Package ‘ComplexHeatmap’

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Type Package

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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.

biocViews Software, Visualization, Sequencing

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ComplexHeatmap-package

Make complex heatmaps

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>
See Also

%v% operator is used for vertical heatmap list.

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
Description

Add Heatmap to the Heatmap List

Usage

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

Arguments

- **object** A `Heatmap-class` object.
- **x** a `Heatmap-class` object, a `HeatmapAnnotation-class` object or a `HeatmapList-class` object.
- **direction** Whether the heatmap is added horizontal or vertically?

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 Annotations or Heatmaps as a Heatmap List

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
```
Description
Add heatmaps and row annotations to the heatmap list

Usage
```r
## 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
```r
# 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

# There is no example
NULL

alter_graphic

Automatically generate alter_fun

Description

Automatically generate alter_fun

Usage

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
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

```r
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.
**AnnotationFunction**

- **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 `SingleAnnotation` or even `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 build-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

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()
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))
Size of the Annotation Legends

Description

Size of the Annotation Legends

Usage

```r
## S4 method for signature 'HeatmapList'
annotation_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 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

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

---

anno_barplot  Barplot Annotation

Description

Barplot Annotation

Usage

```r
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.
**anno_barplot**

- **beside**: When `x` is a matrix, will bars be positioned beside each other or as stacked bars?
- **attach**: When `beside` is `TRUE`, it controls whether bars should be attached.
- **gp**: Graphic 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.

- **ylim**: Data ranges. By default it is `range(x)` if `x` is a vector, or `range(rowSums(x))` if `x` is a matrix.
- **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.
- **add_numbers**: Whether to add numbers to the bars. It only works when `x` is a simple vector.
- **numbers_gp**: Graphics parameters for the numbers.
- **numbers_rot**: Rotation of numbers.
- **numbers_offset**: Offset to the default positions (1mm away the top of the bars).
- **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**

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

m = matrix(runif(4*10), nc = 4)
m = t(apply(m, 1, function(x) x/sum(x)))
anno = anno_barplot(m, gp = gpar(fill = 2:5), bar_width = 1, height = unit(6, "cm"))
draw(anno, test = "proportion matrix")
```
anno_block

---

### 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(labels[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, nn) {
        grid.rect(gp = gpar(fill = col[nn]))
    },
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


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))
```

---

### anno_density

**Density Annotation**

**Description**

Density Annotation

**Usage**

```r
anno_density(x, which = c("column", "row"),
  type = c("lines", "violin", "heatmap"), xlim = NULL, max_density = NULL,
  heatmap_colors = rev(brewer.pal(name = "RdYlBu", n = 11)),
  joyplot_scale = 1, border = TRUE, 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?
- **type**: Type of graphics to represent density distribution. "lines" for normal density plot, "violine" for violin plot and "heatmap" for heatmap visualization of density distribution.
- **xlim**: Range on x-axis.
anno_density

- **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**

```r
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**

**Description**

Empty Annotation

**Usage**

```r
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 the following example, an empty annotation is first created and later points are added:

```r
m = matrix(rnorm(100), 10)
h = Heatmap(m, top_annotation = HeatmapAnnotation(pt = anno_empty()))
h = draw(h)
c = column_order(h)[[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[c], pch = 16, default.units = "native")
  grid.yaxis()
  popViewport()
})
```

And it is similar as using `anno_points`:

```r
Heatmap(m, top_annotation = HeatmapAnnotation(pt = anno_points(pt_value)))
```
Value

An annotation function which can be used in HeatmapAnnotation.

See Also

empty-annotation

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**: Wether 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

```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

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**

```r
l = lapply(1:20, function(x) cumprod(1 + runif(1000, -x/100, x/100)) - 1)
anno = anno_horizon(l, which = "row")
draw(anno, test = "horizon chart")
anno = anno_horizon(l, which = "row",
  gp = gpar(pos_fill = "orange", neg_fill = "darkgreen"))
draw(anno, test = "horizon chart, col")
anno = anno_horizon(l, which = "row", negative_from_top = TRUE)
draw(anno, test = "horizon chart + negative_from_top")
anno = anno_horizon(l, which = "row", gap = unit(1, "mm"))
draw(anno, test = "horizon chart + gap")
anno = anno_horizon(l, 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  

**Description**

Image Annotation

**Usage**

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

**Arguments**

- `image`  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 draw.
- `which`  Whether it is a column annotation or a row annotation?
- `border`  Whether draw borders of the annotation region?
- `gp`  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.
- `space`  The space around the image to the annotation grid borders. The value should be a `unit` object.
- `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**

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`.
anno_joyplot

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

m = matrix(rnorm(5000), nc = 50)
lc = apply(m, 2, function(x) data.frame(density(x)[c("x", "y")]))
anno = anno_joyplot(lc, 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**
  - Whether 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

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", 90, 0), 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

labels_rot  Rotations of labels, scalar.
padding     Padding between neighbouring labels in the plot.
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.

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)
anno_oncoprint_barplot

Barplot Annotation for oncoPrint

Description

Barplot Annotation for oncoPrint

Usage

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)**

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**Examples**

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

---

**anno_points**

Points Annotation

**Description**

Points Annotation

**Usage**

```r
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

```r
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 nrow 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")
```

Description

Summary Annotation

Usage

```r
anno_summary(which = c("column", "row"), border = TRUE, bar_width = 0.8,
axis = TRUE, axis_param = default_axis_param(which),
ylim = NULL, extend = 0.05, outline = TRUE, box_width = 0.6,
pch = 1, size = unit(2, "mm"), gp = gpar(),
width = NULL, height = NULL)
```
**Arguments**

- **which**: Whether it is a column annotation or a row annotation?
- **border**: Whether draw borders of the annotation region?
- **bar_width**: Relative width of the bars. The value should be smaller than one.
- **axis**: Whether to add axis?
- **axis_param**: parameters for controlling axis. See `default_axis_param` for all possible settings and default parameters.
- **ylim**: Data ranges. `ylim` for barplot is enforced to be `c(0, 1)`.
- **extend**: The extension to both side of `ylim`. The value is a percent value corresponding to `ylim[2] - ylim[1]`. This argument is only for boxplot.
- **outline**: Whether draw outline of boxplots?
- **box_width**: Relative width of boxes. The value should be smaller than one.
- **pch**: Point style.
- **size**: Point size.
- **gp**: Graphic 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**

`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
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 innpc 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**

```r
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")
```

---

**anno_textbox**

**Text box annotations**

**Description**

Text box annotations

**Usage**

```r
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

<table>
<thead>
<tr>
<th>anno_zoom</th>
<th>Zoom annotation</th>
</tr>
</thead>
</table>

Description

Zoom annotation

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 func-
            tion must have a 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?

columns    Side of the boxes If it is a column annotation, valid values are "top" and "bot-
          tom"; If it is a row annotation, valid values are "left" and "right".
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)
attach_annotation-Heatmap-method

Attach heatmap annotations to the heatmap

Description

Attach heatmap annotations to the heatmap

Usage

## 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

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

Draw 3D bars

Description

Draw 3D bars

Usage

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.\texttt{ColorMapping} \hspace{1cm} \textit{Concatenate A List of ColorMapping objects}

\textbf{Description}

Concatenate A List of ColorMapping objects

\textbf{Usage}

\begin{verbatim}
## S3 method for class 'ColorMapping'
c(..., name = NULL)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \ldots \hspace{1cm} A list of \texttt{ColorMapping-class} objects.
  \item name \hspace{1cm} Name of the new merged color mapping.
\end{itemize}

\textbf{Details}

Only discrete color mappings can be concatenated.

\textbf{Examples}

\begin{verbatim}
cm1 = ColorMapping(colors = c("A" = "red", "B" = "black"))
cm2 = ColorMapping(colors = c("B" = "blue", "C" = "green"))
c(cm1, cm2)
\end{verbatim}

\textbf{c.\texttt{HeatmapAnnotation} \hspace{1cm} Concatenate Heatmap Annotations}

\textbf{Description}

Concatenate Heatmap Annotations

\textbf{Usage}

\begin{verbatim}
## S3 method for class 'HeatmapAnnotation'
c(..., gap = unit(1, "points"))
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \ldots \hspace{1cm} \texttt{HeatmapAnnotation-class} objects.
  \item gap \hspace{1cm} Gap between the groups of annotations.
\end{itemize}
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

```
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**

`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**

`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,ColorMapping-method`: mapping values to colors.
- `color_mapping_legend,ColorMapping-method`: 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,
```
color_mapping_legend-ColorMapping-method

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.
lables_gp Graphical parameters for legend labels.
lables_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

```r
# 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

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

Value

A `HeatmapAnnotation-class` object.
Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

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

Usage

## 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.
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)
column_dend(ht)
ht = Heatmap(mat, column_km = 2)
ht = draw(ht)
column_dend(ht)
```

Description

Get Column Dendrograms from a hHeatmap 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

```r
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

```r
# no example
NULL
```

---

column_order-Heatmap-method  

*Get Column Order from a Heatmap List*

---

Description

Get Column Order from a Heatmap List
Usage

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

---

Description

Get Column Order from a Heatmap List

Usage

```r
## 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.
**comb_degree**

**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)
```

<table>
<thead>
<tr>
<th>comb_degree</th>
<th>Degrees of the Combination sets</th>
</tr>
</thead>
</table>

**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)
lt = list(a = sample(letters, 10),
          b = sample(letters, 15),
          c = sample(letters, 20))
m = make_comb_mat(lt)
comb_degree(m)
```
comb_name

Names of the Combination sets

Description

Names of the Combination sets

Usage

```
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

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

comb_size

Sizes of the Combination sets

Description

Sizes of the Combination sets

Usage

```
comb_size(m, degree = NULL)
```
compare_heatmap

Arguments

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

- 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)
lc = list(a = sample(letters, 10),
         b = sample(letters, 15),
         c = sample(letters, 20))
m = make_comb_mat(lc)
comb_size(m)
```

Description

Compare heatmaps between `stats::heatmap()` and `ComplexHeatmap::heatmap()`

Usage

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

Arguments

... The same set of arguments passed to `stats::heatmap` and `ComplexHeatmap::heatmap`.

Details

The function plots two heatmaps, one by `stats::heatmap()` and one by `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.
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

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

## 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
## 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
# 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

---

**component_width-Heatmap-method**

*Widths of Heatmap Components*

---

**Description**

Widths of Heatmap Components

**Usage**

```r
## 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

## 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

```r
# 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
**Examples**

```r
# no example
NULL
```

**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(attention, 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)
```

---

decorate_column_dend  Decorate Heatmap Column Dendrograms

Description

Decorate Heatmap Column Dendrograms
**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_names  Decorate Heatmap Column Names**

**Description**

Decorate Heatmap Column Names

**Usage**

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

**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
```

---

**decorate_column_title**  *Decorate Heatmap Column Titles*

**Description**

Decorate Heatmap Column Titles

**Usage**

```r
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**

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

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"))
})
```
**decorator_row_dend**  
*Decorate Heatmap Row Dendrograms*

**Description**  
Decorate Heatmap Row Dendrograms

**Usage**  
`decorator_row_dend(..., envir = new.env(parent = parent.frame()))`

**Arguments**  
- `...` Pass to `decorator_dend`.  
- `envir` Where to look for variables inside code?

**Details**  
This is a helper function which pre-defined which argument in `decorator_dend`.

**Value**  
The function returns no value.

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

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

---

**decorator_row_names**  
*Decorate Heatmap Row Names*

**Description**  
Decorate Heatmap Row Names

**Usage**  
`decorator_row_names(..., envir = new.env(parent = parent.frame()))`
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
```

---

decorate_row_title  Decorate Heatmap Row Titles

Description

Decorate Heatmap Row Titles

Usage

```r
decorate_row_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_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**
**default_axis_param**

Examples

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

---

The Default Parameters for Annotation Axis

Description

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` Graphc 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 invoild 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**

```r
default_get_type(x)
```

**Arguments**

- `x` 
  A strings which encode multiple alterations.

**Details**

It recognizes following separators: ;:, |.

**Examples**

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

---

**dendrogramGrob**  
*Grob for Dendrogram*

**Description**

Grob for Dendrogram

**Usage**

```r
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
```

---

---

---

---

**dend_xy**

**Description**

Coordinates of the Dendrogram

**Usage**

```r
dend_xy(dend)
```

**Arguments**

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

**Examples**

```r
# There is no example
NULL
```
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_quartiles Whether show quartile 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?
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.

Pass to `Heatmap`.

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

Multiple cores for calculating `ks` distance.

Pass to `Heatmap`.

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.

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

Zuguang Gu <z.gu@dkfz.de>


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

```r
# 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

```r
# no example
NULL
```

---

**draw-Heatmap-method**

*Draw a Single Heatmap*

---

**Description**

Draw a Single Heatmap

**Usage**

```r
## 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

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

---

draw-HeatmapAnnotation-method

*Draw the Heatmap Annotations*

Description

Draw the Heatmap Annotations

Usage

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

object  A HeatmapAnnotation-class object.
index  A vector of indices.
k  The current slice index for the annotation if it is split.
n  Total number of slices.
...  Pass to viewport which contains all the annotations.
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 and pass to the draw.SingleAnnotation-method.

Value

No value is returned.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
 NULL

---

draw-HeatmapList-method

\textit{Draw a list of heatmaps}

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,
class_row_sides = 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,
class_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 all 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
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
**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()
```

---

**draw**-**SingleAnnotation**-method

*Draw the Single Annotation*

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.
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

```r
## 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
```
Description
Draw Heatmap Dendrograms

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

Arguments
object Aheatmap-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
```
**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
```
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
```
**draw_heatmap_list-HeatmapList-method**

*Draw the List of Heatmaps*

**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
```
Method dispatch page for \texttt{draw_title}.

**Dispatch**

\texttt{draw_title} can be dispatched on following classes:

- \texttt{draw_title,HeatmapList-method,HeatmapList-class} class method
- \texttt{draw_title,Heatmap-method,Heatmap-class} class method

**Examples**

```r
# no example
NULL
```

---

Draw Heatmap Title

**Description**

Draw Heatmap Title

**Usage**

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

**Arguments**

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

**Details**

A viewport is created which contains heatmap title.
This function is only for internal use.
**draw_title-HeatmapList-method**

**Value**

This function returns no value.

**Author(s)**

Zuguang Gu <z.gu@dkfz.de>

**Examples**

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

---

**Description**

Draw Heatmap List Title

**Usage**

```r
## 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

```r
# 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)
l = list(a = sample(letters, 10),
        b = sample(letters, 15),
        c = sample(letters, 20))
m = make_comb_mat(l)
extract_comb(m, "110")
```

---

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

**Description**

Visualize Frequency Distribution by Heatmap
frequencyHeatmap

Usage

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.
rangle 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)
```

---

full_comb_code  

Full set of code of combination sets

Description

Full set of code of combination sets

Usage

```
full_comb_code(n, complement = FALSE)
```

Arguments

- `n`  
  Number of sets
- `complement`  
  Whether include the code for complement set?
### 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
lt = 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()
```

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)
```
popViewport()

grid.dendrogram(dend, test = TRUE)

require(dendextend)
dend = color_branches(dend, k = 2)
dend = adjust_dend_by_x(dend, unit(sort(runif(10)*10), "cm"))
grid.dendrogram(dend, test = TRUE)

grid.draw.Legends

---

**grid.draw.Legends**  
*Draw the Legends*

---

**Description**

Draw the Legends

**Usage**

```r
## 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**

```r
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>&nbsp;And *italics text.*&nbsp;And some <span style='font-size:18pt; color:black'>large</span> text."),
             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("**Legend title**"),
               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 refer to https://jokergoo.github.io/ComplexHeatmap-reference/book/a-single-heatmap.html#colors.

name Name of the heatmap. By default the heatmap name is used as the title of the heatmap legend.
**Heatmap**

- **na_col**: Color for NA values.

- **rect_gp**: Graphic parameters for drawing rectangles (for heatmap body). The value should be specified by `gpar` and `fill` parameter is ignored.

- **color_space**: The color space in which colors are interpolated. Only used if `matrix` is numeric and `col` is a vector of colors. Pass to `colorRamp2`.

- **border**: Whether draw border. The value can be logical or a string of color.

- **border_gp**: Graphic parameters for the borders. If you want to set different parameters for different heatmap slices, please consider to use `decorate_heatmap_body`.

- **cell_fun**: Self-defined function to add graphics on each cell. Seven parameters will be passed into this function: `j`, `i`, `x`, `y`, `width`, `height`, `fill` which are column index, row index in `matrix`, coordinate of the cell, the width and height of the cell and the filled color. `x`, `y`, `width` and `height` are all `unit` objects.


- **jitter**: Random shifts added to the matrix. The value can be logical or a single numeric value. It it is `TRUE`, 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 `(0, jitter)`. It is mainly to solve the problem of "Error: node stack overflow" 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.

- **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 row title.

- **row_title_rot**: Rotation of 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 column title.

- **column_title_rot**: Rotation of column titles.

- **cluster_rows**: If the value is a logical, it controls whether to make cluster on rows. The value can also be a `hclust` or a `dendrogram` which already contains clustering. Check [https://jokergoo.github.io/ComplexHeatmap-reference/book/a-single-heatmap.html#clustering](https://jokergoo.github.io/ComplexHeatmap-reference/book/a-single-heatmap.html#clustering).

- **cluster_row_slices**: If rows are split into slices, whether perform clustering on the slice means?

- **clustering_distance_rows**: It can be a pre-defined character which is in ("euclidean", "maximum", "manhattan", "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.
bottom_annotation
  A HeatmapAnnotation object.
left_annotation
  It should be specified by rowAnnotation.
right_annotation
  It should be specified by rowAnnotation.
km
  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 dendro-
  gram by cutree.
row_km
  Same as km.
row_km_repeats
  Number of k-means runs to get a consensus k-means clustering. Note if row_km_repeats
  is set to more than one, the final number of groups might be smaller than row_km,
  but this might means the original row_km is not a good choice.
row_split
  Same as split.
column_km
  K-means clustering on columns.
column_km_repeats
  Number of k-means runs to get a consensus k-means clustering. Similar as
  row_km_repeats.
column_split
  Split on columns. For heatmap splitting, please refer to https://jokergoo.
github.io/ComplexHeatmap-reference/book/a-single-heatmap.html#heatmap-split
  .
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

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

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.
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**

```r
# 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

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

Description

3D Heatmap

Usage

```r
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)
```

---

**HeatmapAnnotation**

Constructor Method for HeatmapAnnotation class

**Description**

Constructor Method for HeatmapAnnotation class

**Usage**

```r
HeatmapAnnotation(...,
  df = NULL, name, col, na_col = "grey",
  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.
HeatmapAnnotation

**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 drawn 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
```
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

# There is no example
NULL

heatmap_legend_size-HeatmapList-method

Size of the Heatmap Legends

Description
Size of the Heatmap Legends

Usage

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

## S4 method for signature 'enable_plotting'
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
```

---

**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.
Examples

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

---

**height.heatmap**

*Height of the Heatmap*

**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  

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  

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.
Arguments

x

The `grob` object returned by `Legend` or `packLegend`.

... Other arguments.

Value

The returned unit `x` is always in mm.

Examples

```
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

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

**Assign the Height to the AnnotationFunction Object**

**Description**

Assign the Height to the AnnotationFunction Object

**Usage**

```r
## 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**

```r
## 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**

```
# 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 `HeatmapAnnotation-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.legenda

Grob height for legend_body

Description
Grob height for legend_body

Usage
## S3 method for class 'legend_body'
heightDetails(x)

Arguments
x A legend_body object.

Examples
# There is no example
NULL

heightDetails.packed_legends

Grob height for packed_legends

Description
Grob height for packed_legends

Usage
## S3 method for class 'packed_legends'
heightDetails(x)

Arguments
x A packed_legends object.

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

Examples
# There is no example
NULL

---

ht_opt  Global Options for Heatmaps

Description
Global Options for Heatmaps

Usage
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** whether 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 bottom 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

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

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 \texttt{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 \texttt{<z.gu@dkfz.de>}

Examples

\begin{verbatim}
  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"))
\end{verbatim}

--

\textbf{Legend}

\textit{Make a Single Legend}

Description

Make a Single Legend

Usage

\begin{verbatim}
Legend(at, labels = at, col_fun, name = NULL, grob = NULL, break_dist = NULL, nrow = NULL, ncol = 1, by_row = FALSE, grid_height = unit(4, "mm"), grid_width = unit(4, "mm"), tick_length = unit(0.8, "mm"), gap = unit(2, "mm"), column_gap = gap, row_gap = unit(0, "mm"), labels_gp = gpar(fontsize = 10), labels_rot = 0, border = NULL, background = "#EEEEEE", type = "grid", graphics = NULL, legend_gp = gpar(), pch = 16, size = unit(2, "mm"), legend_height = NULL, legend_width = NULL, direction = c("vertical", "horizontal"), title = ",", title_gp = gpar(fontsize = 10, fontface = "bold"), title_position = c("topleft", "topcenter", "leftcenter", "lefttop", "leftcenter-rot", "lefttop-rot"), title_gap = unit(2, "mm"))
\end{verbatim}
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.

colour
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.
**Legend**

- **size**: Size of points.
- **legend_height**: Height of the whole legend body. It is only used for vertical continuous legend.
- **legend_width**: Width of the whole legend body. It is only used for horizontal continuous 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**

```r
glgd = 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

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
lgd = Legend(at = 1:4)
lgd
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

Description
List All Heatmap Components

Usage
list_components(pattern = NULL)

Arguments
- pattern: A regular expression.

Value
A vector of viewport names.

Examples
# 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
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

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. If it 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.: 
```r
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)
lt = list(a = sample(letters, 10),
         b = sample(letters, 15),
         c = sample(letters, 20))
m = make_comb_mat(lt)

mat = list_to_matrix(lt)
mat
m = make_comb_mat(mat)

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

## 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

```r
# 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 heamtaps/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
   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_order
   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.
column_dend_width
   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
   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.
**make_row_cluster-Heatmap-method**

```r
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**

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

---

**make_row_cluster-Heatmap-method**

*Make Cluster on Rows*

**Description**

Make Cluster on Rows

**Usage**

```r
# 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.
map_to_colors-ColorMapping-method

Map Values to Colors

Description
Map Values to Colors

Usage

```r
## 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>
max_text_height

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))
```
**Description**

Maximum Width of Text

**Usage**

```r
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**

```r
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**

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

**Arguments**

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

**Examples**

```r
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**

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

**Arguments**

- `x` A `HeatmapList-class` object

**Examples**

```r
# There is no example
NULL
```
Assign Annotation Names

## Description

Assign Annotation Names

## Usage

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

## Arguments

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

## Examples

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

---

Number of Columns in the Heatmap

## Description

Number of Columns in the Heatmap

## Usage

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

## Arguments

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

## Examples

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

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

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

Description

Number of Observations

Usage

```r
## 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

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

normalize_comb_mat  Normalize a list of combination matrices

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.
- **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) {
```
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_cnv = GRanges(seqnames = bed[, 1], ranges = IRanges(bed[, 2], bed[, 3]))
    char_mat = cbind(char_mat, normalize_genomic_signals_to_bins(gr_cnv, 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[, 2]))
gr3$gene = paste0("gene_", 1:length(gr3))
meth = as.matrix(findOverlaps(chr_window, gr3))
at = meth[, 1]
labels = mcols(gr3)[meth[, 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

## S3 method for class 'Heatmap'
nrow(x)

Arguments

x  
A Heatmap-class object.

Examples

# There is no example
NULL
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 parameters 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.

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")
Arguments

\[ m \]
A combination matrix returned by \texttt{make_comb_mat}.

\[ \text{on} \]
On sets or on combination sets?

\[ \text{decreasing} \]
Whether the ordering is applied decreasingly.

Details

It first sorts by the degree of the combination sets then by the combination matrix.

Examples

\begin{verbatim}
# There is no example
NULL
\end{verbatim}

Description

Pack Legends

Usage

\texttt{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

\[ \ldots \]
A list of objects returned by \texttt{Legend}.

\[ \text{gap} \]
Gap between two neighbouring legends. The value is a \texttt{unit} object with length of one. It is the same as \texttt{row_gap} if the direction if vertical and the same as \texttt{column_gap} if the direction is horizontal.

\[ \text{row_gap} \]
Horizontal gaps between legends.

\[ \text{column_gap} \]
Vertical gaps between legends.

\[ \text{direction} \]
The direction to arrange legends.

\[ \text{max_width} \]
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.

\[ \text{max_height} \]
Similar as \texttt{max_width}, but for the vertical arrangement of legends.

\[ \text{list} \]
The list of legends can be specified as a list.
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,
borders = 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,
legend_labels = NA,
annotation_row = NA,
annotation_col = NA,
annotation = NA,
annotation_colors = NA,
annotation_legend = TRUE,
annotation_names_row = TRUE,
annotation_names_col = TRUE,
drop_levels = TRUE,
show_rownames = TRUE,
show_colnames = TRUE,
main = NA,
fontsize = 10,
fontsize_row = fontsize,
fontsize_col = fontsize,
angle_col = c("270", "0", "45", "90", "315"),
display_numbers = FALSE,
number_format = "%.2f",
number_color = "grey30",
fontsize_number = 0.8 * fontsize,
gaps_row = NULL,
gaps_col = NULL,
labels_row = NULL,
labels_col = NULL,
filename = NA,
width = NA,
horizontal = FALSE,
silent = FALSE,
na_col = "#DDDDDD",
name = NULL,

# other graphic parameters for fonts
fontfamily = "",
fontfamily_row = fontfamily,
fontfamily_col = fontfamily,
fontface = 1,
fontface_row = fontface,
fontface_col = fontface,

# argument specific for Heatmap()
heatmap_legend_param = list(),
..., 
run_draw = FALSE)

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 `colorRampPalette` are also OK here. E.g. `colorRampPalette(rev(brewer.pal(n = 7, name = "RdYlBu"))(100))` can be simply replaced as `rev(brewer.pal(n = 7, name = "RdYlBu"))`.

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>kmeans_k</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>breaks</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>border_color</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>cellwidth</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>cellheight</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>scale</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>cluster_rows</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>cluster_cols</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>clustering_distance_rows</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>clustering_distance_cols</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>clustering_method</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>clustering_callback</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>cutree_rows</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>cutree_cols</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>treeheight_row</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>treeheight_col</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>legend</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>legend_breaks</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>legend_labels</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>annotation_row</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>annotation_col</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>annotation_colors</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>annotation_legend</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>annotation_names_row</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>annotation_names_col</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>drop_levels</td>
<td>Enforced to be TRUE.</td>
</tr>
<tr>
<td>show_row_names</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
<tr>
<td>show_colnames</td>
<td>The same as in <code>pheatmap</code></td>
</tr>
</tbody>
</table>
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.

fontfamily: Font family for row and column names.

fontfamily_row: Font family for row names.

fontfamily_col: Font family for column names.

fontface: Font face for row and column names.

fontface_row: Font face for row names.

fontface_col: Font face for column names.

heatmap_legend_param: Pass to Heatmap.

...: Other arguments passed to Heatmap.

run_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.
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 \( c(m[i_1, j_1], m[i_2, j_2], \ldots) \).
If m is an array, the value returned is a matrix \( \text{rbind}(m[i_1, j_1, \ldots], m[i_2, j_2, \ldots]) \).

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, ]))
```

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
plot.Heatmap  

Description

Draw heatmap

Usage

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

Arguments

- `x` A `Heatmap-class` object.
- `...` All pass to `draw,Heatmap-method`.

Examples

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

plot.HeatmapAnnotation  

Description

Draw heatmap annotations

Usage

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

Arguments

- `x` A `HeatmapAnnotation-class` object.
- `...` All pass to `draw,HeatmapList-method`.

Examples

```r
# There is no example
NULL
```
**plot.HeatmapList**

*Draw heatmap*

**Description**

Draw heatmap

**Usage**

```r
## S3 method for class 'HeatmapList'
plot(x, ...)
```

**Arguments**

- `x` A `HeatmapList-class` object.
- `...` All pass to `draw.HeatmapList-method`.

**Examples**

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

---

**prepare-Heatmap-method**

*Prepare the Heatmap*

**Description**

Prepare the Heatmap

**Usage**

```r
## 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.
Details

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

# There is no example
NULL

print.comb_mat
Print the comb_mat Object

Description

Print the comb_mat Object

Usage

## S3 method for class 'comb_mat'
print(x, ...)

Arguments

x                   A combination matrix returned by `make_comb_mat`.
...                Other arguments

Examples

# There is no example
NULL
restore_matrix  

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 convenient 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:

```
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 \( j, i, x, y, \ldots \) in \( \text{layer}_\text{fun} \). Now, if we want to add values on the second column in the top-left slice, the code which is put inside \( \text{layer}_\text{fun} \) 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)
        })

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])
        })
```

---

**re_size-HeatmapAnnotation-method**

*Resize the Width or Height of Heatmap Annotations*

**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 \texttt{HeatmapAnnotation-class} object.
annotation_height A vector of annotation heights in \texttt{unit} class.
annotation_width A vector of annotation widths in \texttt{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 \texttt{unit(1, \"null\")}.
3. simple_anno_size is only used when annotation_height is \texttt{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 \texttt{FALSE}, the size of the simple annotations will not change.

Examples

# There is no example
NULL

---

\texttt{rowAnnotation} \hspace{1cm} \textit{Construct Row Annotations}

Description

Construct Row Annotations

Usage

\texttt{rowAnnotation(...)}

Arguments

... Pass to \texttt{HeatmapAnnotation}.
Details

The function is identical to

```
HeatmapAnnotation(..., which = "row")
```

Value

A `HeatmapAnnotation-class` object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

```r
# 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

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

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 `rowAnnotate`.

Value

See help page of `anno_density`.

Examples

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

Description
Text as Row Annotation

Usage
row_anno_text(...)

Arguments
... pass to anno_text.
Details

A wrapper of `anno_text` with pre-defined which to row.

You can directly use `anno_text` for row annotation if you call it in `rowAnnotation`.

Value

See help page of `anno_text`.

Examples

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

---

**row_dend-dispatch**  
*Method dispatch page for row_dend*

---

**Description**

Method dispatch page for `row_dend`.

**Dispatch**

`row_dend` can be dispatched on following classes:

- `row_dend,HeatmapList-method,HeatmapList-class` class method
- `row_dend,Heatmap-method,Heatmap-class` class method

**Examples**

```r
# no example
NULL
```
Get Row Dendrograms from a Heatmap

Description

Get Row Dendrograms from a Heatmap

Usage

```r
## 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)
```

Get Row Dendrograms from a Heatmap List

Description

Get Row Dendrograms from a Heatmap List
Usage

```r
## 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) %v% 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
row_order-Heatmap-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

## 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
```
set_component_width-Heatmap-method

Description

Set Width of Heatmap Component

Usage

## 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

# There is no example
NULL
### set_name

**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)
lit = list(a = sample(letters, 10),
         b = sample(letters, 15),
         c = sample(letters, 20))
m = make_comb_mat(lit)
set_name(m)
```

### set_nameAssign

**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)
lt = list(a = sample(letters, 10),
         b = sample(letters, 15),
         c = sample(letters, 20))
m = make_comb_mat(lt)
set_name(m) = c("A", "B", "C")
m
```

Description

Set Sizes

Usage

`set_size(m)`

Arguments

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

Value

A vector of set sizes.

Examples

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

# 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

# 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 `draw,Heatmap-method`, but only with default parameters. If users want to customize the heatmap, they can pass parameters directly to `draw,Heatmap-method`.

Value

The `HeatmapList-class` object.

Author(s)

Zuguang Gu <z.gu@dkfz.de>

Examples

# There is no example
NULL

show-HeatmapAnnotation-method

Print the HeatmapAnnotation object

Description

Print the HeatmapAnnotation object

Usage

## S4 method for signature 'HeatmapAnnotation'
show(object)

Arguments

object A `HeatmapAnnotation-class` object.

Value

No value is returned.

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**

```r
## 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**

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

**show-SingleAnnotation-method**

*Print the SingleAnnotation object*

**Description**

Print the SingleAnnotation object

**Usage**

```r
## 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
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 stored 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 = local({
    # because there variables outside the function for use, we put it a local environment
    value = 1:10
    function(index, k = 1, n = 1) {
        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
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 `SingleAnnotation-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
```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 rectangle-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

```
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)
omfrow = par("mfrow")
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

```r
## S3 method for class 'comb_mat'
str(object, ...)
```

### Arguments

- **object**
  - A combination matrix returned by `make_comb_mat`.
- **...**
  - Other arguments.

### Examples

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

## subset_gp

### Description

Subset a gpar Object

### Usage

```r
subset_gp(gp, i)
```

### Arguments

- **gp**
  - A `gpar` object.
- **i**
  - A vector of indices.

### Value

A `gpar` object.

### Examples

```r
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**
```r
# 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 of a Heatmap List

**Description**

Summary of a Heatmap List

**Usage**

```r
## S3 method for class 'HeatmapList'
summary(object, ...)
```

**Arguments**

- `object`: A `HeatmapList-class` object.
- `...`: Other arguments.

**Examples**

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

### Transpose the Combination Matrix

**Description**

Transpose the Combination Matrix

**Usage**

```r
## S3 method for class 'comb_mat'
t(x)
```

**Arguments**

- `x`: A combination matrix returned by `make_comb_mat`. 
test_alter_fun 219

Examples

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

test_alter_fun Test alter_fun for oncoPrint()

Description

Test alter_fun for oncoPrint()

Usage

```r
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.rect(x, y, w, h, gp = gpar(lwd = 2)),
  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 sentense 1", "This is a long long long long long long sentense.")
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
```
UpSet is a function for making UpSet plots. It is used for visualizing set intersections and is particularly useful when dealing with a large number of sets or when the relationships between sets are complex.

**Description**

Make the UpSet plot

**Usage**

```r
UpSet(m, 
    comb_col = "black", 
    pt_size = unit(3, "mm"), lwd = 2, 
    bg_col = "#F0F0F0", bg_pt_col = "#CC0000", 
    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)
l1 = list(a = sample(letters, 10),
         b = sample(letters, 15),
         c = sample(letters, 20))
m = make_comb_mat(l1)
UpSet(m)
UpSet(t(m))

m = make_comb_mat(l1, mode = "union")
UpSet(m)
UpSet(m, comb_col = c(rep(2, 3), rep(3, 3), 1))

# compare two UpSet plots
set.seed(123)
l1 = list(a = sample(letters, 10),
         b = sample(letters, 15),
         c = sample(letters, 20))
m1 = make_comb_mat(l1)
set.seed(456)
l2 = list(a = sample(letters, 10),
         b = sample(letters, 15),
         c = sample(letters, 20))
m2 = make_comb_mat(l2)

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")
```

---

**upset_left_annotation  UpSet Left Annotation**

**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(00, 90, 180, 270)`.
- `...`: Passed to `anno_barplot`, e.g. to set `add_numbers`.

Examples

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

upset_right_annotation

Default UpSet Right Annotation

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(),
)```
annotation_name_offset = NULL,
annotation_name_side = "bottom",
annotation_name_rot = NULL,
...)

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

Description

Default UpSet Top Annotation
upset_top_annotation

Usage

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

    # 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.
Examples

# There is no example
NULL

width.HeatmapAnnotation

Width of the HeatmapAnnotation Object

Description

Width of the HeatmapAnnotation Object

Usage

## S3 method for class 'HeatmapAnnotation'
width(x, ...)

Arguments

x The HeatmapAnnotation-class object.
...
Other arguments.

Details

Internally used.

Examples

# There is no example
NULL

width.HeatmapList

Width of the Heatmap List

Description

Width of the Heatmap List

Usage

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

Arguments

x The HeatmapList-class object.
...
Other arguments.
Arguments

x The HeatmapList-class object returned by drawHeatmapList-method.

... Other arguments.

Examples

# There is no example
NULL

width.Legends Width of the Legends

Description

Width of the Legends

Usage

## 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

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

## S3 method for class 'SingleAnnotation'
width(x, ...)

Arguments

x The SingleAnnotation-class object.
...

Other arguments.

Details

Internally used.

Examples

# There is no example
NULL

widthAssign.AnnotationFunction

Assign the Width to the AnnotationFunction Object

Description

Assign the Width to the AnnotationFunction Object

Usage

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

Arguments

x The AnnotationFunction-class object.
...

Other arguments.

value A unit object.
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

## 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

  # There is no example
  NULL

widthDetails.annotation_axis

Width for annotation_axis Grob

Description

  Width for annotation_axis Grob

Usage

  ## 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

# There is no example
NULL

widthDetails.legend_body

Grob width for legend_body

Description

Grob width for legend_body

Usage

## S3 method for class 'legend_body'
widthDetails(x)

Arguments

x A legend_body object.

Examples

# There is no example
NULL

widthDetails.legend

Grob width for packed_legends

Description

Grob width for packed_legends

Usage

## S3 method for class 'legend'
widthDetails(x)

Arguments

x A legend object.

Examples

# There is no example
NULL
widthDetails.packed_legends

Grob width for packed_legends

Description

Grob width for packed_legends

Usage

## S3 method for class 'packed_legends'
widthDetails(x)

Arguments

x  A packed_legends object.

Examples

# There is no example
NULL

widthDetails.textbox

Width for textbox grob

Description

Width for textbox grob

Usage

## 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]
```

`.gridtext  Subset method of gridtext class

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
Details

Internally used.

Examples

# There is no example
NULL

Description

Subset a Heatmap

Usage

## S3 method for class 'Heatmap'
x[i, j]

Arguments

x  A `Heatmap-class` object.
i  Row indices.
j  Column indices.

Details

This functionality is quite experimental. It should be applied before the layout is initialized.

Examples

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
ha = HeatmapAnnotation(foo = 1:10, bar = anno_points(10:1),
                        sth = cbind(1:10, 10:1))
ha[1:5,]
ha[, c("foo", "bar")]
ha[, 1:2]
ha[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])
```

Description

Subset an SingleAnnotation Object

Usage

```r
## 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

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

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

# There is no example
NULL
Index

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