ComplexHeatmap Complete Reference

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last revised on 2018-10-16

Contents

About

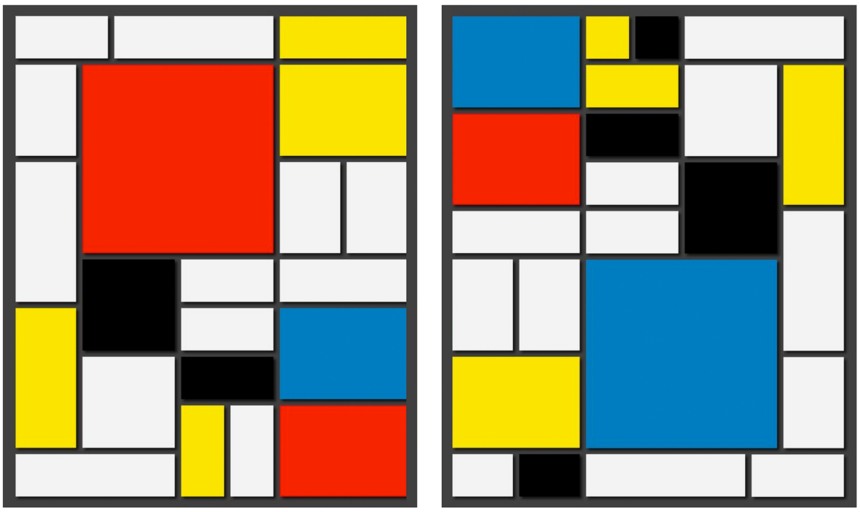
This is the documentation of the **ComplexHeatmap** package. Examples in the book are generated under version 1.99.0.

Please note, this documentation is not completely compatible with older versions (< 1.99.0, before Oct, 2018), the major functionality keeps the same.

If you use **ComplexHeatmap** in your publications, I am appreciated if you can cite:

Gu, Z. (2016) Complex heatmaps reveal patterns and correlations in multidimensional genomic data. DOI: 10.1093/bioinformatics/btw313

ComplexHeatmap Complete Reference



Zuguang Gu

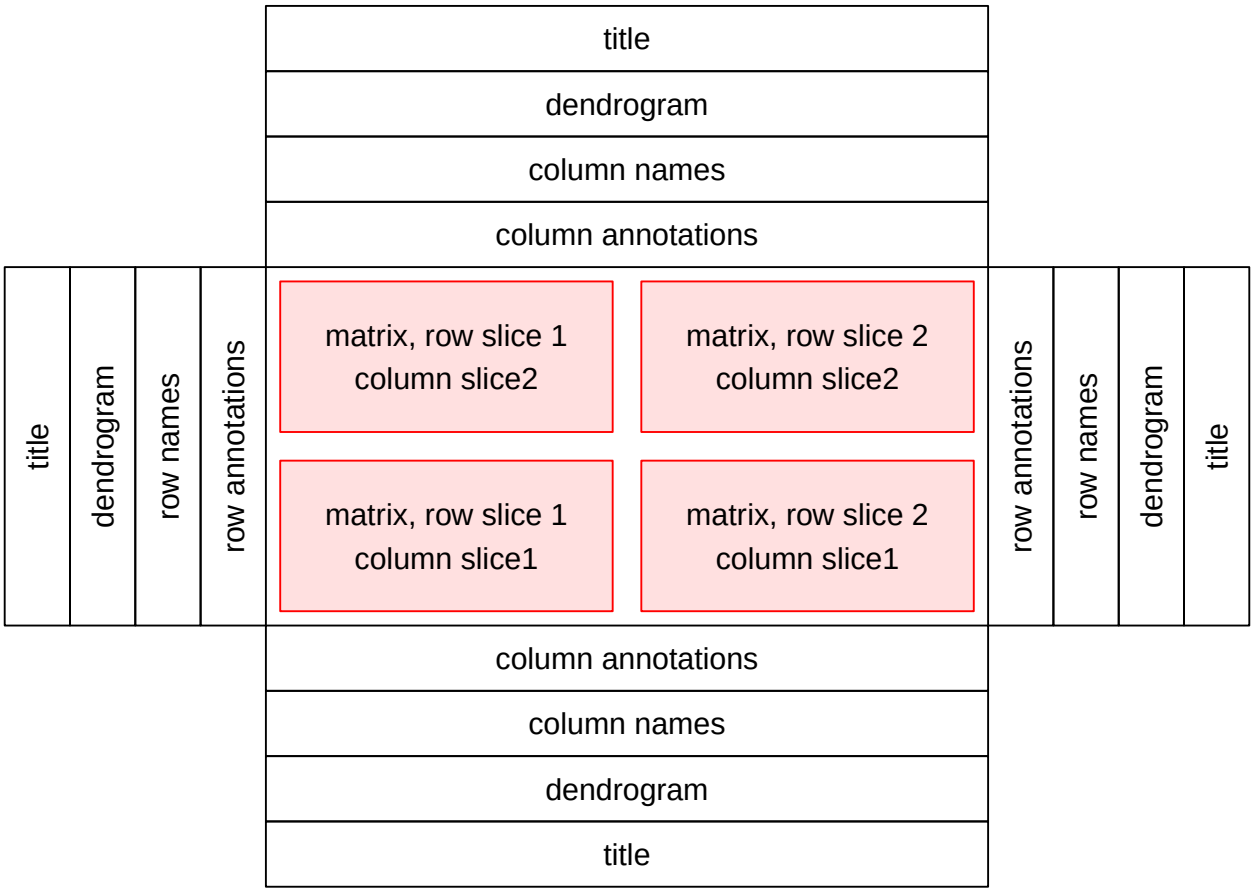
Chapter 1

Introduction

Complex heatmaps are efficient to visualize associations between different sources of data sets and reveal potential structures. Here the **ComplexHeatmap** package provides a highly flexible way to arrange multiple heatmaps and supports self-defined annotation graphics.

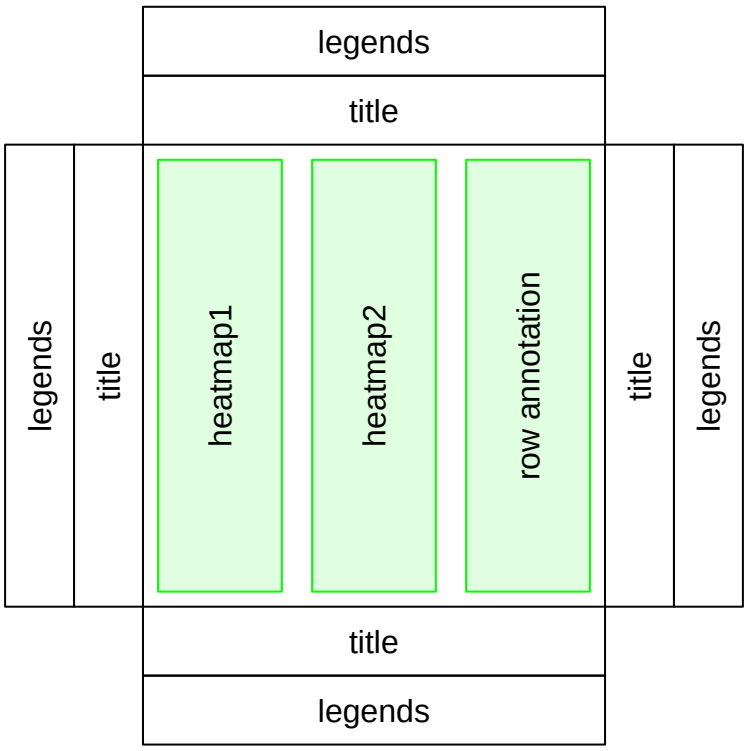
1.1 General design

A single heatmap is composed of the heatmap body and the heatmap components. The heatmap body can be split by rows and columns. The heatmap components are titles, dendrograms, matrix names and annotations, which are put on the four sides of the heamap body.

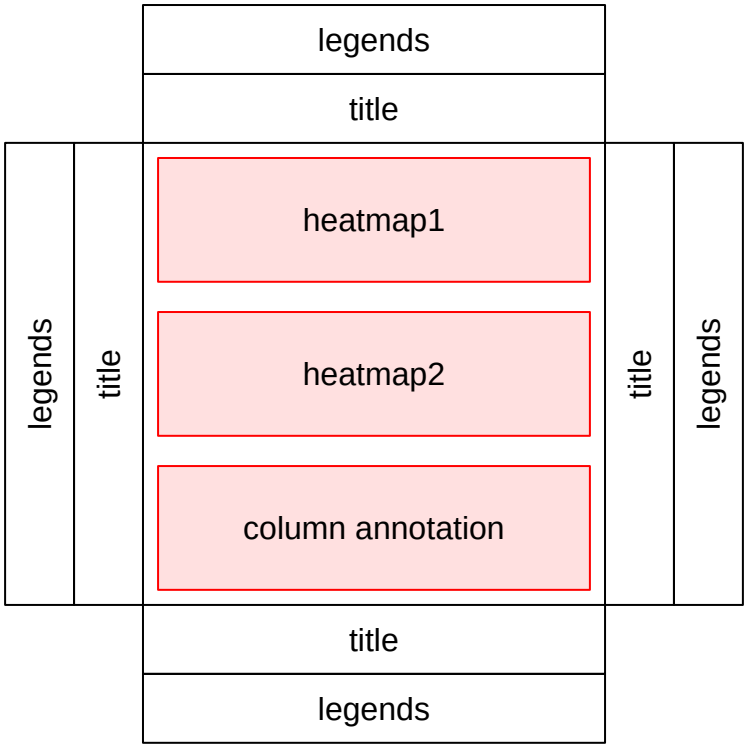


A heatmap list is concatenation of a list of heatmaps and heatmap annotations. Surrounding the heatmap list, there are global-level titles and legends.

One of the important things for the heatmap list is that rows for all heatmaps and annotations (it is row annotation if the heatmap list is horizontal.) are all adusted so that the same row in all heatmaps and annotations corresponds to a same feature.



The heatmaps and annotations can also be arranged vertically.



The **ComplexHeatmap** package is implemented in an object-oriented way. To describe a heatmap list, there are following classes:

- `Heatmap` class: a single heatmap containing heatmap body, row/column names, titles, dendrograms and column annotations.

- `HeatmapList` class: a list of heatmaps and heatmap annotations.
- `HeatmapAnnotation` class: defines a list of row annotations and column annotations. The heatmap annotations can be components of heatmap, also they can be independent as heatmaps.

There are also several internal classes:

- `SingleAnnotation` class: defines a single row annotation or column annotation.
- `ColorMapping` class: mapping from values to colors.
- `AnnotationFunction` class: construct user-defined annotations.

ComplexHeatmap is implemented under **grid** system, so users need to know basic **grid** functionality to get full use of the package.

1.2 A brief description of following chapters

1. **A Single Heatmap**

This chapter describes the configurations of a single heatmap.

2. **Heatmap Annotations**

This chapter describes the concept of the heatmap annotation and demonstrates how to make simple annotations as well as complex annotations. Also, the chapter explains the difference between column annotations and row annotations.

3. **A List of Heatmaps**

This chapter describes how to concatenate a list of heatmaps and annotations and how adjustment is applied to keep the correspondence of the heatmaps.

4. **Legends**

This chapter describes how to configurate the heatmap legends and annotation legends, also how to create self-defined legends.

5. **Heatmap Decoration**

This chapter describes methods to add more self-defined graphics to the heatmaps after the heatmaps are generated.

6. **OncoPrint**

This chapter describes how to make oncoPrints and how to integrate other functionalities from **ComplexHeatmap** to oncoPrints.

7. **Other High-level Plots**

This chapter describes functions implemented in **ComplexHeatmap** for specific use, e.g. visualizing distributions.

8. **More Examples**

More simulated and real-world examples are shown in this chapter.

Chapter 2

A single Heatmap

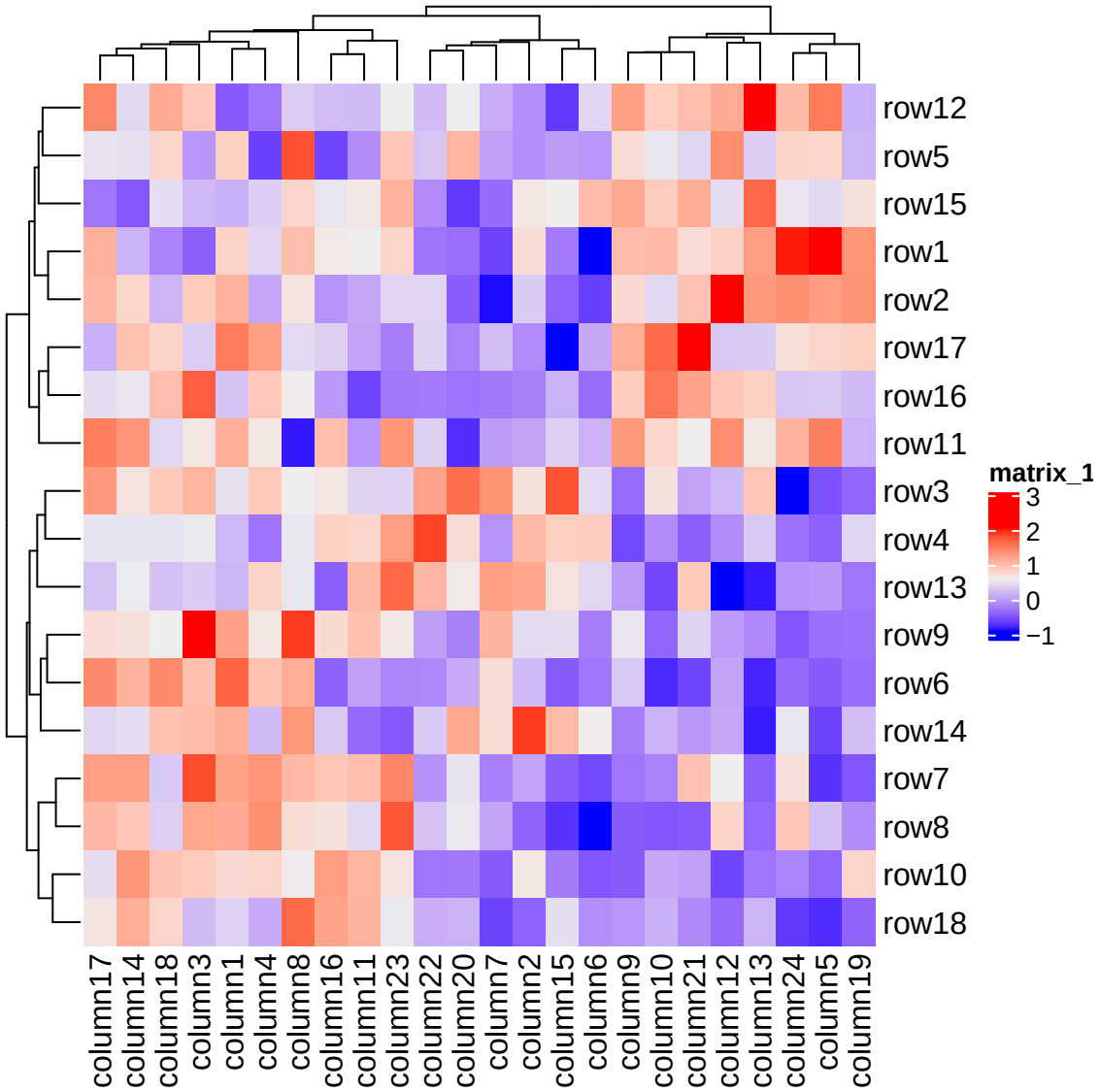
A single heatmap is the most used way for visualizing the data. Although "the shining point" of the **ComplexHeatmap** package is it can visualize a list of heatmaps in parallel, as the basic unit of the heatmap list, it is still very important to have the single heatmap nicely configured.

First let's generate a random matrix where there are three groups by columns and three groups by rows:

```
set.seed(123)
nr1 = 4; nr2 = 8; nr3 = 6; nr = nr1 + nr2 + nr3
nc1 = 6; nc2 = 8; nc3 = 10; nc = nc1 + nc2 + nc3
mat = cbind(rbind(matrix(rnorm(nr1*nc1, mean = 1,   sd = 0.5), nr = nr1),
          matrix(rnorm(nr2*nc1, mean = 0,   sd = 0.5), nr = nr2),
          matrix(rnorm(nr3*nc1, mean = 0,   sd = 0.5), nr = nr3)),
    rbind(matrix(rnorm(nr1*nc2, mean = 0,   sd = 0.5), nr = nr1),
          matrix(rnorm(nr2*nc2, mean = 1,   sd = 0.5), nr = nr2),
          matrix(rnorm(nr3*nc2, mean = 0,   sd = 0.5), nr = nr3)),
    rbind(matrix(rnorm(nr1*nc3, mean = 0.5, sd = 0.5), nr = nr1),
          matrix(rnorm(nr2*nc3, mean = 0.5, sd = 0.5), nr = nr2),
          matrix(rnorm(nr3*nc3, mean = 1,   sd = 0.5), nr = nr3))
   )
mat = mat[sample(nr, nr), sample(nc, nc)] # random shuffle rows and columns
rownames(mat) = paste0("row", seq_len(nr))
colnames(mat) = paste0("column", seq_len(nc))
```

Following command contains the minimal argument for the `Heatmap()` function which just visualizes the matrix as a heatmap with default settings. Very similar as other heatmap tools, it draws the dendrograms, the row/column names and the heatmap legend. The default color schema is "blue-white-red" which is mapped to the minimal-mean-maximal values in the matrix. The title for the legend is assigned by an internal index number.

```
Heatmap(mat)
```



The title for the legend is taken from the "name" of the heatmap by default. Each heatmap has a name which is like a unique identifier for the heatmap, which is important when you have a list of heatmaps. In later chapters, you will find the heatmap name is used for setting the "main heatmap" and is used for decoration of heatmaps. If the name is not assigned, an internal name is assigned to the heatmap in a form of `matrix_%d`. In following examples in this chapter, we give the name `mat` to the heatmap (for which you will see the change of the legend in the next plot).

2.1 Colors

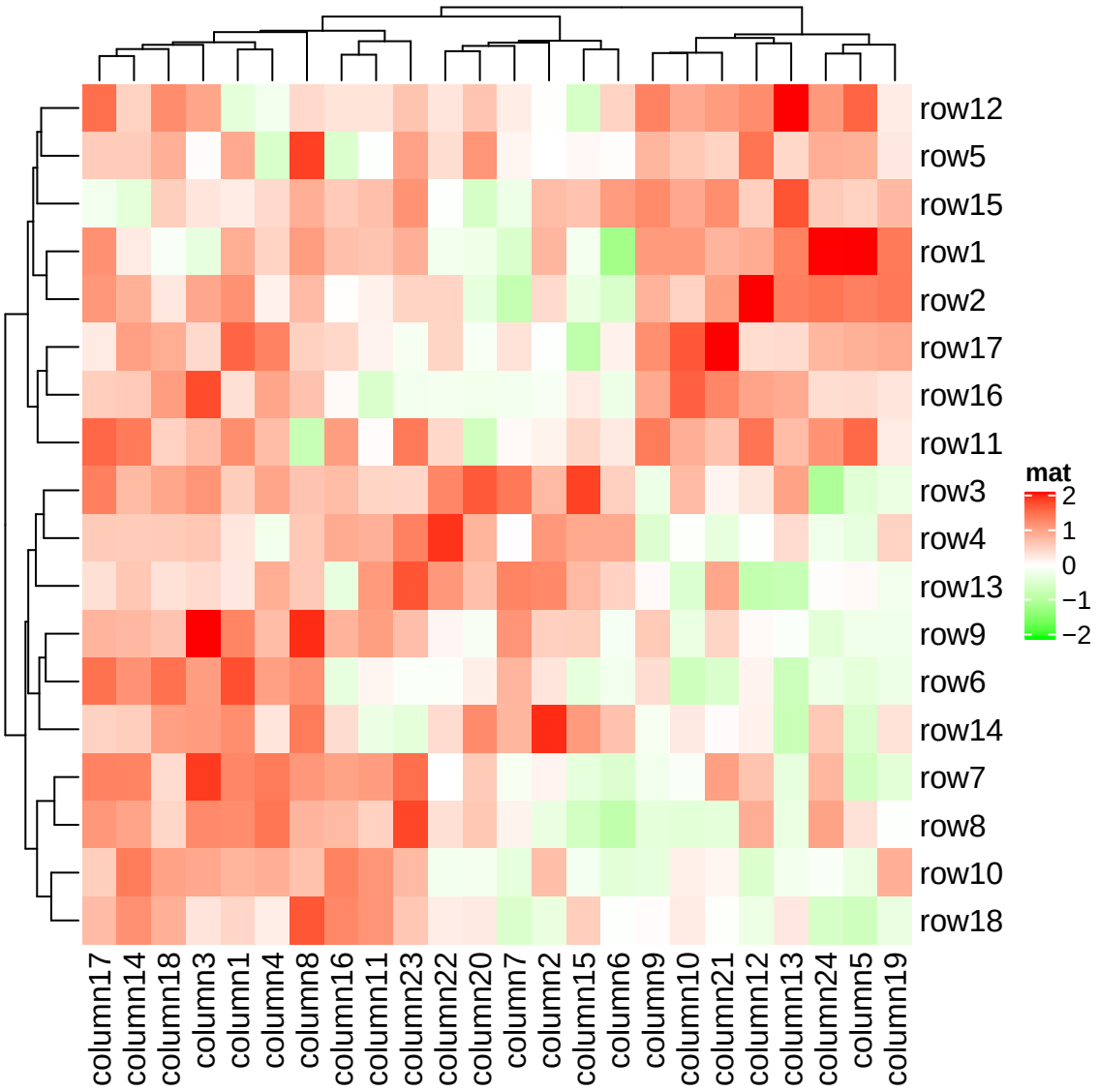
For heatmap visualization, colors are the major representation of the data matrix. In most cases, the heatmap visualizes a matrix with continuous numeric values. In this case, users should provide a color mapping function. A color mapping function should accept a vector of values and return a vector of corresponding colors. **Users should always use `circlize::colorRamp2()` function to generate the color mapping function**. The two arguments for `colorRamp2()` is a vector of break values and a vector of corresponding colors. `colorRamp2()` linearly interpolates colors in every interval through LAB color space. Also using `colorRamp2()` helps to generate a legend with proper tick marks.

In following example, values between -2 and 2 are linearly interpolated to get corresponding colors, values larger than 2 are all mapped to red and values less than -2 are all mapped to green.

```
library(circlize)
col_fun = colorRamp2(c(-2, 0, 2), c("green", "white", "red"))
col_fun(seq(-3, 3))
```

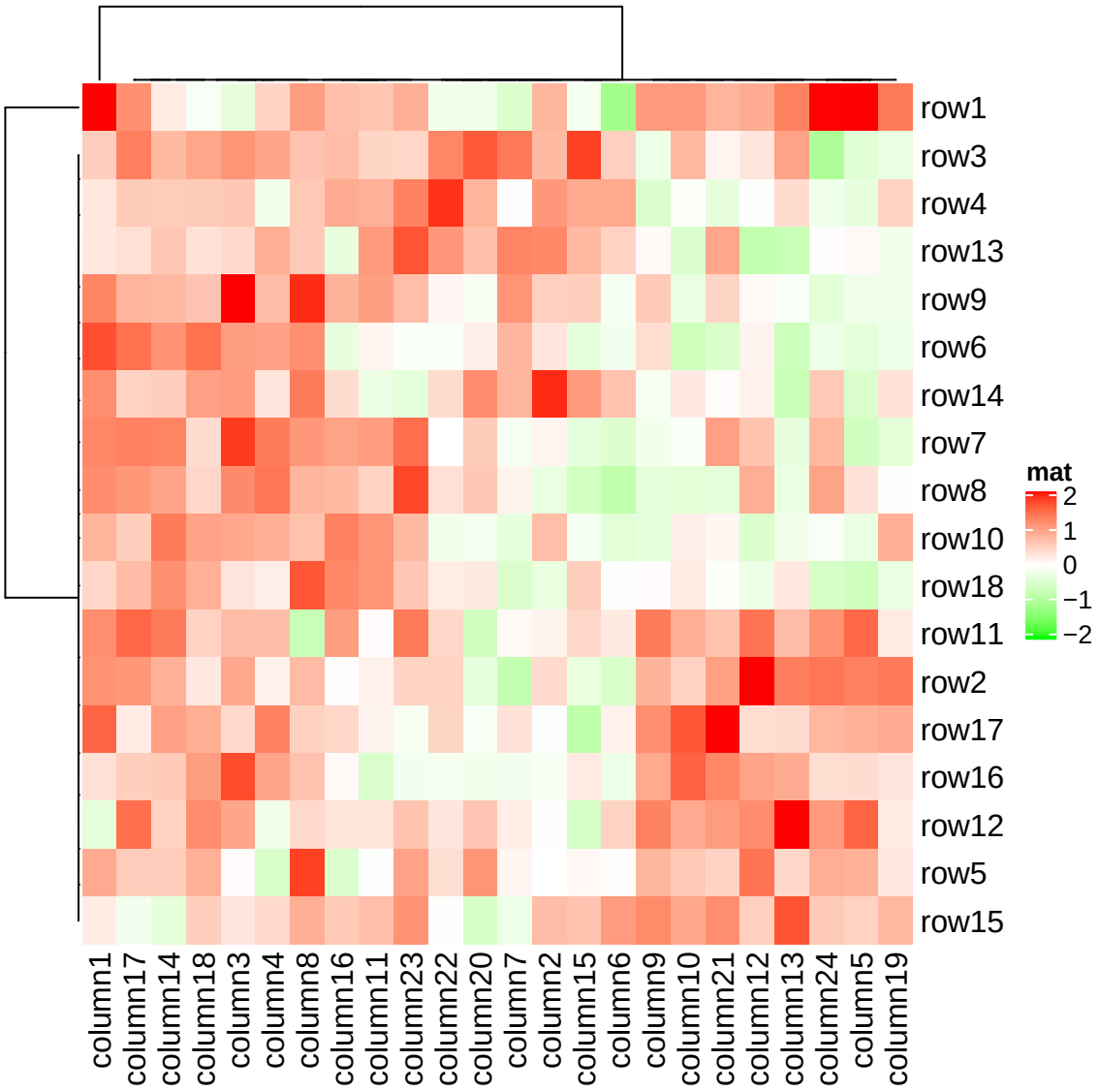
```
## [1] "#00FF00FF" "#00FF00FF" "#B1FF9AFF" "#FFFFFFFF" "#FF9E81FF" "#FF0000FF"
## [7] "#FF0000FF"
```

```
Heatmap(mat, name = "mat", col = col_fun)
```



As you can see, the color mapping function exactly maps negative values to green and positive values to red, even when the distribution of negative values and positive values are not centric to zero. Also this color mapping function is not affected by outliers. In following plot, the clustering is heavily affected by the outlier but not the color mapping.

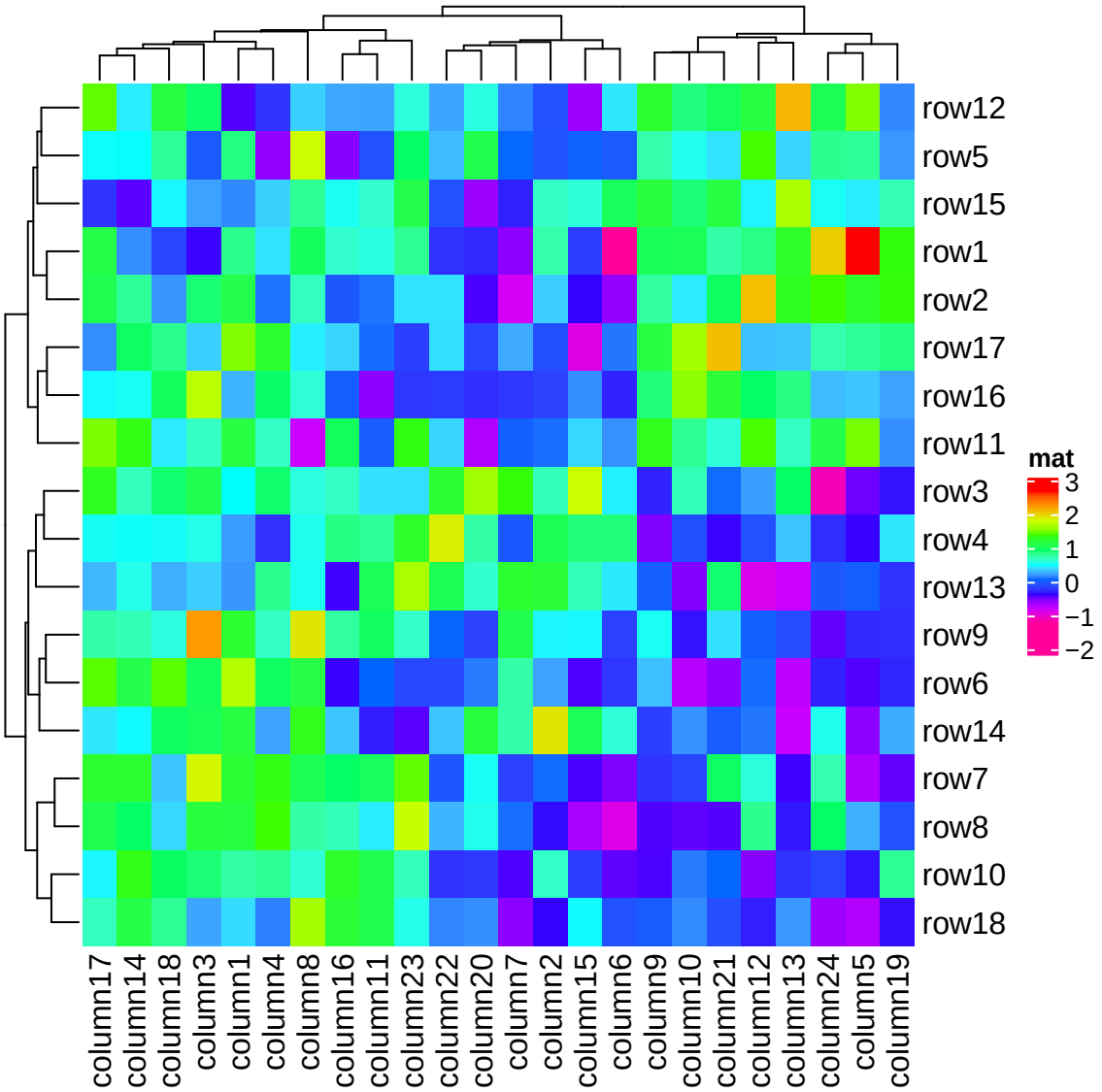
```
mat2 = mat
mat2[1, 1] = 100000
Heatmap(mat2, name = "mat", col = col_fun)
```



More importantly, `colorRamp2()` makes colors in multiple heatmaps comparible if they are set with a same color mapping function.

If the matrix is continuous, you can simply provide a vector of colors and colors will be linearly interpolated. But remember this method is not robust to outliers because the mapping starts from the minimal value in the matrix and ends with the maximal value. Following color mapping setting is identical to `colorRamp2(seq(min(mat), max(mat), length = 10), rev(rainbow(10)))`.

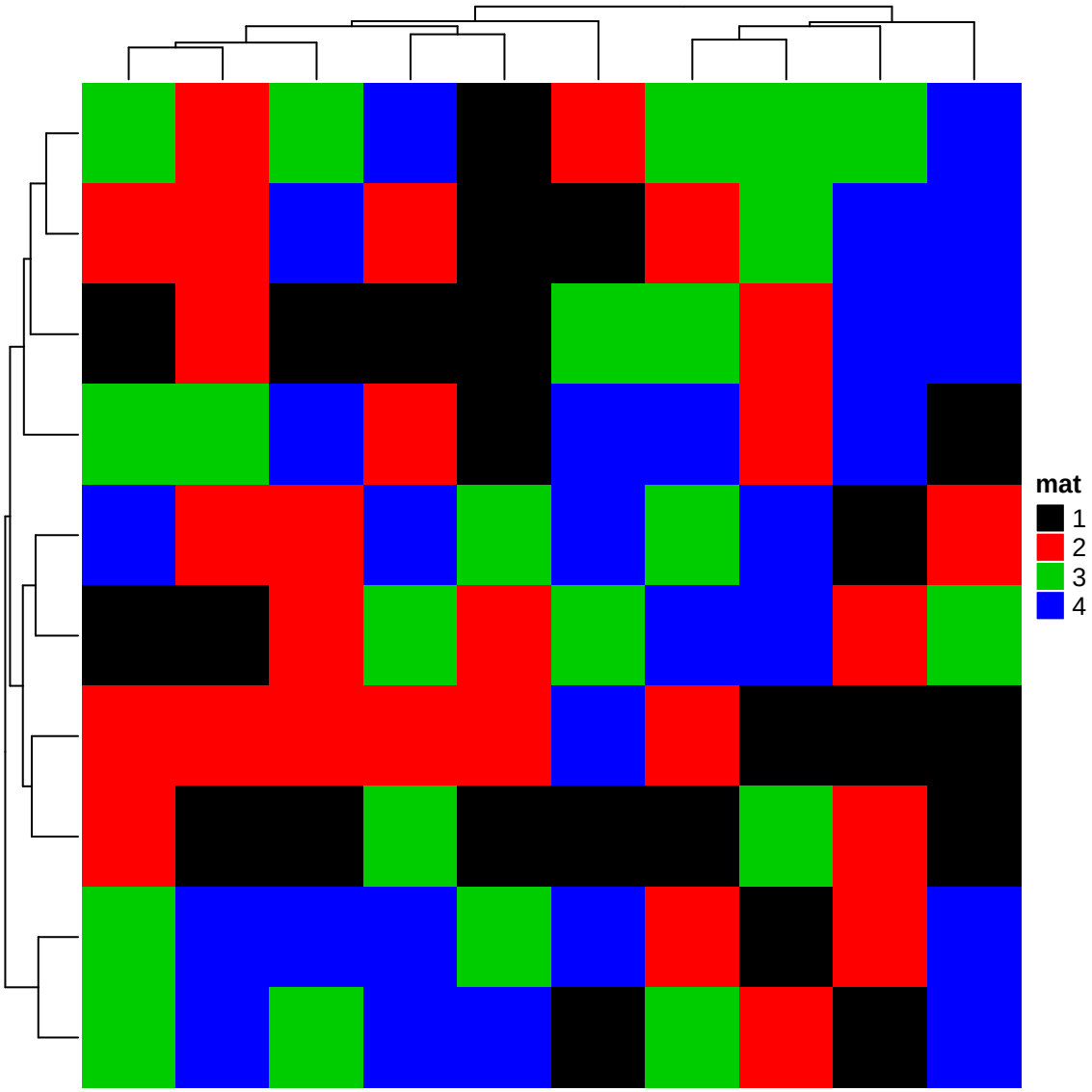
```
Heatmap(mat, name = "mat", col = rev(rainbow(10)))
```



If the matrix contains discrete values (either numeric or character), colors should be specified as a named vector to make it possible for the mapping from discrete values to colors. If there is no name for the color, the order of colors corresponds to the order of `unique(mat)`. Note now the legend is generated from the color mapping vector.

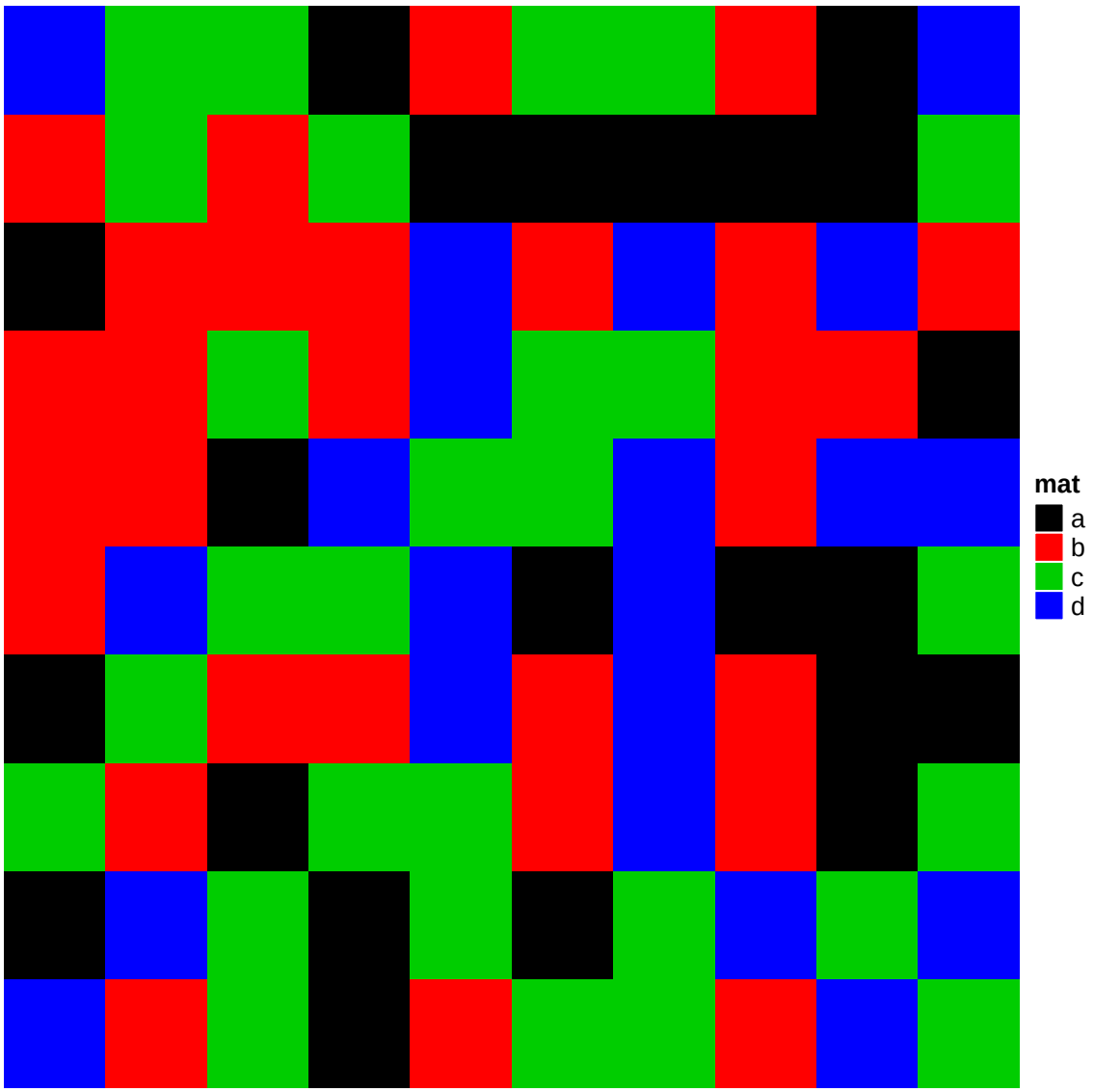
Following sets colors for a discrete numeric matrix (you don't need to convert it to a character matrix).

```
discrete_mat = matrix(sample(1:4, 100, replace = TRUE), 10, 10)
colors = structure(1:4, names = c("1", "2", "3", "4")) # black, red, green, blue
Heatmap(discrete_mat, name = "mat", col = colors)
```



Or a character matrix:

```
discrete_mat = matrix(sample(letters[1:4], 100, replace = TRUE), 10, 10)
colors = structure(1:4, names = letters[1:4])
Heatmap(discrete_mat, name = "mat", col = colors)
```

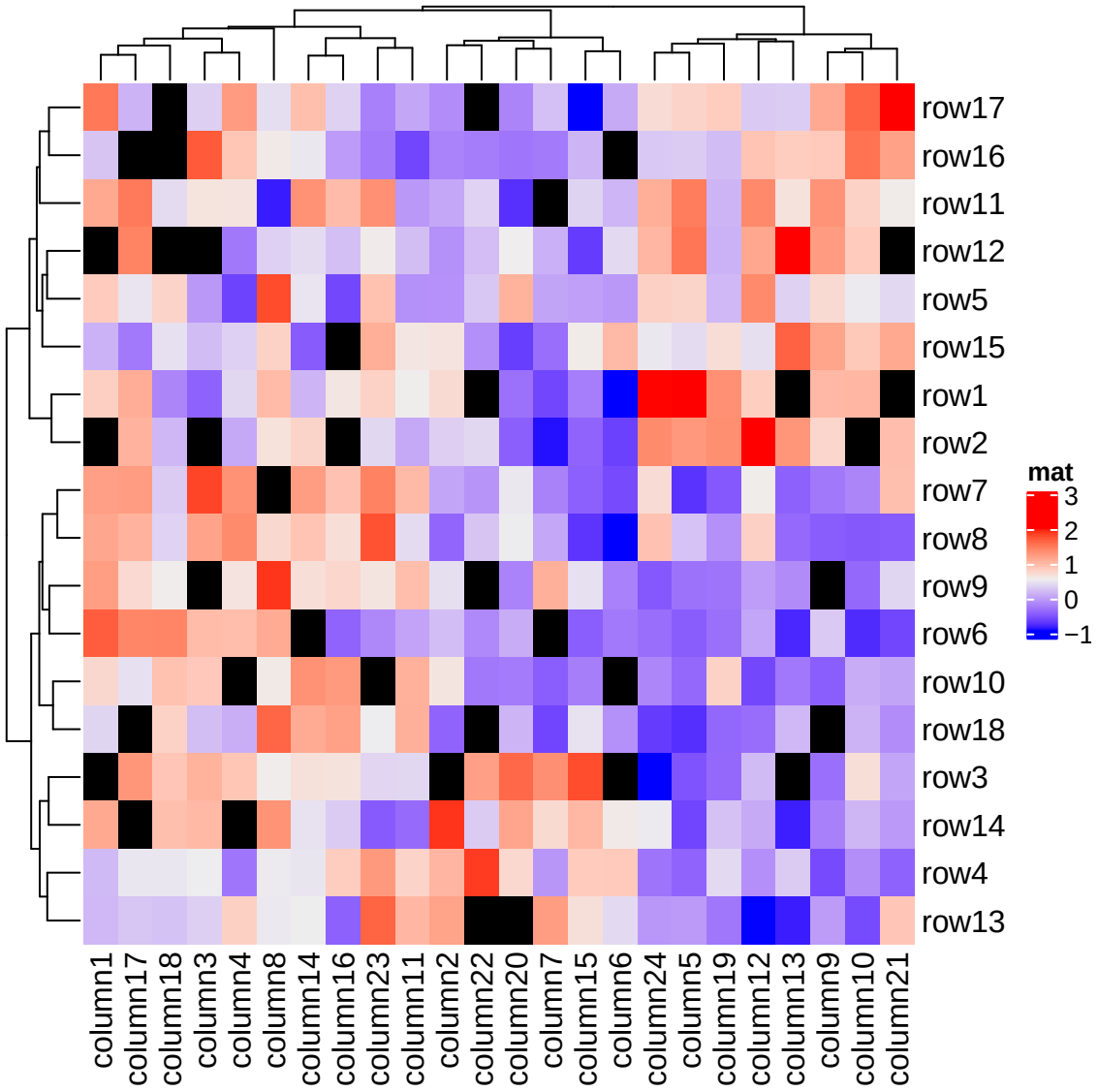


As you see in the two above examples, for the numeric matrix (no matter the color is continuous mapping or discrete mapping), by default clustering is applied on both dimensions while for character matrix, clustering is turned off (but you can still clustering a character matrix if you provide a proper distance metric for two character vectors, see example in Section **??**).

`NA` is allowed in the matrix. You can control the color of `NA` by `na_col` argument (by default it is grey for `NA`). **The matrix that contains `NA` can also be clustered by `Heatmap()`.**

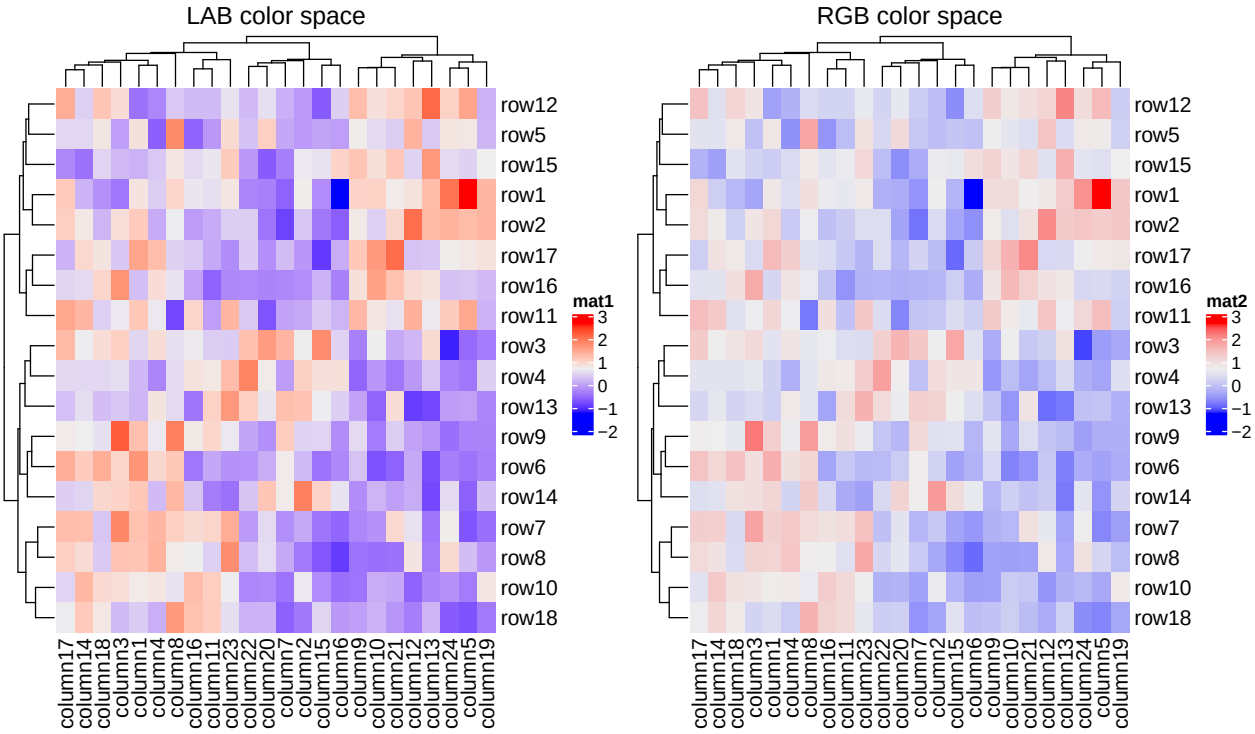
Note the `NA` value is not presended in the legend.

```
mat_with_na = mat
na_index = sample(c(TRUE, FALSE), nrow(mat)*ncol(mat), replace = TRUE, prob = c(1, 9))
mat_with_na[na_index] = NA
Heatmap(mat_with_na, name = "mat", na_col = "black")
```

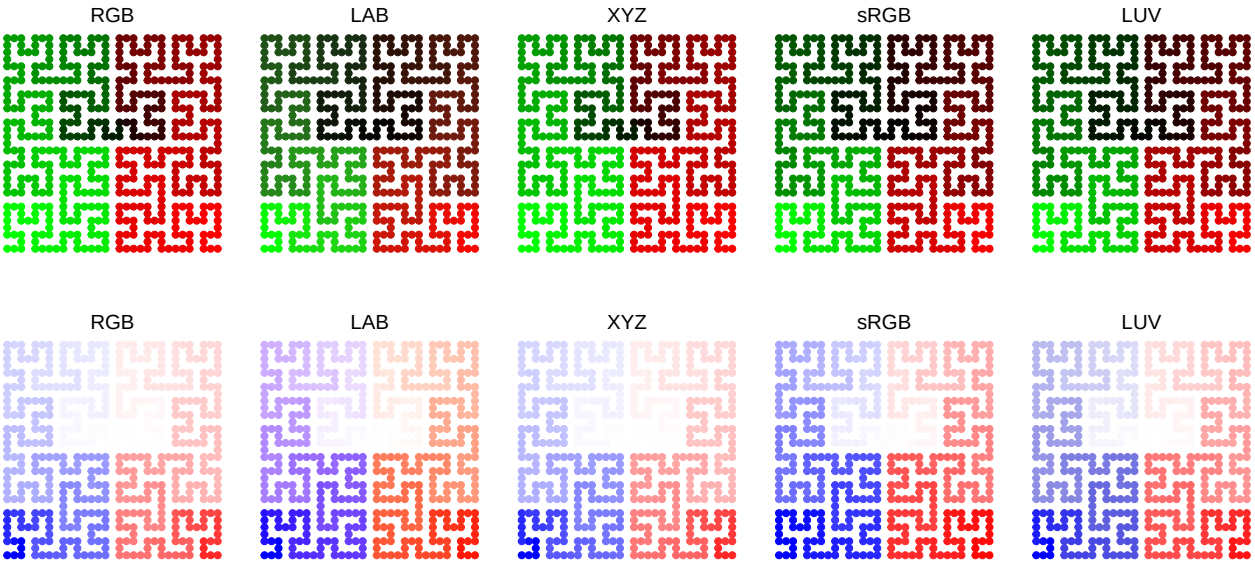


Color space is important for interpolating colors. By default, colors are linearly interpolated in LAB color space, but you can select the color space in `colorRamp2()` function. Compare following two plots. Can you see the difference?

```
f1 = colorRamp2(seq(min(mat), max(mat), length = 3), c("blue", "#EEEEEE", "red"))
f2 = colorRamp2(seq(min(mat), max(mat), length = 3), c("blue", "#EEEEEE", "red"),
    space = "RGB")
Heatmap(mat, name = "mat1", col = f1, column_title = "LAB color space")
Heatmap(mat, name = "mat2", col = f2, column_title = "RGB color space")
```



In following figures, corresponding values change evenly on the folded lines, you can see how colors change under different color spaces (the plot is made by **HilbertCurve** package).

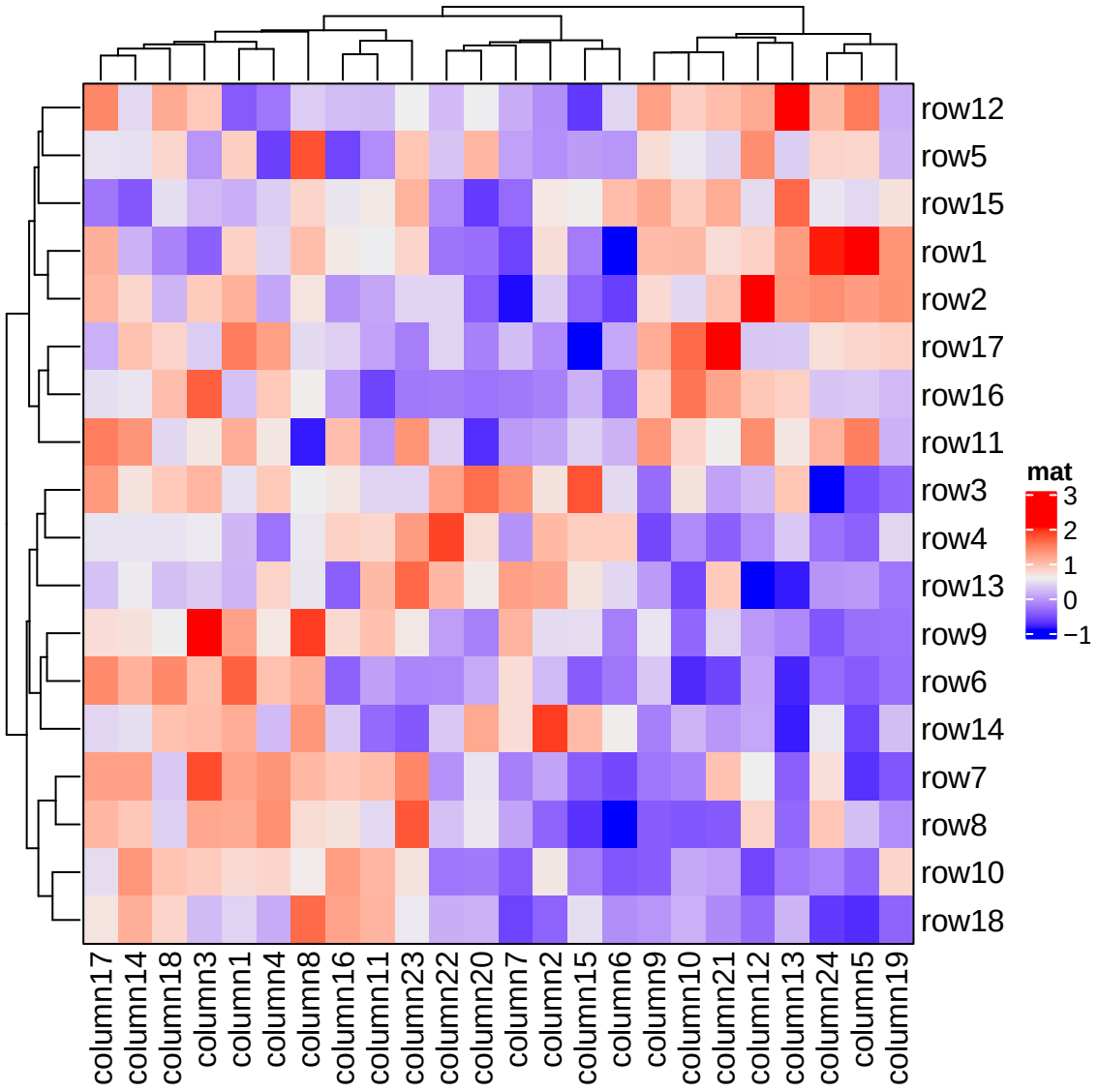


Last but not the least, colors for the heatmap borders can be set by the `border` and `rect_gp` arguments. `border` controls the global border of the heatmap body and `rect_gp` controls the border of the grids in the heatmap.

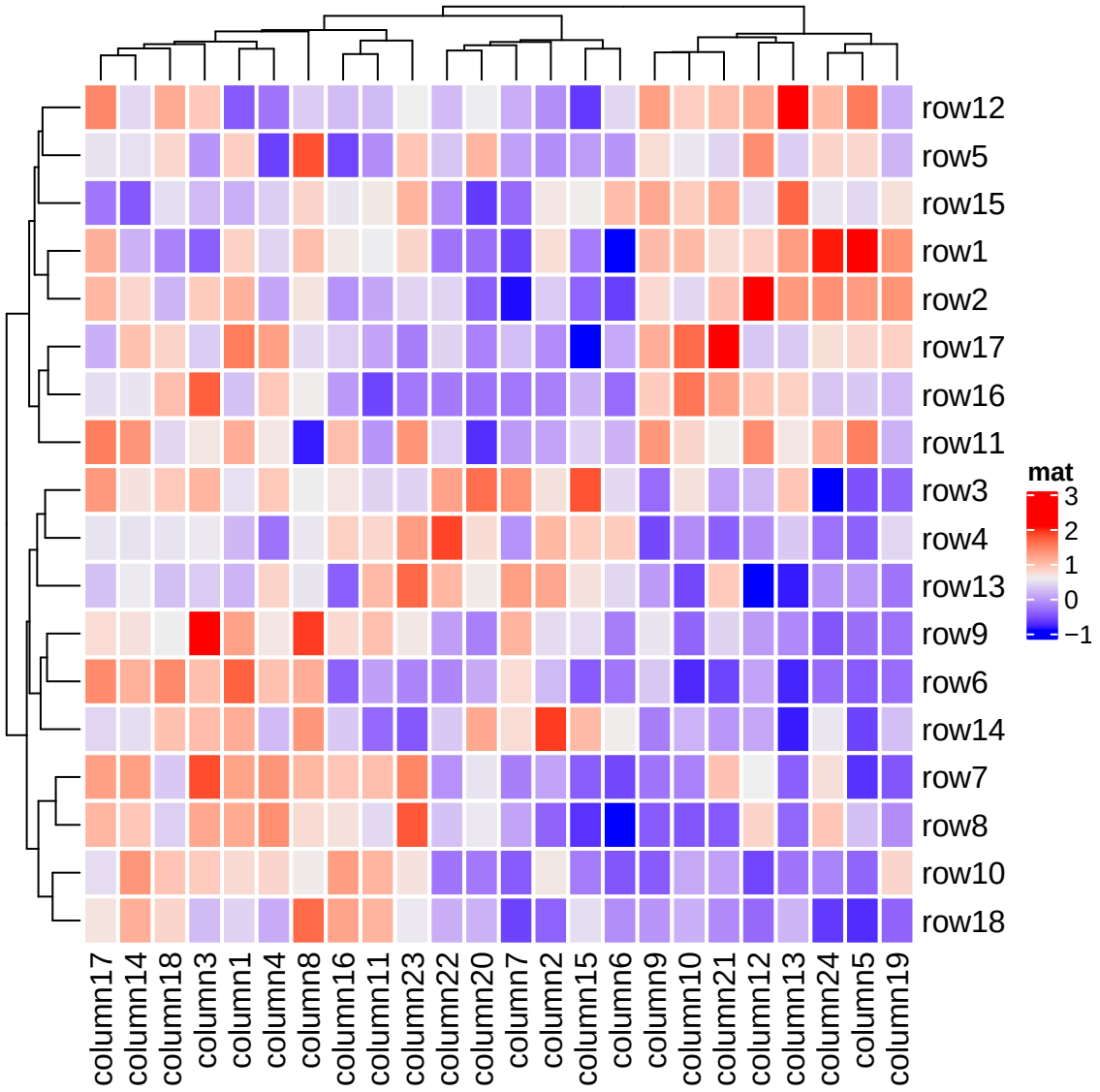
The value of `border` can be logical (`TRUE` corresponds to `black`) or a character of color (e.g. `red`).

`rect_gp` is a `gpar` object which means you can only set it by `grid::gpar()`. Since the filled color is already controlled by the heatmap color mapping, you can only set the `col` parameter in `gpar()` to control the border of the heatmap grids.

```
Heatmap(mat, name = "mat", border = TRUE)
```




```
Heatmap(mat, name = "mat", rect_gp = gpar(col = "white", lwd = 2))
```

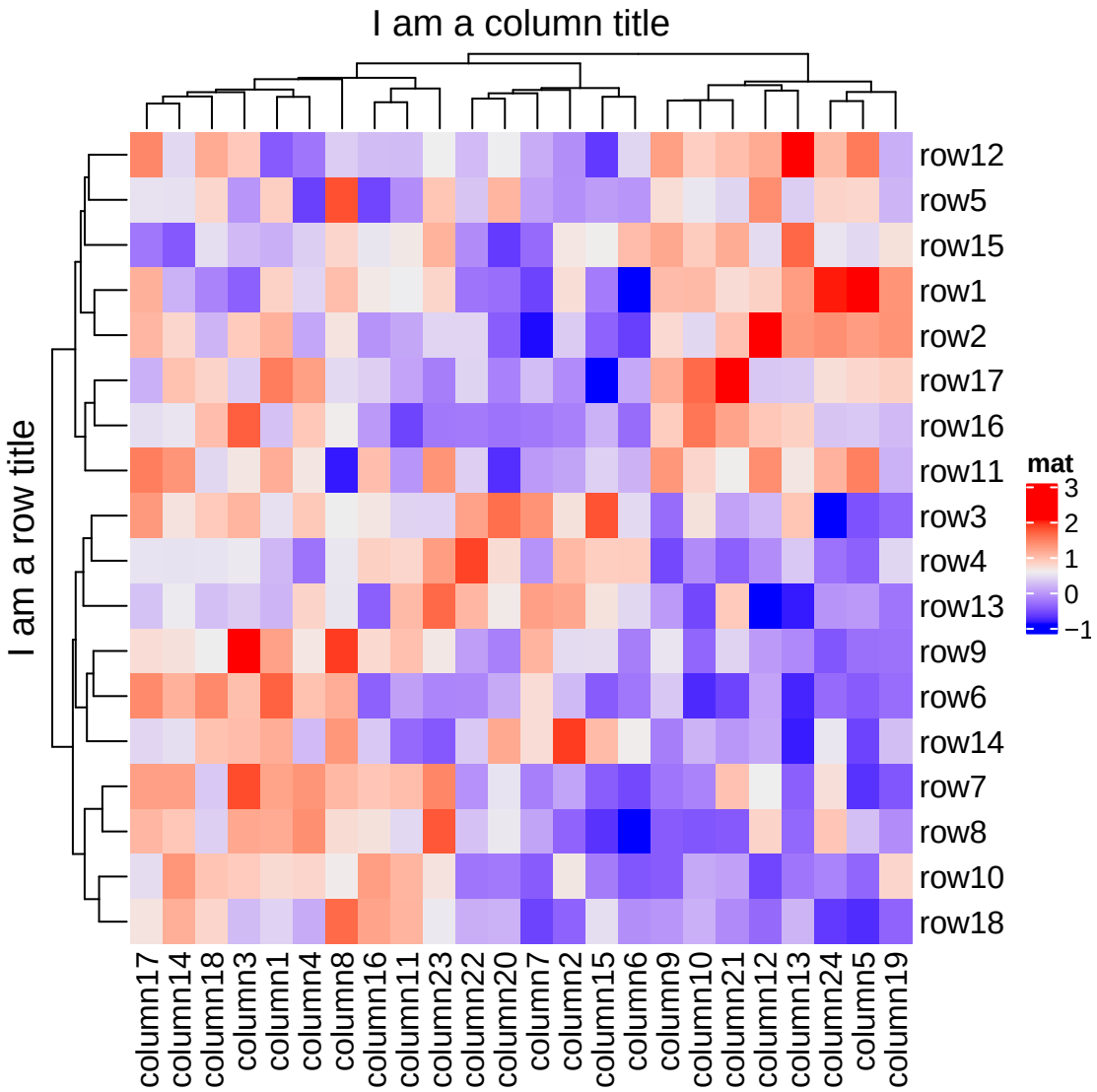


2.2 Titles

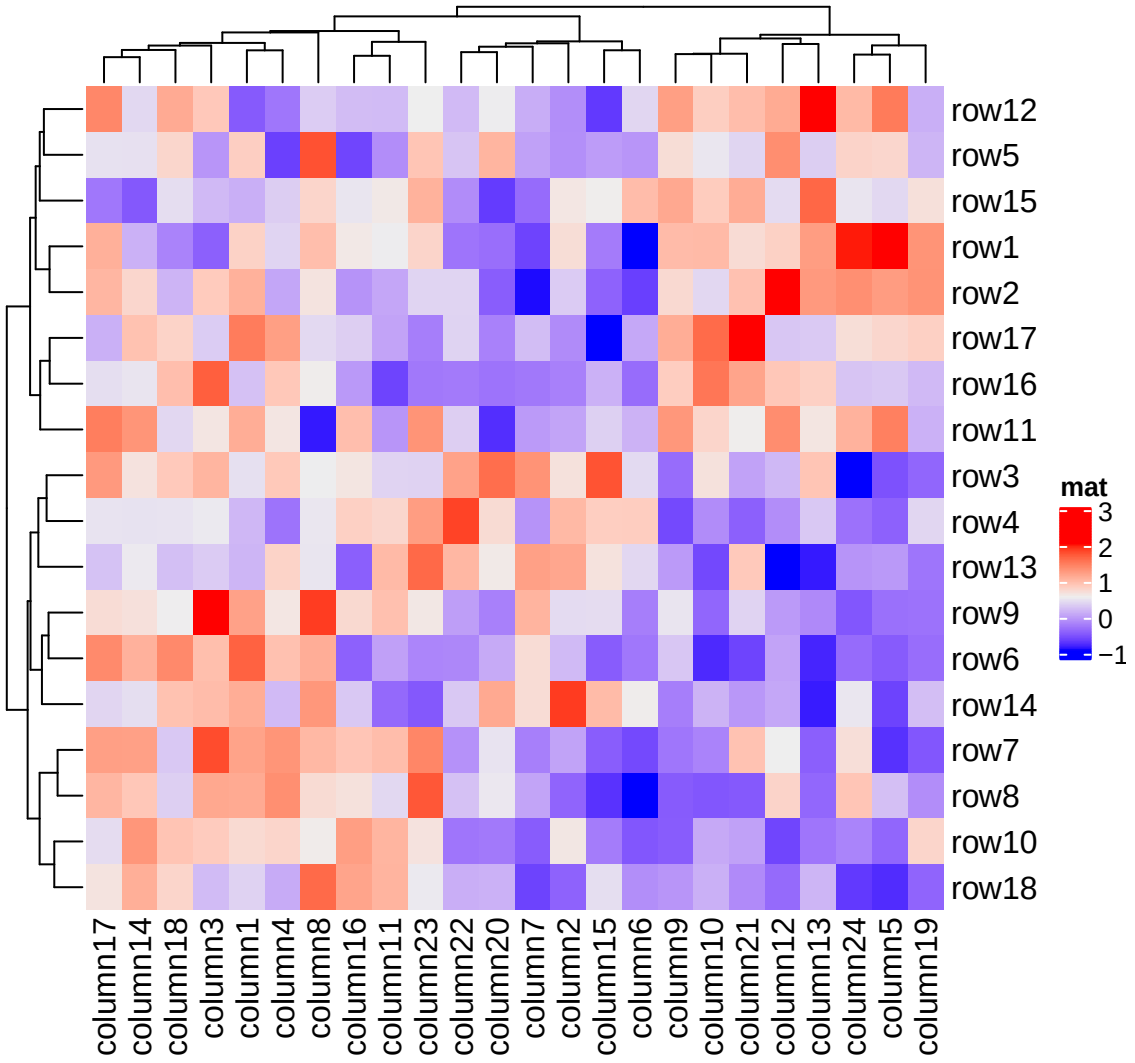
The title of the heatmap basically tells what the plot is about. In **ComplexHeatmap** package, you can set heatmap title either by the row or/and by the column. Note at a same time you can only put e.g. column title either on the top or at the bottom of the heatmap.

The graphic parameters can be set by `row_title_gp` and `column_title_gp` respectively. Please remember you should use `gpar()` to specify graphic parameters.

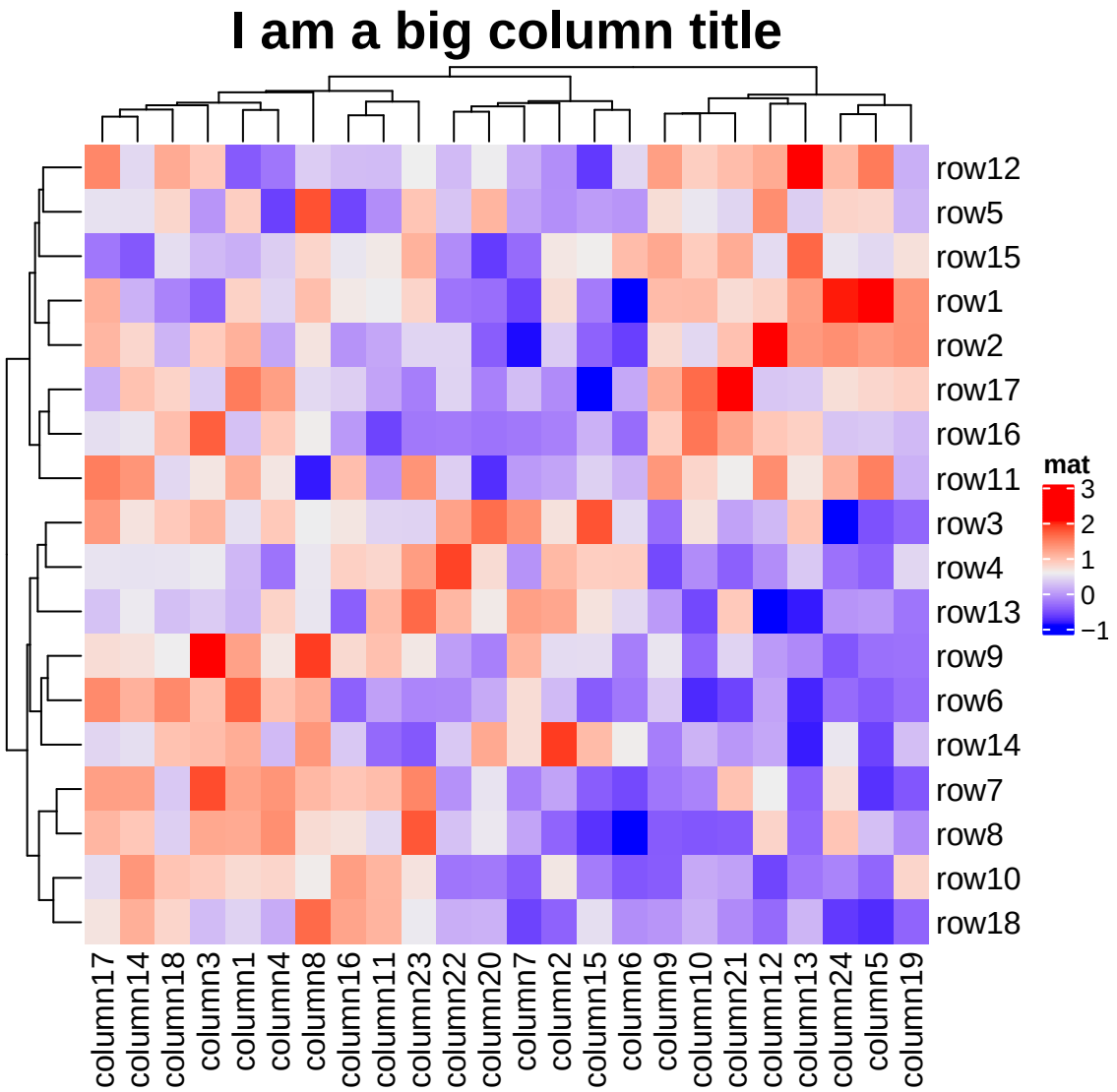
```
Heatmap(mat, name = "mat", column_title = "I am a column title",
    row_title = "I am a row title")
```




```
Heatmap(mat, name = "mat", column_title = "I am a column title at the bottom",
    column_title_side = "bottom")
```

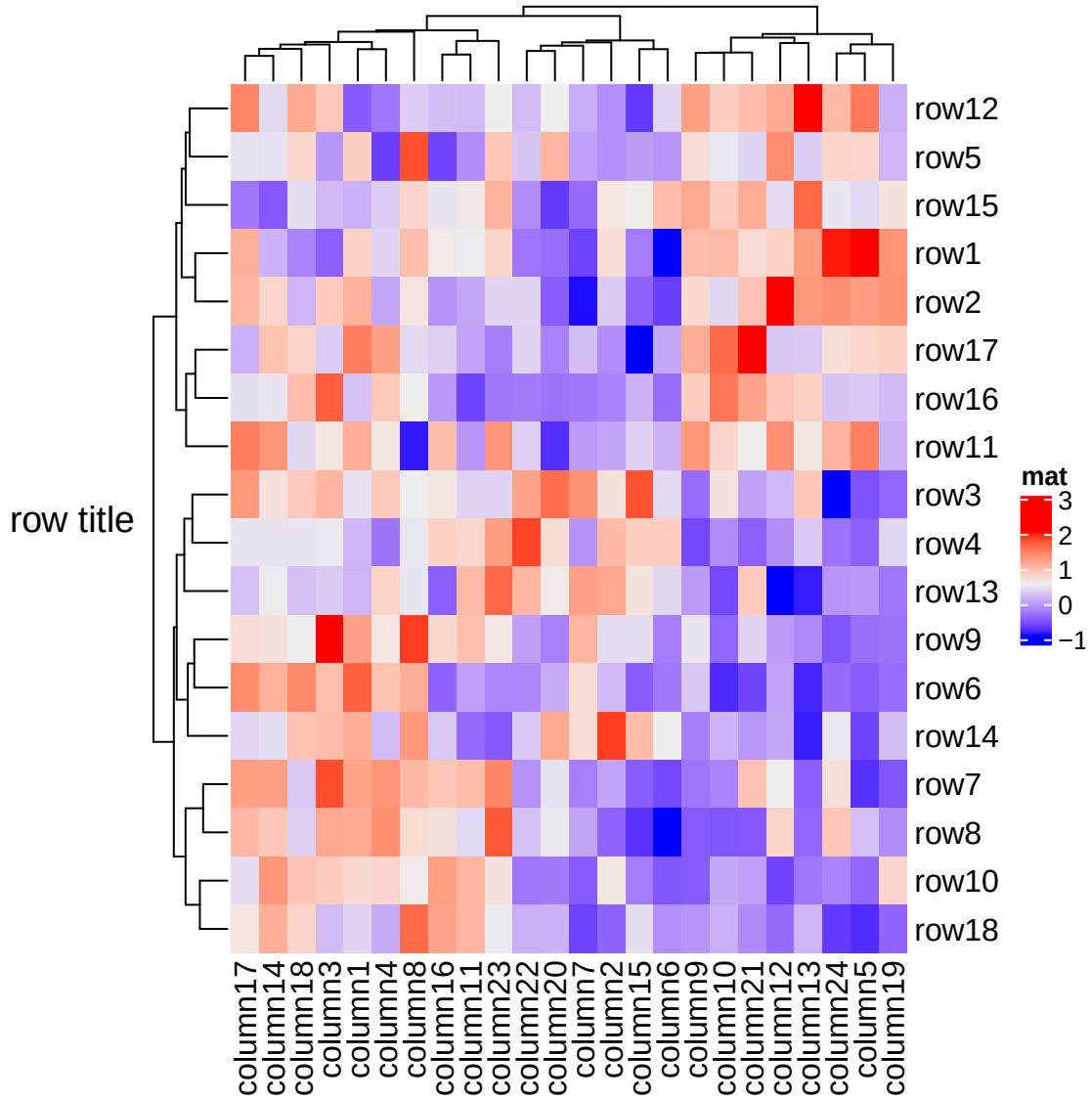



```
Heatmap(mat, name = "mat", column_title = "I am a big column title",
    column_title_gp = gpar(fontsize = 20, fontface = "bold"))
```



Rotations for titles can be set by `row_title_rot` and `column_title_rot`, but only horizontal and vertical rotations are allowed.

```
Heatmap(mat, name = "mat", row_title = "row title", row_title_rot = 0)
```

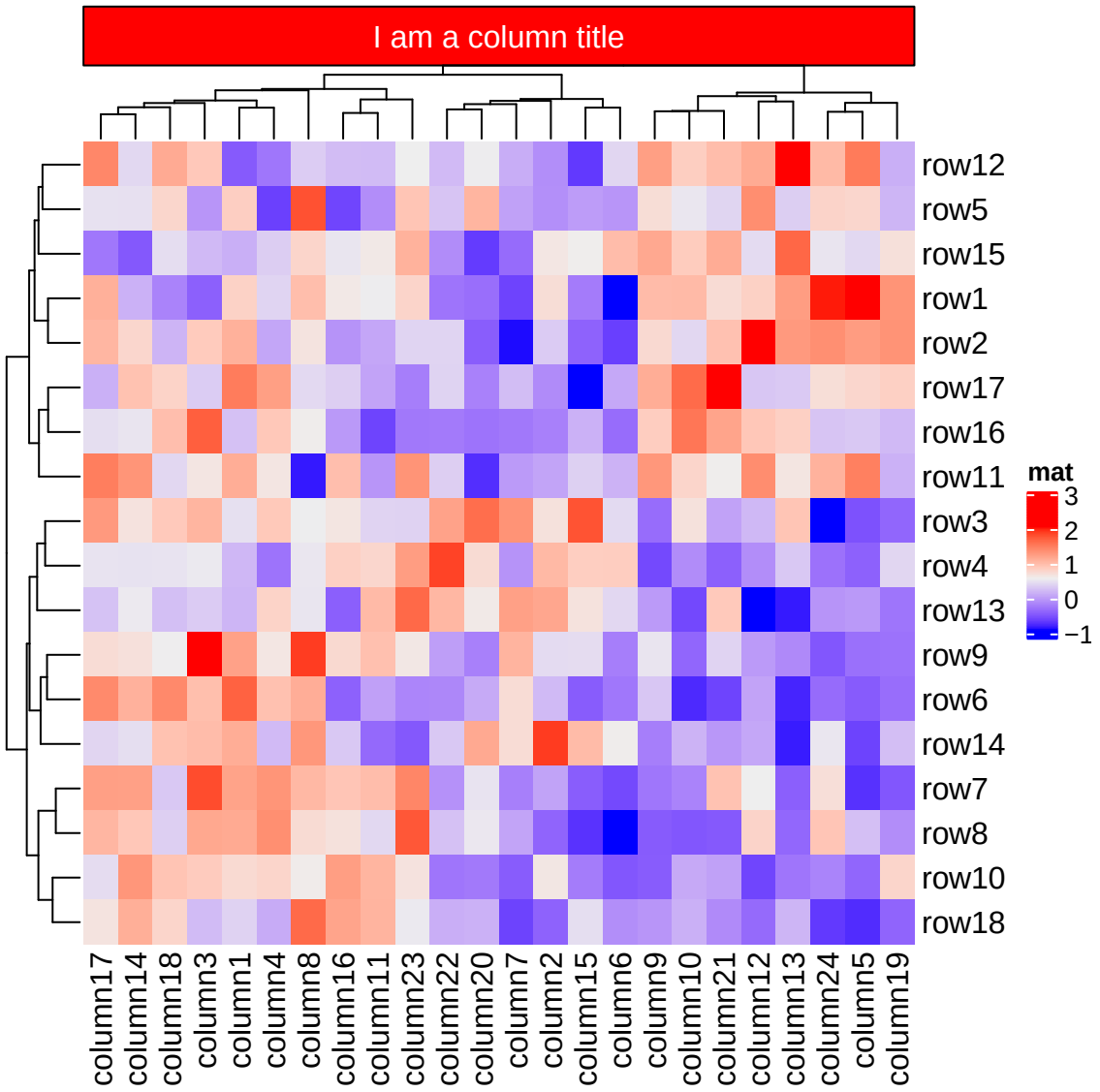


Row or column title supports as a template which is used when rows or columns are split in the heatmap (because there will be multiple row/column titles). This functionality is introduced in Section **??**. A quick example would be:

```
# code only for demonstration
# row title would be cluster_1 and cluster_2
Heatmap(mat, name = "mat", row_km = 2, row_title = "cluster_%s")
```

You can set `fill` parameter in `row_title_gp` and `column_title_gp` to set the background color of titles.

```
Heatmap(mat, name = "mat", column_title = "I am a column title",
    column_title_gp = gpar(fill = "red", col = "white"))
```



2.3 Clustering

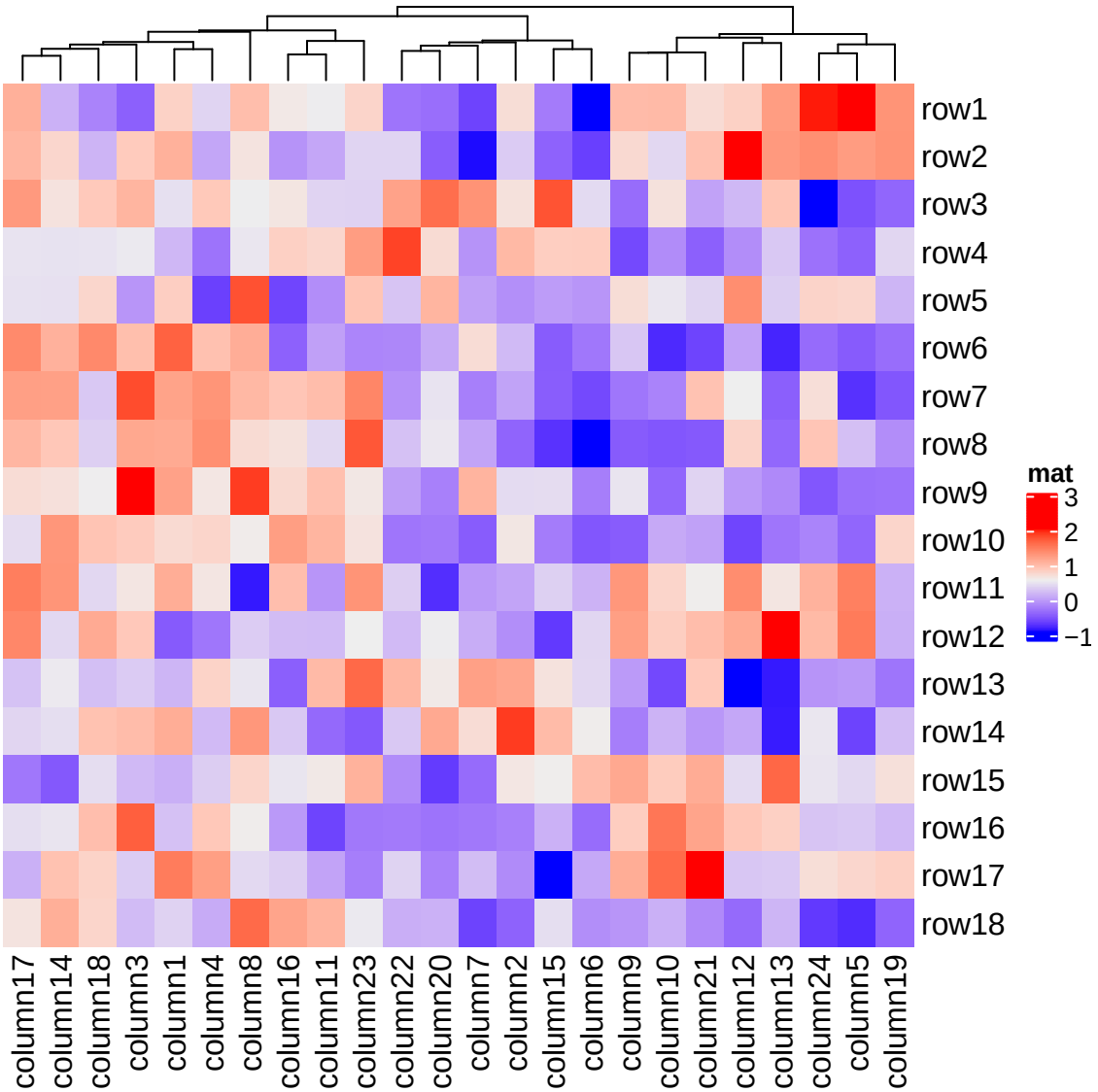
Clustering might be the key component of the heatmap visualization. In **ComplexHeatmap** package, hierarchical clustering is supported with great flexibility. You can specify the clustering either by:

- a pre-defined distance method (e.g. `"eulidean"` or `"pearson"`),
- a distance function,
- a object that already contains clustering (a `hclust` or `dendrogram` object or object that can be coerced to `hclust` or `dendrogram` class),
- a clustering function.

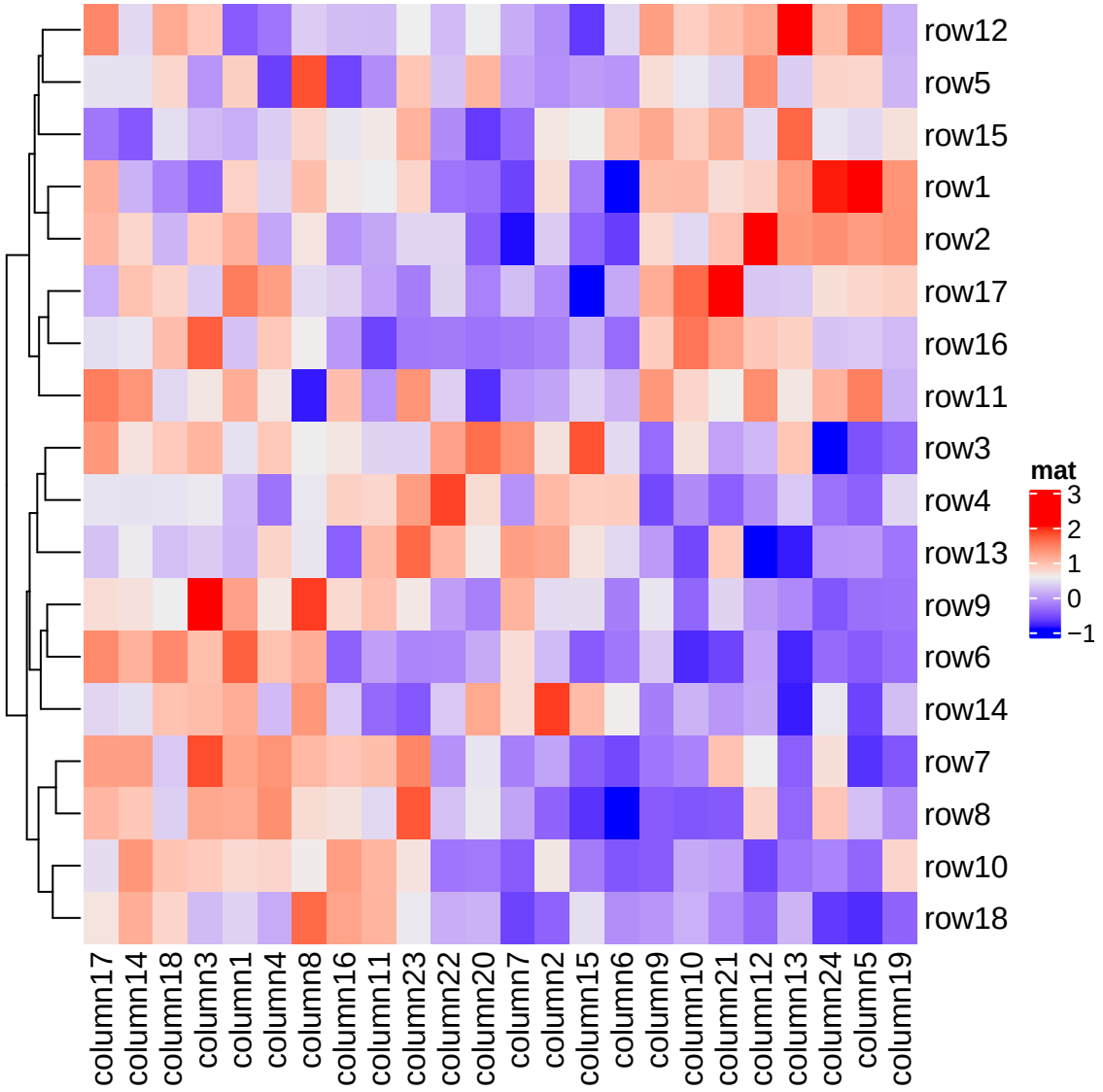
It is also possible to render the dendrograms with different colors and styles for different branches for better revealing structures of your data (e.g. by `dendextend::color_branches()`).

First, there are general settings for the clustering, e.g. whether apply clustering or show dendrograms, the side of the dendrograms and heights of the dendrograms.

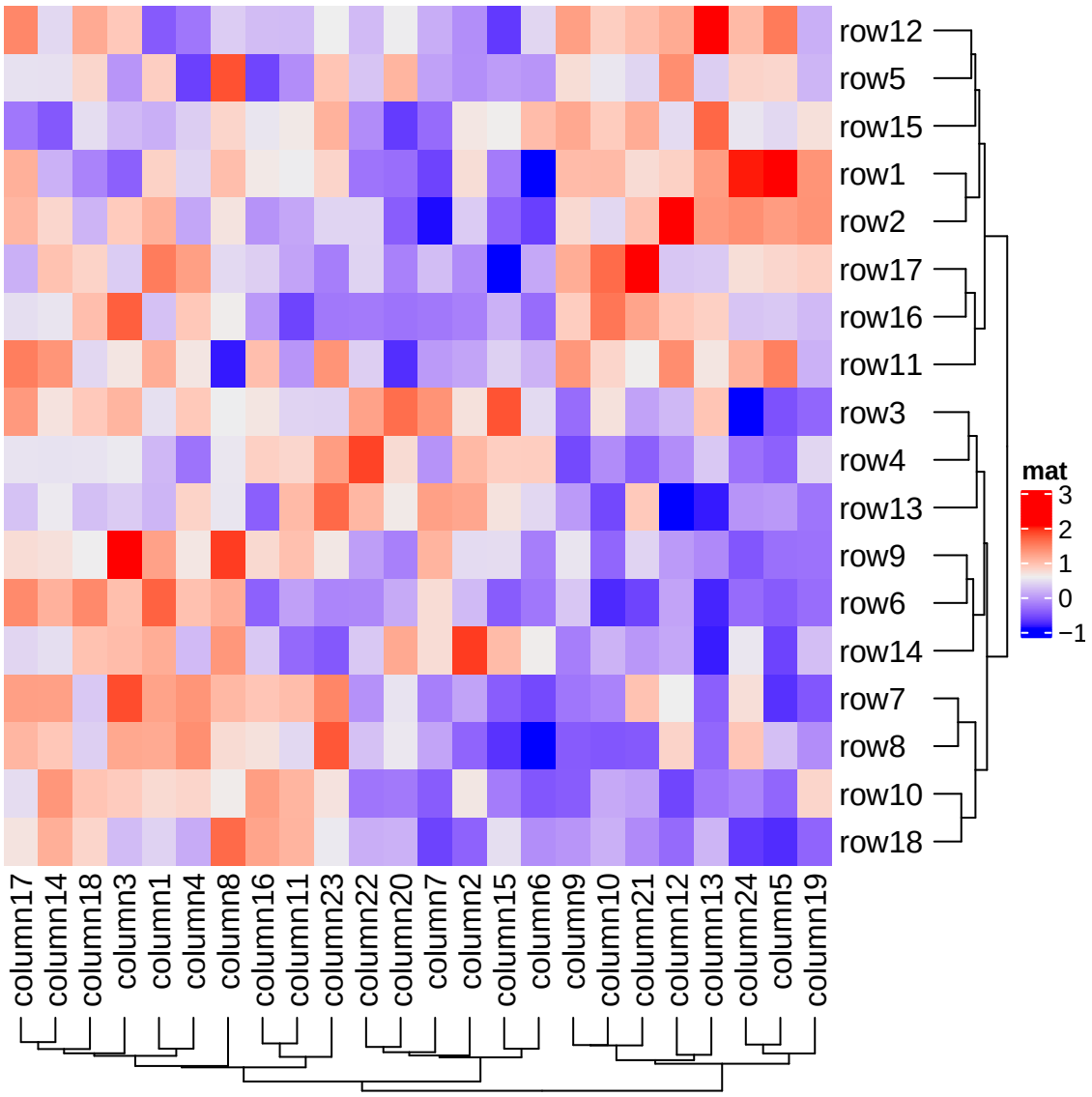
```
Heatmap(mat, name = "mat", cluster_rows = FALSE) # turn off row clustering
```



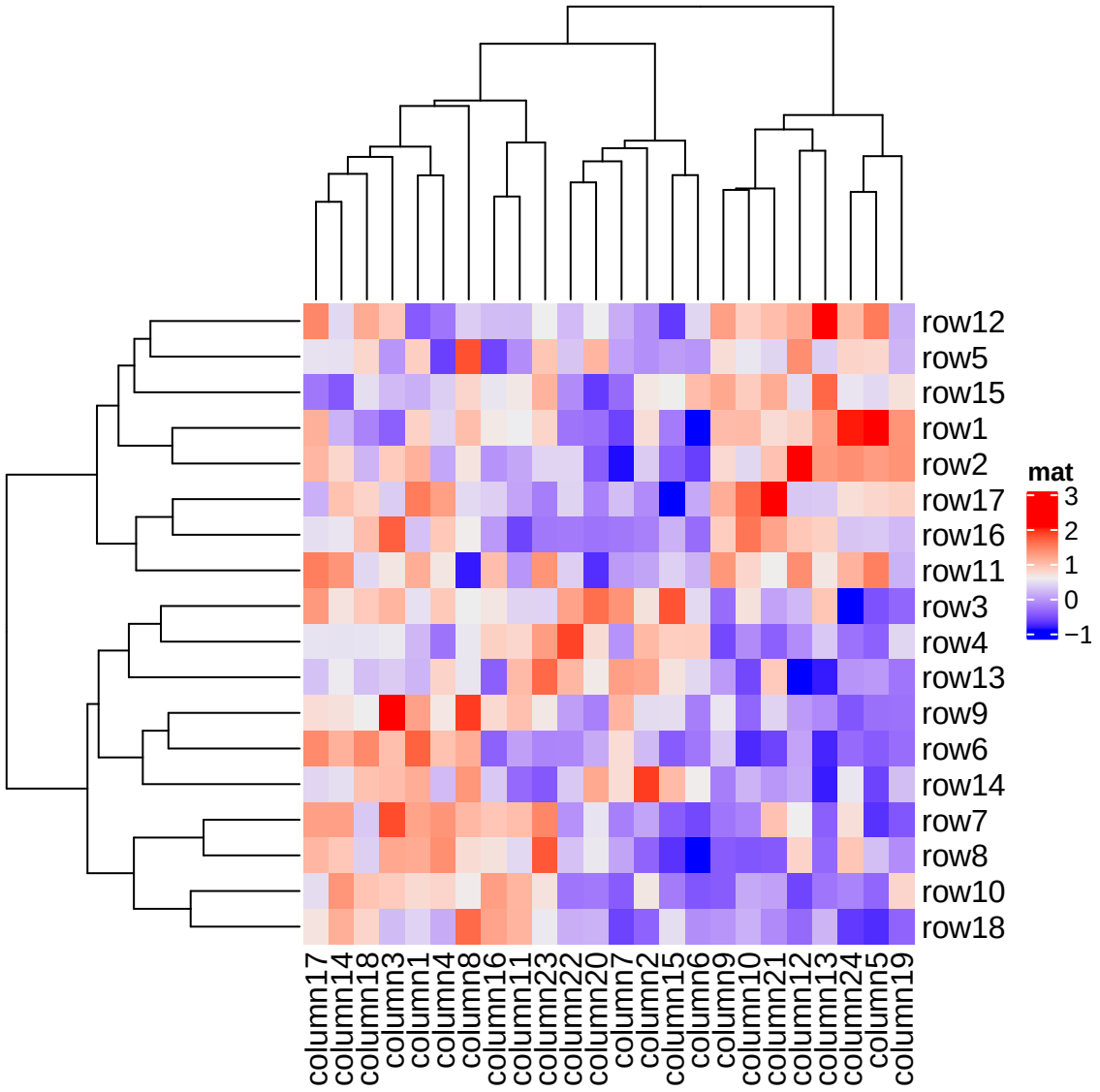

```
Heatmap(mat, name = "mat", show_column_dend = FALSE) # hide column dendrogram
```




```
Heatmap(mat, name = "mat", row_dend_side = "right", column_dend_side = "bottom")
```




```
Heatmap(mat, name = "mat", column_dend_height = unit(4, "cm"),
    row_dend_width = unit(4, "cm"))
```

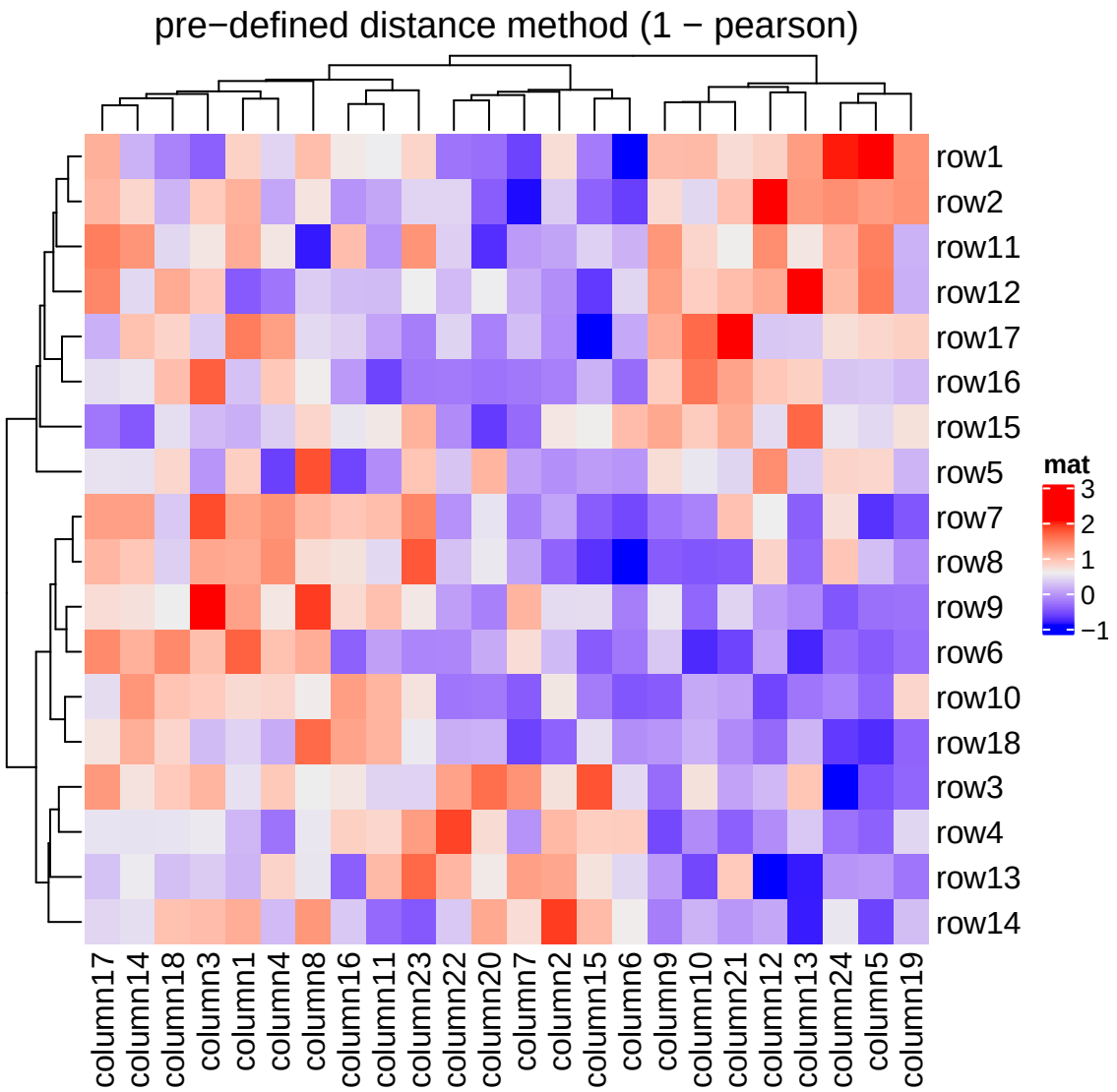


2.3.1 Distance methods

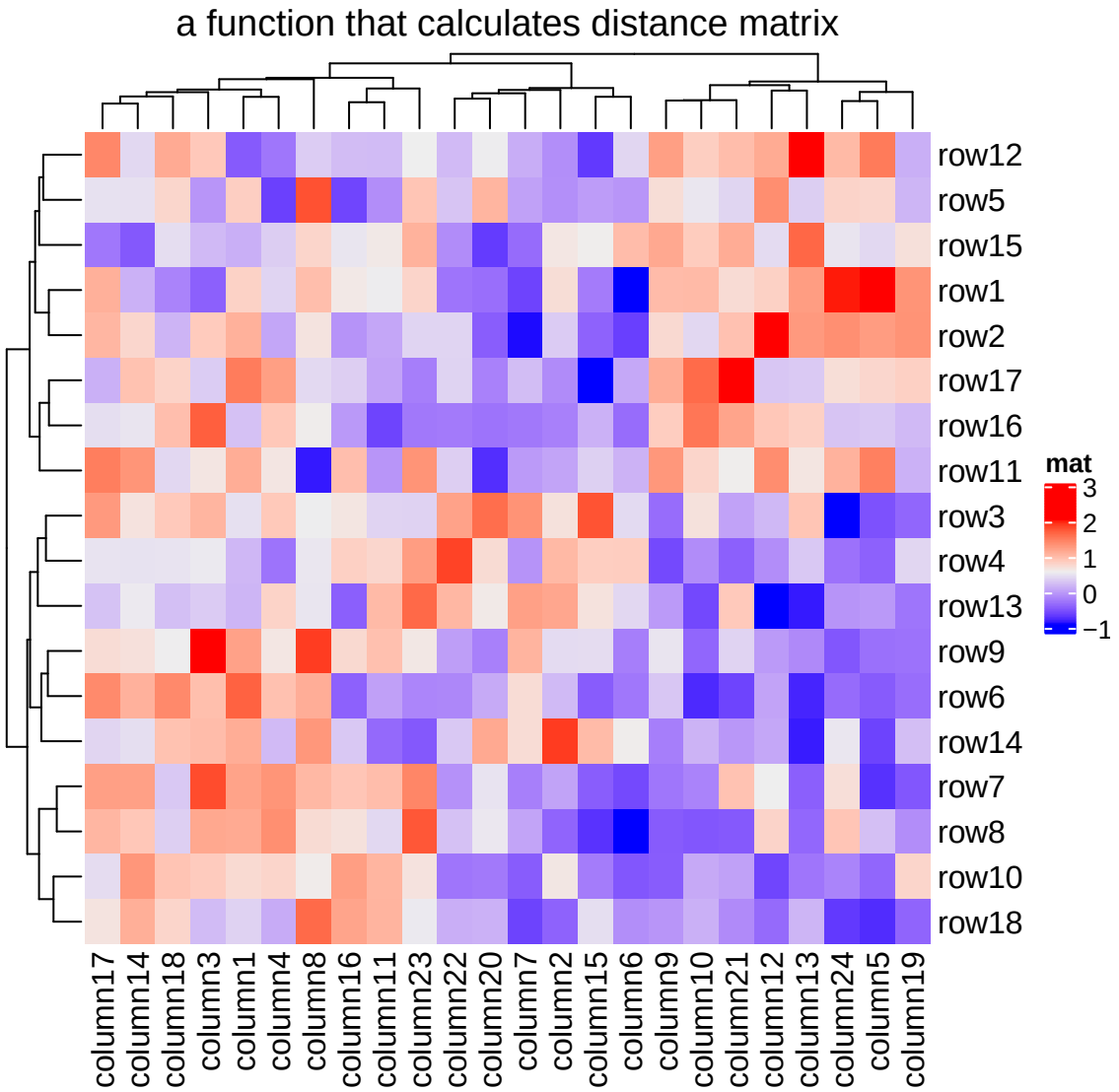
Hierarchical clustering is performed in two steps: calculate the distance matrix and apply clustering. There are three ways to specify distance metric for clustering:

- specify distance as a pre-defined option. The valid values are the supported methods in `dist()` function and in `"pearson"`, `"spearman"` and `"kendall"`. If there is any `NA` values in the matrix, `ComplexHeatmap::dist2()` is used instead which performs pairwise distance calculation by removing `NA` values. The correlation distance is defined as `1 - cor(x, y, method)`.
- a self-defined function which calculates distance from a matrix. The function should only contain one argument. Please note for clustering on columns, the matrix will be transposed automatically.
- a self-defined function which calculates distance from two vectors. The function should only contain two arguments.

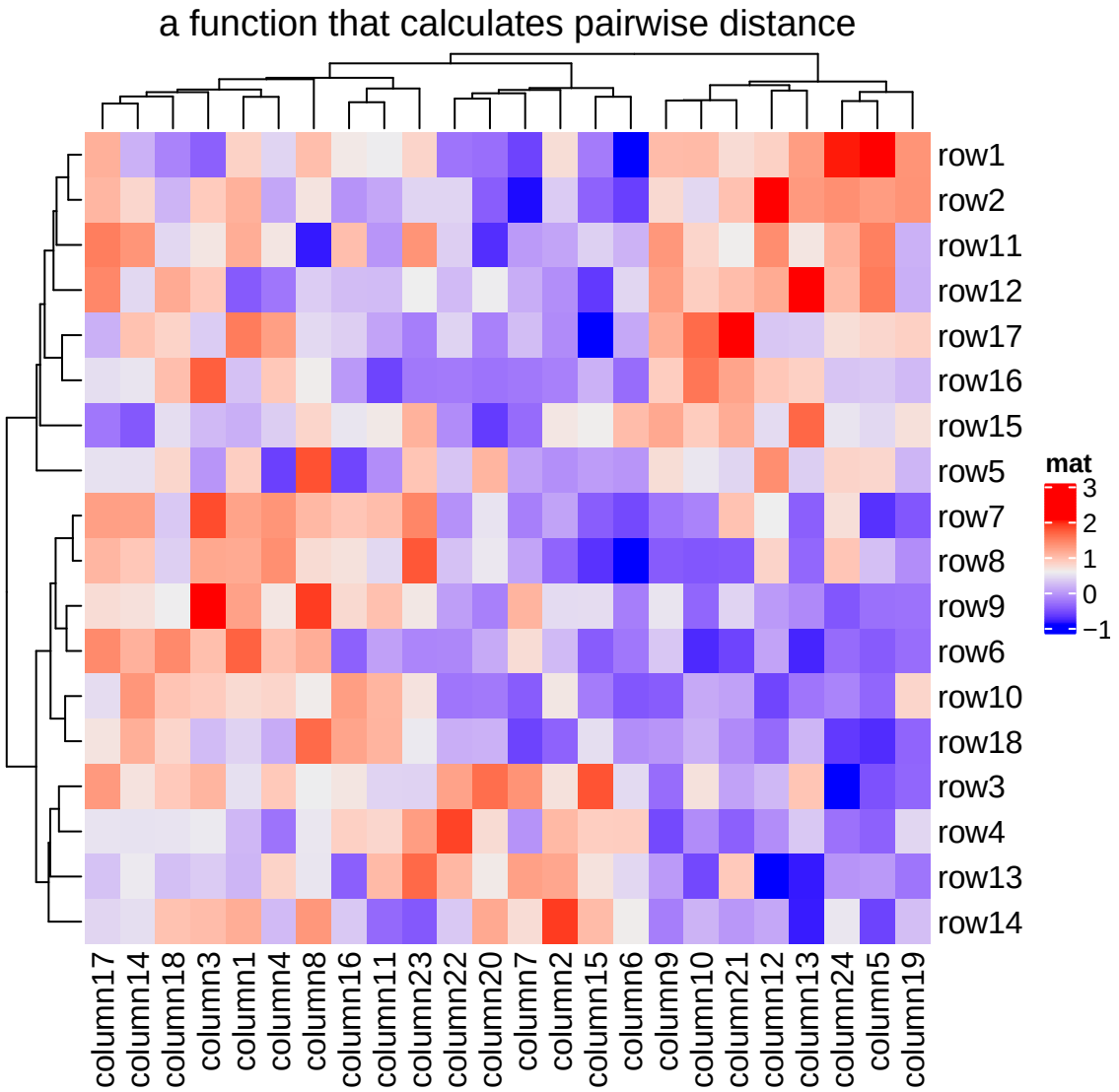
```
Heatmap(mat, name = "mat", clustering_distance_rows = "pearson",
    column_title = "pre-defined distance method (1 - pearson)")
```




```
Heatmap(mat, name = "mat", clustering_distance_rows = function(m) dist(m),
    column_title = "a function that calculates distance matrix")
```




```
Heatmap(mat, name = "mat", clustering_distance_rows = function(x, y) 1 - cor(x, y),
    column_title = "a function that calculates pairwise distance")
```



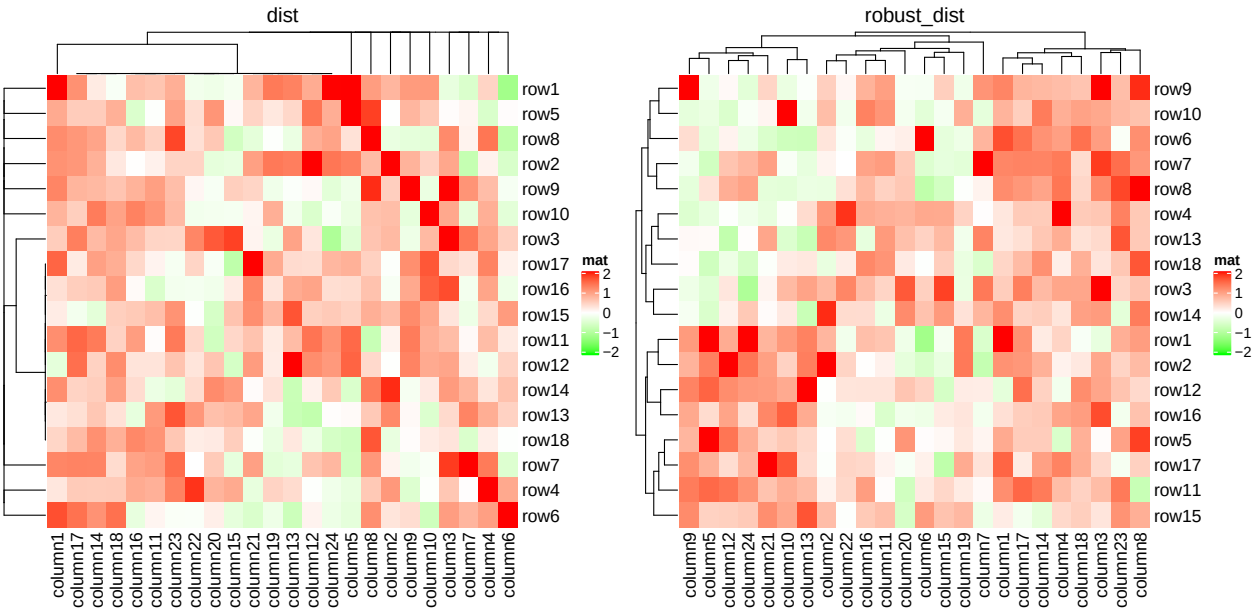
Based on these features, we can apply clustering which is robust to outliers based on the pairwise distance. Note here we set the color mapping function because we don't want outliers affect the colors.

```
mat_with_outliers = mat
for(i in  1:10) mat_with_outliers[i, i] = 1000
robust_dist = function(x, y) {
    qx = quantile(x, c(0.1, 0.9))
    qy = quantile(y, c(0.1, 0.9))
    l = x > qx[1] & x < qx[2] & y > qy[1] & y < qy[2]
    x = x[l]
    y = y[l]
    sqrt(sum((x - y)^2))
}
```

and we compare the two heatmaps with or without the robust distance method:

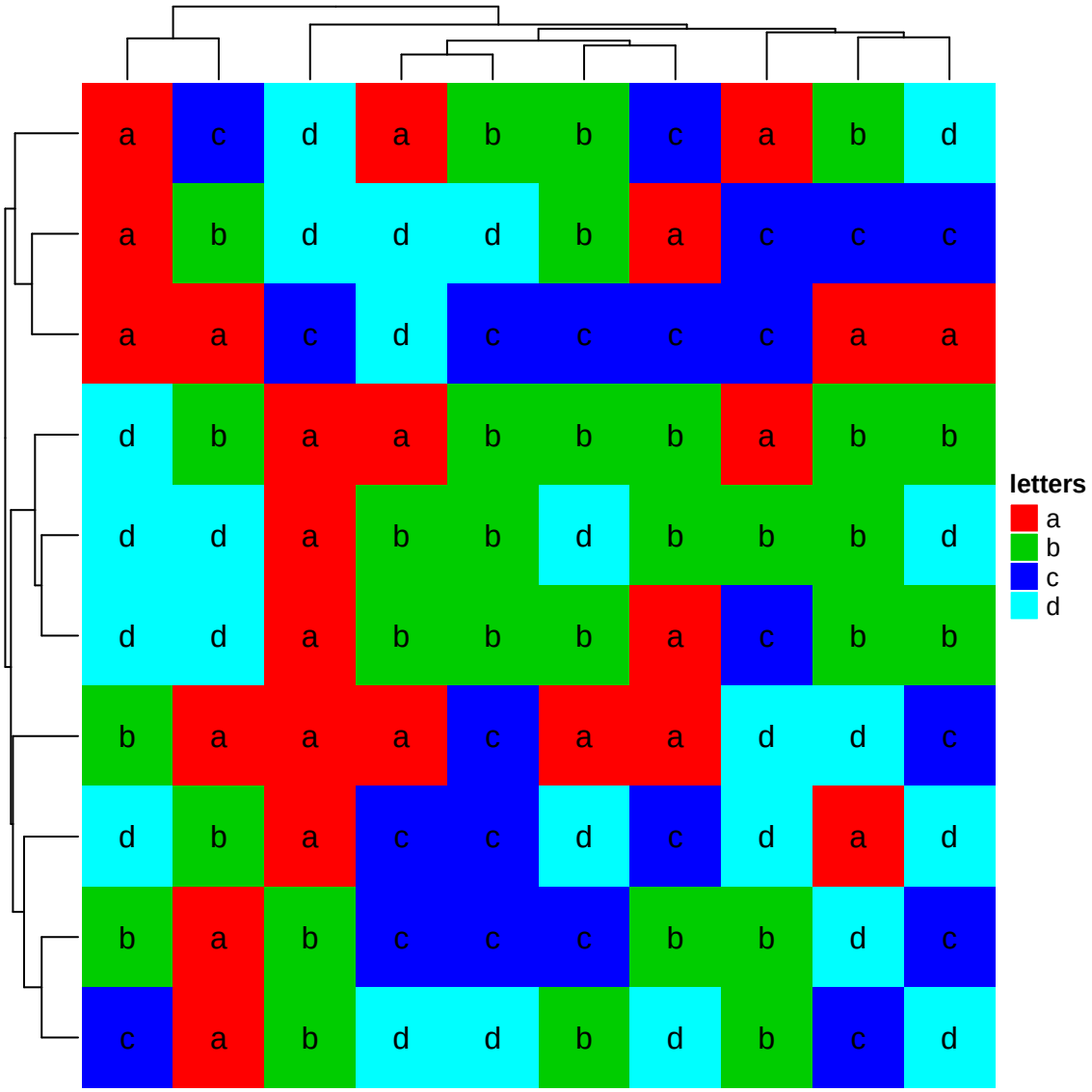
```
Heatmap(mat_with_outliers, name = "mat",
    col = colorRamp2(c(-2, 0, 2), c("green", "white", "red")),
    column_title = "dist")
Heatmap(mat_with_outliers, name = "mat",
```

```
    col = colorRamp2(c(-2, 0, 2), c("green", "white", "red")),
    clustering_distance_rows = robust_dist,
    clustering_distance_columns = robust_dist,
    column_title = "robust_dist")
```



If there are proper distance methods (like methods in **stringdist** package, you can also cluster a character matrix. `cell_fun` argument will be introduced in Section **??**.

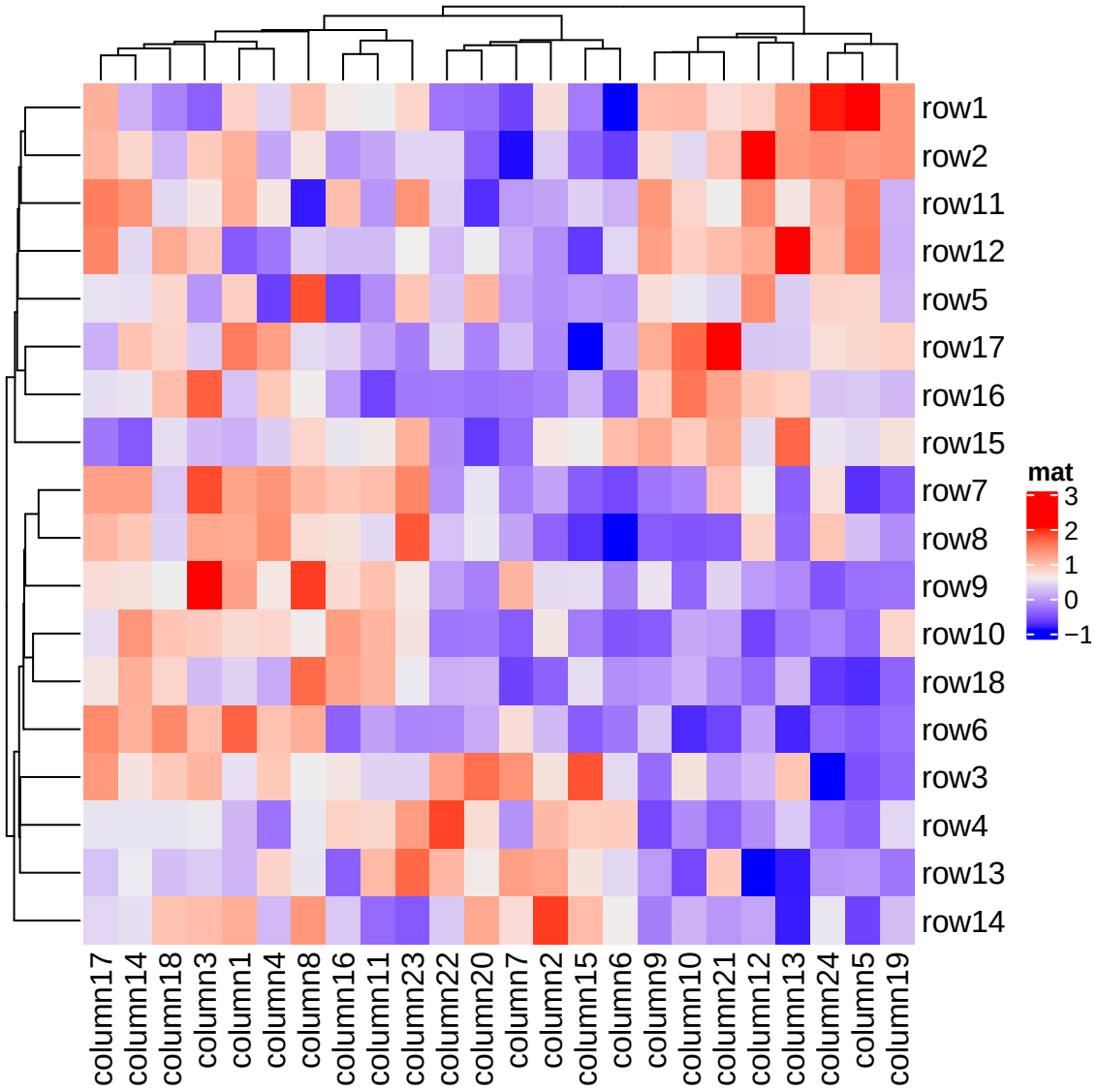
```
mat_letters = matrix(sample(letters[1:4], 100, replace = TRUE), 10)
# distance in the ASCII table
dist_letters = function(x, y) {
    x = strtoi(charToRaw(paste(x, collapse = "")), base = 16)
    y = strtoi(charToRaw(paste(y, collapse = "")), base = 16)
    sqrt(sum((x - y)^2))
}
Heatmap(mat_letters, name = "letters", col = structure(2:5, names = letters[1:4]),
    clustering_distance_rows = dist_letters, clustering_distance_columns = dist_letters,
    cell_fun = function(j, i, x, y, w, h, col) { # add text to each grid
        grid.text(mat_letters[i, j], x, y)
    })
```



2.3.2 Clustering methods

Method to perform hierarchical clustering can be specified by `clustering_method_rows` and `clustering_method_columns`. Possible methods are those supported in `hclust()` function.

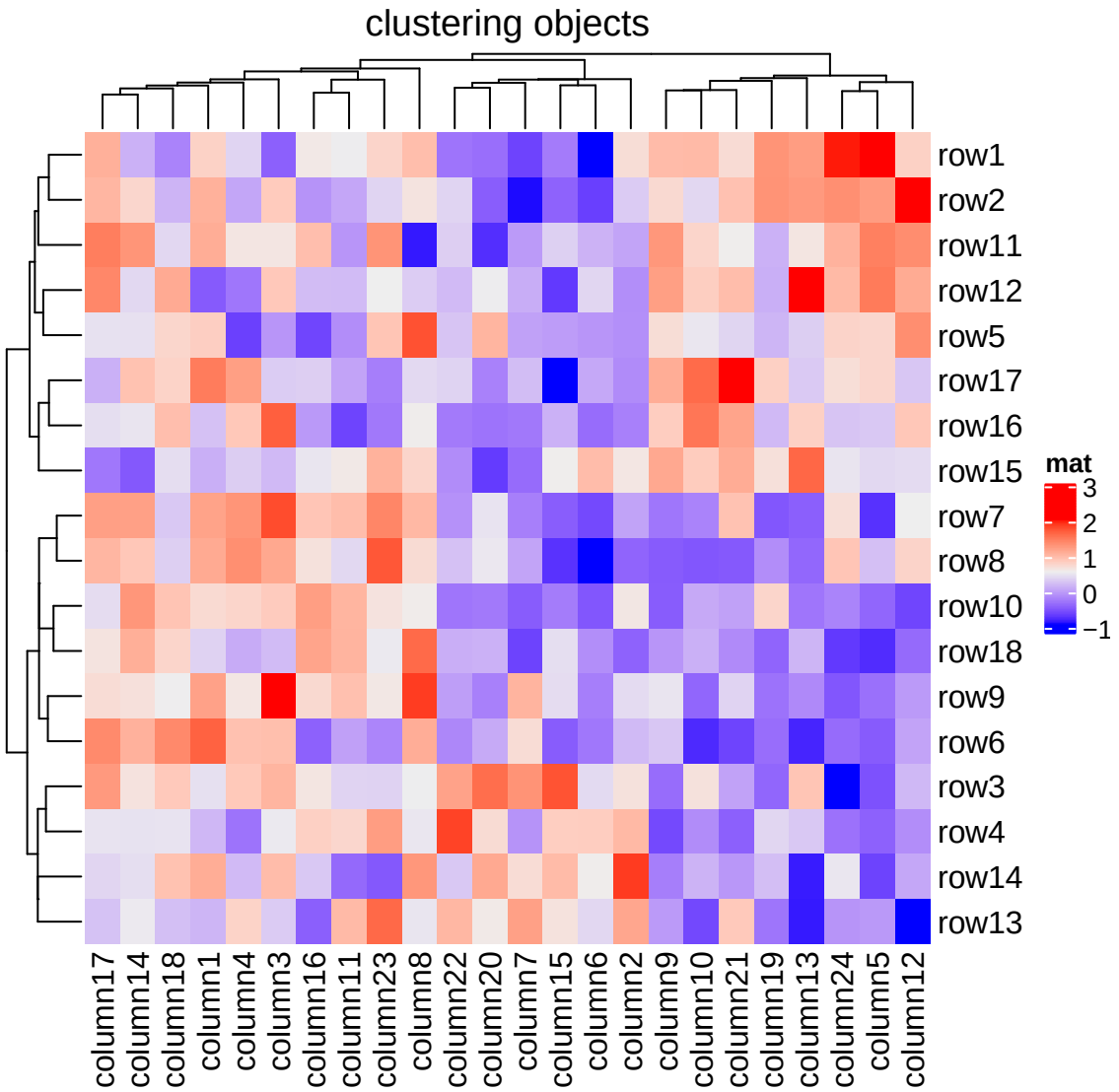
```
Heatmap(mat, name = "mat", clustering_method_rows = "single")
```



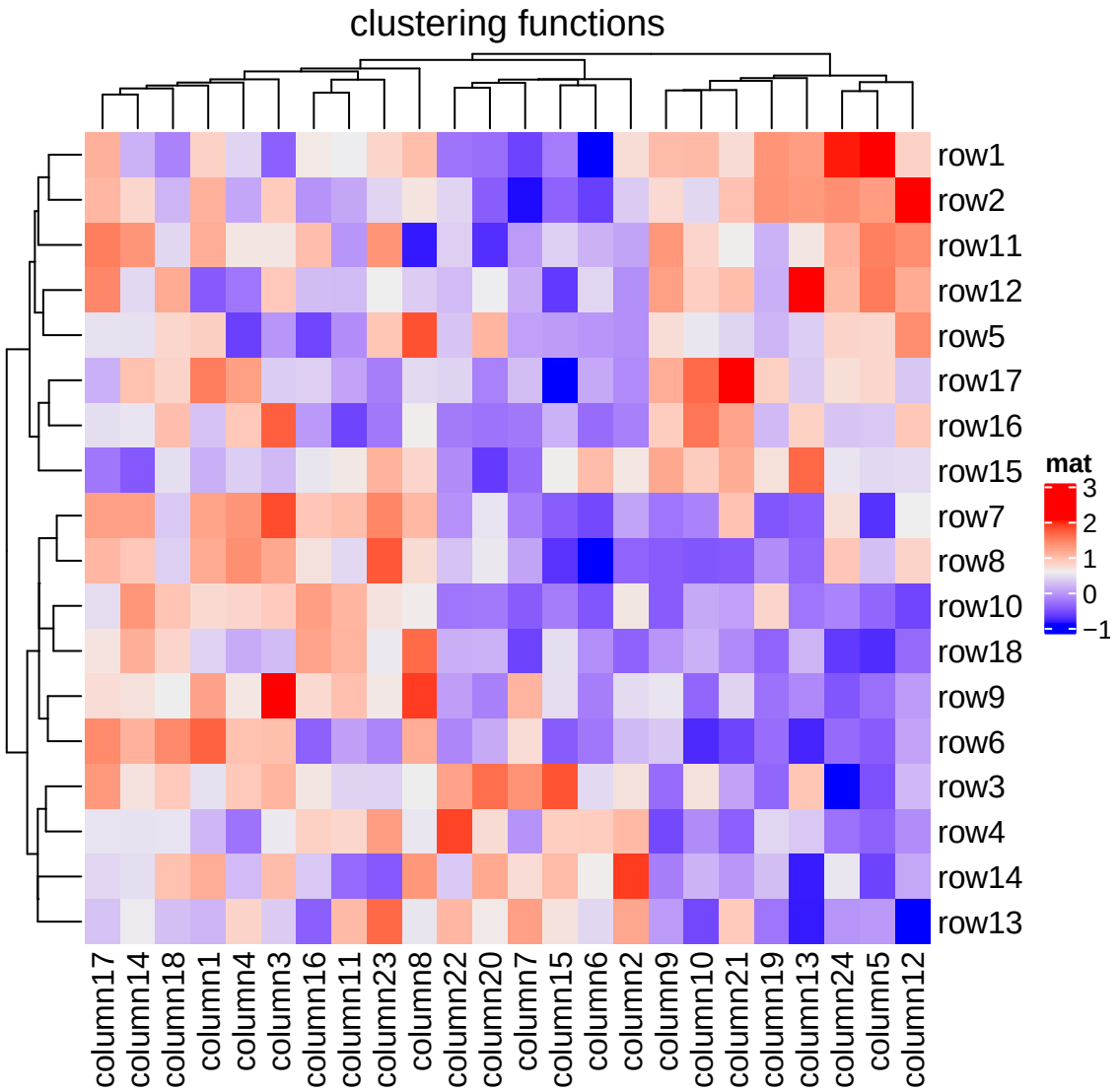
If you already have clustering objects or a function which directly returns a clustering object, you can ignore the distance settings and set `cluster_rows` or `cluster_columns` to the clustering objects or clustering functions. If it is a clustering function, the only argument should be the matrix and it should return a `hclust` or `dendrogram` object or a object that can be coerced to the two classes.

In following example, we perform clustering with methods from **cluster** package either by a pre-calculated clustering object or a clustering function:

```
library(cluster)
Heatmap(mat, name = "mat", cluster_rows = as.dendrogram(diana(mat)),
   cluster_columns = as.dendrogram(agnes(t(mat))), column_title = "clustering objects")
```




```
Heatmap(mat, name = "mat", cluster_rows = diana,
   cluster_columns = agnes, column_title = "clustering functions")
```



The last command is as same as :

```
# code only for demonstration
Heatmap(mat, name = "mat", cluster_rows = function(m) as.dendrogram(diana(m)),
    cluster_columns = function(m) as.dendrogram(agnes(m)), column_title = "clutering functions")
```

Please note, when `cluster_rows` is set as a function, the argument `m` is the input `mat` itself, while for `cluster_columns`, `m` is the transpose of `mat`.

`fastcluster::hclust` implements a faster version of `hclust()`. We can set it to `cluster_rows` and `cluster_columns` to use the faster version of `hclust()`.

```
# code only for demonstration
Heatmap(mat, name = "mat", cluster_rows = fastcluster::hclust,
    cluster_columns = fastcluster::hclust)
```

To make it more convinient to use the faster version of `hclust()` (assuming you have many heatmaps to construct), it can be set as a global option. The usage of `ht_opt` is introduced in Section ??.

```
# code not run when building the vignette
ht_opt$fast_hclust = TRUE
```

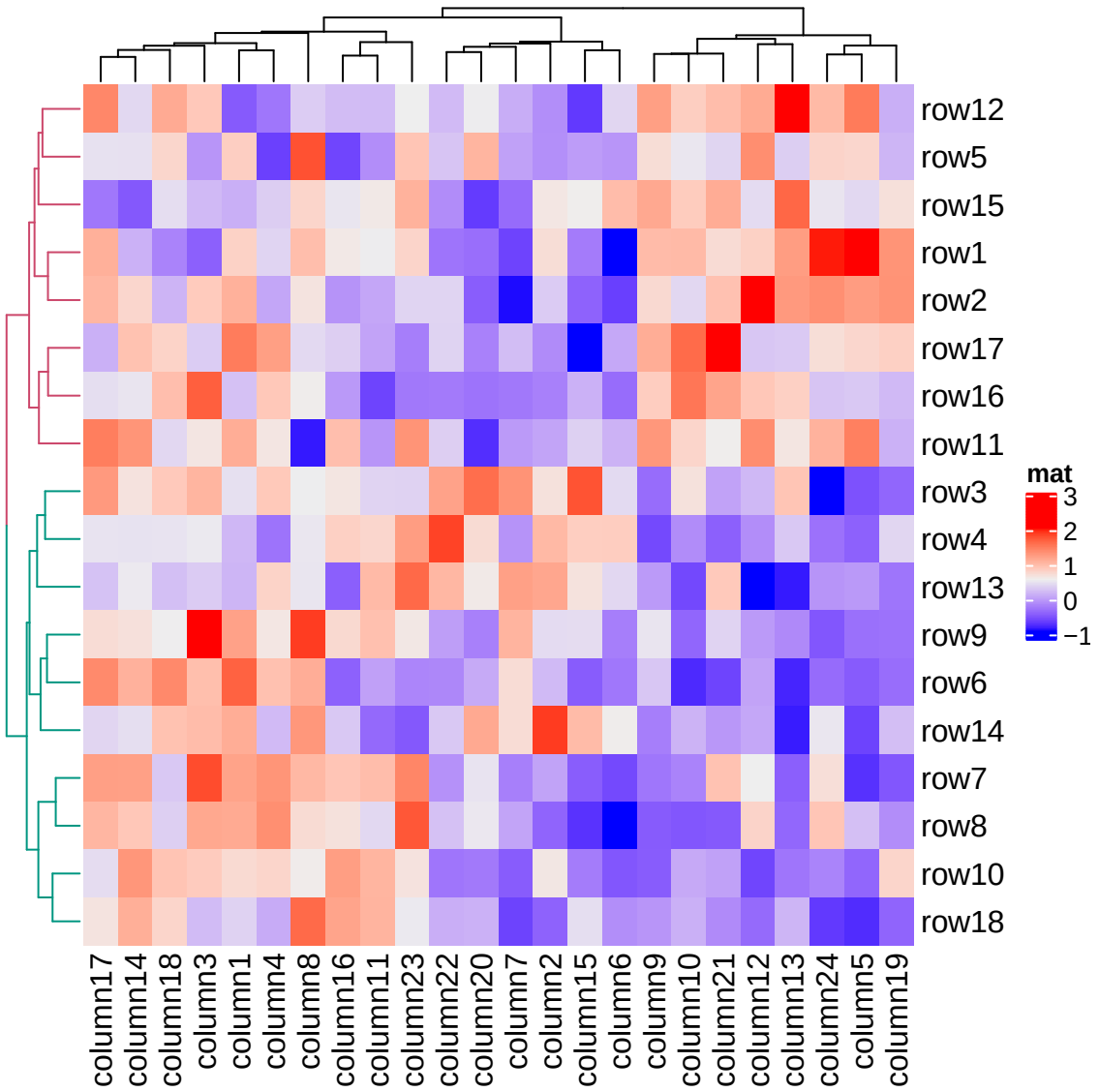
```
# now fastcluster::hclust is used in all heatmaps
```

2.3.3 Render dendrograms

If you want to render the dendrogram, normally you need to generate a `dendrogram` object and render it in the first place, then send it to the `cluster_rows` or `cluster_columns` argument.

You can render your `dendrogram` object by the **dendextend** package to make a more customized visualization of the dendrogram. Note **ComplexHeatmap** only allows rendering on the dendrogram edges.

```
library(dendextend)
row_dend = as.dendrogram(hclust(dist(mat)))
row_dend = color_branches(row_dend, k = 2) # `color_branches()` returns a dendrogram object
Heatmap(mat, name = "mat", cluster_rows = row_dend)
```



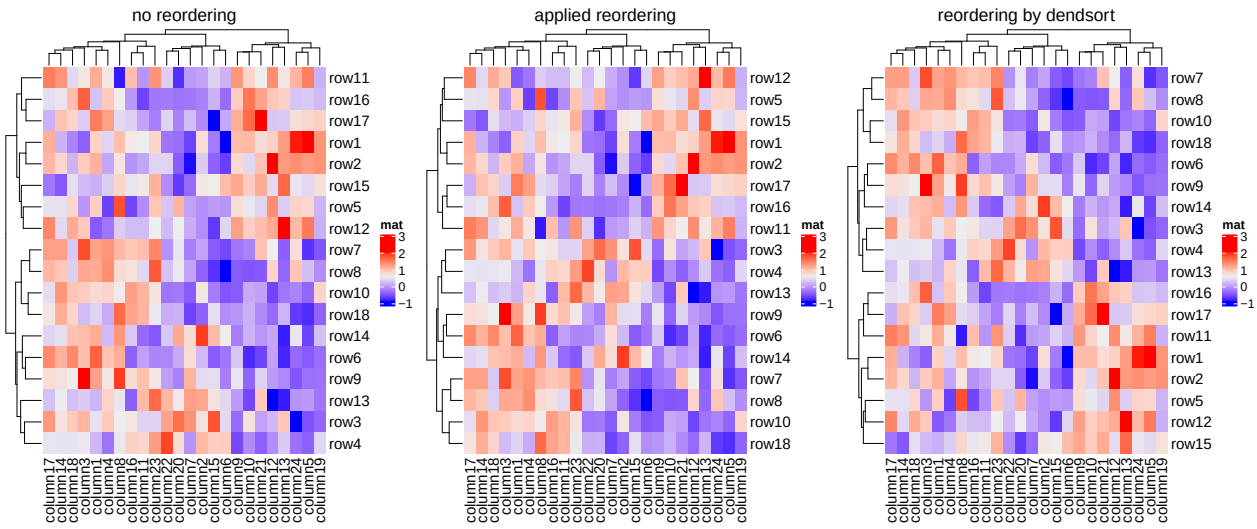
2.3.4 Reorder dendrograms

In the `Heatmap()` function, dendrograms are reordered to make features with larger difference more separated from each others (please refer to the documentation of `reorder.dendrogram()`). Here the difference (or it is called the weight) is measured by the row means if it is a row dendrogram or by the column means if it is a column dendrogram. `row_dend_reorder` and `column_dend_reorder` control whether to apply dendrogram reordering If they are set to `TRUE` or `FALSE`, ot they control the weight for the reordering if they are set to numeric vectors (send to the `wts` argument of `reorder.dendrogram()`). The reordering can be turned off by setting e.g. `row_dend_reorder = FALSE`.

There are many other methods for reordering dendrograms, e.g. the **dendsort** package. Basically, all these methods still return a dendrogram that has been reordered, thus, we can firstly generate the row or column dendrogram based on the data matrix, reorder it by some method, and assign it back to `cluster_rows` or `cluster_columns`.

Compare following three heatmaps:

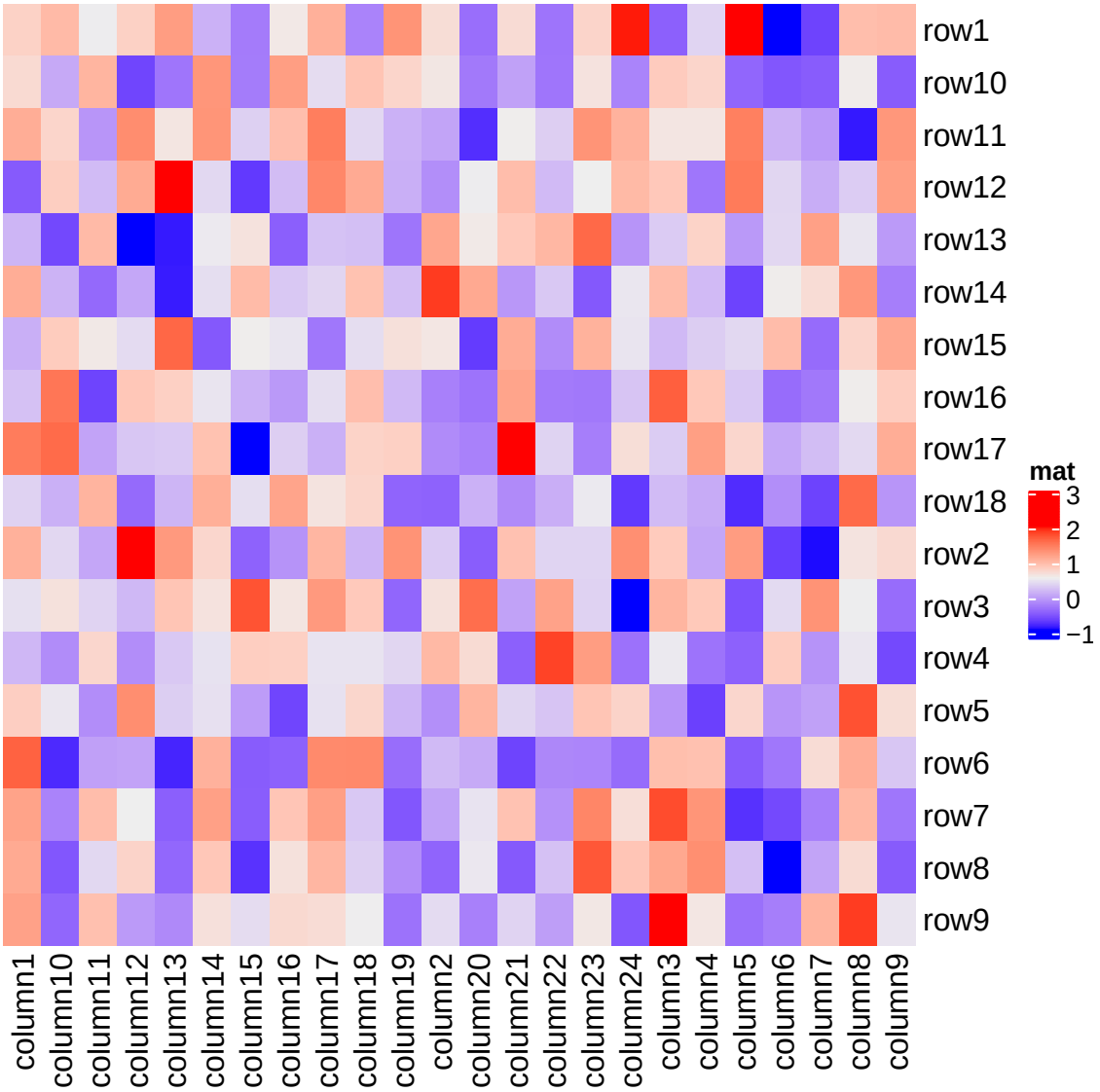
```
Heatmap(mat, name = "mat", row_dend_reorder = FALSE, column_title = "no reordering")
Heatmap(mat, name = "mat", row_dend_reorder = TRUE, column_title = "applied reordering")

library(dendsort)
dend = dendsort(as.dendrogram(hclust(dist(mat))))
Heatmap(mat, name = "mat", cluster_rows = dend, row_dend_reorder = FALSE,
    column_title = "reordering by dendsort")
```



2.4 Row and column orders

Clustering is used to adjust row orders and column orders of the heatmap, but you can still set the order manually by `row_order` and `column_order`. If e.g. `row_order` is set, row clustering is turned off.

```
Heatmap(mat, name = "mat", row_order = order(rownames(mat)),
    column_order = order(colnames(mat)))
```



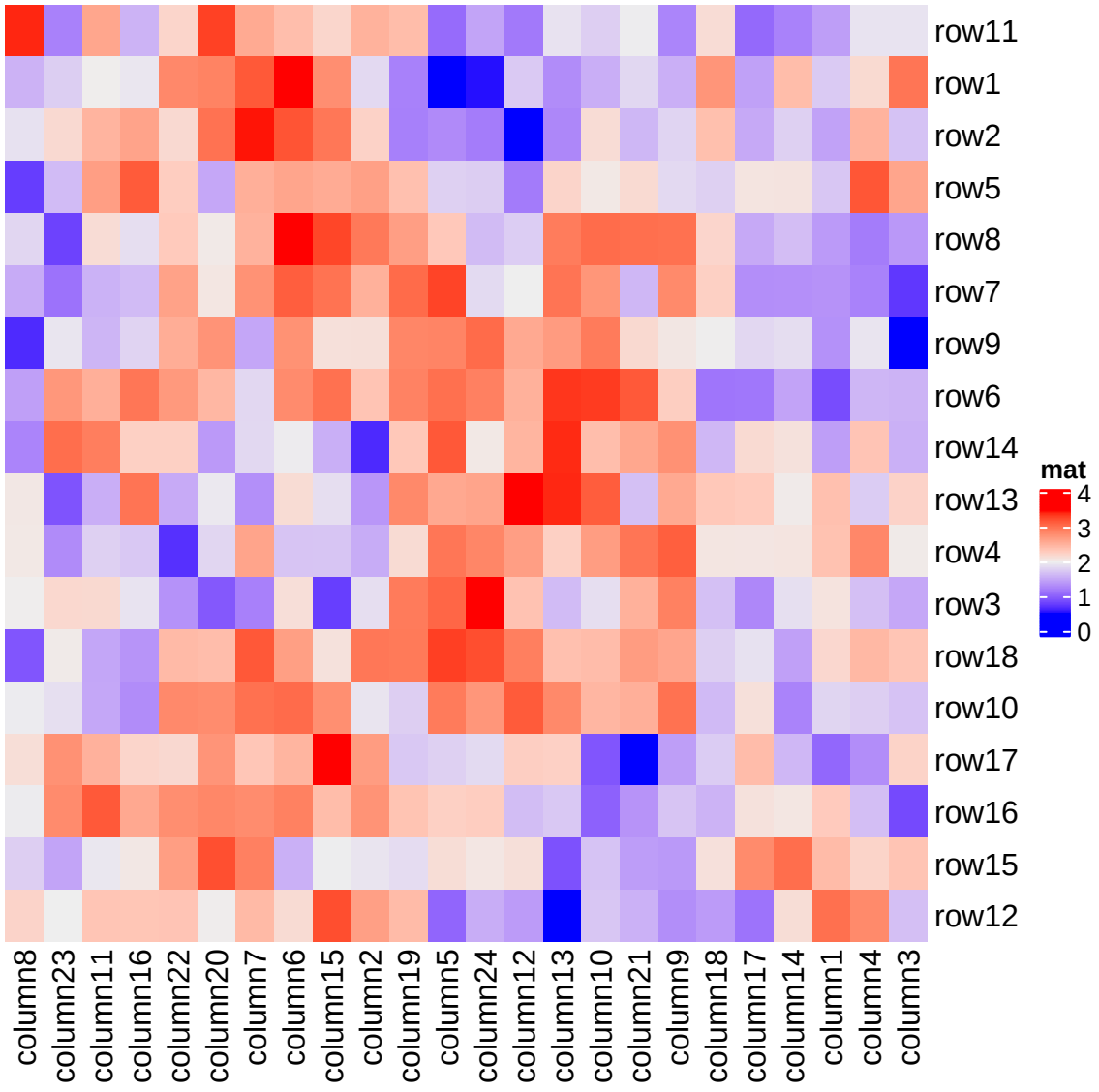
Note `row_dend_reorder` and `row_order` are two different things. `row_dend_reorder` is applied on the dendrogram. For any node in the dendrogram, rotating its two branches actually gives an identical dendrogram, thus, reordering the dendrogram by automatically rotating sub-dendrogram at every node can help to separate elements further from each other which show more difference. As a comparison, `row_order` is simply applied on the matrix and normally dendrograms should be turned off.

2.5 Seriation

Seriation is an interesting technique for ordering the matrix (see this interesting post: http://nicolas.kruchten.com/content/2018/02/seriation/). The powerful **seriation** package implements quite a lot of methods for seriation. Since it is easy to extract row orders and column ordes from the object returned by the core function `seriate()` from **seriation** package. They can be directly assigned to `row_order` and `column_order` to make the heatmap.

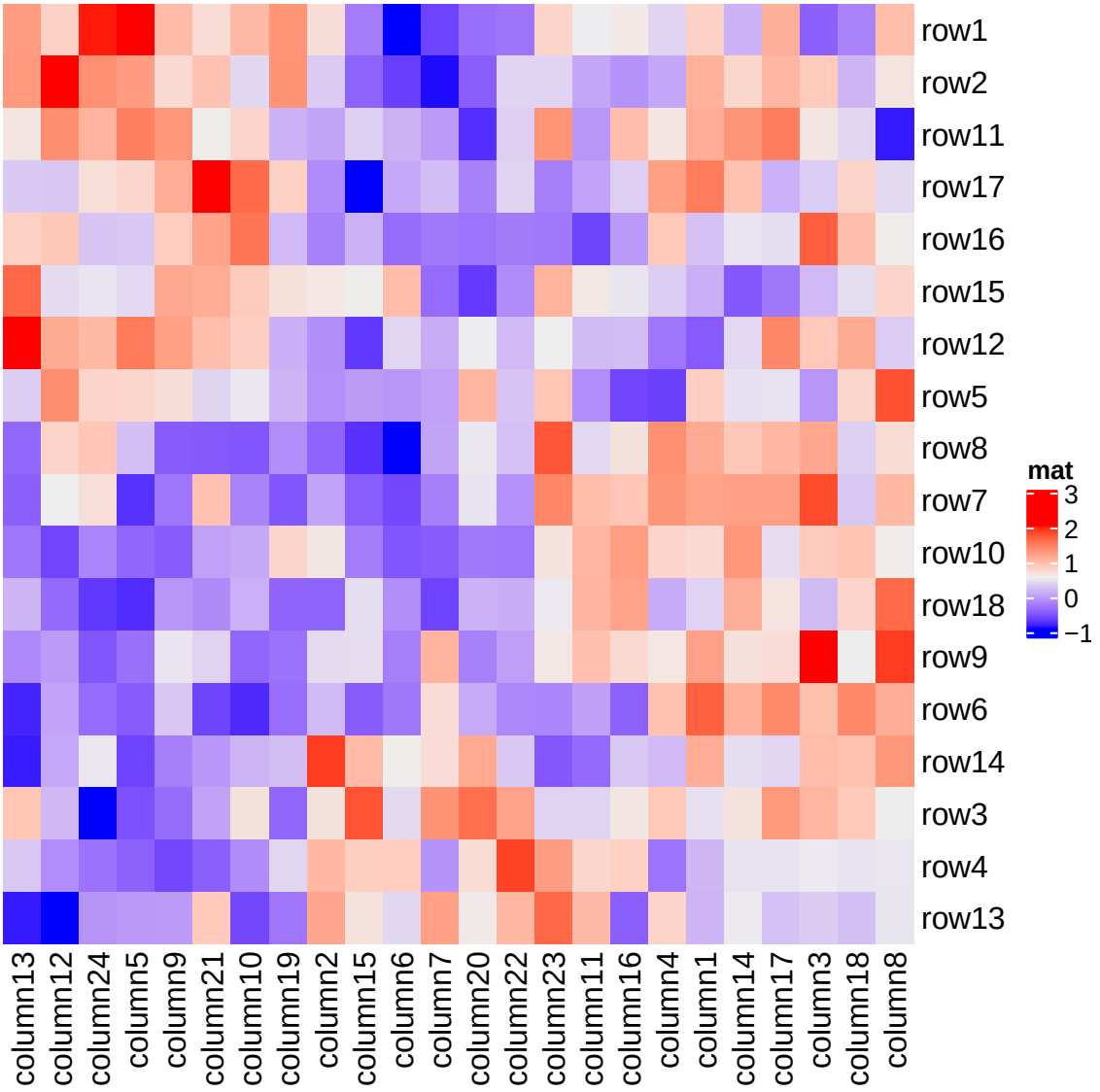
The first example demonstrates to directly apply `seriate()` on the matrix. Since the `"BEA_TSP"` method only allows a non-negative matrix, we modify the matrix to `max(mat) - mat`.

```
library(seriation)
o = seriate(max(mat) - mat, method = "BEA_TSP")
Heatmap(max(mat) - mat, name = "mat",
    row_order = get_order(o, 1), column_order = get_order(o, 2))
```



Or apply `seriate()` to the distance matrix. Now the order for rows and columns needs to be calcualted separatedly (because the distance matrix needs to be calculated separatedly).

```
o1 = seriate(dist(mat), method = "TSP")
o2 = seriate(dist(t(mat)), method = "TSP")
Heatmap(mat, name = "mat", row_order = get_order(o1), column_order = get_order(o2))
```



Some seriation methods also contain the hierarchical clustering information. Let's try:

```
o1 = seriate(dist(mat), method = "GW")
o2 = seriate(dist(t(mat)), method = "GW")
```

`o1` and `o2` are actually mainly composed of `hclust` objects:

```
class(o1[[1]])
```

```
## [1] "ser_permutation_vector" "hclust"
```

And the orders are the same by using `hclust$order` or `get_order()`.

```
o1[[1]]$order
```

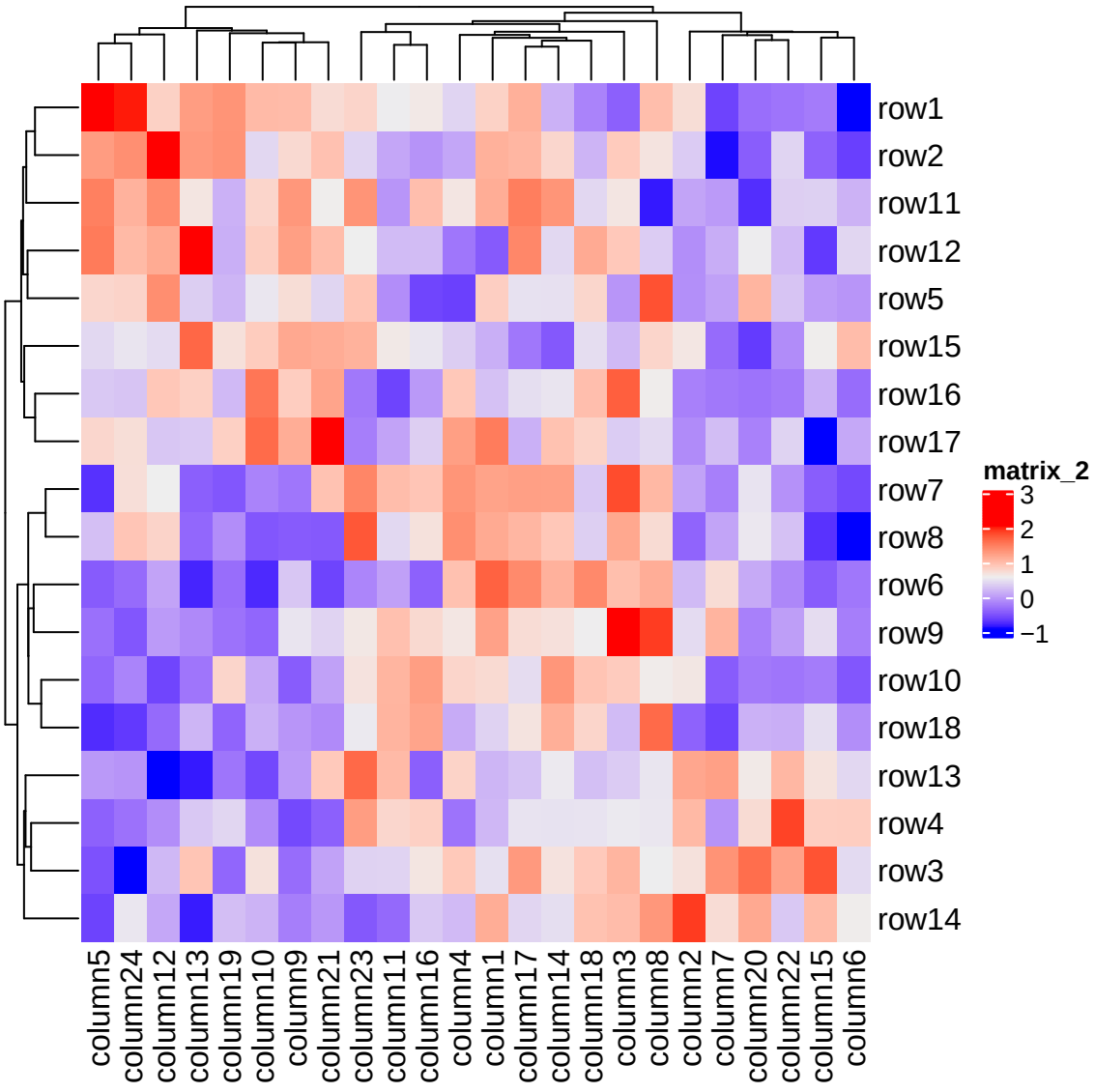
```
##  [1]  1  2 11 12  5 15 16 17  7  8  6  9 10 18 13  4  3 14
```

```
# should be the same as the previous one
get_order(o1)
```

```
##  [1]  1  2 11 12  5 15 16 17  7  8  6  9 10 18 13  4  3 14
```

And we can add the dendrograms to the heatmap (note here we turned off the default reordering because we exactly want the dendrogram order returned from seriation).

```
Heatmap(mat, cluster_rows = as.dendrogram(o1[[1]]), row_dend_reorder = FALSE,
    cluster_columns = as.dendrogram(o2[[1]]), column_dend_reorder = FALSE)
```

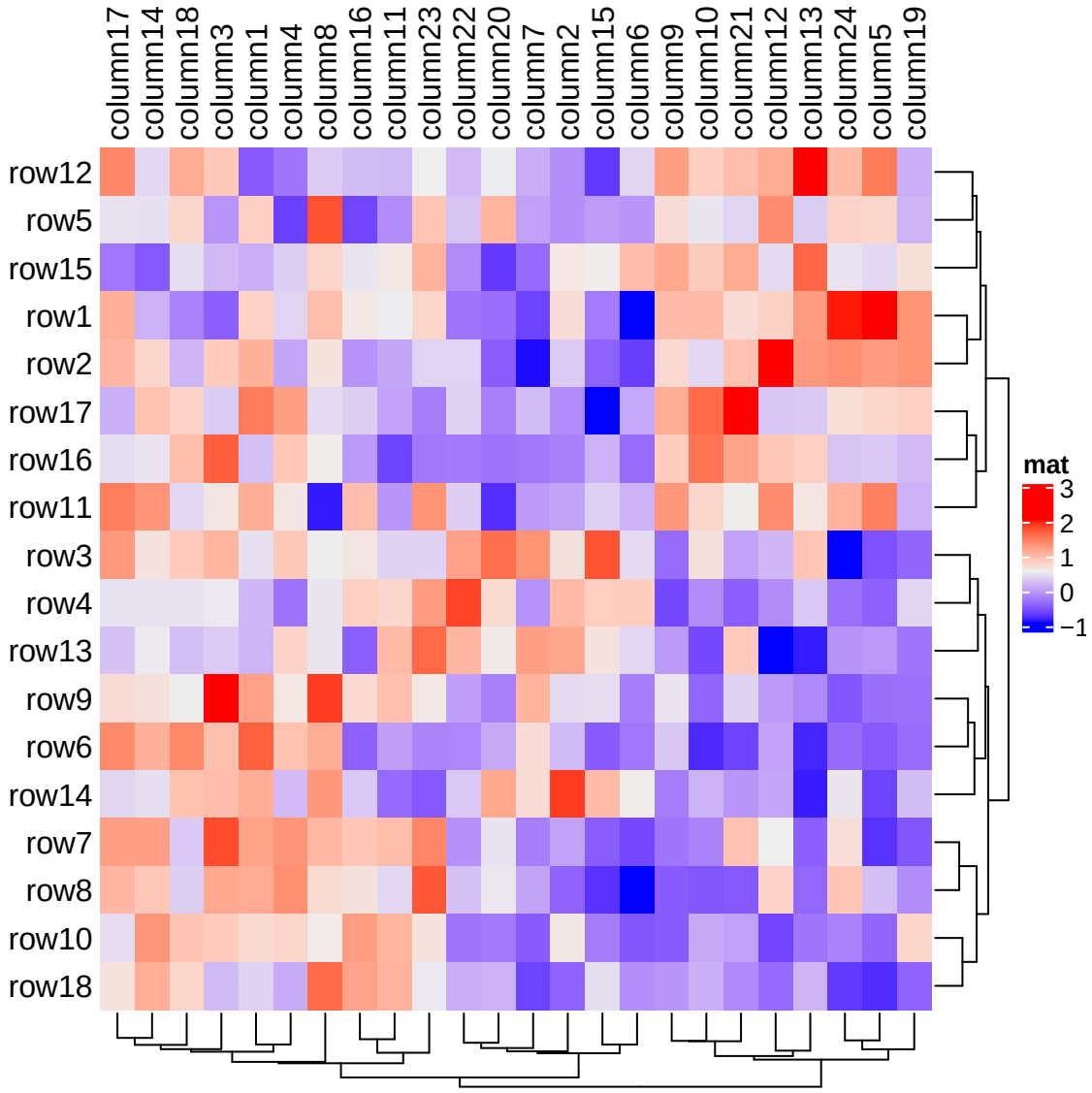


For more use of the `seriate()` function, please refer to the **seriation** package.

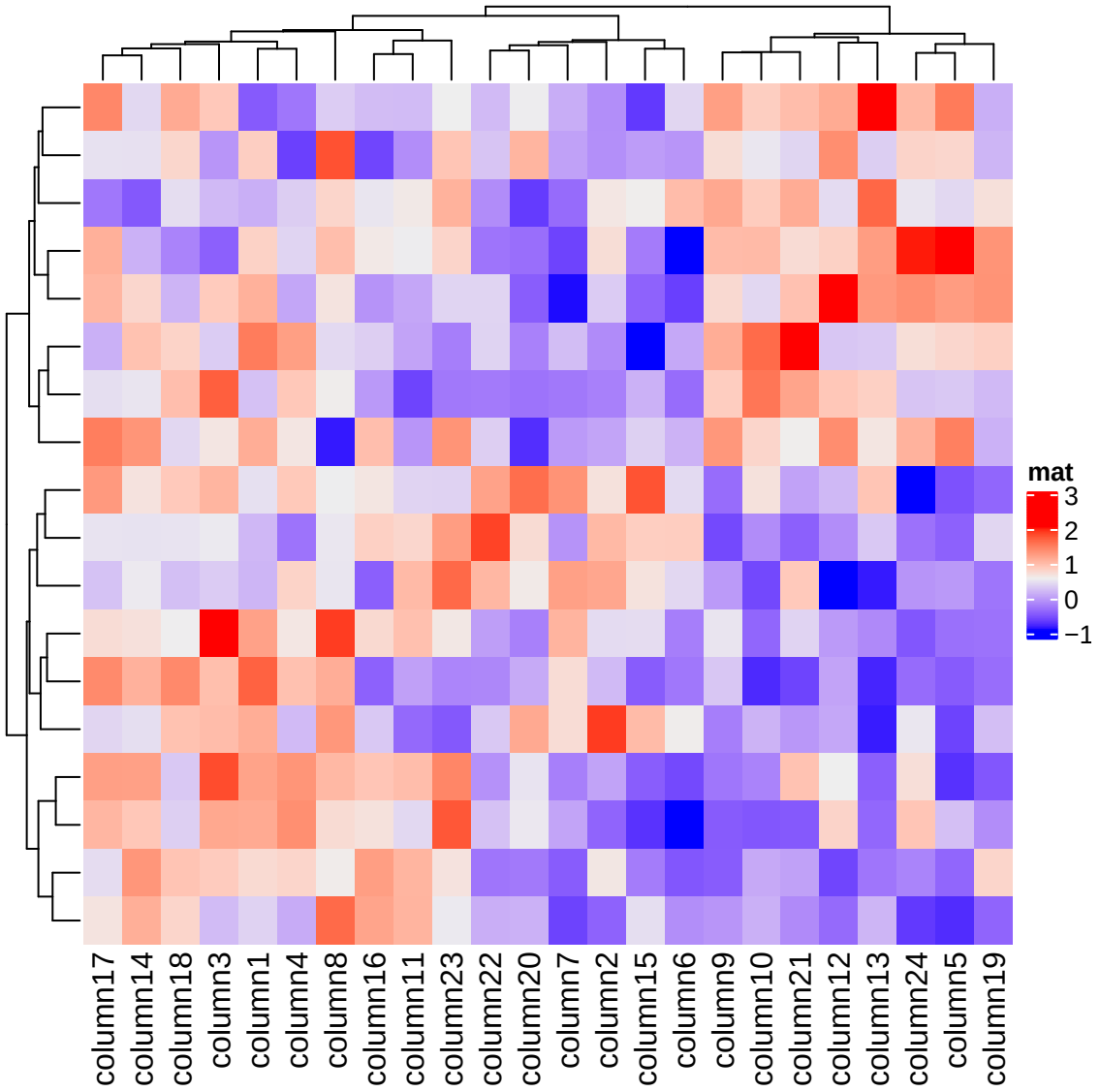
2.6 Dimension names

The row names and column names are drawn on the right and bottom sides of the heatmap by default. Side, visibility and graphic parameters for dimension names can be set as follows:

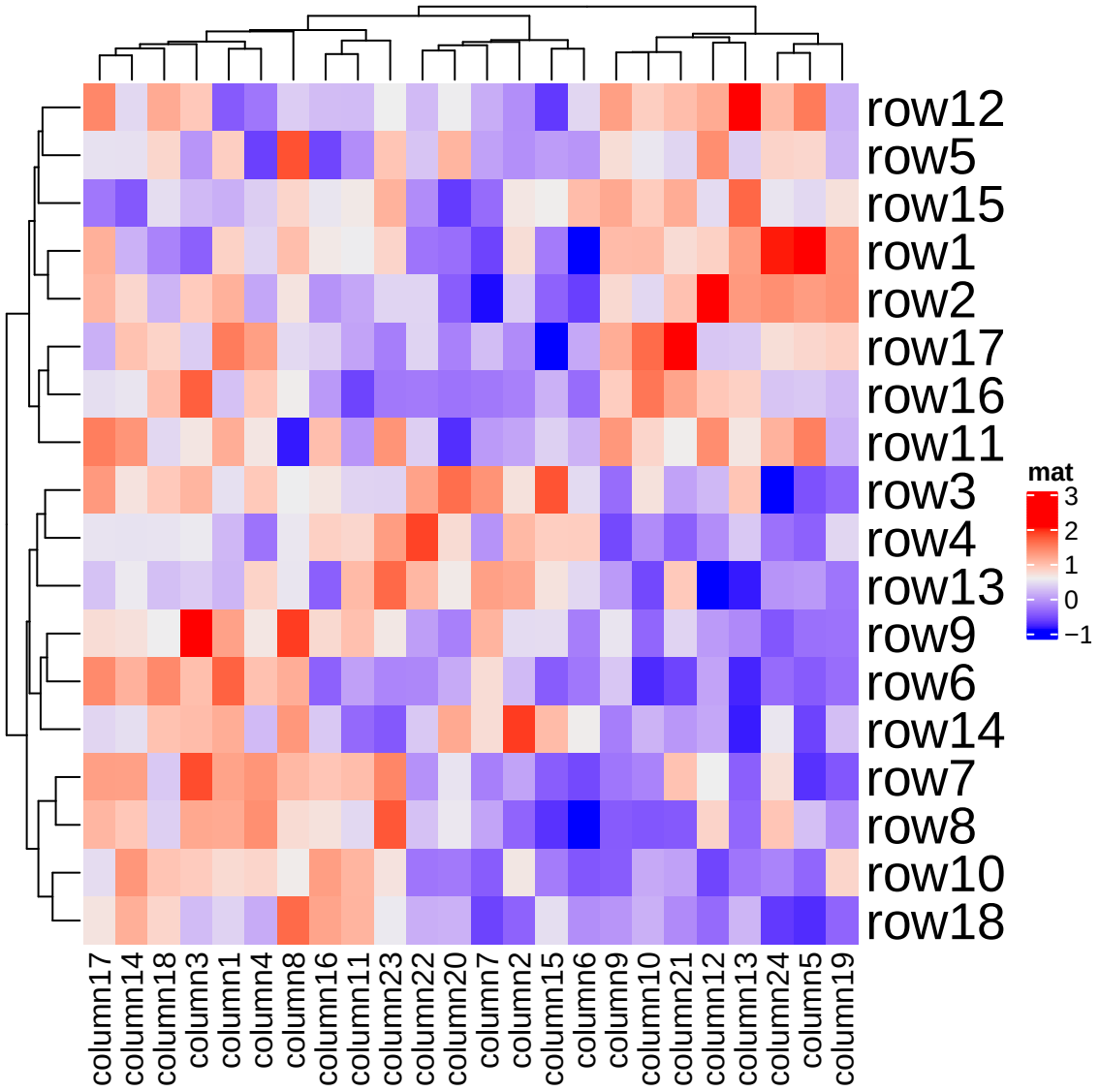
```
Heatmap(mat, name = "mat", row_names_side = "left", row_dend_side = "right",
    column_names_side = "top", column_dend_side = "bottom")
```



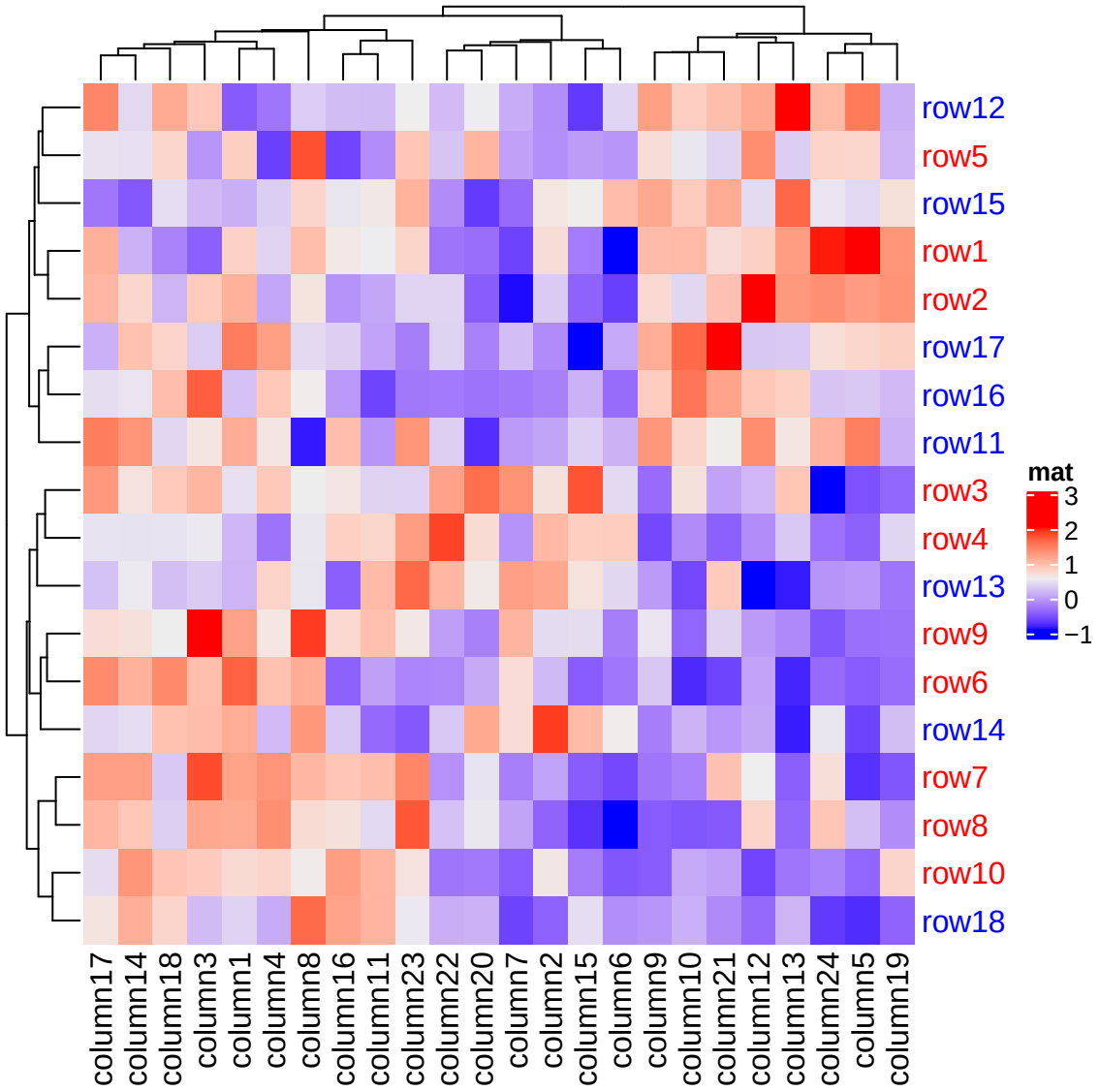

```
Heatmap(mat, name = "mat", show_row_names = FALSE)
```




```
Heatmap(mat, name = "mat", row_names_gp = gpar(fontsize = 20))
```

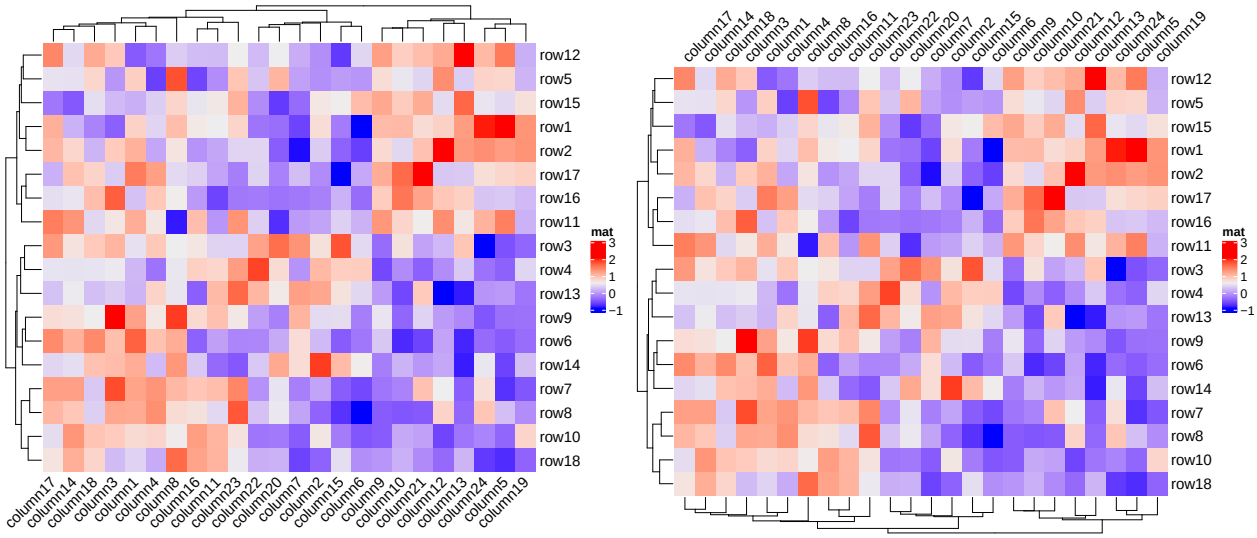



```
Heatmap(mat, name = "mat", row_names_gp = gpar(col = c(rep("red", 10), rep("blue", 8))))
```



The rotation of column names can be set by `column_names_rot`:

```
Heatmap(mat, name = "mat", column_names_rot = 45)
Heatmap(mat, name = "mat", column_names_rot = 45, column_names_side = "top",
    column_dend_side = "bottom")
```



If you have row names or column names which are too long, `row_names_max_width` or `column_names_max_height` can be used to set the maximal space for them.

Instead of directly using the row/column names from the matrix, you can also provide another character vector which corresponds to the rows or columns and set it by `row_labels` or `column_labels`. This is useful because you don't need to change the dimension names of the matrix to change the labels on the heatmap while you can directly provide the new labels.

There is one typical scenario that `row_labels` and `column_labels` are useful. For the gene expression analysis, we might use Ensembl ID as the gene ID which is used as row names of the gene expression matrix. However, the Ensembl ID is for the indexing of the Ensembl database but not for the human reading. Instead, we would prefer to put gene symbol on the heatmap as the row names which is easier to read. To do this, we only need to assign the corresponding gene symbols to `row_labels` without modifying the original matrix.

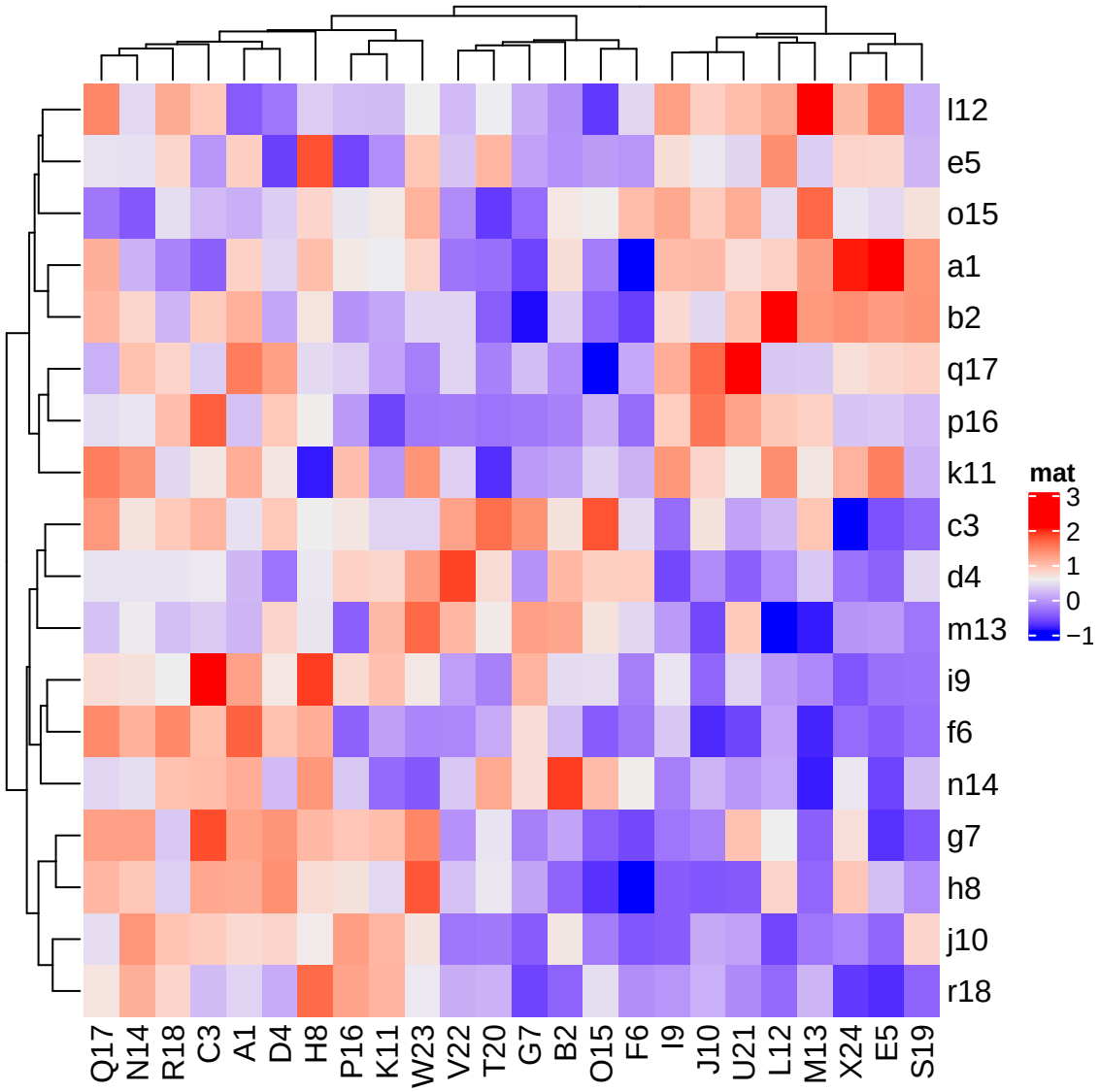
Another advantage is `row_labels` or `column_labels` allows duplicated labels, while duplicated row names or column names are not allowed in the matrix.

Following gives a simple example that we put letters as row labels and column labels:

```
# use named vectors to make sure the correspondance between row names and row labels is correct
row_labels = structure(paste0(letters[1:24], 1:24), names = paste0("row", 1:24))
column_labels = structure(paste0(LETTERS[1:24], 1:24), names = paste0("column", 1:24))
row_labels
```

```
##  row1  row2  row3  row4  row5  row6  row7  row8  row9 row10 row11 row12
##  "a1"  "b2"  "c3"  "d4"  "e5"  "f6"  "g7"  "h8"  "i9" "j10" "k11" "l12"
## row13 row14 row15 row16 row17 row18 row19 row20 row21 row22 row23 row24
## "m13" "n14" "o15" "p16" "q17" "r18" "s19" "t20" "u21" "v22" "w23" "x24"
```

```
Heatmap(mat, name = "mat", row_labels = row_labels[rownames(mat)],
    column_labels = column_labels[colnames(mat)])
```



2.7 Heatmap split

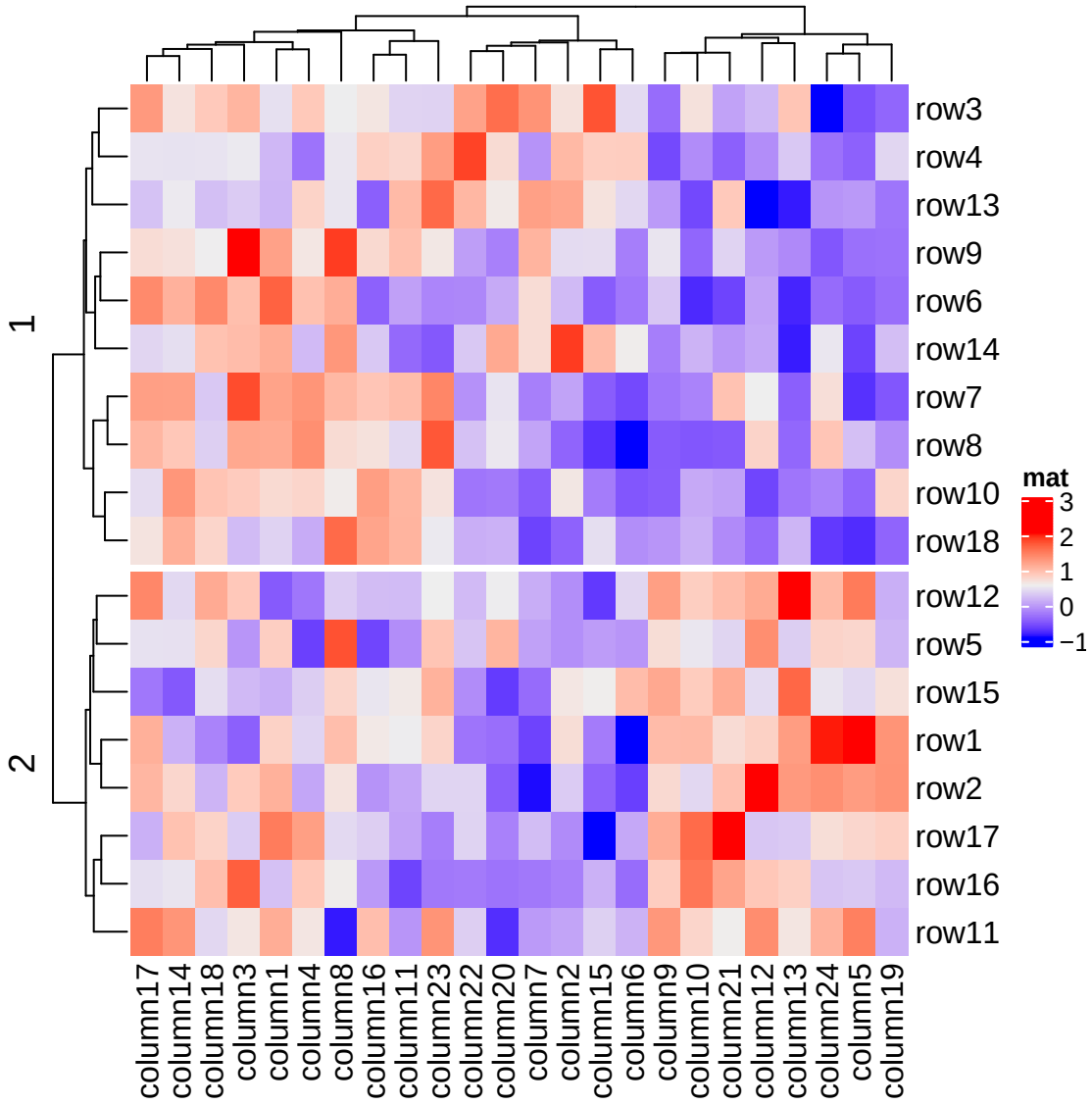
One major advantage of **ComplexHeatmap** package is it supports splitting the heatmap by rows or/and by columns to better group the features and additionally highlight the patterns.

Following arguments control the splitting: `row_km`, `row_split`, `column_km`, `column_split`. In following, we call the sub-clusters generated by splitting "*slices*".

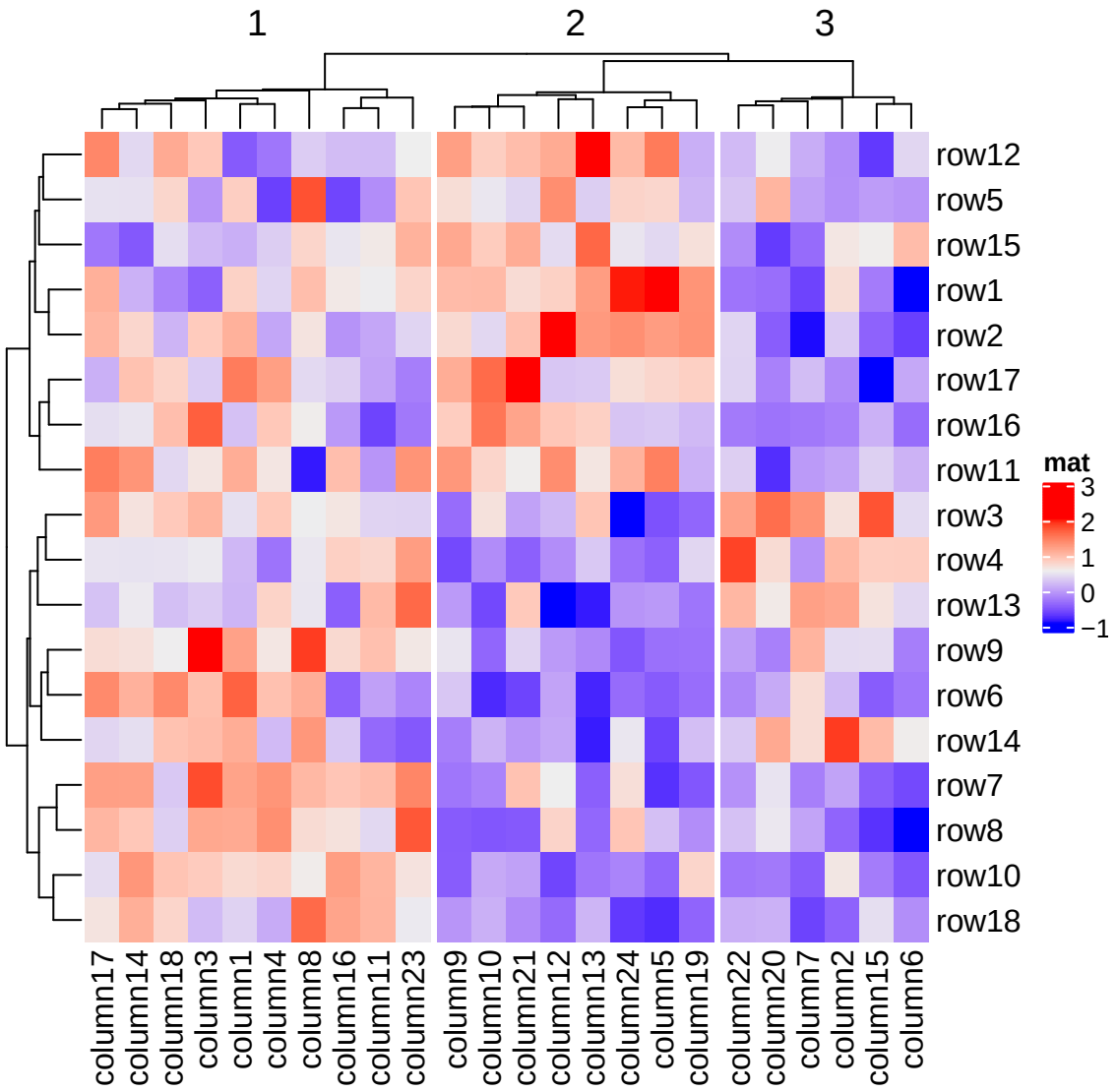
2.7.1 Split by k-means clustering

`row_km` and `column_km` apply k-means partitioning.

```
Heatmap(mat, name = "mat", row_km = 2)
```

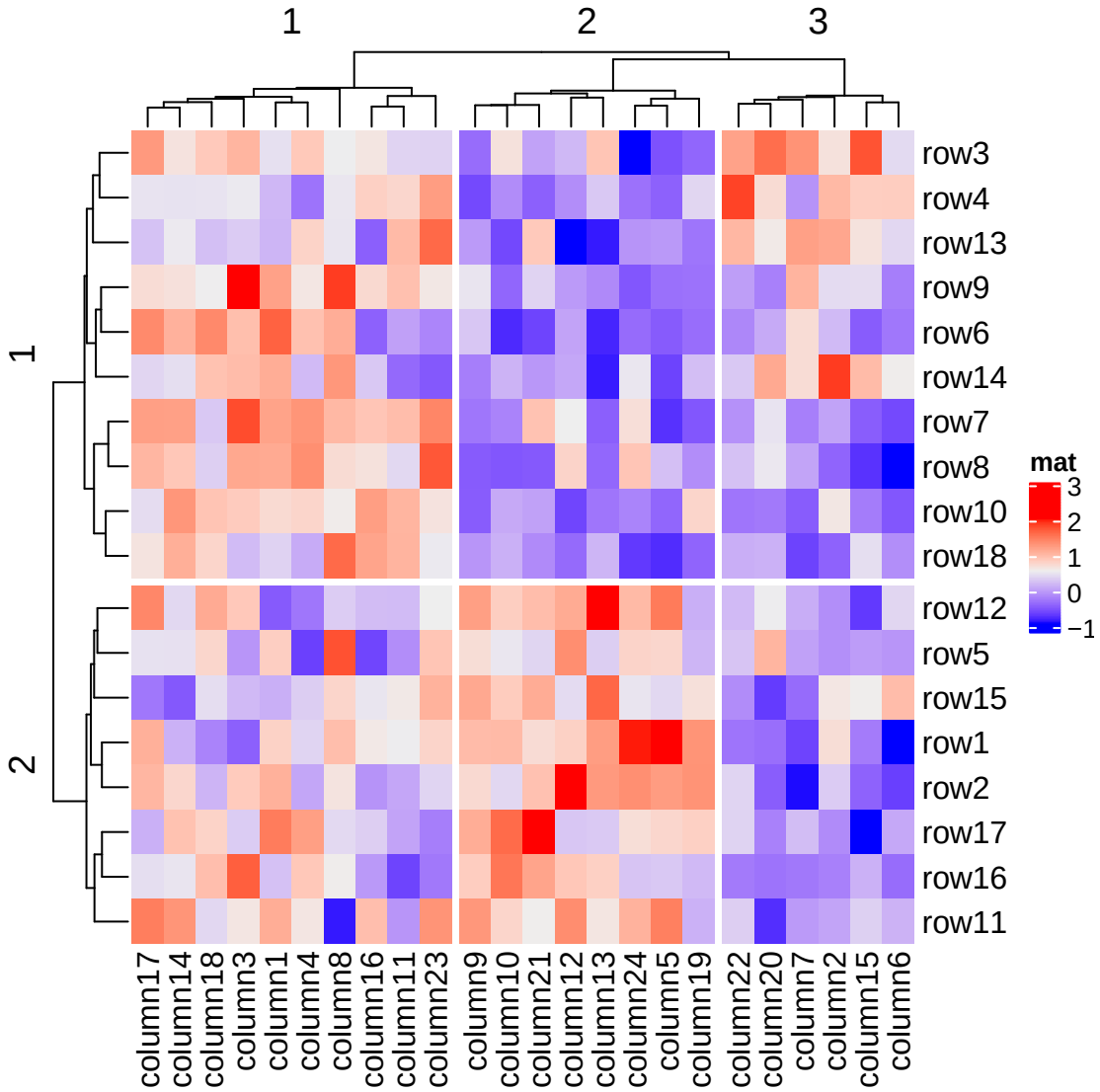



```
Heatmap(mat, name = "mat", column_km = 3)
```



Row splitting and column splitting can be performed simultaneously.

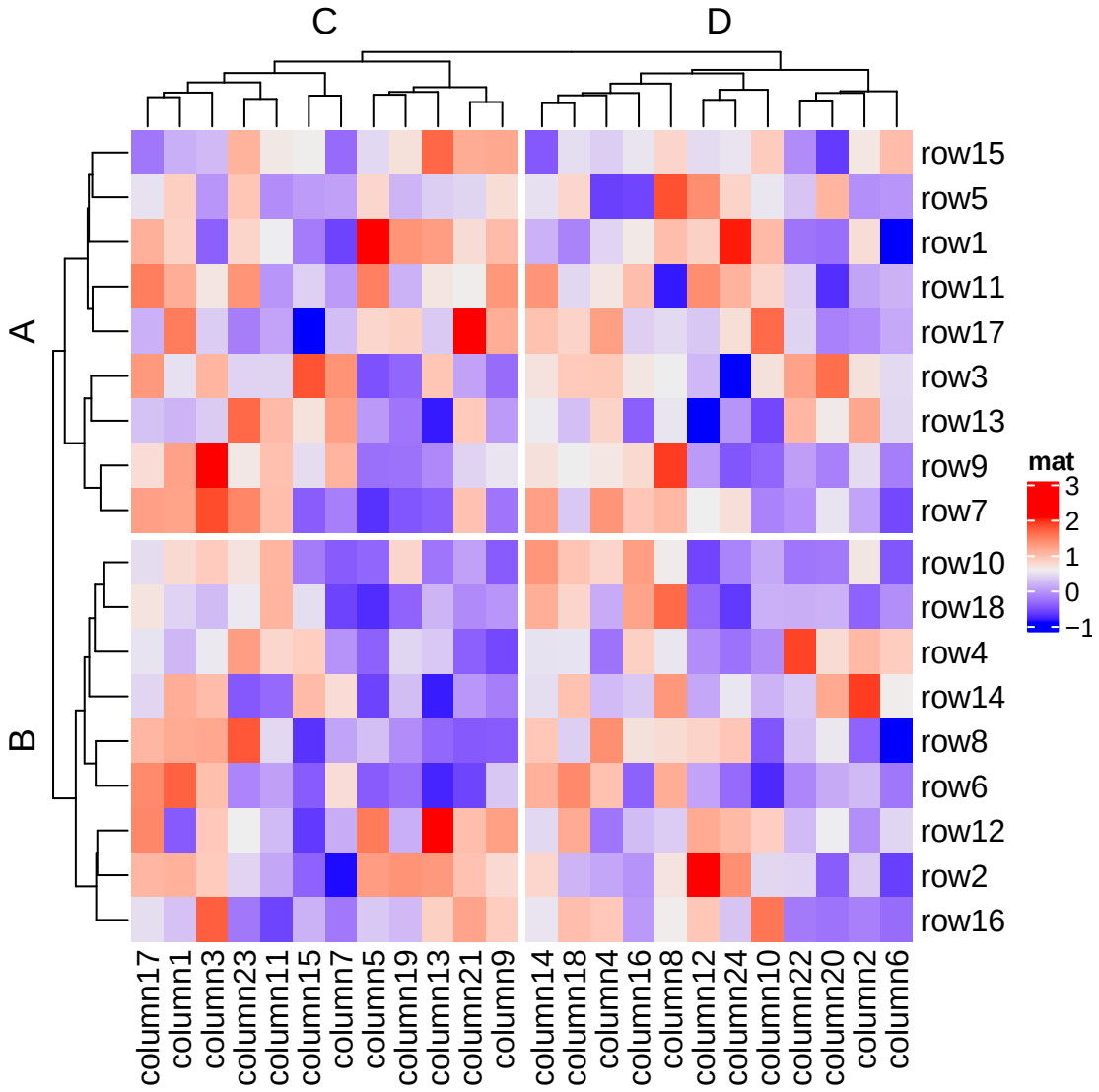
```
Heatmap(mat, name = "mat", row_km = 2, column_km = 3)
```



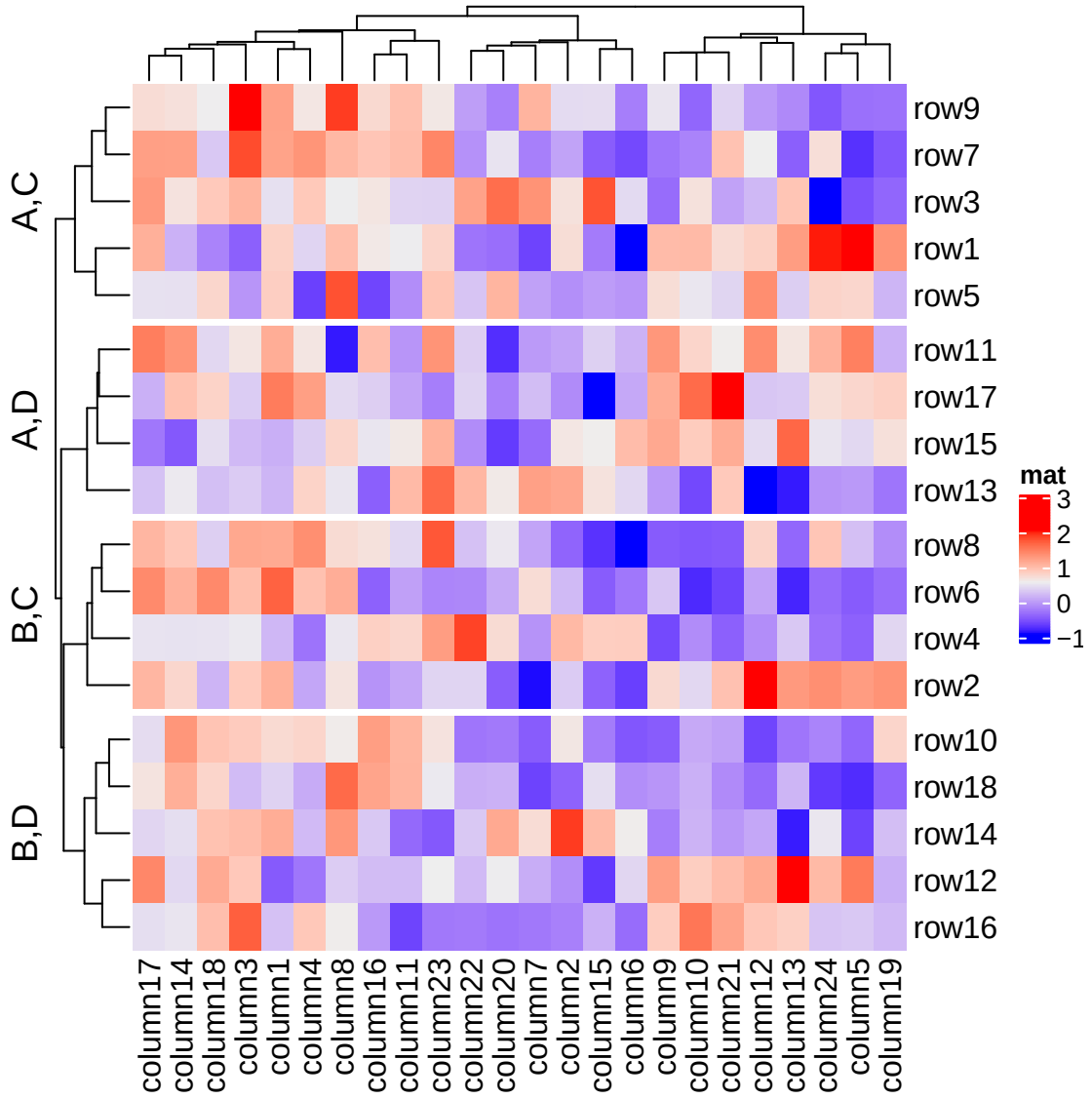
2.7.2 Split by categorical variables

More generally, `row_split` or `column_split` can be set to a categorical vector or a data frame where different combinations of levels split the rows/columns in the heatmap. The order of each slice can be controlled by `levels` of each variable in `split` (in this case, each variable should be a factor). If all variables are characters, the default order is `unique(row_split)` or `unique(column_split)`.

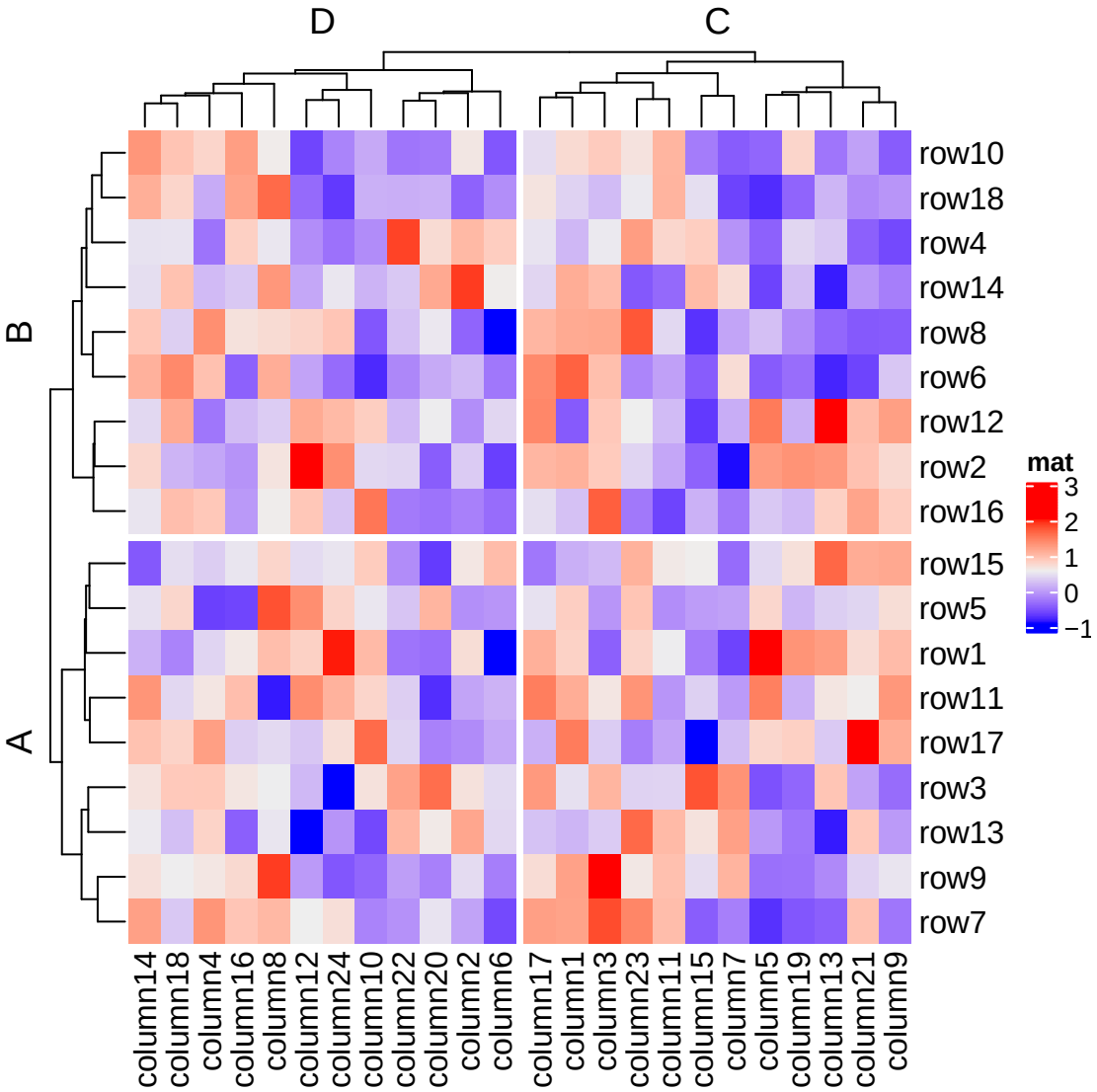
```
Heatmap(mat, name = "mat",
    row_split = rep(c("A", "B"), 9), column_split = rep(c("C", "D"), 12))
```




```
Heatmap(mat, name = "mat",
    row_split = data.frame(rep(c("A", "B"), 9), rep(c("C", "D"), each = 9)))
```

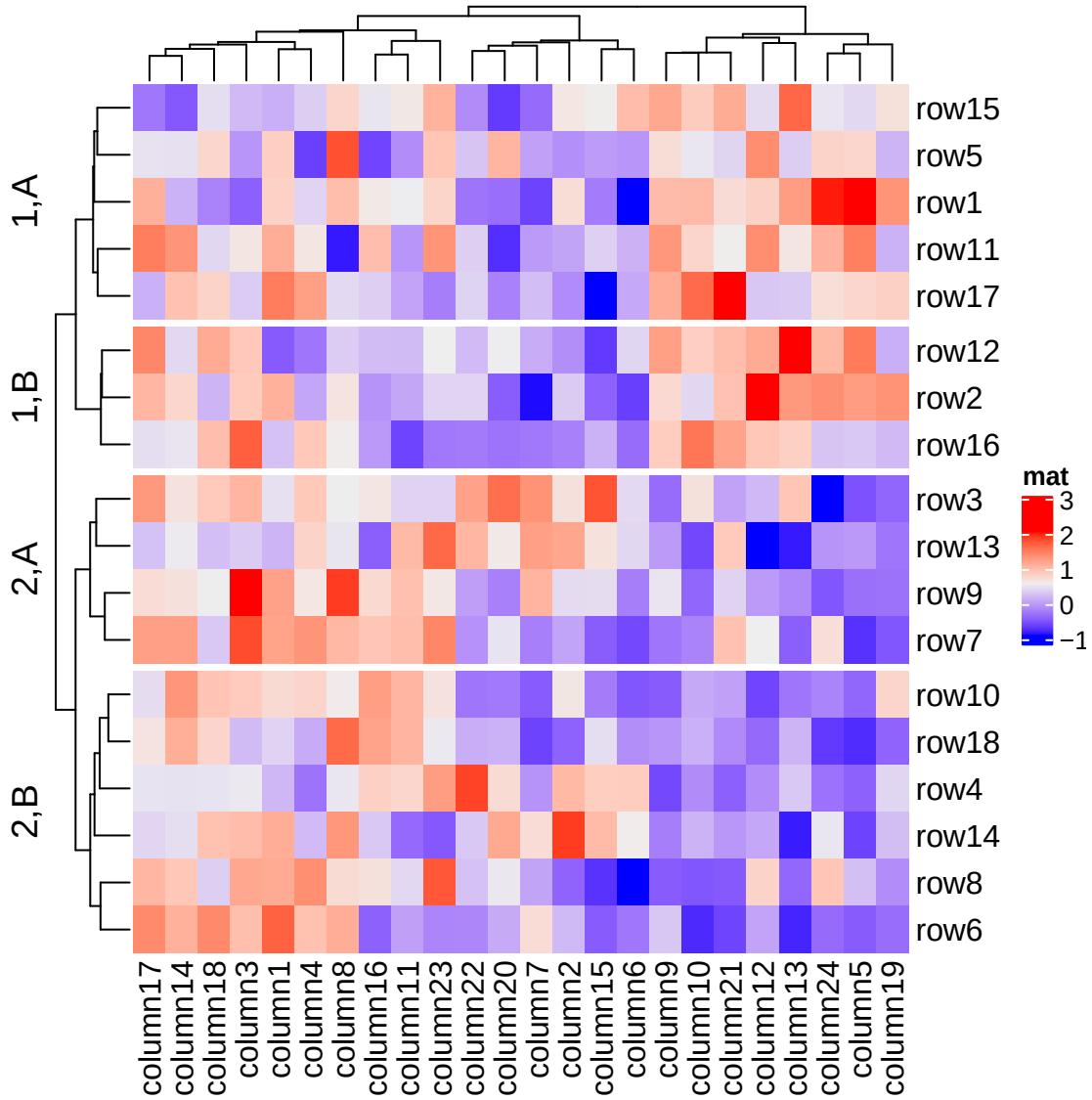



```
Heatmap(mat, name = "mat", row_split = factor(rep(c("A", "B"), 9), levels = c("B", "A")),
    column_split = factor(rep(c("C", "D"), 12), levels = c("D", "C")))
```



Actually, k-means clustering just generates a vector of cluster classes and appends to `row_split` or `column_split`. `row_km`/`column_km` and be used mixed with `row_split` and `column_split`.

```
Heatmap(mat, name = "mat", row_split = rep(c("A", "B"), 9), row_km = 2)
```

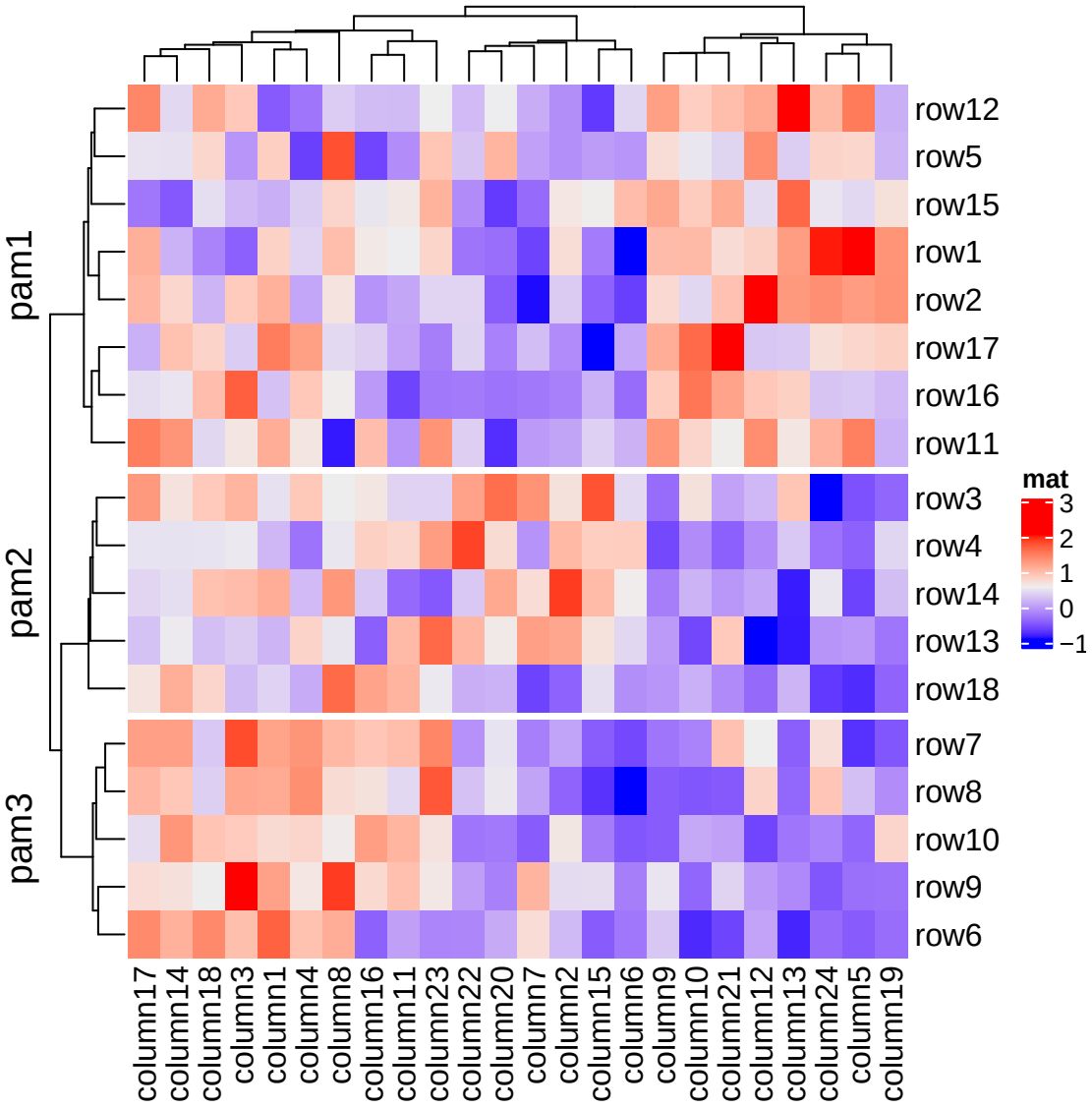


which is as the same as:

```
# code only for demonstration
cl = kmeans(mat, centers = 2)$cluster
# classes from k-means are always put as the first column in `row_split`
Heatmap(mat, name = "mat", row_split = cbind(cl, rep(c("A", "B"), 9)))
```

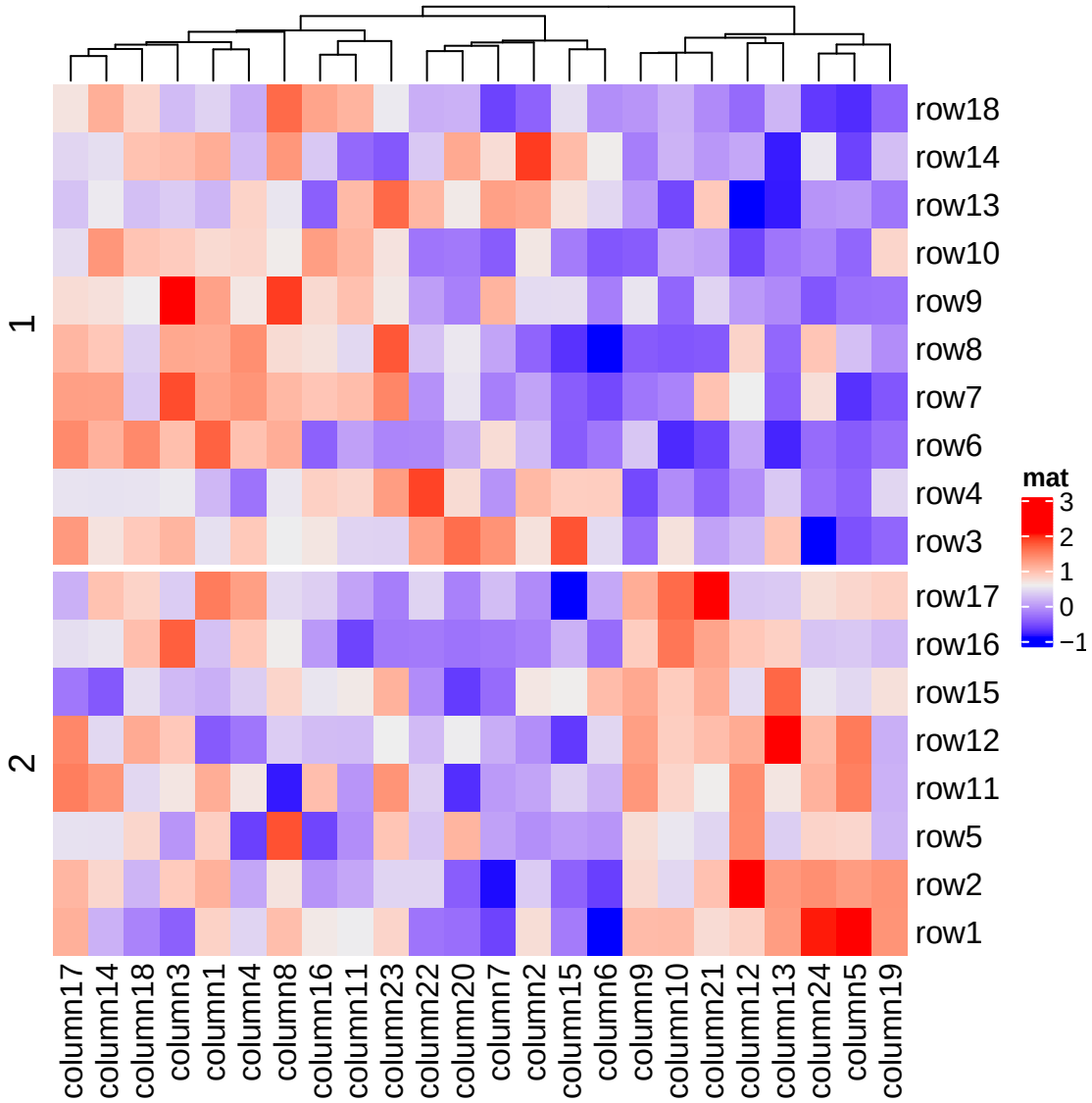
If you are not happy with the default k-means partition, it is easy to use other partition methods by just assigning the partition vector to `row_split`/`column_split`.

```
pa = pam(mat, k = 3)
Heatmap(mat, name = "mat", row_split = paste0("pam", pa$clustering))
```



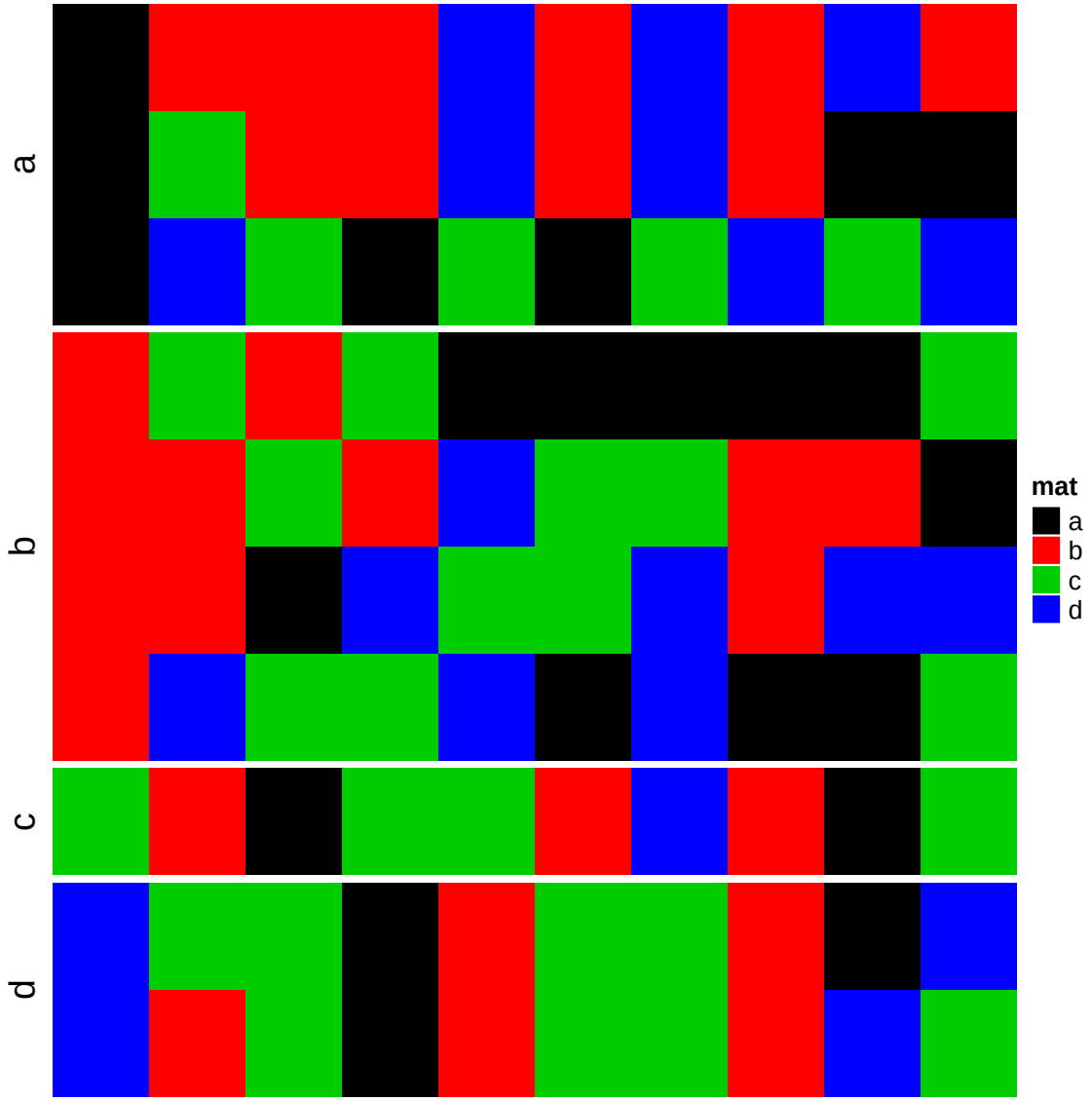
If `row_order` or `column_order` is set, in each row/column slice, it is still ordered.

```
# remember when `row_order` is set, hierarchical clustering on rows is turned off
Heatmap(mat, name = "mat", row_order = 18:1, row_km = 2)
```



Character matrix can only be split by `row_split`/`column_split` argument.

```
# split by the first column in `discrete_mat`
Heatmap(discrete_mat, name = "mat", col = 1:4, row_split = discrete_mat[, 1])
```



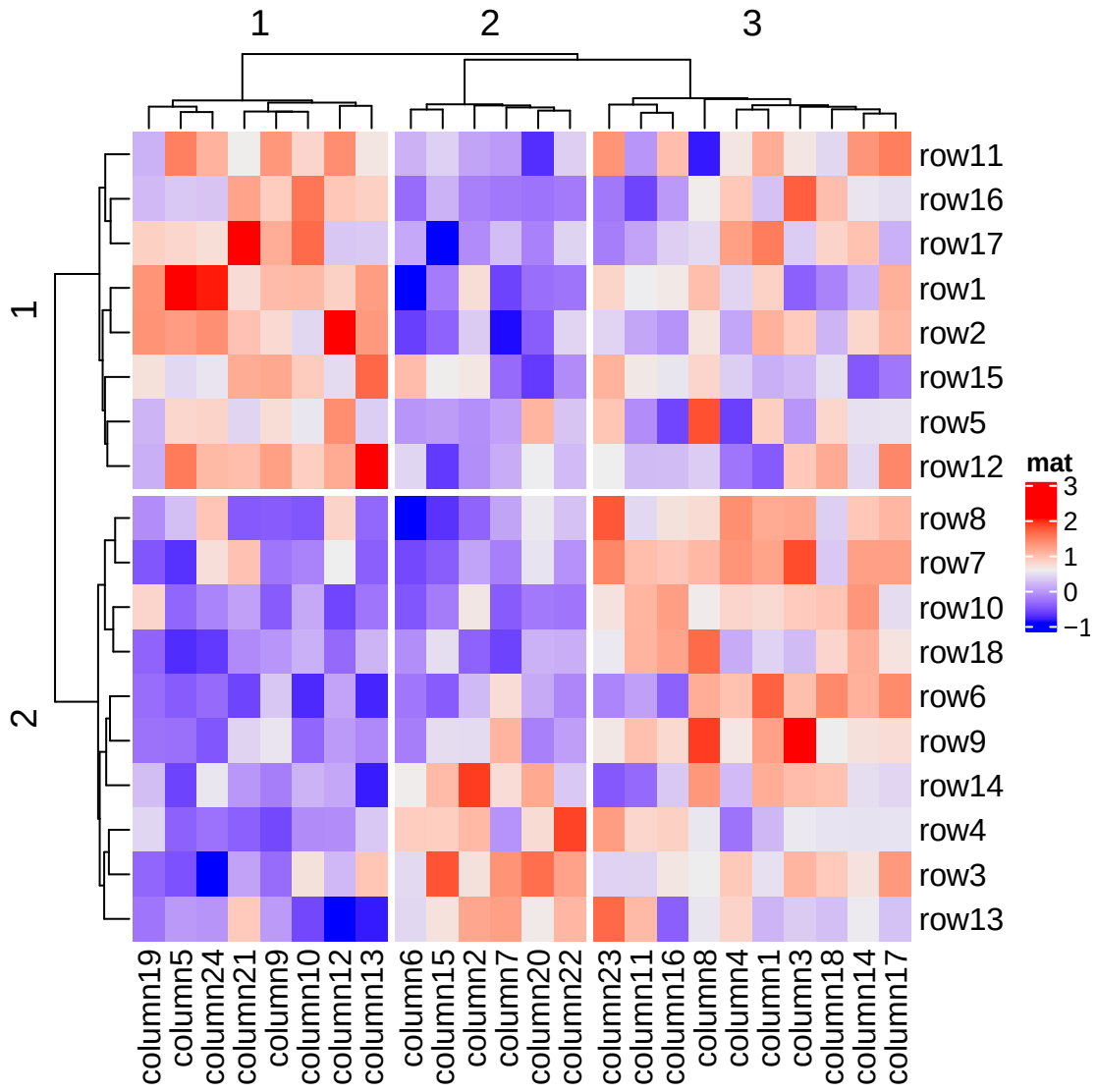
2.7.3 Split by dendrogram

In the scenarios described previously, if `row_km/column_km` is set or `row_split/column_split` is set as a vector or a data frame, hierarchical clustering is first applied to each slice which generates `k` dendrograms, then a parent dendrogram is generated based on the mean value of each slice. **The height of the parent dendrogram is adjusted by adding the maximal height of the dendrograms in all children slices and the parent dendrogram is added on top of the children dendrograms to form a single global dendrogram.**

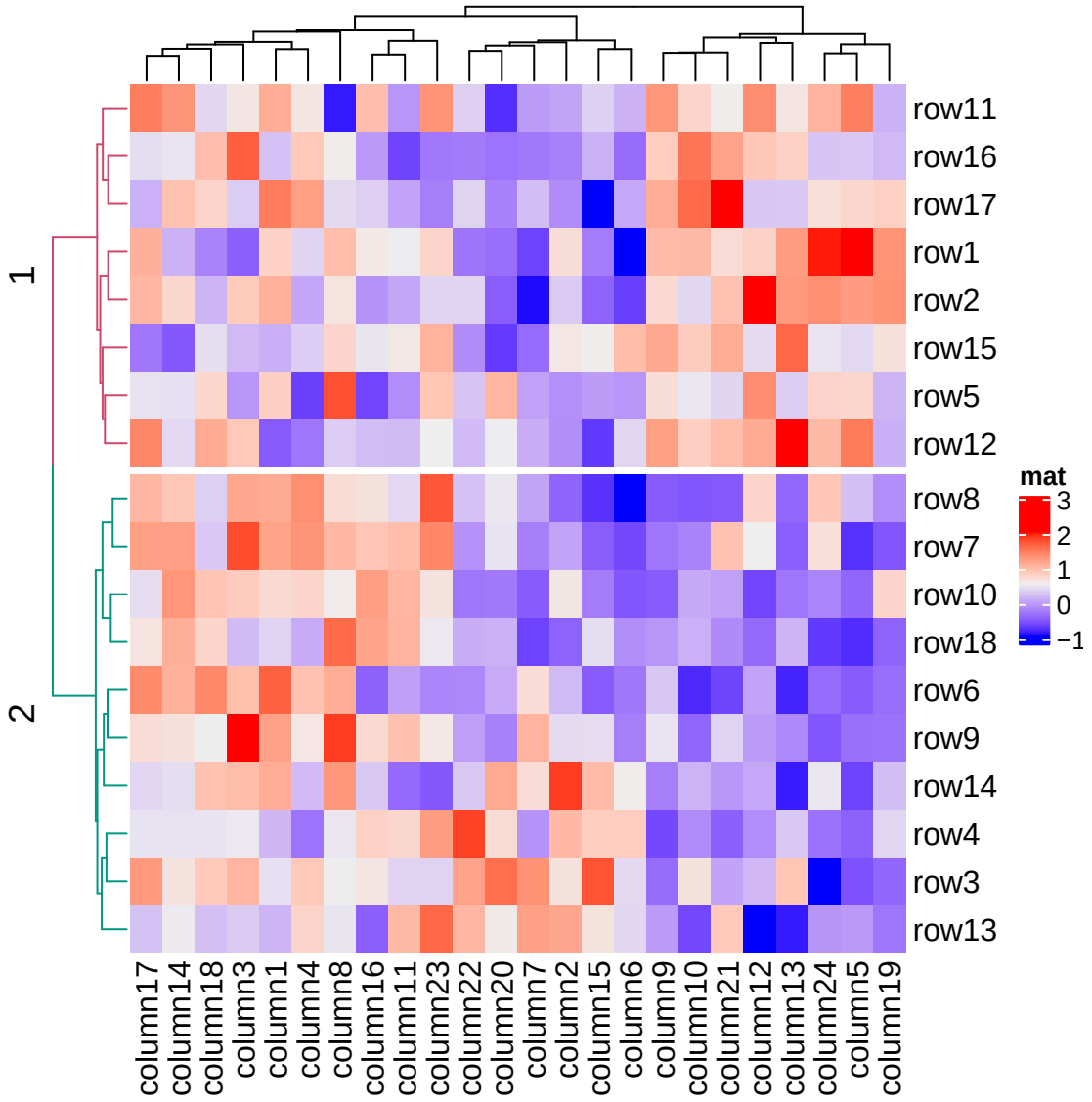
A second scenario for splitting is that users may still want to keep the global dendrogram which is generated from the complete matrix while not split it in the first place. In this case, `row_split/column_split` can be set to a single number which will apply `cutree()` on the row/column dendrogram. This works when `cluster_rows/cluster_columns` is set to `TRUE` or is assigned with a `hclust/dendrogram` object.

For this case, the dendrogram is still as same as the original one, expect the positions of dendrogram leaves are slightly adjusted by the gaps between slices.

```
Heatmap(mat, name = "mat", row_split = 2, column_split = 3)
```




```
dend = hclust(dist(mat))
dend = color_branches(dend, k = 2)
Heatmap(mat, name = "mat", cluster_rows = dend, row_split = 2)
```



If you want to combine splitting from `cutree()` and other categorical variables, you need to generate the classes from `cutree()` in the first place, append to e.g. `row_split` as a data frame and then send it to `row_split` argument.

```
# code only for demonstration
split = data.frame(cutree(hclust(dist(mat)), k = 2), rep(c("A", "B"), 9))
Heatmap(mat, name = "mat", row_split = split)
```

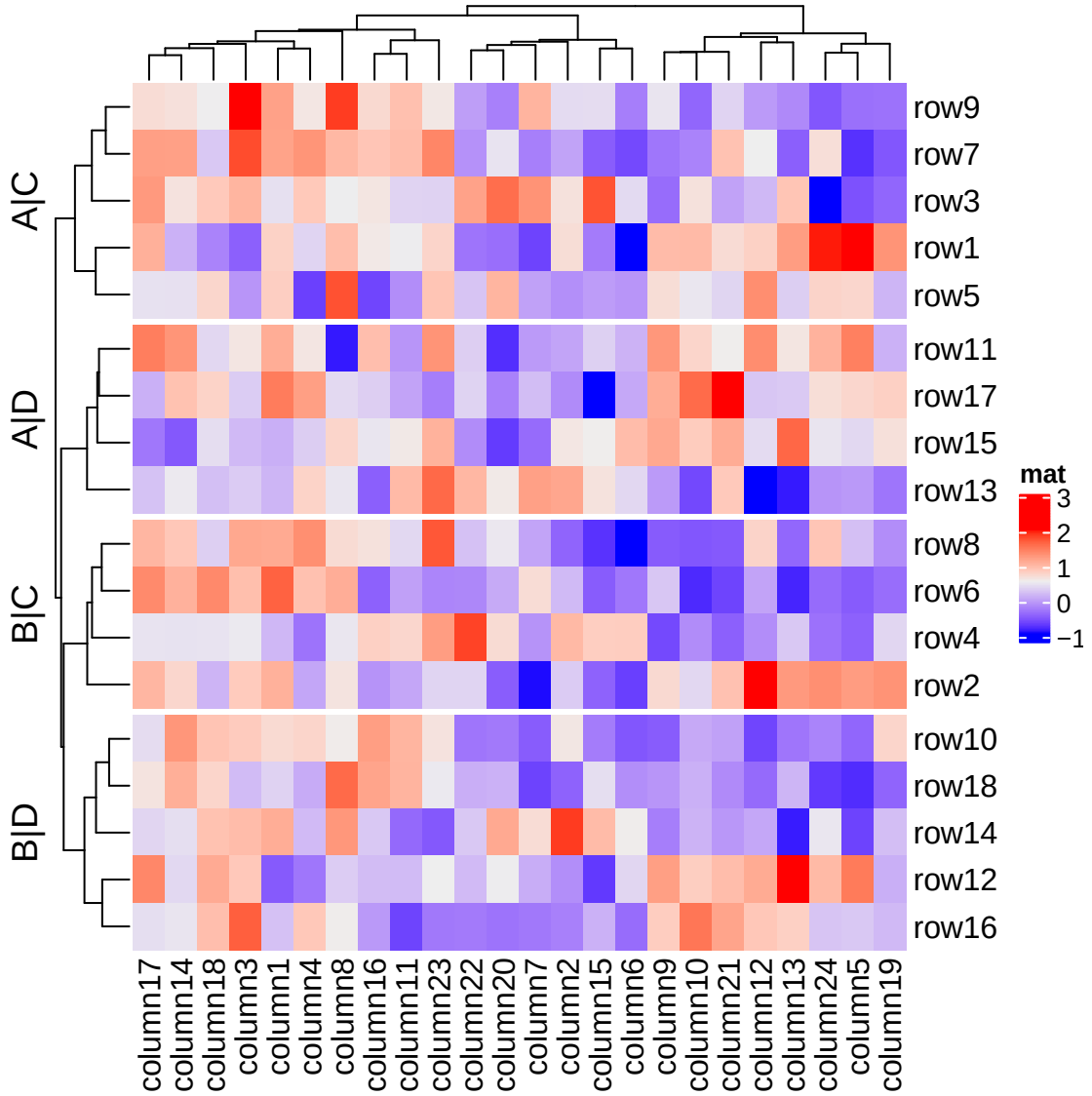
2.7.4 Titles for splitting

When `row_split/column_split` is set as a single number, there is only one categorical variable, while when `row_km/column_km` is set and/or `row_split/column_split` is set as categorical variables, there will be multiple categorical variables. By default, the titlea are in a form of `"level1,level2,..."` which corresponds to every combination of levels in all categorical variables. The titles for splitting can be controlled by "a title template".

ComplexHeatmap supports three types of templates. The first one is by `sprintf()` where the `%s` is replaced by the corresponding level. In following example, since all combinations of `split` are `A,C`, `A,D`, `B,C`

and `B,D`, if `row_title` is set to `%s|%s`, the four row titles will be `A|C`, `A|D`, `B|C`, `B|D`.

```
split = data.frame(rep(c("A", "B"), 9), rep(c("C", "D"), each = 9))
Heatmap(mat, name = "mat", row_split = split, row_title = "%s|%s")
```



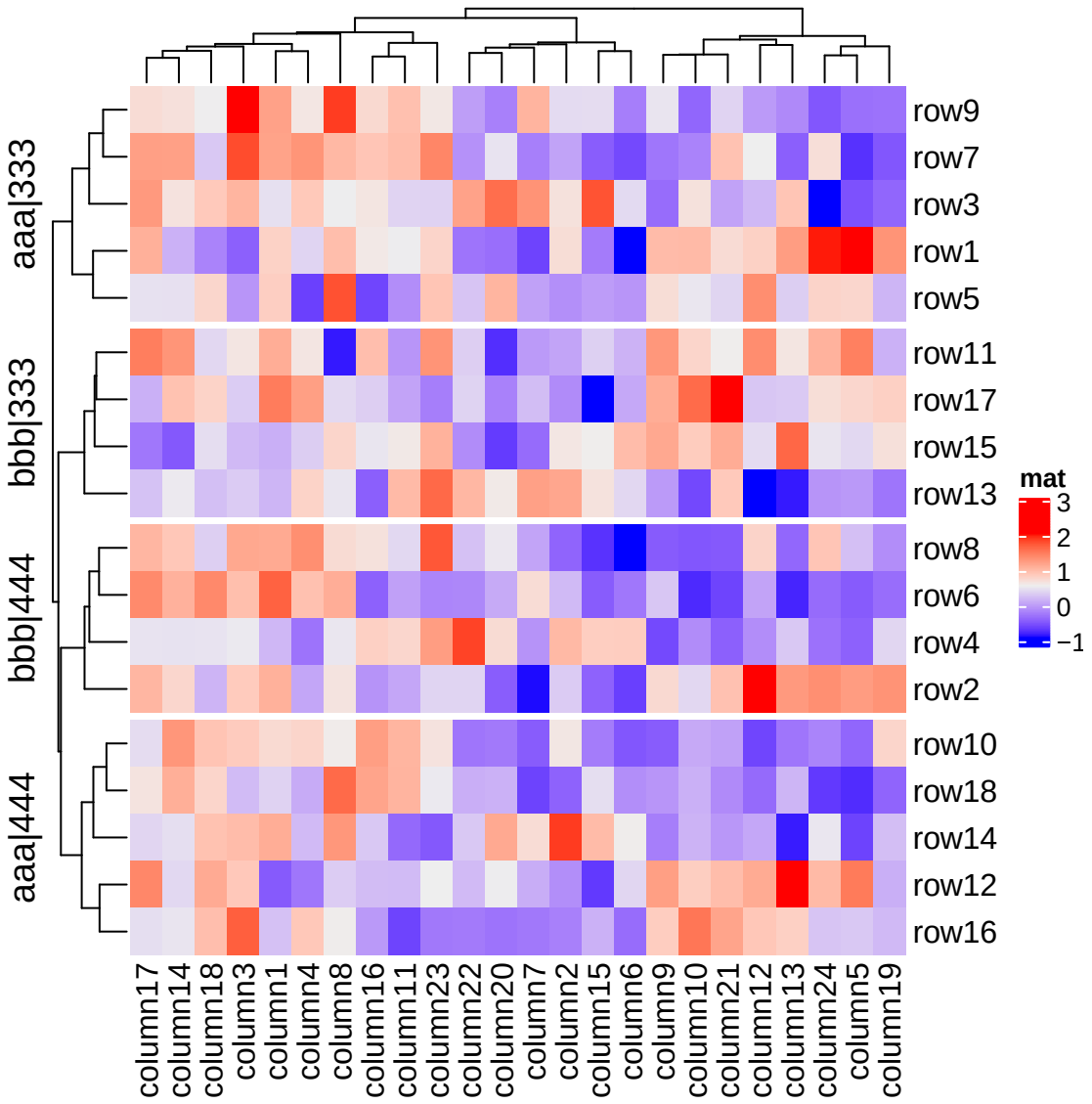
For the `sprintf()` template, you can only put the levels which are `A,B,C,D` in the title. However, when making the heatmap, you might want to put more meaningful text instead of the internal levels. Once you know how to correspond the text to the level, you can add it by following two template methods.

In the following two template methods, special marks are used to mark the R code which is executable (it is called variable interpolation where the code is extracted and executed and the returned value in put back to the string). There are two types of template marks `@{}` and `{}`. The first one is from **GetoptLong** package which should already be installed when you install the **ComplexHeatmap** package and the second one is from **glue** package which you need to install to support it.

There is an internal variable `x` you should use when you use the latter two templates. `x` is just a simple vector which contains current category levels (e.g. `c("A", "C")`).

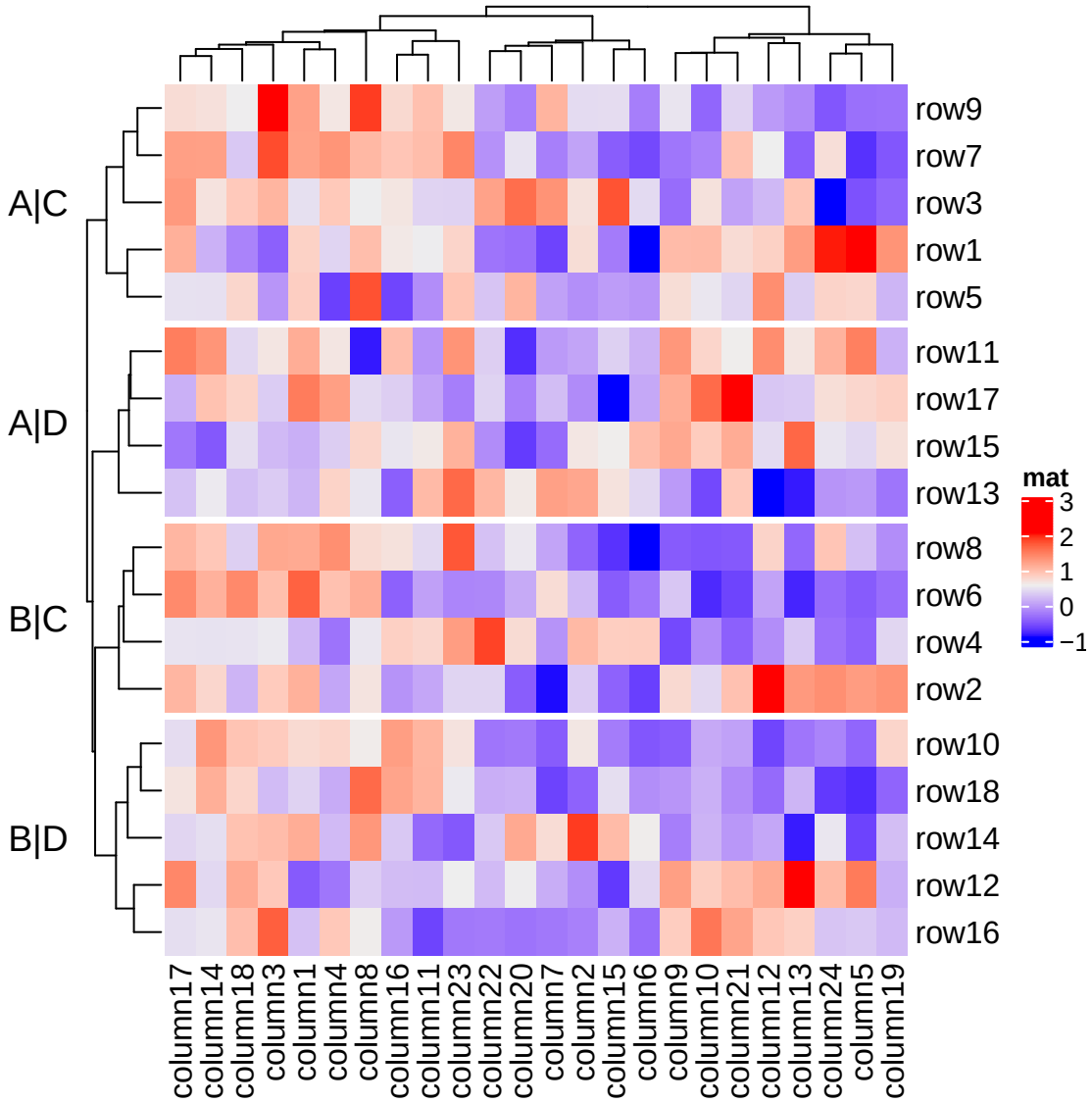
```
# code only for demonstration
map = c("A" = "aaa", "B" = "bbb", "C" = "333", "D" = "444")
```

```
Heatmap(mat, name = "mat", row_split = split, row_title = "@{map[ x[1] ]}|@{map[ x[2] ]}")
Heatmap(mat, name = "mat", row_split = split, row_title = "{map[ x[1] ]}|{map[ x[2] ]}")
```



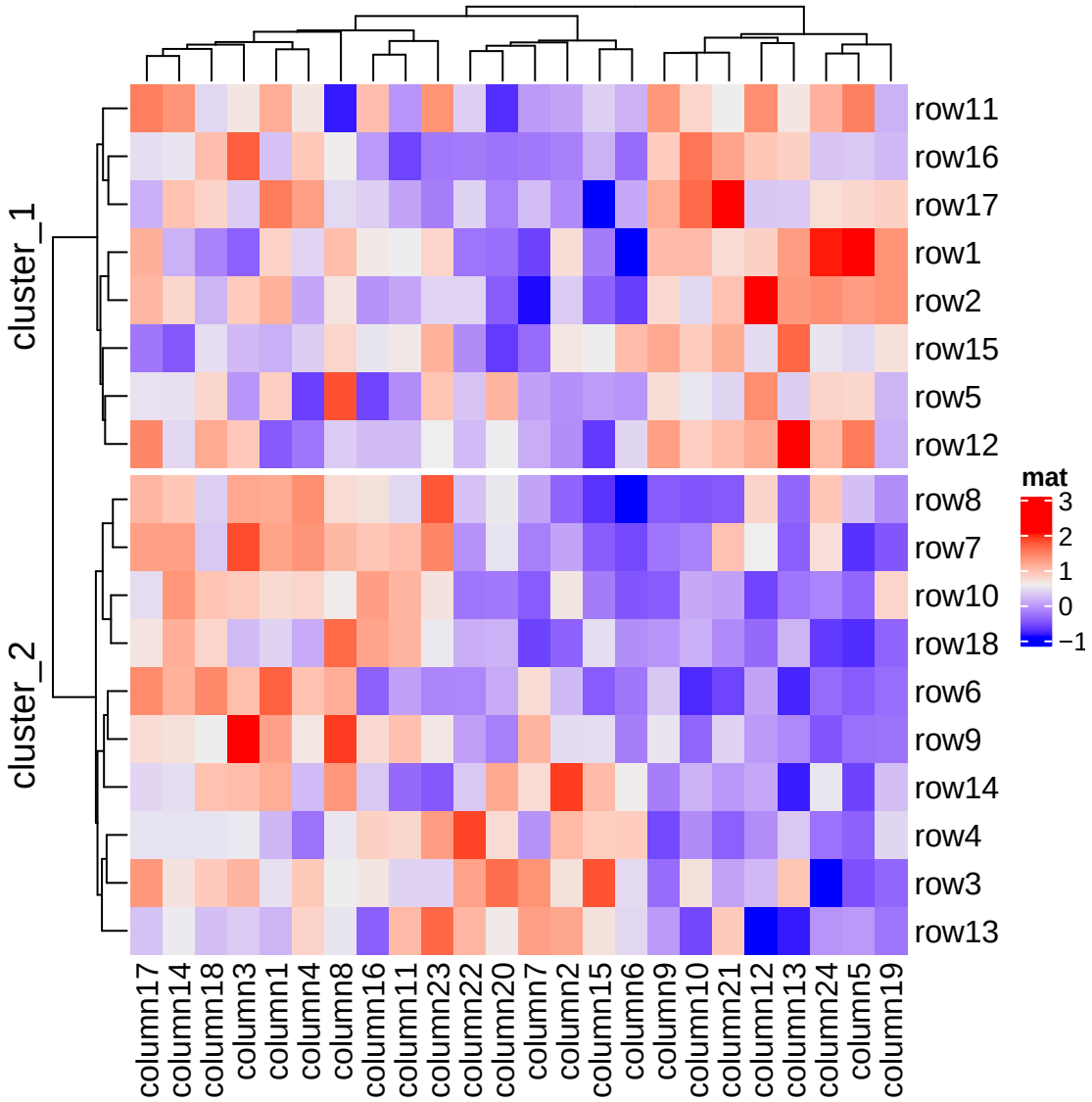
The row title is rotated by default, you can set `row_title_rot = 0` to make it horizontal:

```
Heatmap(mat, name = "mat", row_split = split, row_title = "%s|%s", row_title_rot = 0)
```



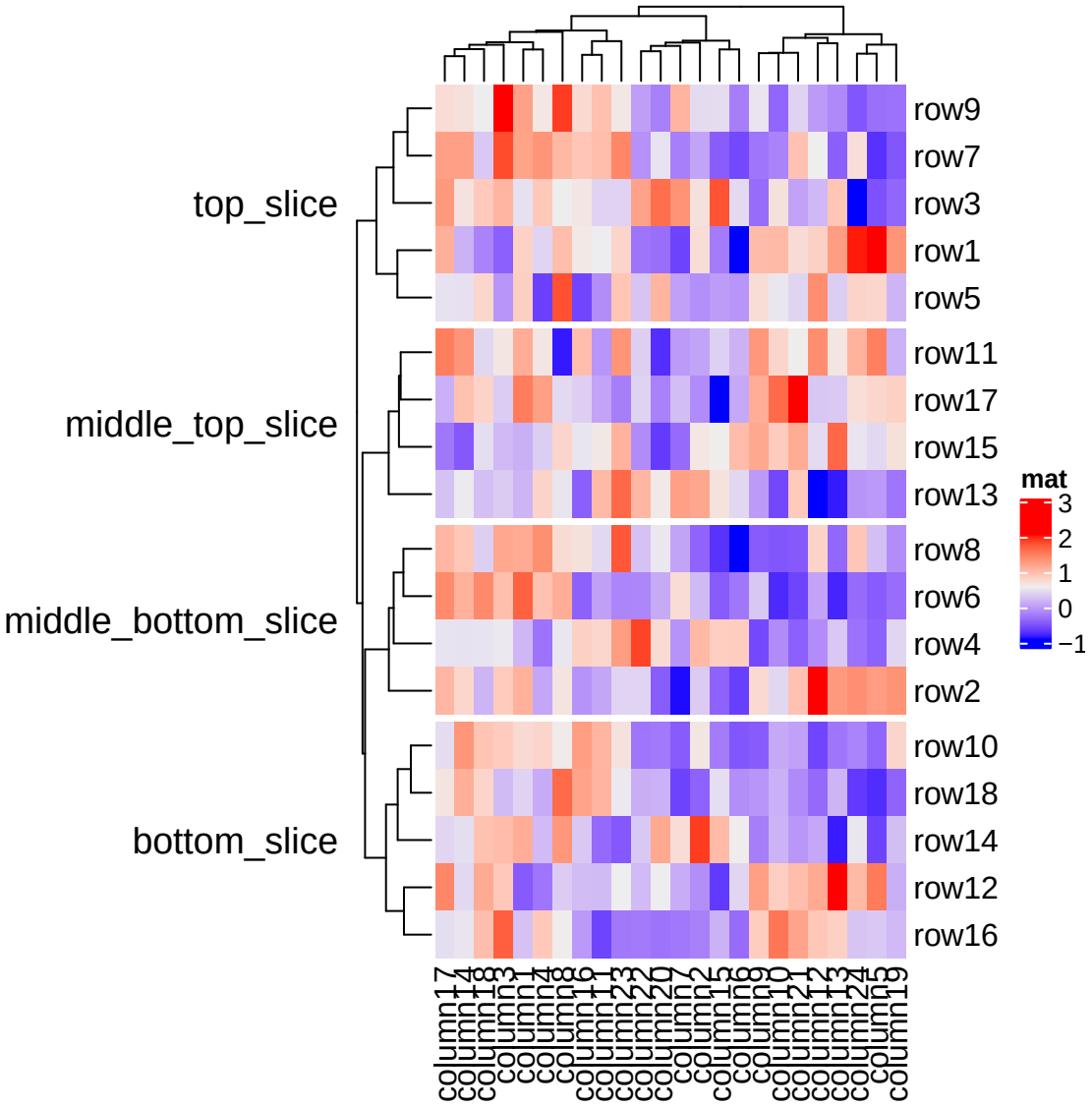
When `row_split`/`column_split` is set as a number, you can also use template to adjust the titles for slices.

```
Heatmap(mat, name = "mat", row_split = 2, row_title = "cluster_%s")
```



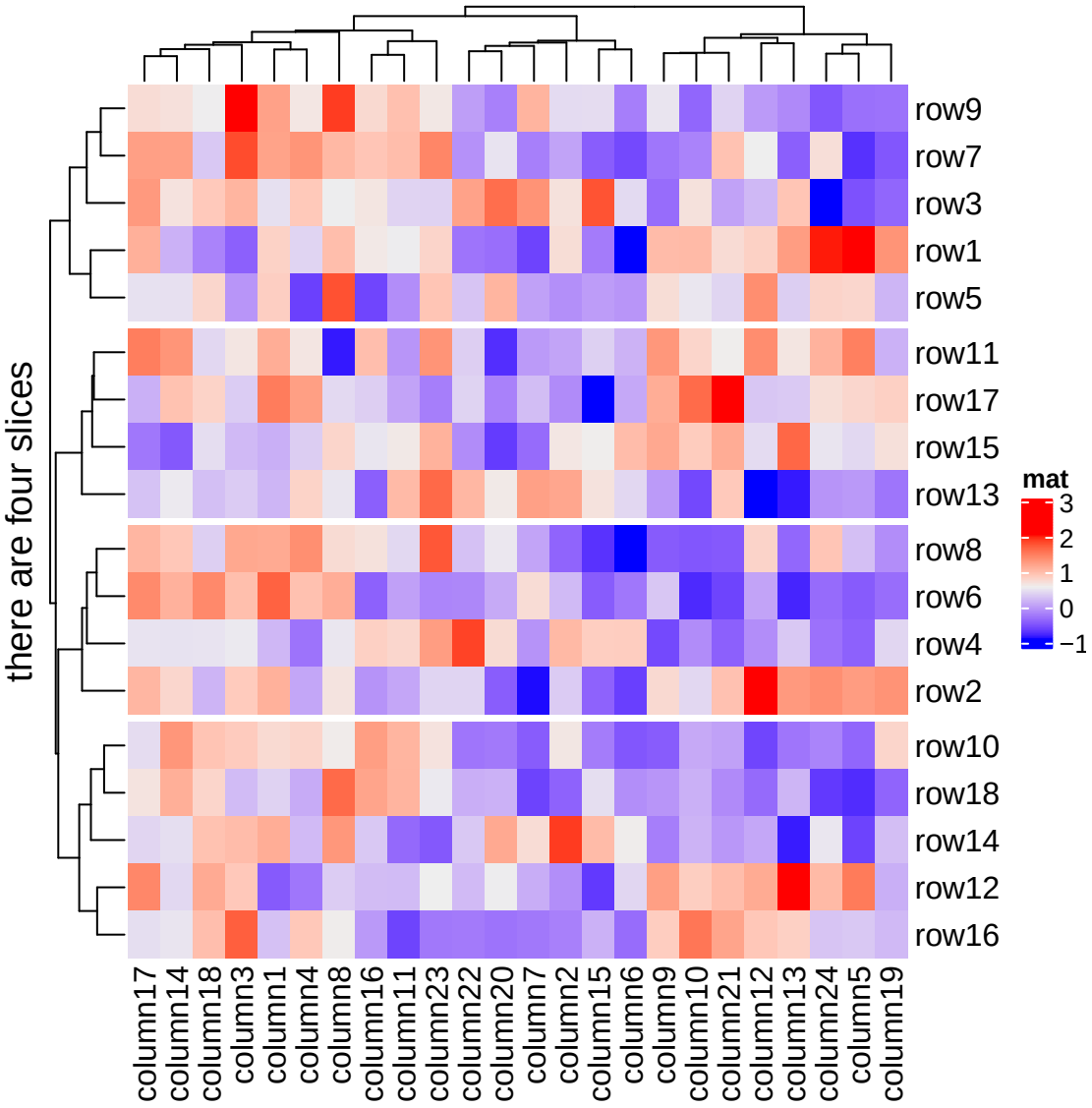
If you know the final number of row slices, you can directly set a vector of titles to `row_title`. Be careful the number of row slices is not always identical to `nlevel_1*nlevel_2*...`.

```
Heatmap(mat, name = "mat", row_split = split,
    row_title = c("top_slice", "middle_top_slice", "middle_bottom_slice", "bottom_slice"),
    row_title_rot = 0)
```



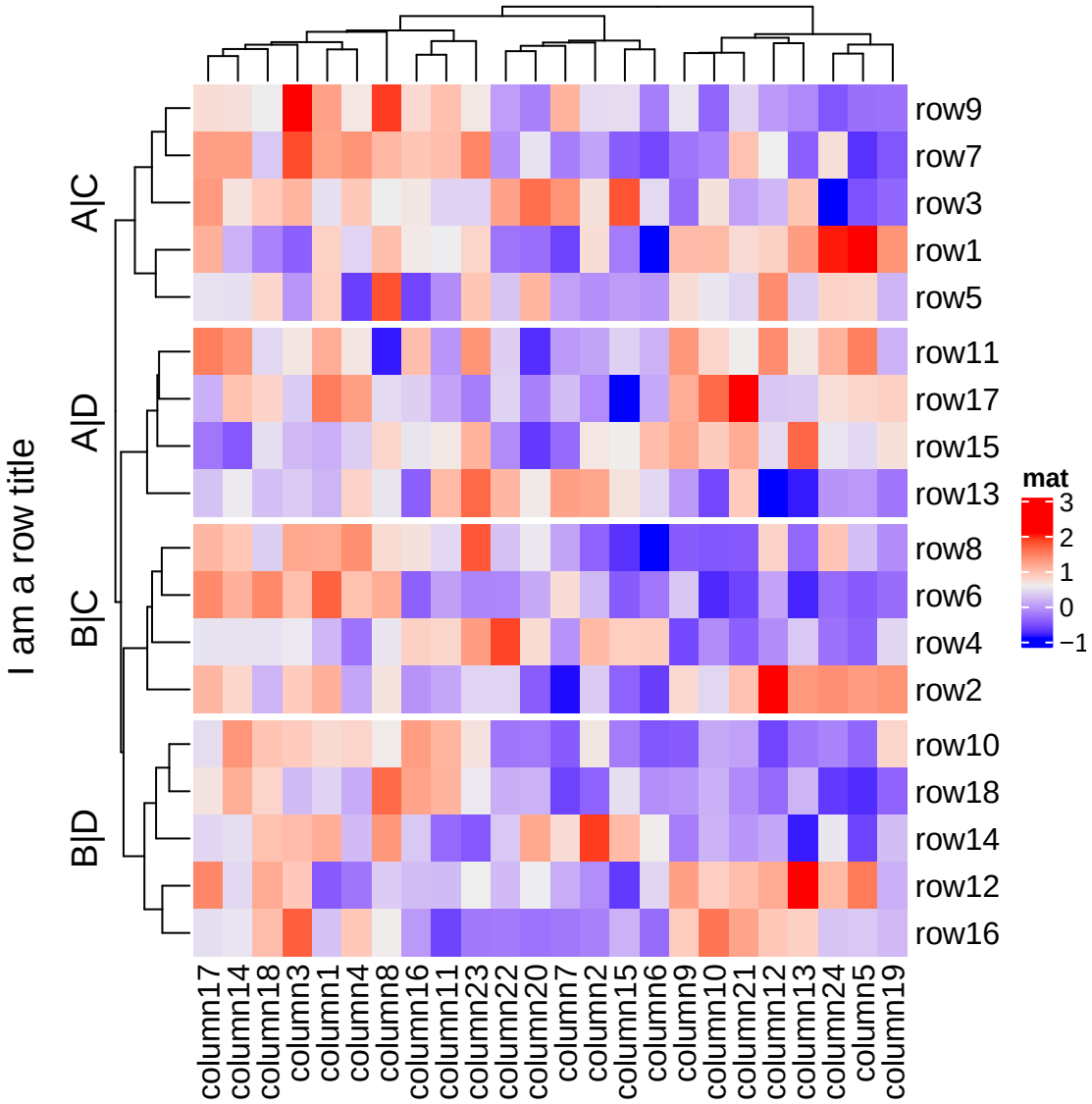
If the length of `row_title` is specified as a single string, it will be like a title for all slices.

```
Heatmap(mat, name = "mat", row_split = split, row_title = "there are four slices")
```



If you still want titles for each slice, but also a global title, you can do as follows.

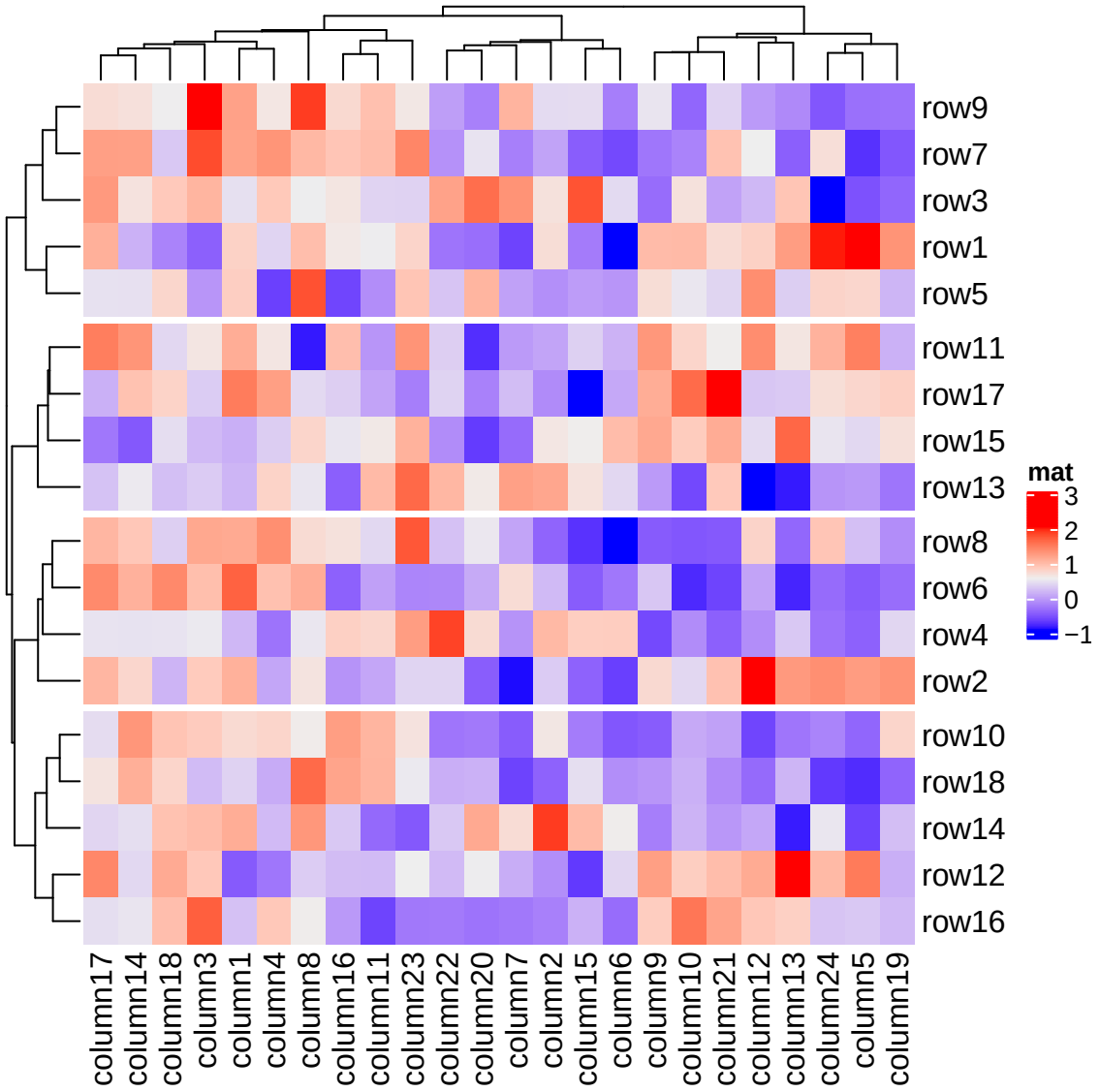
```
ht = Heatmap(mat, name = "mat", row_split = split, row_title = "%s|%s")
draw(ht, row_title = "I am a row title")
```



Actually the `row_title` used in `draw()` function is the row title of the heatmap list, although in the example there is only one heatmap. The `draw()` function and the heatmap list will be introduced in Chapter **??**.

If `row_title` is set to `NULL` or `""`, no row title will be drawn.

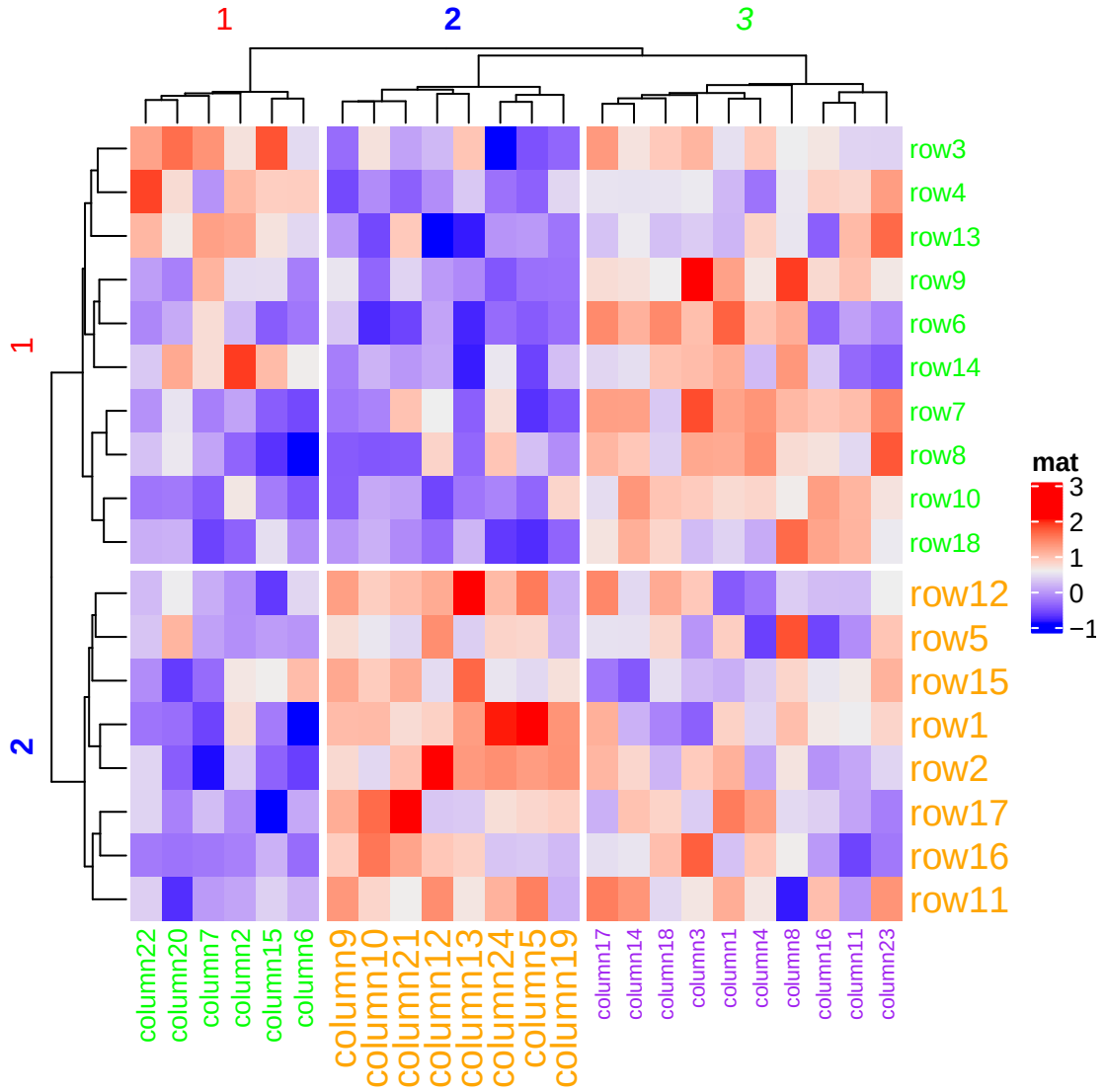
```
Heatmap(mat, name = "mat", row_split = split, row_title = NULL)
```



2.7.5 Graphic parameters for splitting

When splitting is applied on rows/columns, graphic parameters for row/column title and row/column names can be specified as same length as number of slices.

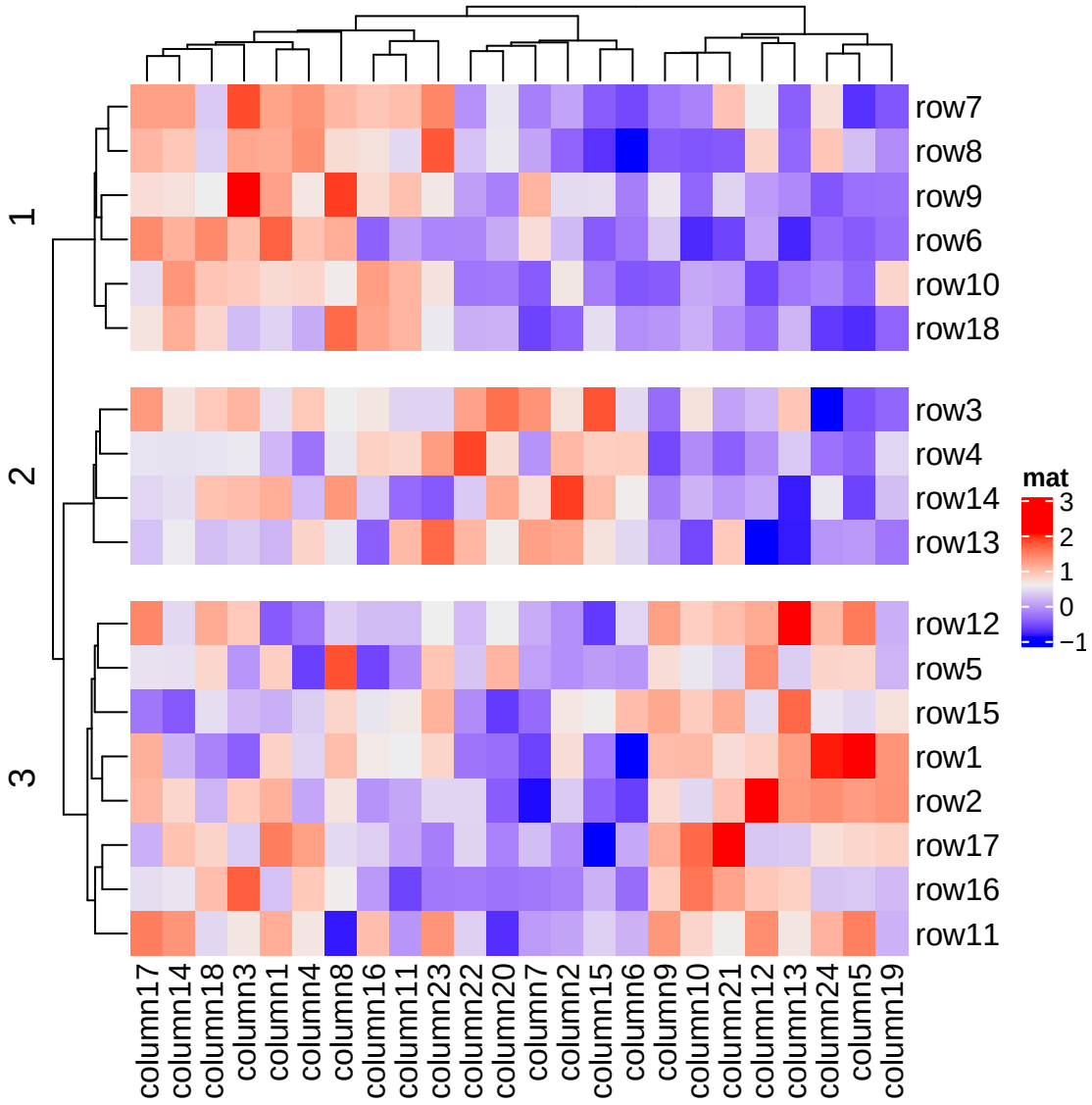
```
Heatmap(mat, name = "mat",
    row_km = 2, row_title_gp = gpar(col = c("red", "blue"), font = 1:2),
    row_names_gp = gpar(col = c("green", "orange"), fontsize = c(10, 14)),
    column_km = 3, column_title_gp = gpar(col = c("red", "blue", "green"), font = 1:3),
    column_names_gp = gpar(col = c("green", "orange", "purple"), fontsize = c(10, 14, 8)))
```



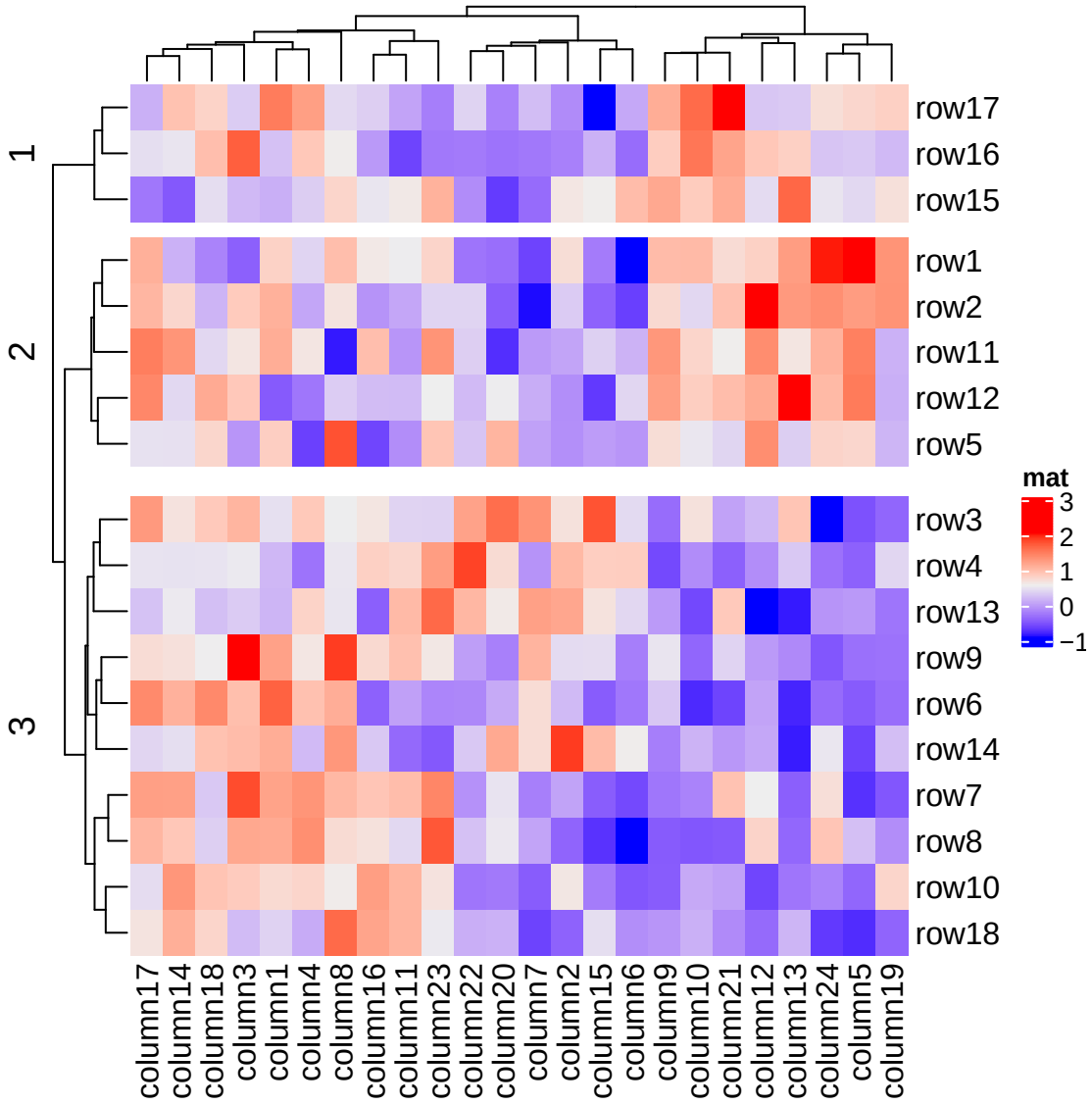
2.7.6 Gaps between slices

The space of gaps between row/column slices can be controlled by `row_gap`/`column_gap`. The value can be a single unit or a vector of units.

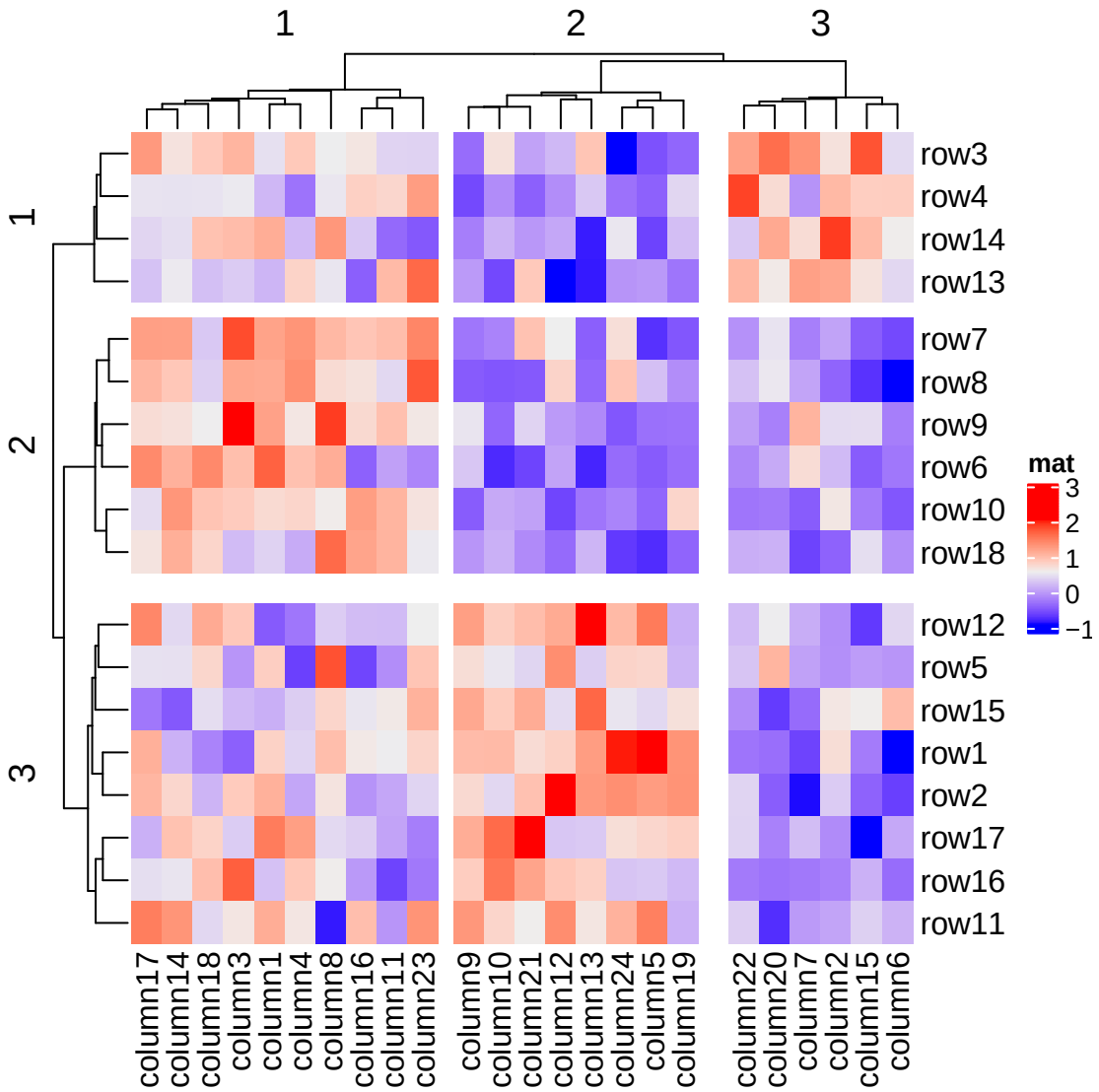
```
Heatmap(mat, name = "mat", row_km = 3, row_gap = unit(5, "mm"))
```




```
Heatmap(mat, name = "mat", row_km = 3, row_gap = unit(c(2, 4), "mm"))
```

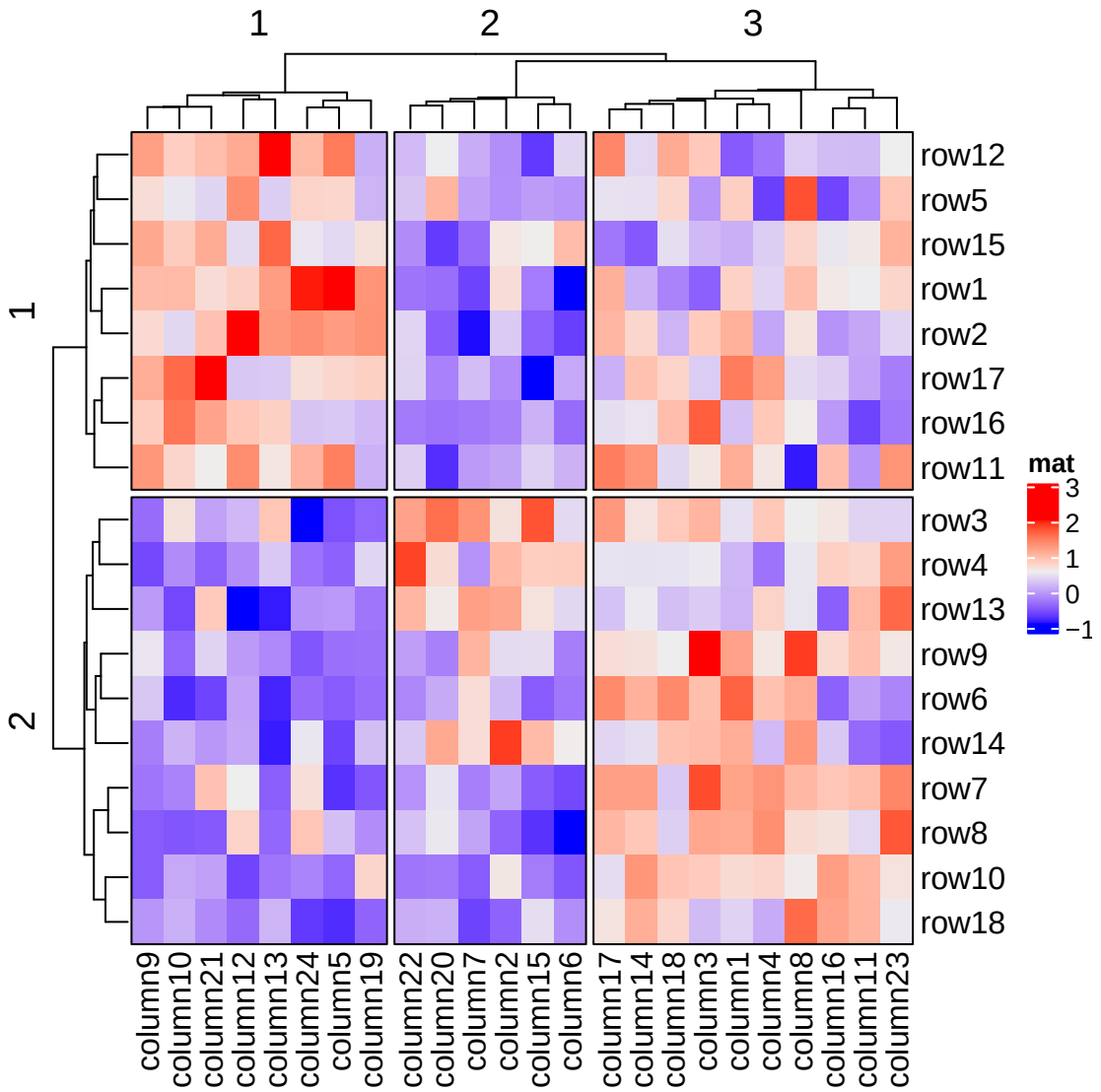



```
Heatmap(mat, name = "mat", row_km = 3, row_gap = unit(c(2, 4), "mm"),
    column_km = 3, column_gap = unit(c(2, 4), "mm"))
```



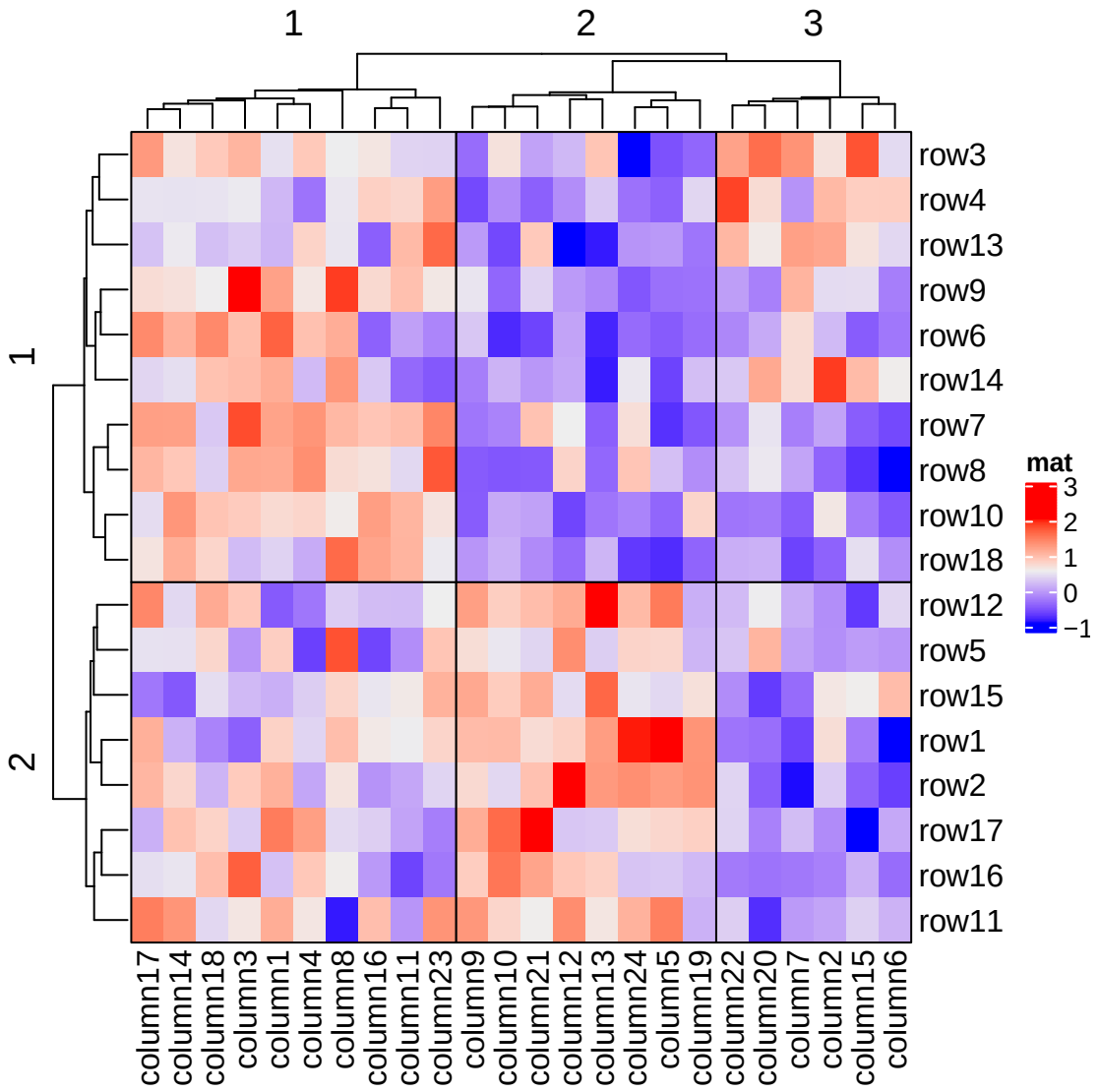
When heatmap border is added by setting `border = TRUE`, the border of every slice is added.

```
Heatmap(mat, name = "mat", row_km = 2, column_km = 3, border = TRUE)
```



If you set gap size to zero, the heatmap will look like it is partitioned by vertical and horizontal lines.

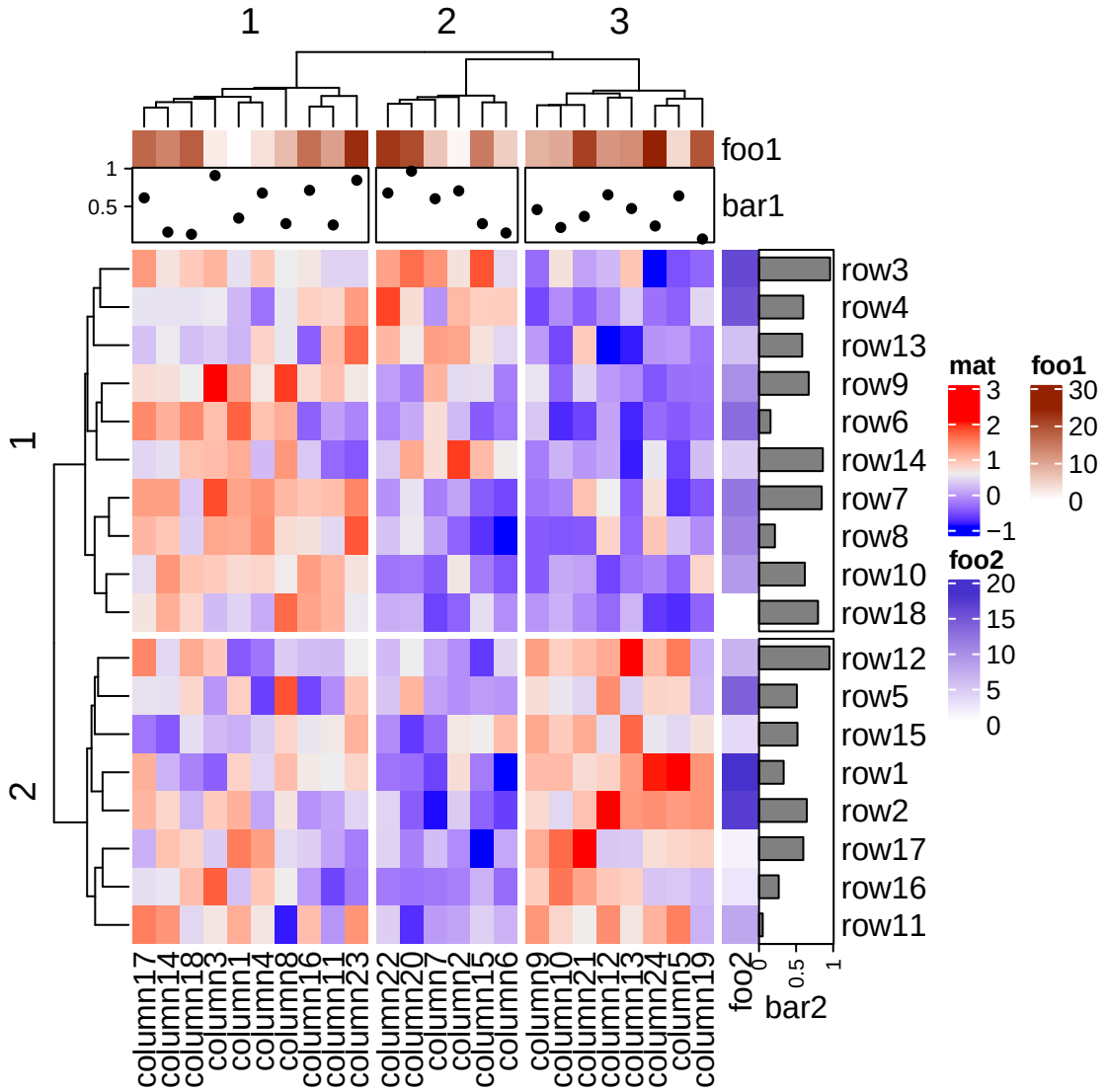
```
Heatmap(mat, name = "mat", row_km = 2, column_km = 3,
    row_gap = unit(0, "mm"), column_gap = unit(0, "mm"), border = TRUE)
```



2.7.7 Split heatmap annotations

When the heatmap is split, all the heatmap components are split accordingly. Following gives you a simple example and the heatmap annotation will be introduced in Chapter **??**.

```
Heatmap(mat, name = "mat", row_km = 2, column_km = 3,
    top_annotation = HeatmapAnnotation(foo1 = 1:24, bar1 = anno_points(runif(24))),
    right_annotation = rowAnnotation(foo2 = 18:1, bar2 = anno_barplot(runif(18)))
)
```



2.8 Heatmap as raster image

Saving plots in PDF format is kind like best parctice to preserve the quality. However, when there are too many rows (say, > 10000), the output PDF file would be huge and it takes long time and memory to read the whole plot. On the other hand, details of the huge matrix will not be seen in limited size of PDF file. Rendering heatmaps (the heatmap body) as raster images will effectively reduce the file size while the plot looks exactly the same for your screen or if you print it out. In `Heatmap()` function, there are four options which control how to generate the raster image: `use_raster`, `raster_device`, `raster_quality`, `raster_device_param`.

You can choose graphic device (`png`, `jpeg` and `tiff`) by `raster_device`, control the quality of the raster image by `raster_quality`, and pass further parameters for a specific device by `raster_device_param`.

If `raster_quality` is set to 1, internally, a PNG (if `raster_device` is set to `png`) file is generated with the same physical size as the heatmap body and refit into the heatmap body as a raster image. The png file generated has the size of `raster_quality*width` and `raster_quality*height`. So a larger `raster_quality` value gives you a better reservation of the original resolution.

In **Complexheatmap**, `use_raster` is by default turned on if the number of rows or columns is more than 2000.

```
# code only for demonstration
Heatmap(mat, use_raster = TRUE, raster_quality = 2)
```

2.9 Customize the heatmap body

The heatmap body can be self-defined to add more types of graphics. By default the heatmap body is composed by an array of rectangles (it might be called grids in other parts of this documentation, but it is called "*cells*" here) with different filled colors. However, it is also possible to add more graphics or symbols as additional layers on the heatmap. There are two arguments `cell_fun` and `layer_fun` which both should be user-defined functions.

`cell_fun` draws in each cell repeatedly, which is internally executed in two nested `for` loops, while `layer_fun` is the vectorized version of `cell_fun`. `cell_fun` is easier to understand but `layer_fun` is faster to execute.

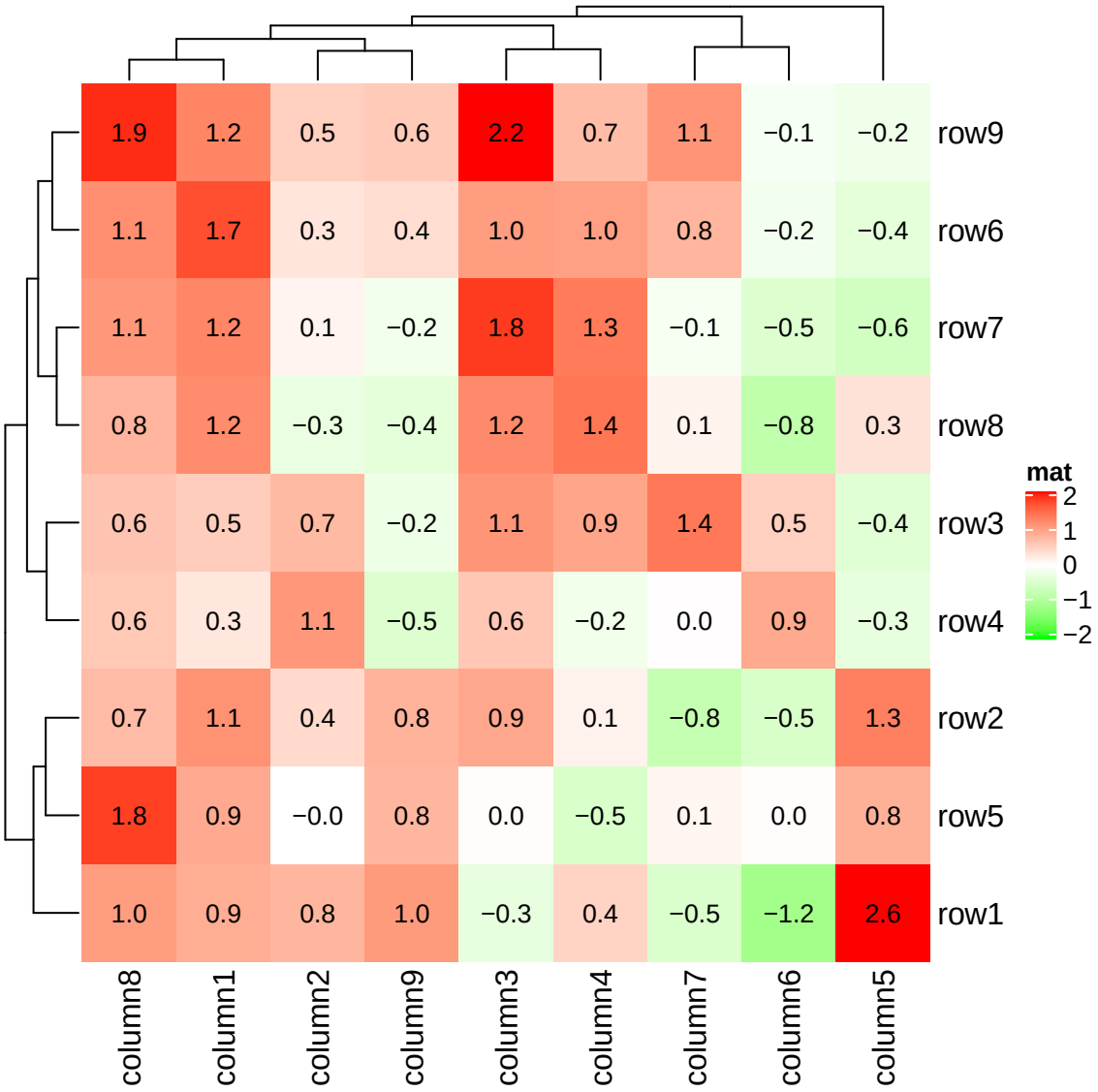
`cell_fun` expects a function with 7 arguments (the argument names can be different from following, but the order must be the same), which are:

- `j`: column index in the matrix. Column index corresponds to the x-direction in the viewport, that's why `j` is put as the first argument.
- `i`: row index in the matrix.
- `x`: x coordinate of middle point of the cell which is measured in the viewport of the heatmap body.
- `y`: y coordinate of middle point of the cell which is measured in the viewport of the heatmap body.
- `width`: width of the cell. The value is `unit(1/ncol(mat), "npc")`.
- `height`: height of the cell. The value is `unit(1/nrow(mat), "npc")`.
- `fill`: color of the cell.

The values for the seven arguments are automatically sent to the function when executed in each cell.

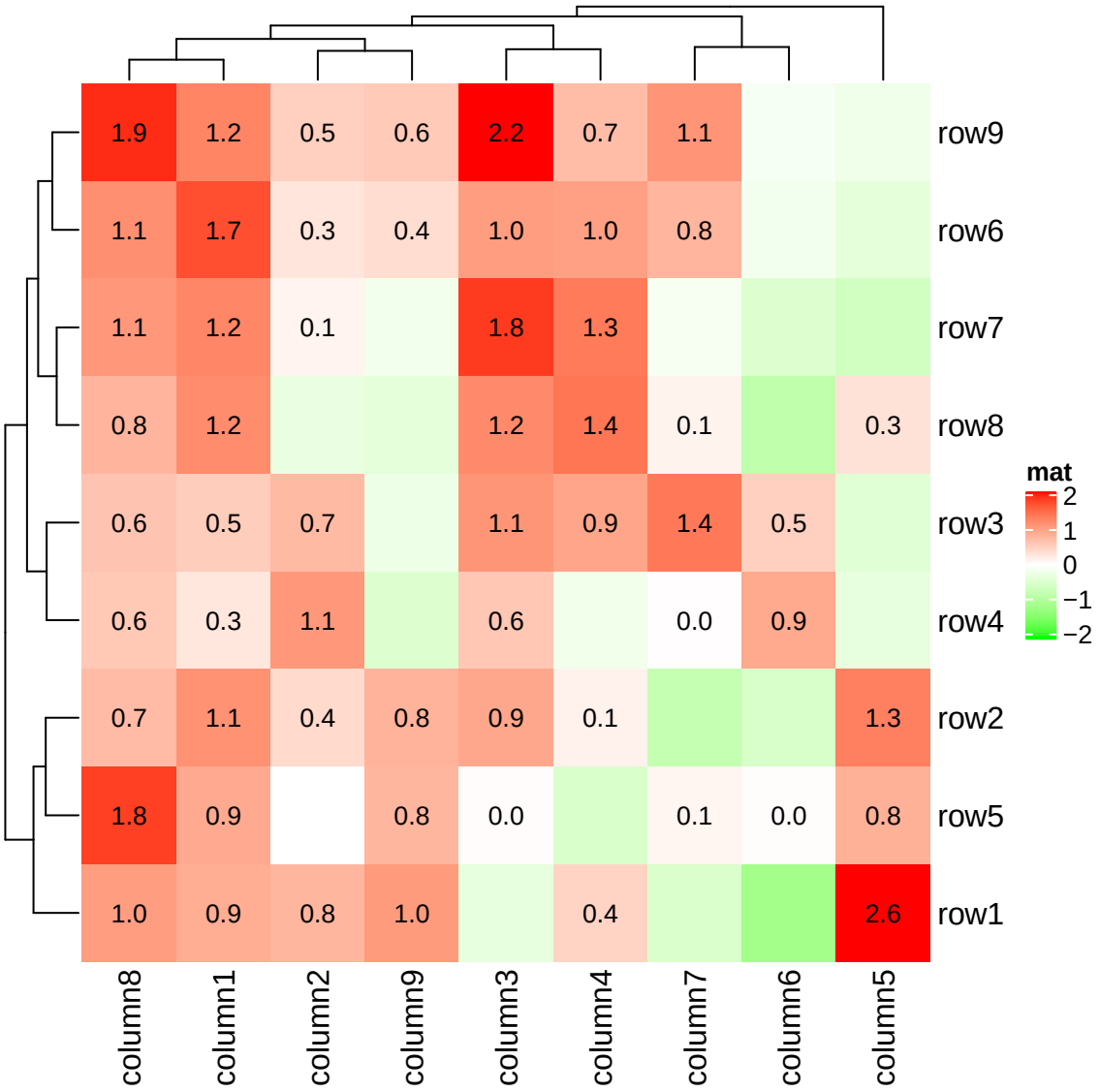
The most common use is to add values in the matrix onto the heatmap:

```
small_mat = mat[1:9, 1:9]
col_fun = colorRamp2(c(-2, 0, 2), c("green", "white", "red"))
Heatmap(small_mat, name = "mat", col = col_fun,
    cell_fun = function(j, i, x, y, width, height, fill) {
        grid.text(sprintf("%.1f", mat[i, j]), x, y, gp = gpar(fontsize = 10))
})
```



and we can also choose only to add text for the cells with positive values:

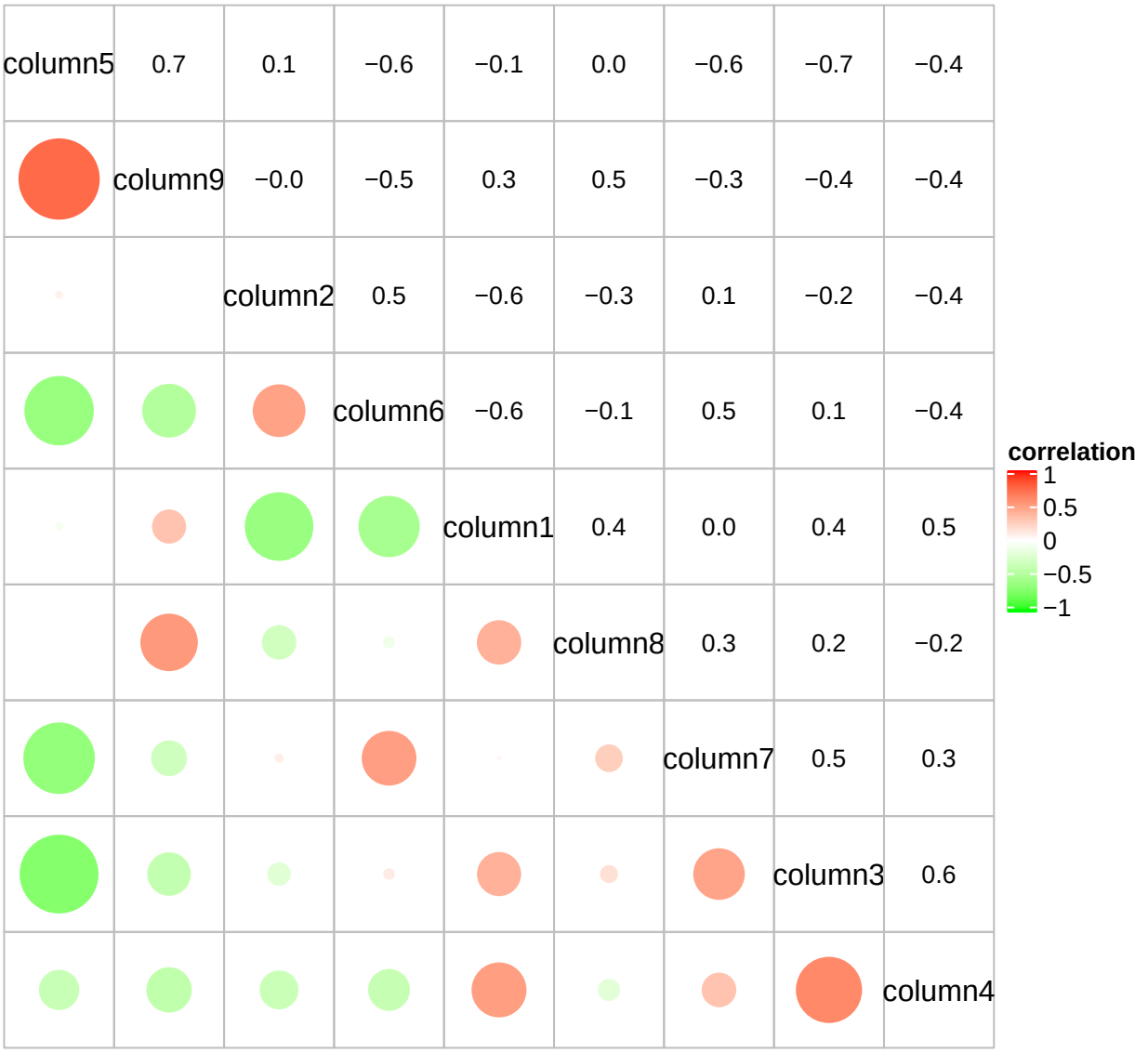
```
Heatmap(small_mat, name = "mat",  col = col_fun,
    cell_fun = function(j, i, x, y, width, height, fill) {
        if(small_mat[i, j] > 0)
            grid.text(sprintf("%.1f", mat[i, j]), x, y, gp = gpar(fontsize = 10))
})
```



In following example, we make a heatmap which shows correlation matrix similar as the **corrplot** package:

```
cor_mat = cor(small_mat)
od = hclust(dist(cor_mat))$order
cor_mat = cor_mat[od, od]
nm = rownames(cor_mat)
col_fun = circlize::colorRamp2(c(-1, 0, 1), c("green", "white", "red"))
# `col = col_fun` here is used to generate the legend
Heatmap(cor_mat, name = "correlation", col = col_fun, rect_gp = gpar(type = "none"),
    cell_fun = function(j, i, x, y, width, height, fill) {
        grid.rect(x = x, y = y, width = width, height = height, gp = gpar(col = "grey", fill = NA))
        if(i == j) {
            grid.text(nm[i], x = x, y = y)
        } else if(i > j) {
            grid.circle(x = x, y = y, r = abs(cor_mat[i, j])/2 * min(unit.c(width, height)),
                gp = gpar(fill = col_fun(cor_mat[i, j]), col = NA))
        } else {
            grid.text(sprintf("%.1f", cor_mat[i, j]), x, y, gp = gpar(fontsize = 10))
        }
```

```
    }, cluster_rows = FALSE, cluster_columns = FALSE,
    show_row_names = FALSE, show_column_names = FALSE)
```



As you may see, when setting the non-standard parameter `rect_gp = gpar(type = "none")`, the clustering is performed but nothing is drawn on the heatmap body.

Similar as `cell_fun`, `layer_fun` also needs seven arguments, but they are all in vector form:

```
# code only for demonstration
Heatmap(..., layer_fun = function(j, i, x, y, w, h, fill) {...})
# on you can capitalize the arguments to mark they are vectors
Heatmap(..., layer_fun = function(J, I, X, Y, W, H, F) {...})
```

Since `j` and `i` are vectors, to get corresponding values in the matrix, we cannot use the form as `mat[j, i]` because it gives you a sub-matrix with `length(i)` rows and `length(j)` columns, instead we can use `pindex()` function from **ComplexHeatmap** which is like pairwise indexing. See follow example:

```
mfoo = matrix(1:9, nr = 3)
mfoo[1:2, c(1, 3)]
```

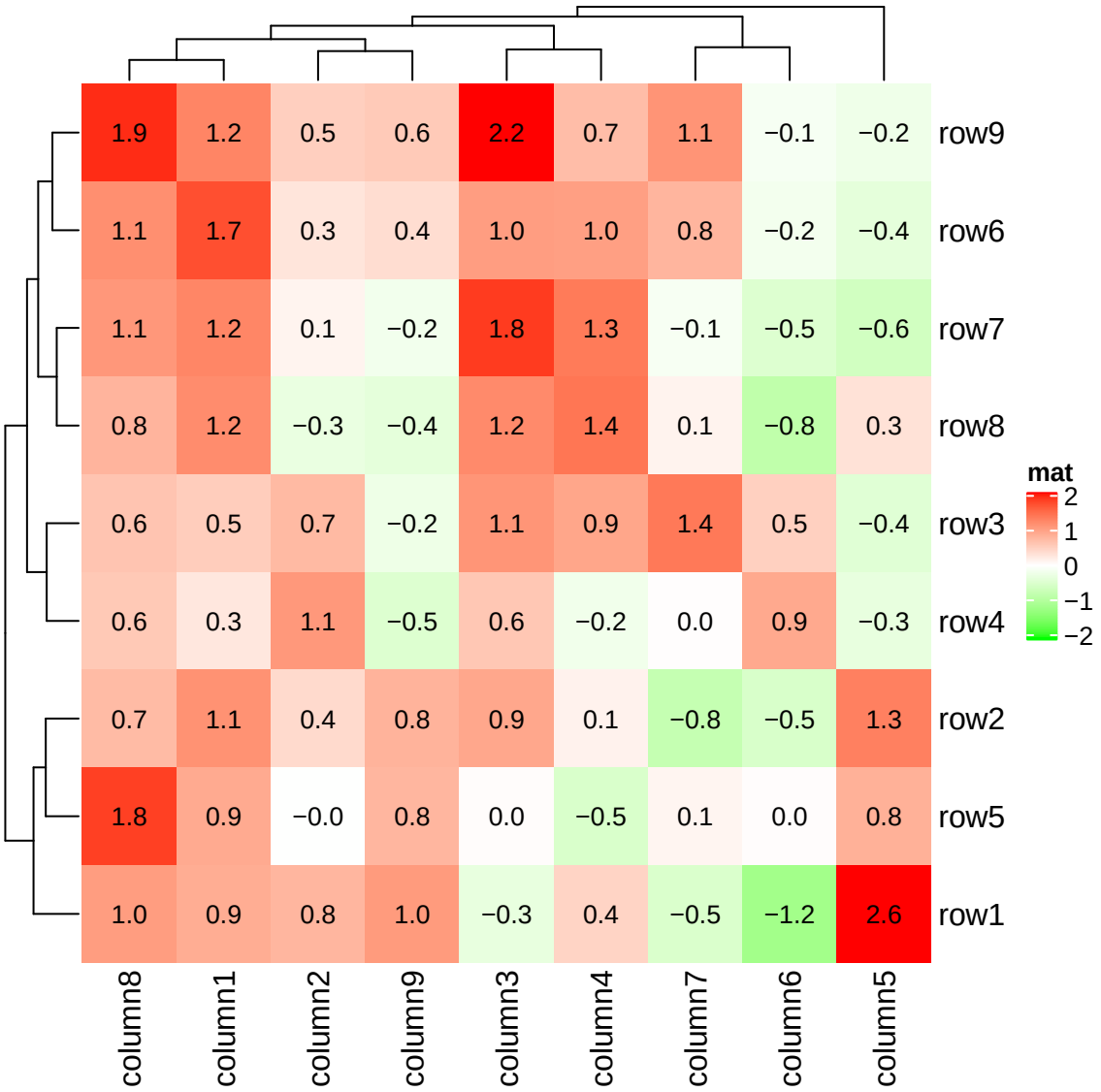
```
##      [,1] [,2]
## [1,]    1    7
## [2,]    2    8
```

```
# but we actually want mfoo[1, 1] and mfoo[2, 3]
pindex(mfoo, 1:2, c(1, 3))
```

```
## [1] 1 8
```

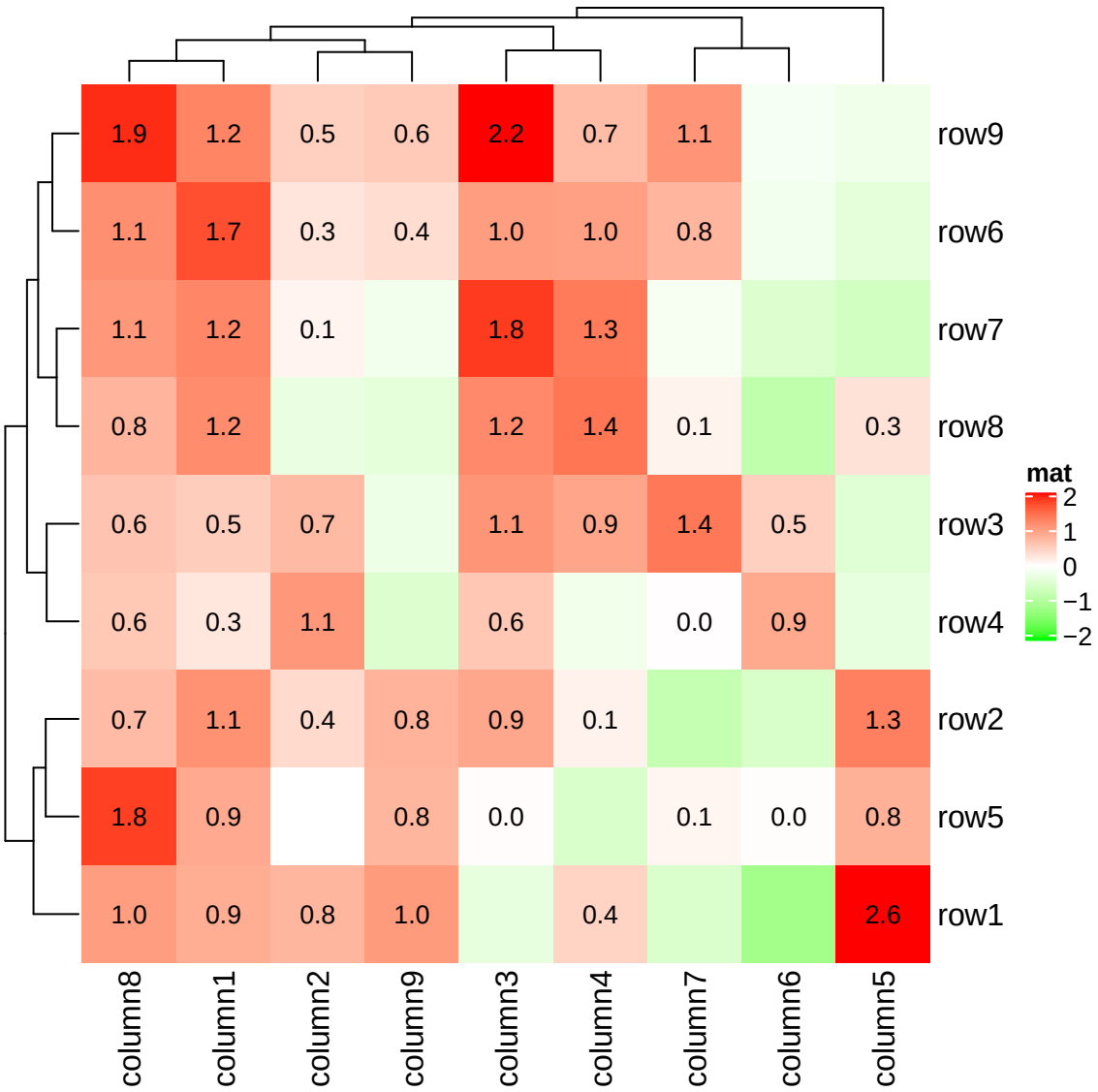
Next example shows the `layer_fun` version of adding text on heatmap. It's basically the same as the `cell_fun` version.

```
col_fun = colorRamp2(c(-2, 0, 2), c("green", "white", "red"))
Heatmap(small_mat, name = "mat", col = col_fun,
    layer_fun = function(j, i, x, y, width, height, fill) {
        # since grid.text can also be vectorized
        grid.text(sprintf("%.1f", pindex(mat, i, j)), x, y, gp = gpar(fontsize = 10))
})
```



And only add text to cells with positive values:

```
Heatmap(small_mat, name = "mat", col = col_fun,
    layer_fun = function(j, i, x, y, width, height, fill) {
        v = pindex(mat, i, j)
        l = v > 0
        grid.text(sprintf("%.1f", v[l]), x[l], y[l], gp = gpar(fontsize = 10))
})
```



One last example is to visualize a GO game. The input data takes records of moves in the game.

```
str = "B[cp];W[pq];B[dc];W[qd];B[eq];W[od];B[de];W[jc];B[qk];W[qn]
;B[qh];W[ck];B[ci];W[cn];B[hc];W[je];B[jq];W[df];B[ee];W[cf]
;B[ei];W[bc];B[ce];W[be];B[bd];W[cd];B[bf];W[ad];B[bg];W[cc]
;B[eb];W[db];B[ec];W[lq];B[nq];W[jp];B[iq];W[kq];B[pp];W[op]
;B[po];W[oq];B[rp];W[ql];B[oo];W[no];B[pl];W[pm];B[np];W[qq]
;B[om];W[ol];B[pk];W[qp];B[on];W[rm];B[mo];W[nr];B[rl];W[rk]
;B[qm];W[dp];B[dq];W[ql];B[or];W[mp];B[nn];W[mq];B[qm];W[bp]
;B[co];W[ql];B[no];W[pr];B[qm];W[dd];B[pn];W[ed];B[bo];W[eg]
;B[ef];W[dg];B[ge];W[gh];B[gf];W[gg];B[ek];W[ig];B[fd];W[en]
;B[bn];W[ip];B[dm];W[ff];B[cb];W[fe];B[hp];W[ho];B[hq];W[el]
```

```
;B[dl];W[fk];B[ej];W[fp];B[go];W[hn];B[fo];W[em];B[dn];W[eo]
;B[gp];W[ib];B[gc];W[pg];B[qg];W[ng];B[qc];W[re];B[pf];W[of]
;B[rc];W[ob];B[ph];W[qo];B[rn];W[mi];B[og];W[oe];B[qe];W[rd]
;B[rf];W[pd];B[gm];W[gl];B[fm];W[fl];B[lj];W[mj];B[lk];W[ro]
;B[hl];W[hk];B[ik];W[dk];B[bi];W[di];B[dj];W[dh];B[hj];W[gj]
;B[li];W[lh];B[kh];W[lg];B[jn];W[do];B[cl];W[ij];B[gk];W[bl]
;B[cm];W[hk];B[jk];W[lo];B[hi];W[hm];B[gk];W[bm];B[cn];W[hk]
;B[il];W[cq];B[bq];W[ii];B[sm];W[jo];B[kn];W[fq];B[ep];W[cj]
;B[bk];W[er];B[cr];W[gr];B[gk];W[fj];B[ko];W[kp];B[hr];W[jr]
;B[nh];W[mh];B[mk];W[bb];B[da];W[jh];B[ic];W[id];B[hb];W[jb]
;B[oj];W[fn];B[fs];W[fr];B[gs];W[es];B[hs];W[gn];B[kr];W[is]
;B[dr];W[fi];B[bj];W[hd];B[gd];W[ln];B[lm];W[oi];B[oh];W[ni]
;B[pi];W[ki];B[kj];W[ji];B[so];W[rq];B[if];W[jf];B[hh];W[hf]
;B[he];W[ie];B[hg];W[ba];B[ca];W[sp];B[im];W[sn];B[rm];W[pe]
;B[qf];W[if];B[hk];W[nj];B[nk];W[lr];B[mn];W[af];B[ag];W[ch]
;B[bh];W[lp];B[ia];W[ja];B[ha];W[sf];B[sg];W[se];B[eh];W[fh]
;B[in];W[ih];B[ae];W[so];B[af]"
```

We convert it into a matrix:

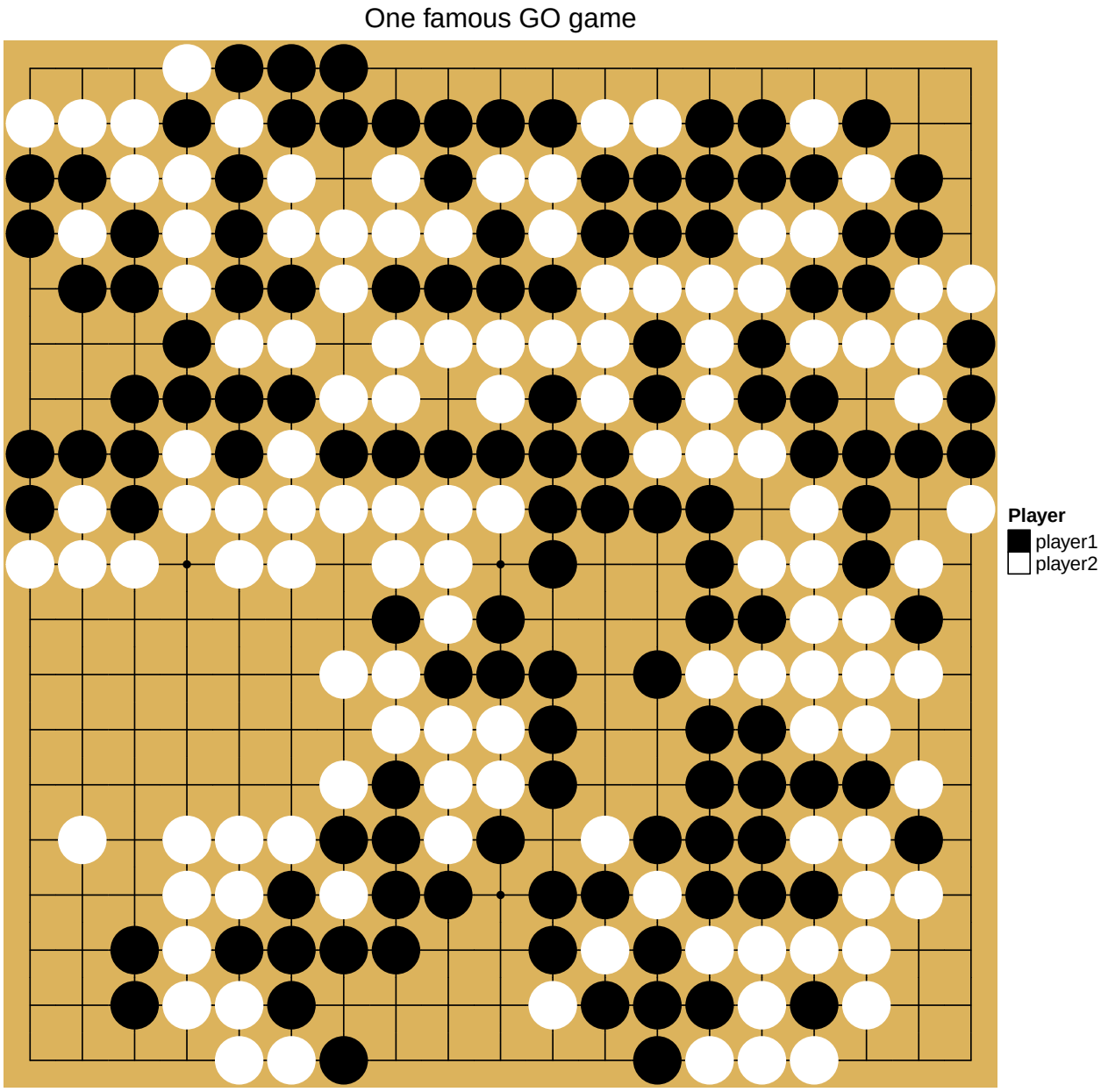
```
str = gsub("\\n", "", str)
step = strsplit(str, ";")[[1]]
type = gsub("(B|W).*", "\\1", step)
row = gsub("(B|W)\\[(.).\\]", "\\2", step)
column = gsub("(B|W)\\[.(.)\\]", "\\2", step)

go_mat = matrix(nrow = 19, ncol = 19)
rownames(go_mat) = letters[1:19]
colnames(go_mat) = letters[1:19]
for(i in seq_along(row)) {
    go_mat[row[i], column[i]] = type[i]
}
go_mat[1:4, 1:4]
```

```
##   a   b   c   d
## a NA  NA  NA  "W"
## b "W" "W" "W" "B"
## c "B" "B" "W" "W"
## d "B" "W" "B" "W"
```

Black and white stones are put based on the values in the matrix:

```
Heatmap(go_mat, name = "go", rect_gp = gpar(type = "none"),
    cell_fun = function(j, i, x, y, w, h, col) {
        grid.rect(x, y, w, h, gp = gpar(fill = "#dcb35c", col = NA))
        if(i == 1) {
            grid.segments(x, y-h*0.5, x, y)
        } else if(i == nrow(go_mat)) {
            grid.segments(x, y, x, y+h*0.5)
        } else {
            grid.segments(x, y-h*0.5, x, y+h*0.5)
        }
        if(j == 1) {
            grid.segments(x, y, x+w*0.5, y)
        } else if(j == ncol(go_mat)) {
```

```
            grid.segments(x-w*0.5, y, x, y)
        } else {
            grid.segments(x-w*0.5, y, x+w*0.5, y)
        }

        if(i %in% c(4, 10, 16) & j %in% c(4, 10, 16)) {
            grid.points(x, y, pch = 16, size = unit(2, "mm"))
        }

        r = min(unit.c(w, h))*0.45
        if(is.na(go_mat[i, j])) {
        } else if(go_mat[i, j] == "W") {
            grid.circle(x, y, r, gp = gpar(fill = "white", col = "white"))
        } else if(go_mat[i, j] == "B") {
            grid.circle(x, y, r, gp = gpar(fill = "black", col = "black"))
        }
    },
    col = c("B" = "black", "W" = "white"),
    show_row_names = FALSE, show_column_names = FALSE,
    column_title = "One famous GO game",
    heatmap_legend_param = list(title = "Player", at = c("B", "W"),
        labels = c("player1", "player2"), border = "black")
)
```

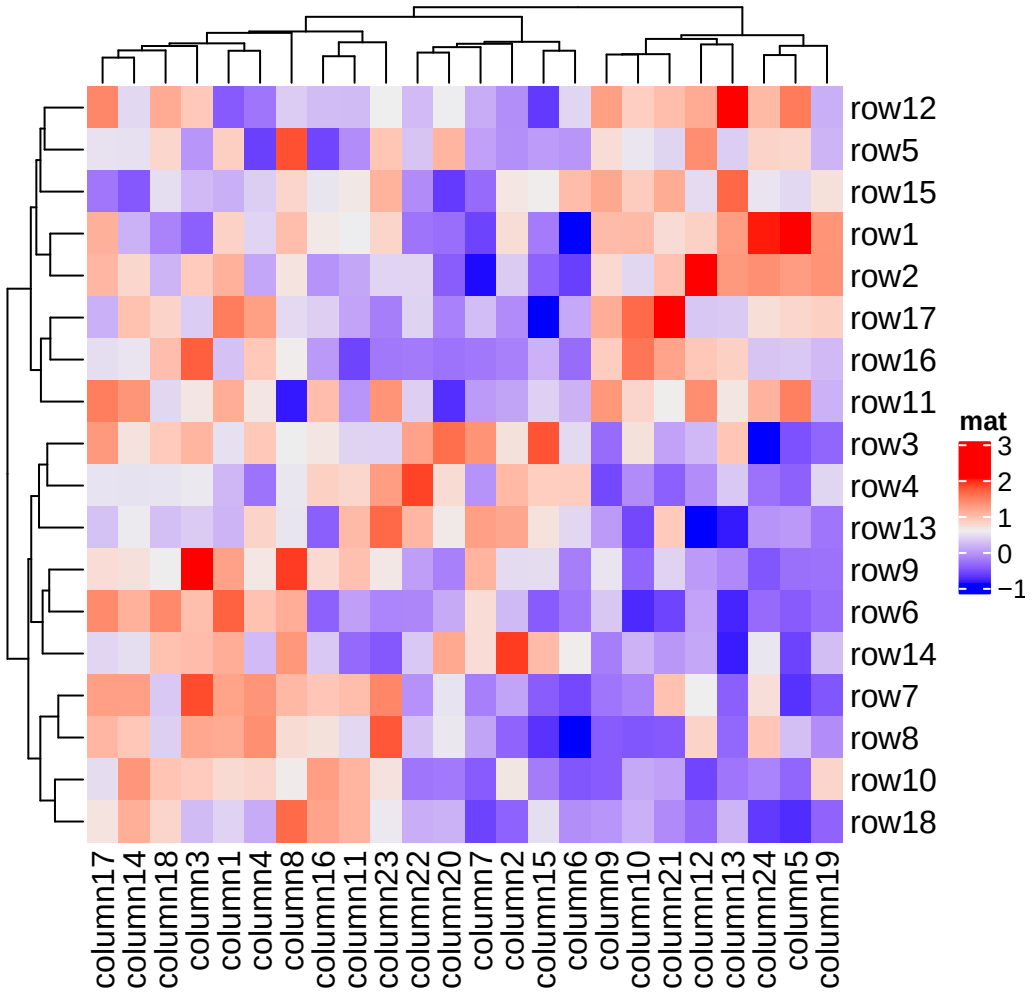


2.10 Size of the heatmap

`width`, `heatmap_width`, `height` and `heatmap_height` control the size of the heatmap. By default, all heatmap components have fixed width or height, e.g. the width of row dendrogram is `1cm`. The width or the height of the heatmap body fill the rest area of the final plotting region, which means, if you draw it in an interactive graphic window and you change the size of the window by draging it, the size of the heatmap body is automatically adjusted.

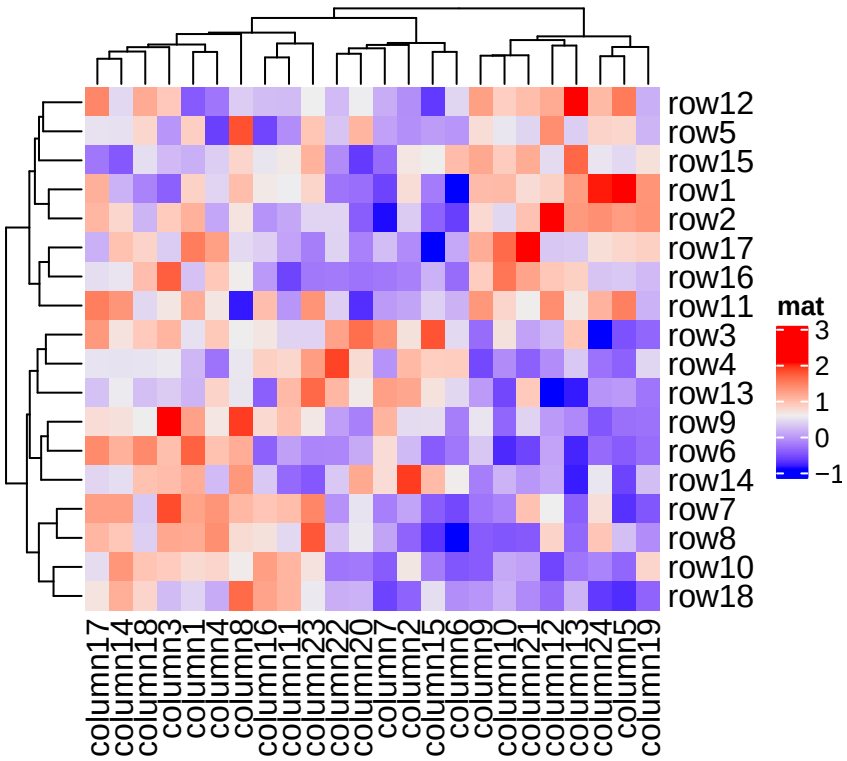
`heatmap_width` and `heatmap_height` control the width/height of the complete heatmap while `width` and `height` only control the width/height of the heamtap body. All these four arguments can be set as absolute units.

```
Heatmap(mat, name = "mat", width = unit(10, "cm"), height = unit(10, "cm"))
```




```
## Since all heatmaps/annotations have absolute units, the total width of the plot is 139mm
## Since all heatmaps/annotations have absolute units, the total height of the plot is 135mm
```

```
Heatmap(mat, name = "mat", heatmap_width = unit(10, "cm"), heatmap_height = unit(10, "cm"))
```




```
## Since all heatmaps/annotations have absolute units, the total width of the plot is 115mm
## Since all heatmaps/annotations have absolute units, the total height of the plot is 104mm
```

There will be message showing the size of the whole plot.

These four arguments are more important when adjust the size in a list of heatmaps (see Section **??**).

2.11 Plot the heatmap {plot-the-heatmap}

`Heatmap()` function actually is only a constructor, which means it only puts all the data and configurations into the object in the `Heatmap` class. The clustering will only be performed when the `draw()` method is called. Under interactive mode (e.g. the interactive R terminal where you can type your R code line by line), directly calling `Heatmap()` without returning to any object prints the object and the print method (or the S4 `show()` method) for the `Heatmap` class object calls `draw()` internally. So if you type `Heatmap(...)` in your R terminal, it looks like it is a plotting function like `plot()`, you need to be aware of that it is actually not true and in the following cases you might see nothing plotted.

- you put `Heatmap(...)` inside a function,
- you put `Heatmap(...)` in a code chunk like `for` or `if-else`
- you put `Heatmap(...)` in an Rscript and you run it under command line.

The reason is in above three cases, the `show()` method WILL NOT be called and thus `draw()` method is not executed either. So, to make the plot, you need to call `draw()` explicitly: `draw(Heatmap(...))` or:

```
# code only for demonstration
ht = Heatmap(...)
draw(ht)
```

The `draw()` function actually is applied to a list of heatmaps in `HeatmapList` class. The `draw()` method for the single `Heatmap` class constructs a `HeatmapList` with only one heatmap and call `draw()` method of the

`HeatmapList` class. The `draw()` function accpets a lot of more arguments which e.g. controls the legends. It will be discussed in Chapter ??.

```
draw(ht, heatmap_legend_side, padding, ...)
```

2.12 Get orders and dendrograms

The row/column orders of the heatmap can be obtained by `row_order()`/`column_order()` functions. You can directly apply to the heatmap object returned by `Heatmap()` or to the object returned by `draw()`. In following, we take `row_order()` as example.

```
small_mat = mat[1:9, 1:9]
ht1 = Heatmap(small_mat)
row_order(ht1)
```

```
## [1] 9 6 7 8 3 4 2 5 1
```

```
ht2 = draw(ht1)
row_order(ht2)
```

```
## [1] 9 6 7 8 3 4 2 5 1
```

As explained in previous section, `Heatmap()` function does not perform clustering, thus, when directly apply `row_order()` on `ht1`, clustering will be performed. Later when making the heatmap by `draw(ht1)`, the clustering will be applied again. This might be a problem that if you set k-means clustering in the heatmap. Since the clustering is applied twice, k-means might give you different clustering, which means, you might have different results from `row_order()` and you might have different heatmap.

In following chunk of code, `o1`, `o2` and `o3` might be different because each time, k-means clustering is performed.

```
ht1 = Heatmap(small_mat, row_km = 2)
o1 = row_order(ht1)
o2 = row_order(ht1)
ht2 = draw(ht1)
o3 = row_order(ht2)
o4 = row_order(ht2)
```

`draw()` function returns the heatmap (or more precisely, the heatmap list) which has been reordered, and applying `row_order()` just extracts the row order from the object, which ensures the row order is exactly the same as the one shown in the heatmap. In above code, `o3` is always identical to `o4`.

So, the preferable way to get row/column orders is as follows.

```
# code only for demonstration
ht = Heatmap(small_mat)
ht = draw(ht)
row_order(ht)
column_order(ht)
```

If rows/columns are split, row order or column order will be a list.

```
ht = Heatmap(small_mat, row_km = 2, column_km = 3)
ht = draw(ht)
row_order(ht)
```

```
## $`1`
## [1] 9 6 7 8 3 4
```

```
##
## $`2`
## [1] 2 5 1
```

```
column_order(ht)
```

```
## $`1`
## [1] 5 9
##
## $`2`
## [1] 8 1 3 4
##
## $`3`
## [1] 2 7 6
```

Similarly, the `row_dend()`/`column_dend()` functions return the dendrograms. It returns a single dendrogram or a list of dendrograms depending on whether the heatmap is split.

```
ht = Heatmap(small_mat, row_km = 2)
ht = draw(ht)
row_dend(ht)
```

```
## $`1`
## 'dendrogram' with 2 branches and 6 members total, at height 3.109169
##
## $`2`
## 'dendrogram' with 2 branches and 3 members total, at height 2.718561
```

```
column_dend(ht)
```

```
## 'dendrogram' with 2 branches and 9 members total, at height 5.191887
```

`row_order()`, `column_order()`, `row_dend()` and `column_dend()` also work for a list of heatmaps, it will be expalined in Section **??**.

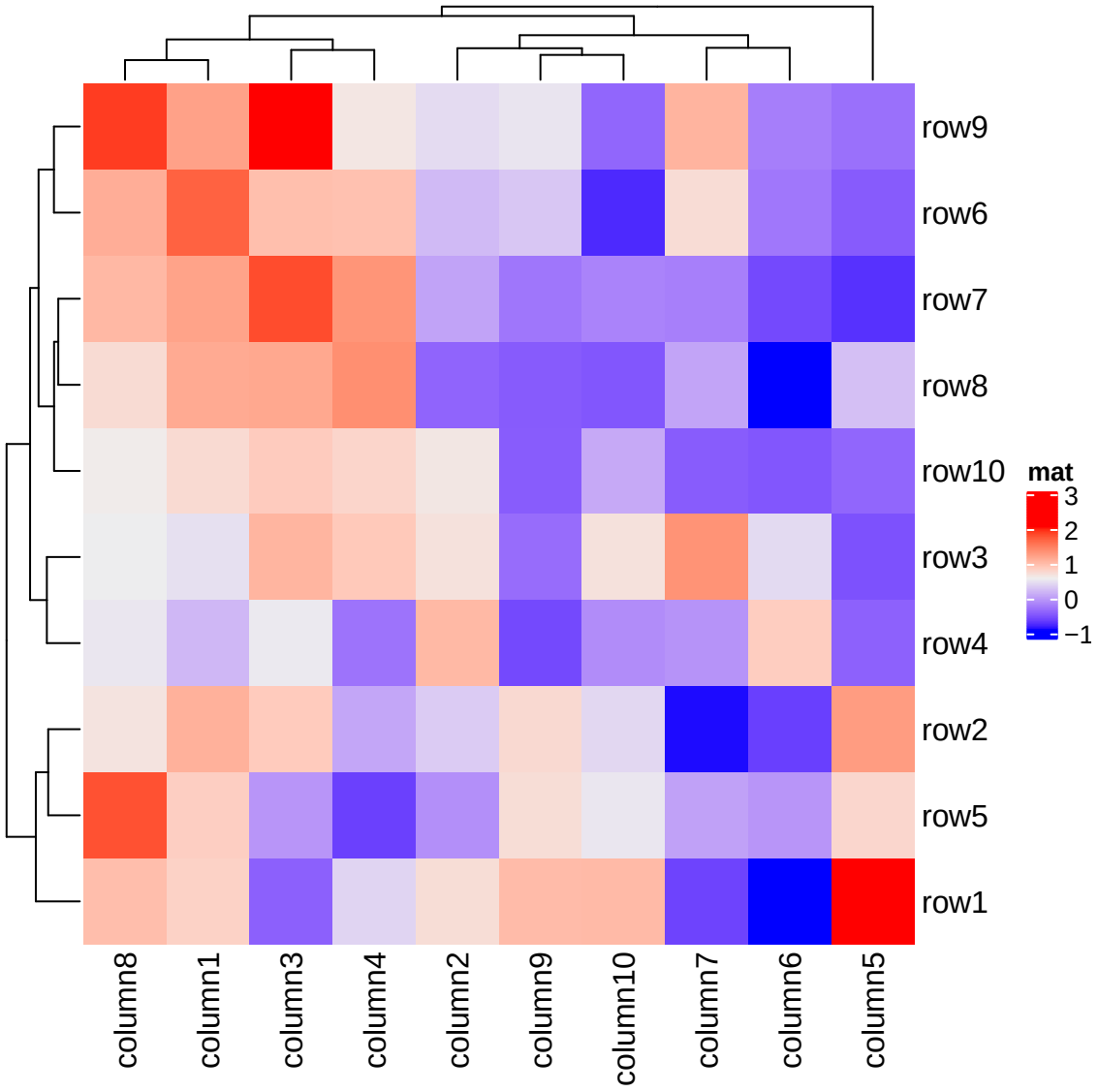
2.13 Subset a heatmap

Since heatmap is a representation of a matrix, there is also subset method for the `Heatmap` class.

```
ht = Heatmap(mat, name = "mat")
dim(ht)
```

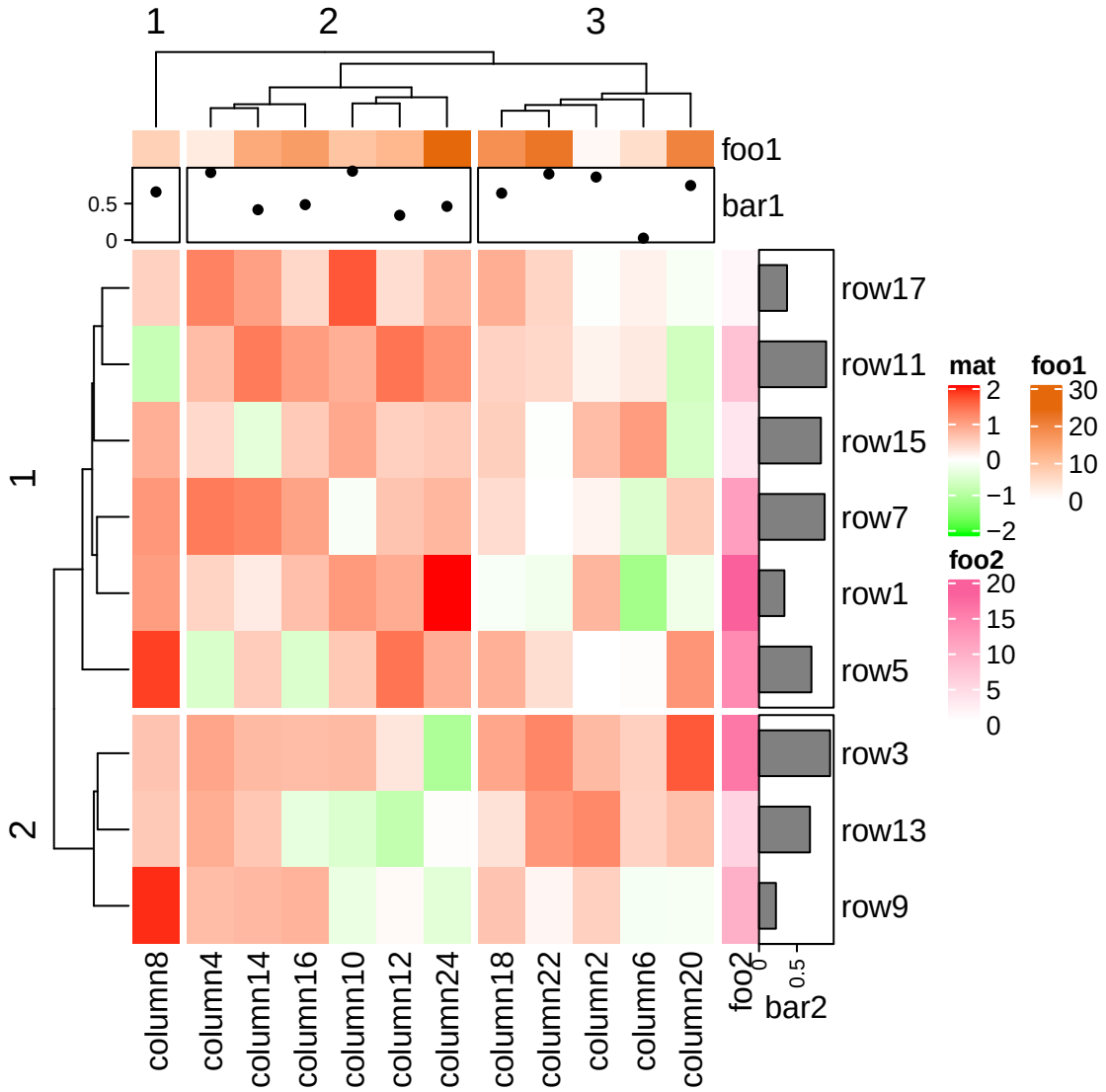
```
## [1] 18 24
```

```
ht[1:10, 1:10]
```



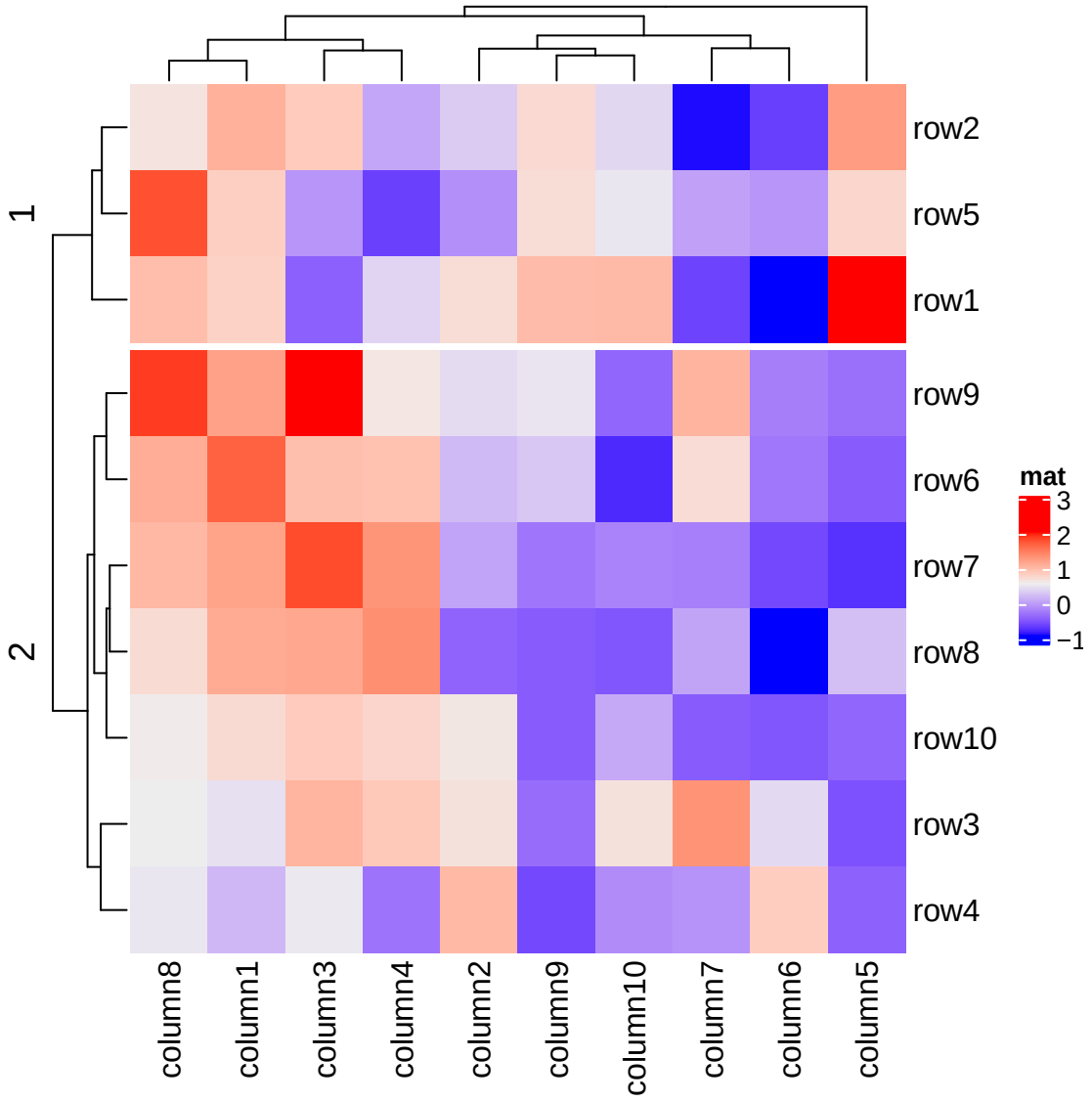
The annotations are subsetted accordingly as well.

```
ht = Heatmap(mat, name = "mat", row_km = 2, column_km = 3,
    col = colorRamp2(c(-2, 0, 2), c("green", "white", "red")),
    top_annotation = HeatmapAnnotation(foo1 = 1:24, bar1 = anno_points(runif(24))),
    right_annotation = rowAnnotation(foo2 = 18:1, bar2 = anno_barplot(runif(18)))
)
ht[1:9*2 - 1, 1:12*2] # odd rows, even columns
```



The heatmap components are subsetted if they present as vector-like. Some configurations in the heatmap keep the same when subsetting, e.g. if `row_km` is set in the original heatmap, the configuration of k-means is kept and it is performed in the sub-heatmap. So in following example, k-means clustering is only performed when making heatmap for `ht2`.

```
ht = Heatmap(mat, name = "mat", row_km = 2)
ht2 = ht[1:10, 1:10]
ht2
```



The implementation of subsetting heatmaps is very experimental. If you have problems or comments, please let me know.

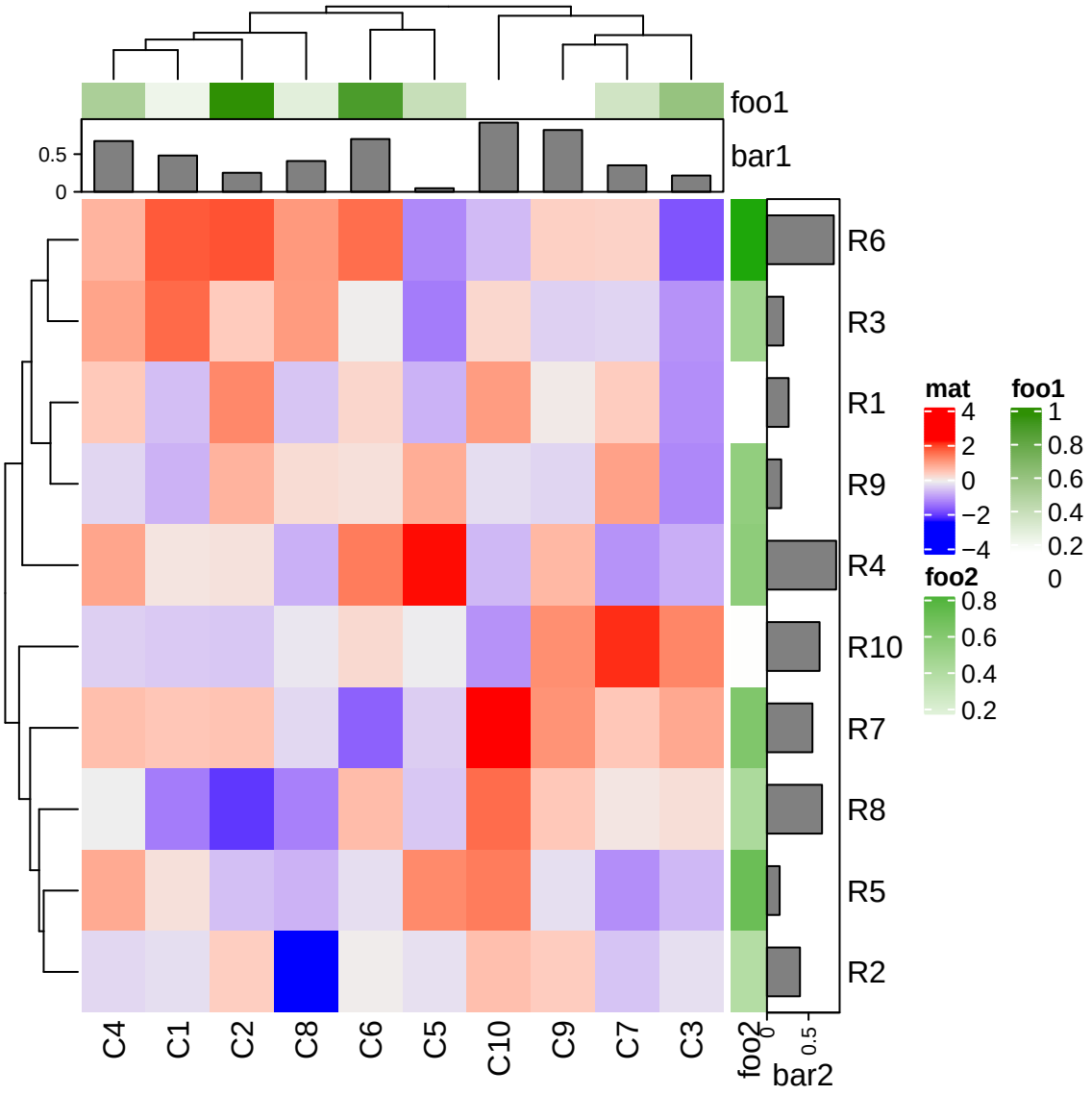
Chapter 3

Heatmap Annotations

Heatmap annotations are important components of a heatmap that it shows additional information that associates with rows or columns in the heatmap. **ComplexHeatmap** package provides very flexible supports for setting annotations or defining new annotation graphics. The annotations can be put on the four sides of the heatmap, by `top_annotation`, `bottom_annotation`, `left_annotation` and `right_annotation` arguments.

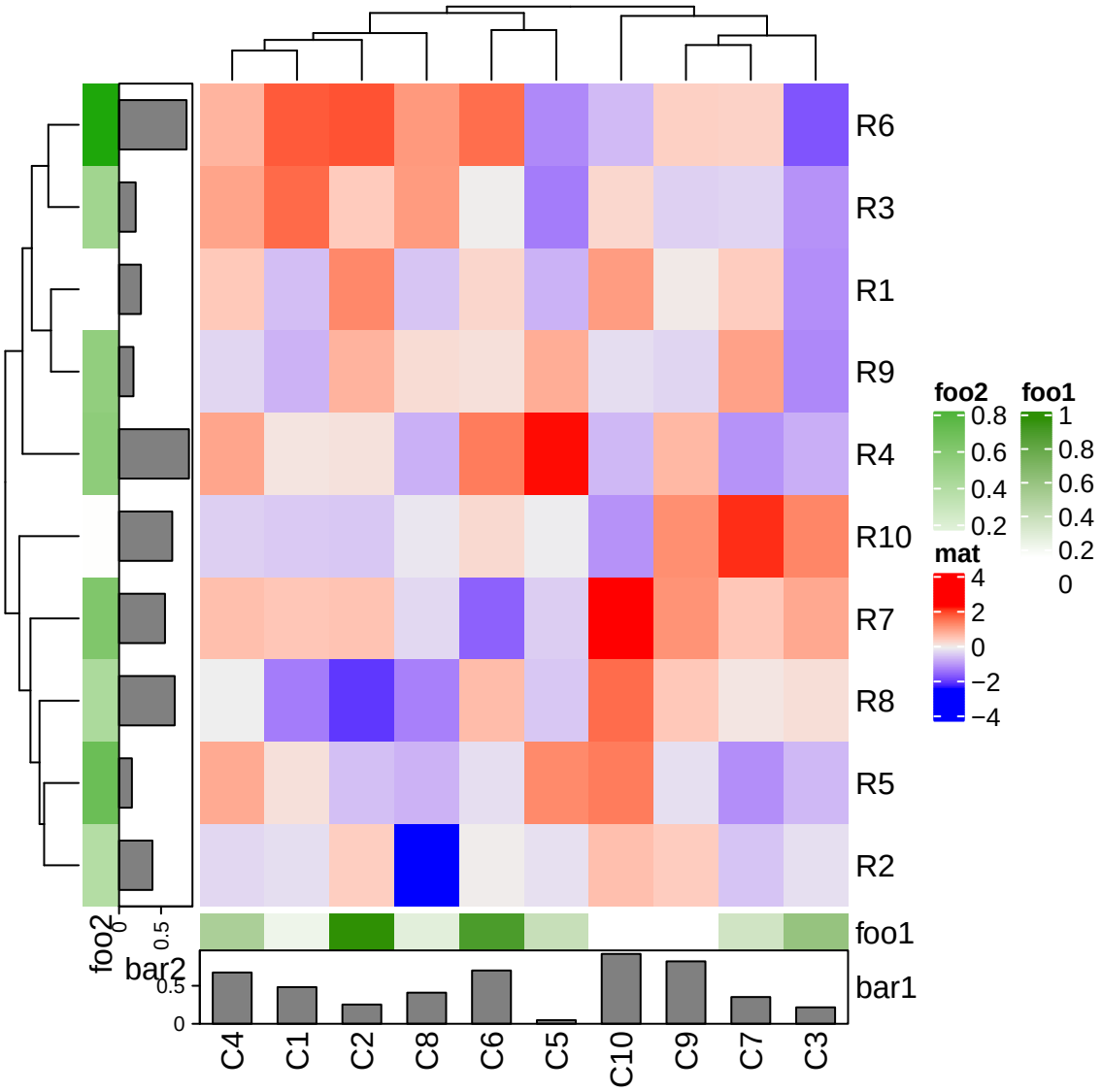
The value for the four arguments should be in the `HeatmapAnnotation` class and should be constructed by `HeatmapAnnotation()`, or by `rowAnnotation()` function if it is a row annotation. (`rowAnnotation()` is just a helper function which is identical to `HeatmapAnnotation(..., which = "row")`) A simple usage of heatmap annotations is as follows.

```
set.seed(123)
mat = matrix(rnorm(100), 10)
rownames(mat) = paste0("R", 1:10)
colnames(mat) = paste0("C", 1:10)
column_ha = HeatmapAnnotation(foo1 = runif(10), bar1 = anno_barplot(runif(10)))
row_ha = rowAnnotation(foo2 = runif(10), bar2 = anno_barplot(runif(10)))
Heatmap(mat, name = "mat", top_annotation = column_ha, right_annotation = row_ha)
```



Or assign as bottom annotation and left annotation.

```
Heatmap(mat, name = "mat", bottom_annotation = column_ha, left_annotation = row_ha)
```



In above examples, `column_ha` and `row_ha` both have two annotations where `foo1` and `foo2` are numeric vectors and `bar1` and `bar2` are barplots. The vector-like annotation is called *"simple annotation"* here and the barplot annotation is called *"complex annotation"*. You can already see the annotations must be defined as name-value pairs (e.g. `foo = ...`).

Heatmap annotations can also be independent of the heatmaps. They can be concatenated to the heatmap list by `+` if it is horizontal or `%v%` if it is vertical. Chapter **??** will discuss how to concatenate heatmaps and annotations.

```
# code only for demonstration
Heatmap(...) + rowAnnotation() + ...
Heatmap(...) %v% HeatmapAnnotation(...) + ...
```

`HeatmapAnnotation()` returns a `HeatmapAnnotation` class object. The object is usually composed of several annotations. If following sections of this chapter, we first introduce settings for individual annotation, and later we show how to put them toghether.

You can see the information of the `column_ha` and `row_ha` objects: