

# Package: gapmap (via r-universe)

September 18, 2024

**Title** Drawing Gapped Cluster Heatmaps with 'ggplot2'

**Version** 1.0.0

**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

**Encoding** UTF-8

**Depends** ggplot2, reshape2

**Imports** grid

**Suggests** knitr, dendsort, RColorBrewer, rmarkdown

**VignetteBuilder** knitr

**URL** <https://github.com/evanbiederstedt/gapmap>

**BugReports** <https://github.com/evanbiederstedt/gapmap/issues>

**RoxygenNote** 7.2.3

**NeedsCompilation** no

**Maintainer** Evan Biederstedt <evan.biederstedt@gmail.com>

**Repository** <https://evanbiederstedt.r-universe.dev>

**RemoteUrl** <https://github.com/evanbiederstedt/gapmap>

**RemoteRef** HEAD

**RemoteSha** e5664e487abd0032b4b5533cacb4cc18317b4eff

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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

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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

*Generate a gapdata class object from a dendrogram object*

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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              |

**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 Vestein Thorsson from the Institute for Systems Biology for sharing this sample data set.

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