Package ‘gapmap’

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Title Drawing Gapped Cluster Heatmap with 'ggplot2'
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Description The gap encodes the distance between clusters and improves interpretation of cluster heatmaps. The gaps can be of the same distance based on a height threshold to cut the dendrogram. Another option is to vary the size of gaps based on the distance between clusters.
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gapmap-package

Draws gapped heatmap (gapmap) and gapped dendrograms using ggplot2 in [R].

Description

Functions for drawing gapped cluster heat map with ggplot2

Details

This is a set of tools for drawing gap maps using ggplot

gap.data extracts data from a dendrogram object. Make sure to convert hclust object to dendrogram object by calling as.dendrogram(). This method generates an object class gapdata, consisting of a list of data.frames. The general workflow is as following:

1. Hierarchical clustering hclust()
2. Convert the hclust output class into dendrogram by calling as.dendrogram()
3. Generate a gapped cluster heatmap by specifying a matrix and dendrogram objects for rows and columns in gapmap() function

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gapmap

Function to draw a gapped cluster heatmap

Description

This function draws a gapped cluster heatmap using the ggplot2 package. The input for the function is the a matrix, two dendrograms, and parameters for gaps.

Usage

```r
 gapmap(
   m,
   d_row,
   d_col,
   mode = c("quantitative", "threshold"),
   mapping = c("exponential", "linear"),
   ratio = 0.2,
   scale = 0.5,
   threshold = 0,
   row_threshold = NULL,
) ```
col_threshold = NULL,
rotate_label = TRUE,
verbose = FALSE,
left = "dendrogram",
top = "dendrogram",
right = "label",
bottom = "label",
col = c("#053061", "#2166AC", "#4393C3", "#92C5DE", "#D1E5F0", "#F7F7F7", "#F2DBC7",
        "#F4A582", "#D6604D", "#B2182B", "#67001F"),
h_ratio = c(0.2, 0.7, 0.1),
v_ratio = c(0.2, 0.7, 0.1),
label_size = 5,
show_legend = FALSE,
...)

Arguments

m                        matrix
d_row                     a dendrogram class object for rows
d_col                     a dendrogram class object for columns
mode                      gap mode, either "threshold" or "quantitative"
mapping                  in case of quantitative mode, either "linear" or "exponential" mapping
ratio                     the percentage of width allocated for the sum of gaps.
scale                     the scale log base for the exponential mapping
threshold                 the height at which the dendrogram is cut to infer clusters
row_threshold             the height at which the row dendrogram is cut
col_threshold             the height at which the column dendrogram is cut
rotate_label              a logical to rotate column labels or not
verbose                   logical for whether in verbose mode or not
left                      a character indicating "label" or "dendrogram" for composition
top                       a character indicating "label" or "dendrogram" for composition
right                     a character indicating "label" or "dendrogram" for composition
bottom                    a character indicating "label" or "dendrogram" for composition
col                       colors used for heatmap
h_ratio                   a vector to set the horizontal ratio of the grid. It should add up to 1. top, center, bottom.
v_ratio                   a vector to set the vertical ratio of the grid. It should add up to 1. left, center, right.
label_size                a numeric to set the label text size
show_legend               a logical to set whether to show a legend or not
...                       ignored
Value

a ggplot object

Examples

```r
set.seed(1234)
#generate sample data
x <- rnorm(10, mean=rep(1:5, each=2), sd=0.4)
y <- rnorm(10, mean=rep(c(1,2), each=5), sd=0.4)
dataFrame <- data.frame(x=x, y=y, row.names=c(1:10))
#calculate distance matrix. default is Euclidean distance
distxy <- dist(dataFrame)
#perform hierarchical clustering. default is complete linkage.
hc <- hclust(distxy)
dend <- as.dendrogram(hc)
#make a cluster heatmap plot
gapmap(m = as.matrix(distxy), d_row= rev(dend), d_col=dend)
```

---

**gap_data**

Generate a gapdata class object from a dendrogram object

**Description**

This function takes a dendrogram class object as an input, and generate a gapdata class object as an output. By parsing the dendrogram object based on parameters for gaps, gaps between leaves in a dendrogram are introduced, and the coordinates of the leaves are adjusted. The gaps can be based on the a height (or distance) threshold to to introduce the gaps of the same width, or quantitative mapping of distance values mapped linearly or exponentially.

**Usage**

```r
gap_data(
  d,
  mode = c("quantitative", "threshold"),
  mapping = c("exponential", "linear"),
  ratio = 0.2,
  scale = 0.5,
  threshold = 0,
  verbose = FALSE,
  ...
)
```

**Arguments**

d dendrogram class object

mode gap mode, either "threshold" or "quantitative"
**gap_dendrogram**

- **mapping**: in case of quantitative mode, either "linear" or "exponential" mapping
- **ratio**: the percentage of width allocated for the sum of gaps.
- **scale**: the scale log base for the exponential mapping
- **threshold**: the height at which the dendrogram is cut to infer clusters
- **verbose**: logical for whether in verbose mode or not
- **...**: ignored

**Value**

a list of data frames that contain coordinates for drawing a gapped dendrogram

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**Description**

This function draws a gapped dendrogram using the ggplot2 package. The input for the function is the gapdata class object, generated from gap_data() function.

**Usage**

```r
gap_dendrogram(
  data,
  leaf_labels = TRUE,
  rotate_label = FALSE,
  orientation = c("top", "right", "bottom", "left"),
  ...
)
```

**Arguments**

- **data**: gapdata class object
- **leaf_labels**: a logical to show labels or not
- **rotate_label**: a logical to rotate labels or not
- **orientation**: a character to set the orientation of dendrogram. Choices are "top", "right", "bottom", "left".
- **...**: ignored

**Value**

a ggplot object
**Description**

This function draws a gapped heatmap using the ggplot2 package. The input for the function are the gapdata class objects, generated from gap_data() function, and the data matrix.

**Usage**

```r
gap_heatmap(
m,  
row_gap = NULL,  
col_gap = NULL,  
row_labels = TRUE,  
col_labels = TRUE,  
rotate = FALSE,  
col = c("#053061", "#2166AC", "#4393C3", "#92C5DE", "#D1E5F0", "#F7F7F7", "#FDDBC7",  
        "#F4A582", "#D6604D", "#B2182B", "#67001F")
)
```

**Arguments**

- `m` : data matrix
- `row_gap` : a gapdata class object for rows
- `col_gap` : a gapdata class object for columns
- `row_labels` : a logical to show labels for rows
- `col_labels` : a logical to show labels for columns
- `rotate` : a logical to rotate row labels
- `col` : colors used for heatmap

**Value**

a ggplot object

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**Description**

This function draws a gapped labels using the ggplot2 package. The input for the function is the gapdata class object, generated from gap_data() function.

---

**Description**

This function draws a gapped labels using the ggplot2 package. The input for the function is the gapdata class object, generated from gap_data() function.
Usage

gap_label(data, orientation, label_size = 5)

Arguments

data gapdata class object
orientation orientation of the labels, "left", "top", "right", or "bottom"
label_size a numeric to set the label text size

Value

a ggplot object

---

sample_tcga

Sample data matrix from the integrated pathway analysis of gastric cancer from the Cancer Genome Atlas (TCGA) study.

Description

A multivariate table obtained from the integrated pathway analysis of gastric cancer from the Cancer Genome Atlas (TCGA) study. In this data set, each column represents a pathway consisting of a set of genes and each row represents a cohort of samples based on specific clinical or genetic features. For each pair of a pathway and a feature, a continuous value of between 1 and -1 is assigned to score positive or negative association, respectively.

Usage

data(sample_tcga)

Format

A data frame with 215 rows and 117 variables

Details

We would like to thank Sheila Reynolds and Vesteinn Thorsson from the Institute for Systems Biology for sharing this sample data set.
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