

# Package ‘gapmap’

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**Type** Package

**Title** Functions for Drawing Gapped Cluster Heatmap with ggplot2

**Version** 0.0.4

**URL** <https://bitbucket.org/vda-lab/gapmap>

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**Author** Ryo Sakai

**Maintainer** Ryo Sakai <ryo@vda-lab.be>

**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.

**License** GPL-2 | GPL-3

**Depends** ggplot2, reshape2

**Imports** grid

**Suggests** knitr, dendsort, RColorBrewer

**VignetteBuilder** knitr

**RoxygenNote** 5.0.1

**NeedsCompilation** no

**Repository** CRAN

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gapmap-package	<i>Draws gapped heatmap (gapmap) and gapped dendrograms using ggplot2 in [R].</i>
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**Description**

Functions for drawing gapped cluster heatmap with ggplot2

**Details**

This is a set of tools for drawing gapmaps 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

**Author(s)**

Ryo Sakai <[ryo.sakai@esat.kuleuven.be](mailto:ryo.sakai@esat.kuleuven.be)>

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gapmap	<i>Function to draw a gapped cluster heatmap</i>
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**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**

```
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",
              "#FDDBC7", "#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 sclae 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**

```
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)
```

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gap_data	<i>Generate a gapdata class object from a dendrogram object</i>
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### 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

```
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"
mapping	in case of quantitative mode, either "linear" or "exponential" mapping
ratio	the percentage of width allocated for the sum of gaps.
scale	the sclae log base for the exponential mapping
threshold	the height at which the dendrogram is cult 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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gap_dendrogram	<i>Function to draw a gapped dendrogram</i>
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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

```
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

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gap_heatmap	<i>Function to draw a gapped heatmap</i>
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**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**

```
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
...	ignored

**Value**

a ggplot object

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gap_label	<i>Function to draw a gapped labels</i>
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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.

**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

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sample_tcga	<i>Sample data matrix from the integrated pathway analysis of gastric cancer from the Cancer Genome Atlas (TCGA) study.</i>
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**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 Vesteynn Thorsson from the Institute for Systems Biology for sharing this sample data set.

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