),
          c = sample(letters, 20))
m = make_comb_mat(l t)
UpSet(m)
UpSet(t(m))

m = make_comb_mat(l t, mode = "union")
UpSet(m)
UpSet(m, comb_col = c(rep(2, 3), rep(3, 3), 1))

# compare two UpSet plots
set.seed(123)
l t1 = list(a = sample(letters, 10),
           b = sample(letters, 15),
           c = sample(letters, 20))
m1 = make_comb_mat(l t1)
set.seed(456)
l t2 = list(a = sample(letters, 10),
           b = sample(letters, 15),
           c = sample(letters, 20))
m2 = make_comb_mat(l t2)

max1 = max(c(set_size(m1), set_size(m2)))
max2 = max(c(comb_size(m1), comb_size(m2)))

UpSet(m1, top_annotation = upset_top_annotation(m1, ylim = c(0, max2)),
      right_annotation = upset_right_annotation(m1, ylim = c(0, max1)),
      column_title = "UpSet1") +
UpSet(m2, top_annotation = upset_top_annotation(m2, ylim = c(0, max2)),
      right_annotation = upset_right_annotation(m2, ylim = c(0, max1)),
      column_title = "UpSet2")
```

Description

UpSet Left Annotation

Usage

```r
upset_left_annotation(m,
gp = gpar(fill = "black"),
axis_param = list(direction = "reverse"),
width = unit(ifelse(set_on_rows, 2, 3), "cm"),
show_annotation_name = TRUE,
```
Arguments

- `m`: A combination matrix which is as same as the one for `UpSet`.
- `gp`: Graphic parameters for bars.
- `axis_param`: Parameters for axis.
- `width`: Width of the left annotation.
- `show_annotation_name`: Whether show annotation names?
- `annotation_name_gp`: Graphic parameters for annotation names.
- `annotation_name_offset`: Offset to the annotation name, a `unit` object.
- `annotation_name_side`: Side of the annotation name.
- `annotation_name_rot`: Rotation of the annotation name, it can only take values in `c(0, 90, 180, 270)`.
- `...`: Passed to `anno_barplot`, e.g. to set `add_numbers`.

Examples

```r
# There is no example
NULL
```

Description

Default UpSet Right Annotation

Usage

```r
upset_right_annotation(m,
  gp = gpar(fill = "black"),
  width = unit(ifelse(set_on_rows, 2, 3), "cm"),
  show_annotation_name = TRUE,
  annotation_name_gp = gpar(),
)```
Arguments

m  A combination matrix which is as same as the one for UpSet.
gp Graphic parameters for bars.
width Width of the right annotation.
show_annotation_name Whether show annotation names?
annotation_name_gp Graphic parameters for annotation names.
annotation_name_offset Offset to the annotation name, a unit object.
annotation_name_side Side of the annotation name.
annotation_name_rot Rotation of the annotation name, it can only take values in c(00, 90, 180, 270).
... Passed to anno_barplot, e.g. to set add_numbers.

Details

The default right annotation is actually barplot implemented by anno_barplot. For how to set the right annotation or left annotation in UpSet, please refer to UpSet.

If you want to use decorate_annotation function, the annotation name for the "sets" is set_size and the annotation name for the "intersection sets" are intersection_size and if under the union mode, it is union_size.

Examples

# There is no example
NULL
Usage

```r
upset_top_annotation(m,
    gp = gpar(fill = "black"),
    height = unit(ifelse(set_on_rows, 3, 2), "cm"),
    show_annotation_name = TRUE,
    annotation_name_gp = gpar(),
    annotation_name_offset = NULL,
    annotation_name_side = "left",
    annotation_name_rot = 0,
    ...)
```  

Arguments

- **m**: A combination matrix which is as same as the one for `UpSet`.
- **gp**: Graphic parameters for bars.
- **height**: The height of the top annotation.
- **show_annotation_name**: Whether show annotation names?
- **annotation_name_gp**: Graphic parameters for annotation names.
- **annotation_name_offset**: Offset to the annotation name, a `unit` object.
- **annotation_name_side**: Side of the annotation name.
- **annotation_name_rot**: Rotation of the annotation name, it can only take values in `c(00, 90, 180, 270)`.
- **...**: Passed to `anno_barplot`.

Details

The default top annotation is actually barplot implemented by `anno_barplot`. For how to set the top annotation or bottom annotation in `UpSet`, please refer to `UpSet`.

If you want to use `decorate_annotation` function, the annotation name for the "sets" is `set_size` and the annotation name for the "intersection sets" are `intersection_size` and if under the union mode, it is `union_size`.

Examples

```r
# There is no example
NULL
```
width.AnnotationFunction

*Width of the AnnotationFunction Object*

**Description**

Width of the AnnotationFunction Object

**Usage**

```r
## S3 method for class 'AnnotationFunction'
width(x, ...)
```

**Arguments**

- `x` A `AnnotationFunction-class` object.
- `...` Other arguments.

**Details**

Internally used.

**Examples**

```r
anno = anno_points(1:10)
ComplexHeatmap::width(anno)
anno = anno_points(1:10, which = "row")
ComplexHeatmap::width(anno)
```

---

width.Heatmap

*Width of the Heatmap*

**Description**

Width of the Heatmap

**Usage**

```r
## S3 method for class 'Heatmap'
width(x, ...)
```

**Arguments**

- `x` The `HeatmapList-class` object returned by `draw.Heatmap-method`.
- `...` Other arguments.
width.HeatmapAnnotation

Description

Width of the HeatmapAnnotation Object

Usage

## S3 method for class 'HeatmapAnnotation'
width(x, ...)

Arguments

x              The HeatmapAnnotation-class object.
...

Details

Internally used.

Examples

# There is no example
NULL

width.HeatmapList

Description

Width of the Heatmap List

Usage

## S3 method for class 'HeatmapList'
width(x, ...)

Examples

# There is no example
NULL
Arguments

x The **HeatmapList-class** object returned by `draw.HeatmapList-method`.

... Other arguments.

Examples

```r
# There is no example
NULL
```

---

**width.Legends**

*Width of the Legends*

Description

Width of the Legends

Usage

```r
## S3 method for class 'Legends'
width(x, ...)
```

Arguments

x The grob object returned by `Legend` or `packLegend`.

... Other arguments.

Value

The returned unit x is always in mm.

Examples

```r/lgd = Legend(labels = 1:10, title = "foo", legend_gp = gpar(fill = "red"))
ComplexHeatmap::width(lgd)
```
width.SingleAnnotation

*Width of the SingleAnnotation Object*

**Description**

Width of the SingleAnnotation Object

**Usage**

```r
## S3 method for class 'SingleAnnotation'
width(x, ...)
```

**Arguments**

- `x` The `SingleAnnotation-class` object.
- `...` Other arguments.

**Details**

Internally used.

**Examples**

```r
# There is no example
NULL
```

widthAssign.AnnotationFunction

*Assign the Width to the AnnotationFunction Object*

**Description**

Assign the Width to the AnnotationFunction Object

**Usage**

```r
## S3 replacement method for class 'AnnotationFunction'
width(x, ...) <- value
```

**Arguments**

- `x` The `AnnotationFunction-class` object.
- `...` Other arguments.
- `value` A `unit` object.
widthAssign.HeatmapAnnotation

Assign the Width to the HeatmapAnnotation Object

Details
Internally used.

Examples
# There is no example
NULL

widthAssign.HeatmapAnnotation

## S3 replacement method for class 'HeatmapAnnotation'
width(x, ...) <- value

Arguments
x The HeatmapAnnotation-class object.
value A unit object.
... Other arguments.

Details
Internally used.

Examples
# There is no example
NULL
widthAssign.SingleAnnotation

Assign the Width to the SingleAnnotation Object

Description

Assign the Width to the SingleAnnotation Object

Usage

```r
## S3 replacement method for class 'SingleAnnotation'
width(x, ...) <- value
```

Arguments

- `x`  
  The `SingleAnnotation-class` object.
- `value`  
  A `unit` object.
- `...`  
  Other arguments.

Details

Internally used.

Examples

```r
# There is no example
NULL
```

widthDetails.annotation_axis

Width for annotation_axis Grob

Description

Width for annotation_axis Grob

Usage

```r
## S3 method for class 'annotation_axis'
widthDetails(x)
```

Arguments

- `x`  
  The annotation_axis grob returned by `annotation_axis_grob`.
Details

The physical width of the grob can be get by `convertWidth(grobWidth(axis_grob), "mm"`).

Examples

```r
# There is no example
NULL
```

---

widthDetails.legend

**Grob width for packed_legends**

Description

Grob width for packed_legends

Usage

```r
## S3 method for class 'legend'
widthDetails(x)
```

Arguments

- `x` A legend object.

Examples

```r
# There is no example
NULL
```

---

widthDetails.legend_body

**Grob width for legend_body**

Description

Grob width for legend_body

Usage

```r
## S3 method for class 'legend_body'
widthDetails(x)
```

Arguments

- `x` A legend_body object.
widthDetails.packed_legends

Grob width for packed_legends

Description

Grob width for packed_legends

Usage

```r
## S3 method for class 'packed_legends'
widthDetails(x)
```

Arguments

- `x`: A packed_legends object.

Examples

```r
# There is no example
NULL
```

widthDetails.textbox

Width for textbox grob

Description

Width for textbox grob

Usage

```r
## S3 method for class 'textbox'
widthDetails(x)
```

Arguments

- `x`: The textbox grob returned by `textbox_grob`.

Value

A `unit` object.
Examples

# There is no example
NULL

### [.AnnotationFunction

Subset an AnnotationFunction Object

Description

Subset an AnnotationFunction Object

Usage

## S3 method for class 'AnnotationFunction'
x[i]

Arguments

x An AnnotationFunction-class object.
i A vector of indices.

Details

One good thing for designing the AnnotationFunction-class is it can be subsetted, and this is the base for the splitting of the annotations.

Examples

anno = anno_simple(1:10)
anno[1:5]
draw(anno[1:5], test = "subset of column annotation")

### [.comb_mat

Subset the Combination Matrix

Description

Subset the Combination Matrix

Usage

## S3 method for class 'comb_mat'
x[i, j, drop = FALSE]
Arguments

- **x**: A combination matrix returned by `make_comb_mat`.
- **i**: Indices on rows.
- **j**: Indices on columns.
- **drop**: It is always reset to `FALSE` internally.

Details

If sets are on rows of the combination matrix, the row indices correspond to sets and column indices correspond to combination sets, and if sets are on columns of the combination matrix, rows correspond to the combination sets.

If the index is one-dimension, e.g. `x[i]`, the index always corresponds to the combination sets.

You should not subset by the sets. It will give you wrong combination set size. The subsetting on sets are only used internally.

This subsetting method is mainly for subsetting combination sets, i.e., users can first use `comb_size` to get the size of each combination set, and filter them by the size.

Examples

```r
set.seed(123)
l <- list(a = sample(letters, 10),
         b = sample(letters, 15),
         c = sample(letters, 20))
m = make_comb_mat(l)
m2 = m[, comb_size(m) >= 3]
comb_size(m2)
m[comb_size(m) >= 3]
```

Description

Subset method of gridtext class

Usage

```r
## S3 method for class 'gridtext'
x[index]
```

Arguments

- **x**: A vector of labels generated by `gt_render`.
- **index**: Index
## Subset a Heatmap

### Description

Subset a Heatmap

### Usage

```r
## S3 method for class 'Heatmap'
ht[i, j]
```

### Arguments

- `x`  
  A `Heatmap-class` object.
- `i`  
  Row indices.
- `j`  
  Column indices.

### Examples

```r
m = matrix(rnorm(100), nrow = 10)
rownames(m) = letters[1:10]
colnames(m) = LETTERS[1:10]
ht = Heatmap(m)
ht[1:5, ]
ht[1:5]
ht[, 1:5]
ht[, 1:5]
ht[1:5, 1:5]
```
### .HeatmapAnnotation

Subset the HeatmapAnnotation object

**Description**

Subset the HeatmapAnnotation object

**Usage**

```r
## S3 method for class 'HeatmapAnnotation'
x[i, j]
```

**Arguments**

- `x`: A `HeatmapAnnotation-class` object.
- `i`: Index of observations.
- `j`: Index of annotations.

**Examples**

```r
test <- HeatmapAnnotation(foo = 1:10, bar = anno_points(10:1),
sth = cbind(1:10, 10:1))
test[1:5, ]
test[, c("foo", "bar")]
test[, 1:2]
test[1:5, c("foo", "sth")]
```

### .HeatmapList

Subset a HeatmapList object

**Description**

Subset a HeatmapList object

**Usage**

```r
## S3 method for class 'HeatmapList'
x[i, j]
```

**Arguments**

- `x`: A `HeatmapList-class` object
- `i`: row indices
- `j`: column indices
Details

If the heatmap list is horizontal, i is the row indices and j corresponds to heatmap names and single annotation names. and if the heatlist is vertical, i corresponds to heatmap/annotation names and j is the column indices.

Examples

```r
ht_list = Heatmap(matrix(rnorm(100), 10), name = "rnorm") +
  rowAnnotation(foo = 1:10, bar = anno_points(10:1)) +
  Heatmap(matrix(runif(100), 10), name = "runif")
summary(ht_list[1:5, ])
summary(ht_list[1:5, 1])
summary(ht_list[1:5, "rnorm"])
summary(ht_list[1:5, c("rnorm", "foo")])

ht_list = Heatmap(matrix(rnorm(100), 10), name = "rnorm") %v%
  columnAnnotation(foo = 1:10, bar = anno_points(10:1)) %v%
  Heatmap(matrix(runif(100), 10), name = "runif")
summary(ht_list[, 1:5])
summary(ht_list[1, 1:5])
summary(ht_list["rnorm", 1:5])
summary(ht_list[c("rnorm", "foo"), 1:5])
```

[.SingleAnnotation  Subset an SingleAnnotation Object

Description

Subset an SingleAnnotation Object

Usage

```
## S3 method for class 'SingleAnnotation'

x[i]
```

Arguments

x  An SingleAnnotation-class object.
i  A vector of indices.

Details

The SingleAnnotation class object is subsettable only if the containing AnnotationFunction-class object is subsettable. All the anno_* functions are subsettable, so if the SingleAnnotation object is constructed by one of these functions, it is also subsettable.
Examples

```r
ha = SingleAnnotation(value = 1:10)
ha[1:5]
draw(ha[1:5], test = "ha[1:5]")
```

Vertically Add Heatmaps or Annotations to a Heatmap List

Description

Vertically Add Heatmaps or Annotations to a Heatmap List

Usage

```r
x %v% y
```

Arguments

- `x`: A `Heatmap-class` object, a `HeatmapAnnotation-class` object or a `HeatmapList-class` object.
- `y`: A `Heatmap-class` object, a `HeatmapAnnotation-class` object or a `HeatmapList-class` object.

Details

It is only a helper function. It actually calls `add_heatmap,Heatmap-method`, `add_heatmap,HeatmapList-method` or `add_heatmap,HeatmapAnnotation-method` depending on the class of the input objects.

The `HeatmapAnnotation-class` object to be added should only be column annotations.

`x` and `y` can also be `NULL`.

Value

A `HeatmapList-class` object.

Author(s)

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See Also

`.AdditiveUnit` operator is used for horizontal heatmap list.

Examples

```r
# There is no example
NULL
```
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