ggalign: Bridging the Grammar of Graphics and Complex layout

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Preface

Welcome to ggalign documents. Examples in the book are generated under version `0.0.5.9000`.

In the world of data visualization, aligning multiple plots in a coherent and organized layout is often a challenging task, especially when dealing with complex datasets that require precise alignment across rows, columns, and even within plot elements. While existing tools provide some solutions, they often fall short in offering the flexibility, control, and simplicity that users need to create intricate and beautiful plots. This is where `ggalign` comes in.

The `ggalign` package, built on top of the powerful ggplot2 framework, is designed to solve this very problem. It offers a suite of functions specifically crafted for aligning and organizing plots with minimal effort. Whether you need to align observations based on statistical measures, group plots by categorical factors, or fine-tune the layout to match the precise needs of your data, `ggalign` gives you the tools you need to create polished, publication-ready visualizations.

This book serves as both an introduction to the `ggalign` package and a comprehensive guide to mastering its features. Whether you're a beginner or an experienced user of ggplot2, you'll find detailed explanations, step-by-step tutorials, and real-world examples to help you leverage the full potential of `ggalign` in your work.

Throughout this book, we will cover everything from basic concepts to advanced layout customizations, focusing on key functions like `stack_layout()`, `align_*` series (including `align_group()`, `align_order()`, and `align_hclust()`), and how to combine them with other ggplot2 layers to create aligned plots. Additionally, you'll learn how to adapt `ggalign` for different data types and scenarios, allowing you to develop flexible, dynamic visualizations tailored to your specific needs.

By the end of this book, you will be equipped to use `ggalign` effectively in your own projects, whether for scientific research, data analysis, or any other field where data visualization is key. Our goal is to provide you with the knowledge and confidence to tackle complex visualization challenges and transform your datasets into clear, impactful, and visually appealing plots.

Thank you for choosing `ggalign`. We hope this book will inspire you to explore the endless possibilities that come with aligned data visualization.

Part I

Basics

1 Introduction

`ggalign` extends `ggplot2` by providing advanced tools for aligning and organizing multiple plots, particularly those that automatically reorder observations, such as dendrogram. It offers fine control over layout adjustment and plot annotations, enabling you to create complex visualizations while leveraging the familiar grammar of `ggplot2`.

1.1 Installation

You can install `ggalign` from `CRAN` using:

```
install.packages("ggalign")
```

Alternatively, install the development version from r-universe with:

```
install.packages("ggalign",
    repos = c("https://yunuuuu.r-universe.dev", "https://cloud.r-project.org")
)
```

or from GitHub with:

```
# install.packages("remotes")
remotes::install_github("Yunuuuu/ggalign")
```

1.2 General design

The core feature of `ggalign` lies in its integration of the `grammar of graphics` into advanced visualization through its object-oriented `Layout` system. The package provides three main `Layout` classes:

- the `StackLayout` class: Put plots horizontally or vertically.
- the `QuadLayout` class: Arranges plots in the four quadrants (top, left, bottom, right) around a main plot. This layout is ideal for designs that require supplementary plots or annotations surrounding a central figure.

- the `CircleLayout` class: Positions plots in a circular arrangement.

Each `Layout` class supports the alignment of both discrete (ordinal) and continuous variables. Depending on the desired alignment across multiple plots within a layout, the following variants are available:

For `StackLayout`:

- `stack_discrete()`: Align discrete variable along the stack.
- `stack_continuous()`: Align continuous variable along the stack.

`stack_layout()` integrates the functionalities of `stack_discrete()` and `stack_continuous()` into a single interface. For simplicity, throughout this book, I will refer to both variants as `stack_layout()`.

For `QuadLayout`:

- `quad_continuous/ggside`: Align continuous variables in both horizontal and vertical directions.
- `quad_discrete`: Align discrete variables in both horizontal and vertical directions.
- `quad_layout`: Aligns discrete or continuous variables either horizontally or vertically.

The functions `quad_continuous()` and `quad_discrete()` are specialized versions of `quad_layout()` (Section 7.5): `quad_continuous()` sets both `xlim` and `ylim` arguments, while `quad_discrete()` does not set `xlim` or `ylim`. For simplicity, throughout this book, I will refer to all of the variants as `quad_layout()`.

For `CircleLayout`:

- `circle_discrete()`: Align discrete variable in the circle.
- `circle_continuous()`: Align continuous variable in the circle.

`circle_layout()` integrates the functionalities of `circle_discrete()` and `circle_continuous()` into a single interface. For simplicity, throughout this book, I will refer to both variants as `circle_layout()`.

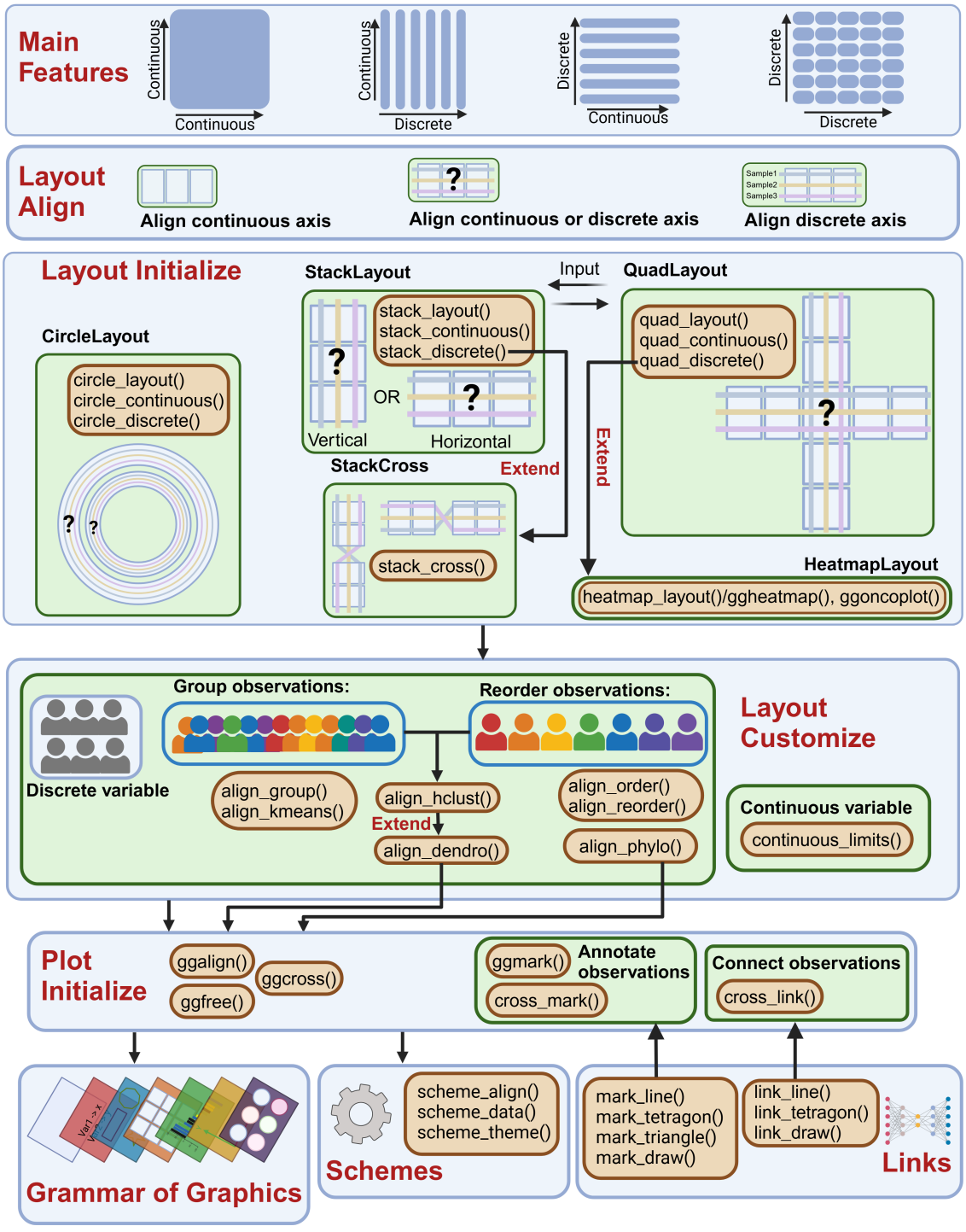


Figure 1.1: General design of ggalign

1.3 Align axes in ggplot

Before introducing the package, let's first discuss how to align axes in ggplot2. For continuous axes, alignment is straightforward because we just need to ensure that all plots have the same `limits`. This can be achieved in the `*_continuous()` function by setting the `limits` (or `xlim`/`ylim`) argument.

Aligning discrete axes is more challenging because we must first ensure that the number of unique discrete values is the same across all plots, and that the ordering is consistent. In ggplot2, it's difficult to align discrete axes, since some plots may self-ordered. This issue is compounded when working with long-formatted data frames, which is required by ggplot2.

To address this, the `ggalign` package typically uses matrix input for layouts that require aligning discrete axes (`*_discrete()` functions). Each row of the matrix represents a unique discrete value (observation), and the number of rows corresponds to the total number of unique values (number of observations). To ensure consistent ordering across plots, the internal just need to reorder the rows. This approach is also well-suited for functions like `quad_layout()`/`ggheatmap()`, where axes need to be aligned in both directions simultaneously, as matrices can be transposed (i.e., switching rows to columns and columns to rows). When drawing the plot, the `ggalign` package will melt the `matrix` into a long-formatted data frame. You may worry about that the matrix format may not fully support all input requirements for plots, the `ggalign` package provides a function (`scheme_data()`) to transform the plot data as needed to fit your specific use case.

We often refer to "observations" when discussing discrete axes. Observations typically correspond to discrete variables, such as data points or samples. In the rest of the book, I will use "observations" and "discrete variables" interchangeably. You can assume that any reference to "observations" also applies to discrete variables.

1.4 Getting Started

```
library(ggalign)
#> Loading required package: ggplot2
```

The usage of `ggalign` is simple if you're familiar with `ggplot2` syntax, the typical workflow includes:

1. Initialize the layout.
2. Customize the layout with:

    - `align_group()`: Group observations into panel with a group variable.
    - `align_kmeans()`: Group observations into panel by kmeans.

- `align_order()`: Reorder layout observations based on statistical weights or by manually specifying the observation index.
- `align_reorder`: Reorder observations using an arbitrary statistical function
- `align_hclust()`: Reorder or group observations based on hierarchical clustering.

3. Adding plots with:

    - `align_dendro()`: Add a dendrogram to the plot, and reorder or group observations based on hierarchical clustering.
    - `ggalign()`: Initialize a ggplot object and align the axes.
    - `ggmark()`: Add a plot to annotate selected observations.
    - `ggcross()`: Initialize a ggplot object to connect two different layout crosswise
    - `ggfree()`: Initialize a ggplot object without aligning the axes.

4. Layer additional `ggplot2` elements such as geoms, stats, or scales.

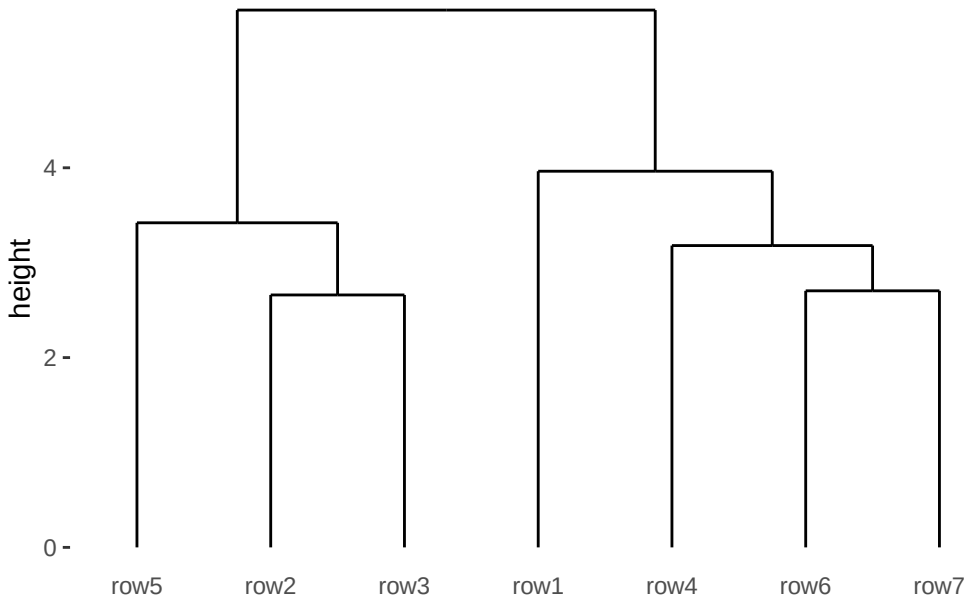
```
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

Every `*_layout()` function accepts default data, which will be inherited by all plots within the layout.

Here's a simple example:

```
stack_discretev(small_mat) +                                    ①
    align_dendro() +                                            ②
    theme(axis.text.x = element_text())                         ③
```

① We initialize a vertical stack.
② Reorder the observations based on hierarchical clustering and add a dendrogram tree.
③ Add x-axis text.

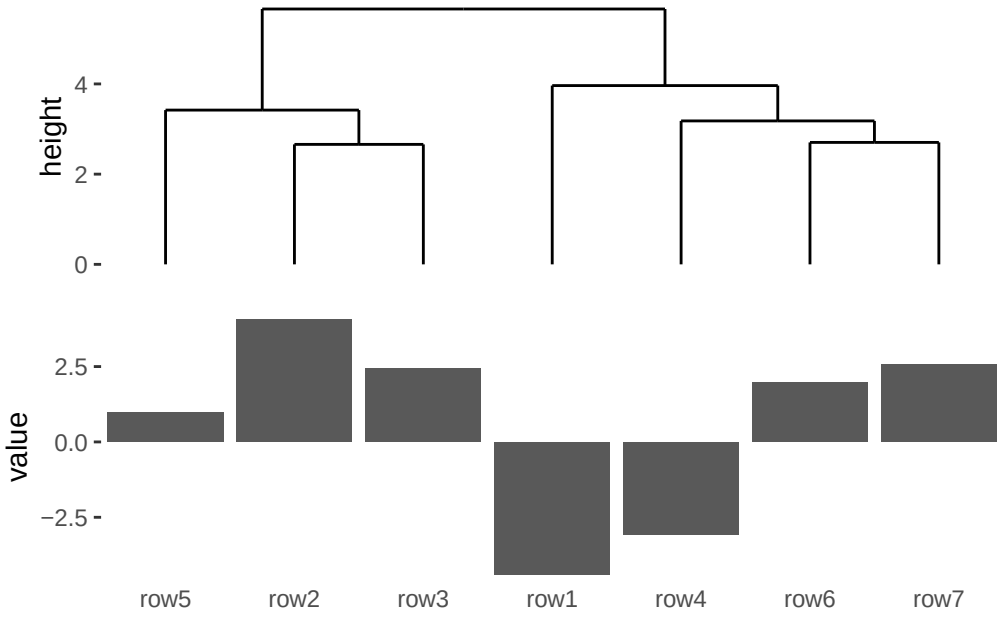


This function produces a simple dendrogram. The `stack_discretev()` function initializes a vertical stack and aligns discrete variables. It is simply an alias for `stack_discrete("v")`. By default, the axis text on the axis used for alignment is removed. This is because it's often unclear which plot should display the axis text, as typically, we want it to appear in only one plot. However, you can easily use the `theme()` function to control where the axis text appears.

Internally, `align_dendro()` will reorder the observations based on the dendrogram, and other plots in the layout will follow this ordering.

```
stack_discretev(small_mat) +                                          ①
    align_dendro() +                                                  ②
    ggalign(data = rowSums) +                                         ③
    geom_bar(aes(.discrete_x, value), stat = "identity") +            ④
    theme(axis.text.x = element_text())                               ⑤
```

① We initialize a vertical stack.
② Reorder the observations based on hierarchical clustering and add a dendrogram tree.
③ Create a new ggplot in the layout, and use data based on the sum of the layout data.
④ Add a bar layer.
⑤ Add x-axis text.



The data in the underlying `ggplot` object of `ggalign()` function contains following columns (more details will be introduced in the Section 5.1):

- `.panel`: the group panel for the aligned axis. It means `x-axis` for vertical stack layout, `y-axis` for horizontal stack layout.
- `.x`/`.y` and `.discrete_x`/`.discrete_y`: an integer index of `x`/`y` coordinates and a factor of the data labels (only applicable when names exists).
- `.names` and `.index`: A character names (only applicable when names exists) and an integer of index of the original data.
- `value`: the actual value (only applicable if `data` is a `matrix` or atomic vector).

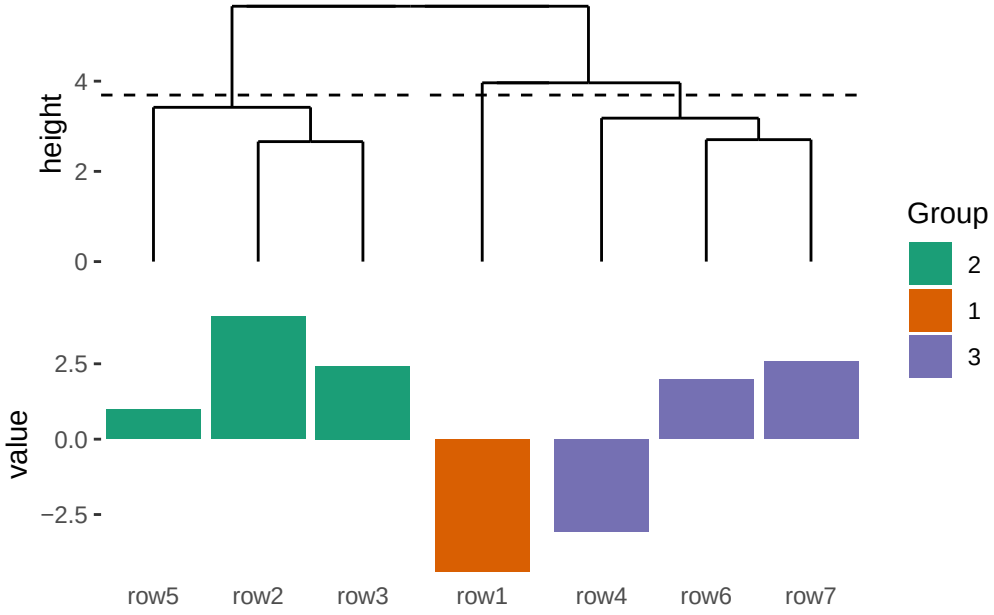
  It is recommended to use `.x`/`.y`, or `.discrete_x`/`.discrete_y` as the `x`/`y` mapping.

`align_dendro()` can also split the observations into groups.

```
stack_alignv(small_mat) +                                                    ①
    align_dendro(k = 3) +                                                    ②
    ggalign(data = rowSums) +                                                ③
    geom_bar(aes(.discrete_x, value, fill = .panel), stat = "identity") +    ④
    scale_fill_brewer(palette = "Dark2", name = "Group") +                   ⑤
    theme(axis.text.x = element_text())                                      ⑥
```

① We initialize a vertical stack.

② Reorder and group the observations based on hierarchical clustering, and add a dendrogram tree.
③ Create a new ggplot in the layout, and use data based on the sum of the layout data.
④ Add a bar layer.
⑤ Set fill scale palette.
⑥ Add x-axis text.

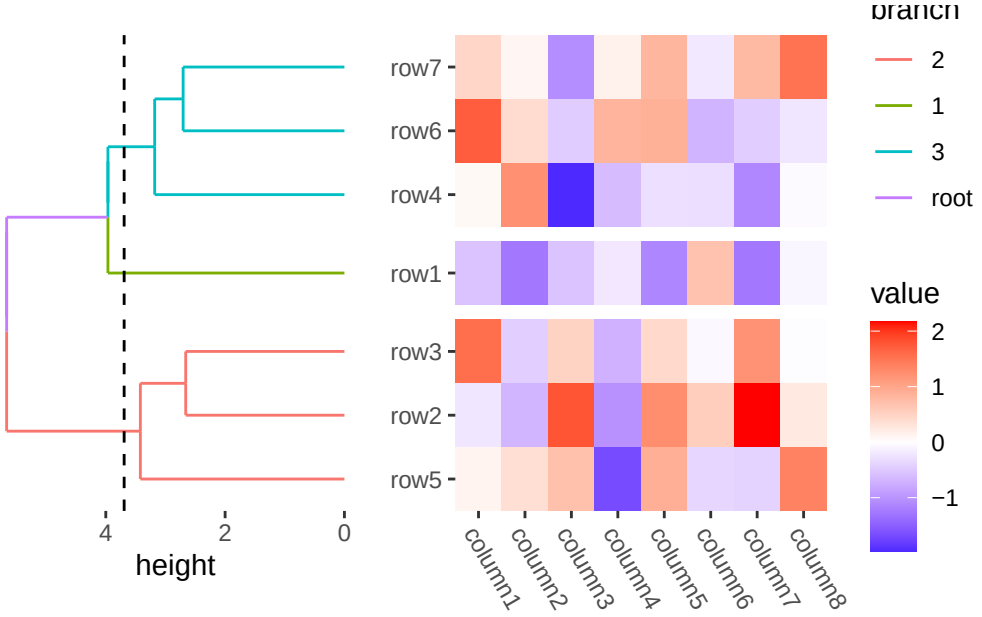


One common visualization associated with the dendrogram is the heatmap. You can use `ggheatmap()` to initialize a heatmap layout. When grouping the observations using `align_dendro(k = 3)`, a special column named `branch` is added, which you can use to color the dendrogram tree.

```
ggheatmap(small_mat) +                                                    ①
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +           ②
    anno_left() +                                                         ③
    align_dendro(aes(color = branch), k = 3) +                            ④
    scale_fill_brewer(palette = "Dark2")                                  ⑤
#> > heatmap built with `geom_tile()`
```

① We initialize a heatmap layout.
② adjust the x-axis label theme element.
③ we initialize an annotation in the left side of the heatmap body, and set it as the active context, in this way, all following addition will be directed to the left annotation.

④ Reorder and group the observations based on hierarchical clustering, and add a dendrogram tree, coloring the tree by `branch`.
⑤ Set fill scale palette.



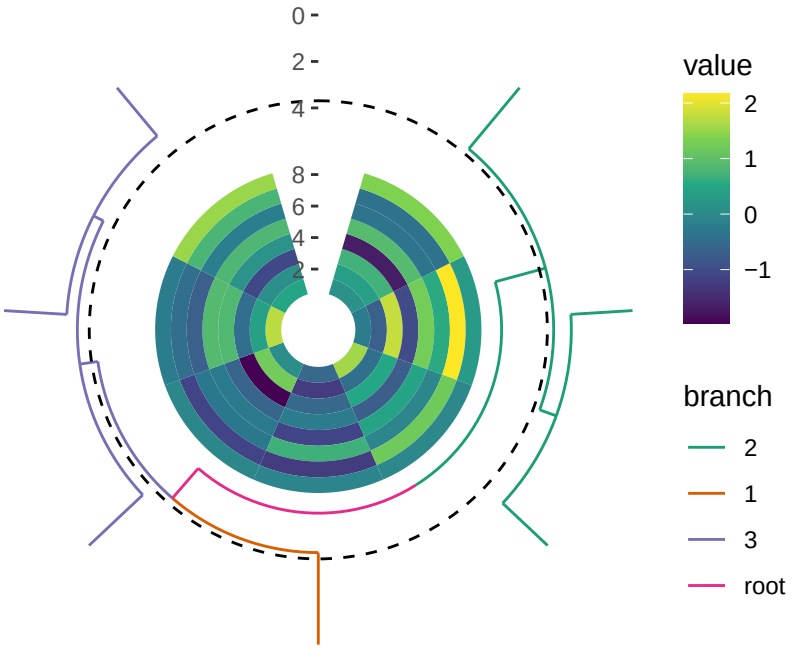
`ggheatmap()` will automatically add axis text in the heatmap body, so you don't need to manually adjust axis text visibility using `theme(axis.text.x = element_text())`/`theme(axis.text.y = element_text())`.

We can also arrange the dendrogram in a circular layout to visualize hierarchical relationships in a more compact and aesthetically pleasing way.

```
circle_discrete(small_mat, radial = coord_radial(inner.radius = 0.1)) +      ①
    ggalign() +                                                               ②
    geom_tile(aes(y = .column_index, fill = value)) +                         ③
    scale_fill_viridis_c() +                                                  ④
    align_dendro(aes(color = branch), k = 3L) +                               ⑤
    scale_color_brewer(palette = "Dark2")                                     ⑥
```

① We initialize a circle layout and set the inner radius.
② Create a new ggplot in the layout, and use data the same with the layout data.
③ Add a tile layer, the matrix input will be converted into a long formated data frame with column `.column_index` indicates the column index of the original matrix.
④ Set fill scale palette.

⑤ Reorder and group the observations based on hierarchical clustering, and add a dendrogram tree, coloring the tree by `branch`.
⑥ Set color scale palette.



Having explored the core principles of `ggalign`, you should now be familiar with its basic workflow. In the next chapter, we'll introduce the `StackLayout`, a powerful tool for arranging multiple plots in a stacked fashion—either horizontally or vertically—while maintaining full control over their alignment. We'll explore how `StackLayout` and its various functions can give you even greater flexibility in creating sophisticated layouts.

2 stack layout

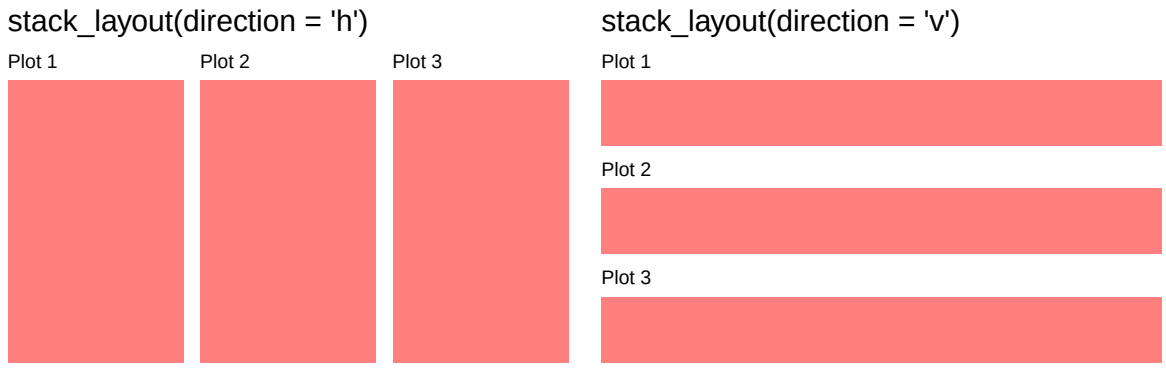
`stack_layout()` arranges plots either horizontally or vertically. Based on whether we want to align the discrete or continuous variables, there are two types of stack layouts:

- `stack_discrete()`: Align discrete variable along the stack.
- `stack_continuous()`: Align continuous variable along the stack.

`stack_layout()` integrates the functionalities of `stack_discrete()` and `stack_continuous()` into a single interface. The first argument for these three functions is `direction` which should be a single string indicating the direction of the stack layout, either `"h"`(`horizontal`) or `"v"`(`vertical`).

Several aliases are available for convenience:

- `stack_discretev`: A special case of `stack_discrete` that sets `direction = "v"`.
- `stack_discreteh`: A special case of `stack_discrete` that sets `direction = "h"`.
- `stack_continuousv()`: A special case of `stack_continuous` that sets `direction = "v"`.
- `stack_continuoush()`: A special case of `stack_continuous` that sets `direction = "h"`.




```
library(ggalign)
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

2.1 Input data

As discussed in Section 1.3, when aligning discrete variables, we typically use a matrix. For continuous axes, we can still use the long-formatted data frame, which is the same as in ggplot2.

- For `stack_continuous()`, a data frame is required, and the input will be automatically converted using `fortify_data_frame()` if needed.
- For `stack_discrete()`, a matrix is required, and the input will be automatically converted using `fortify_matrix()` if needed.

By default, `fortify_data_frame()` will invoke the `ggplot2::fortify()` function for conversion. Note, for matrix, it will be converted to a long-formatted data frame which is different from the `ggplot2::fortify()`.

`stack_discrete()`/`stack_continuous()` will set up the layout, but no plot will be drawn until you add a plot element:

```
stack_discretev(small_mat) +                                                    ①
    layout_annotation(                                                          ②
        theme = theme(plot.background = element_rect(color = "red"))
    )
# the same for `stack_continuous()`
```

① initialize a vertical stack layout.
② Add a plot background in for the entire layout.

In this example, we use `layout_annotation()` to insert a plot background in the entire layout, it can also be used to control the theme of title, subtitle, caption (`layout_title()`), guides, margins, panel.border, panel.spacing.

2.2 Layout Customize

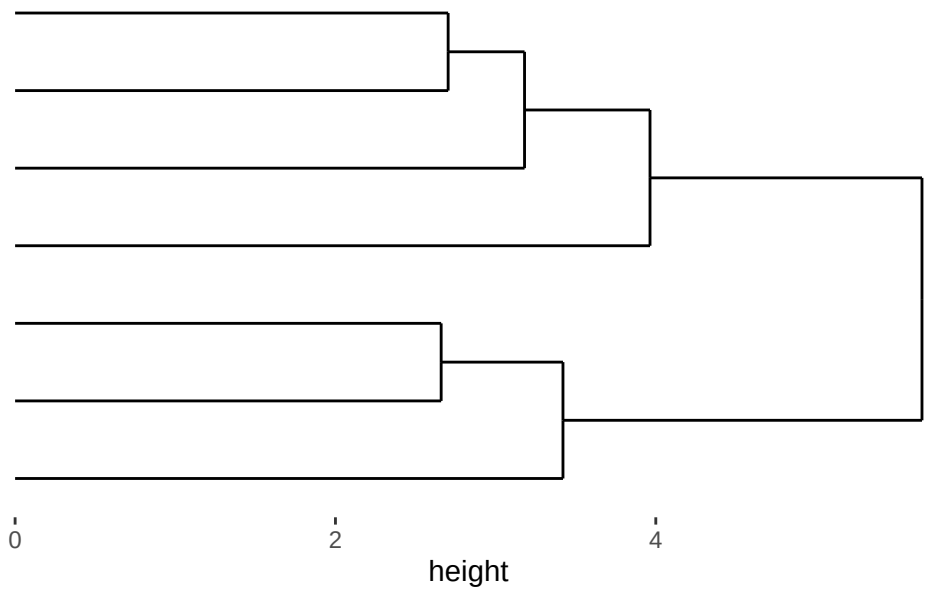
When aligning discrete variables, the package offers a suite of `align_*` functions designed to give you precise control over the ordering and groups. Instead of detailing each `align_*` function individually, we will focus on the general usage and how to combine them with `stack_discrete()`.

Here, we remain take `align_dendro()` as an example, it can reorder the observations, split them into groups, and can add a plot for visualization.

When used for `stack_discreteh()`, the observations are aligned along the `y-axis`:

```
stack_discreteh(small_mat) +                                    ①
    align_dendro()                                              ②
```

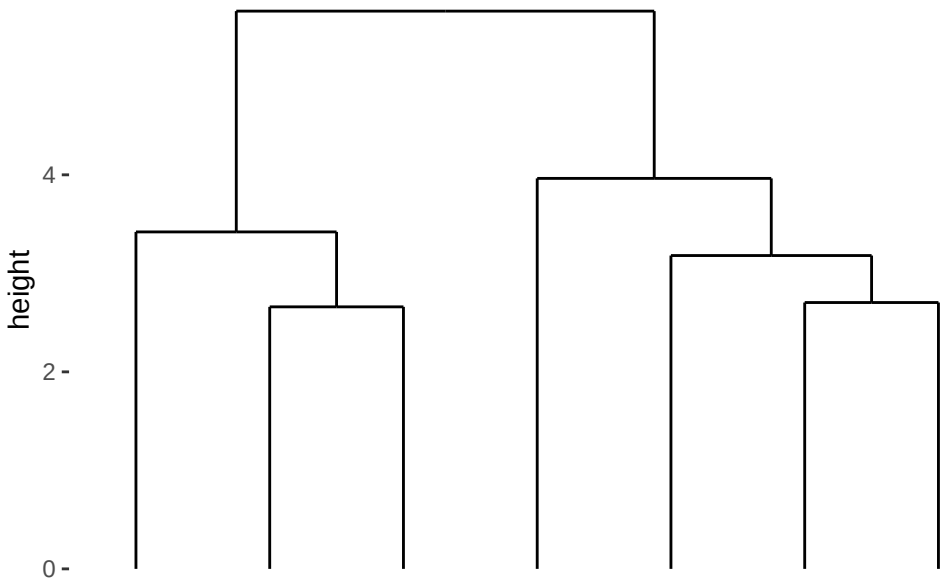
① initialize a horizontal stack layout.
② reorder the observations based on the hierarchical clustering, add a dendrogram tree, and set the active plot to this plot.



When used for `stack_discretev()`, the observations are aligned along the `x-axis`:

```
stack_discretev(small_mat) +                                    ①
    align_dendro()                                              ②
```

① initialize a vertical stack layout.
② reorder the observations based on the hierarchical clustering, add a dendrogram tree, and set the active plot to this plot.



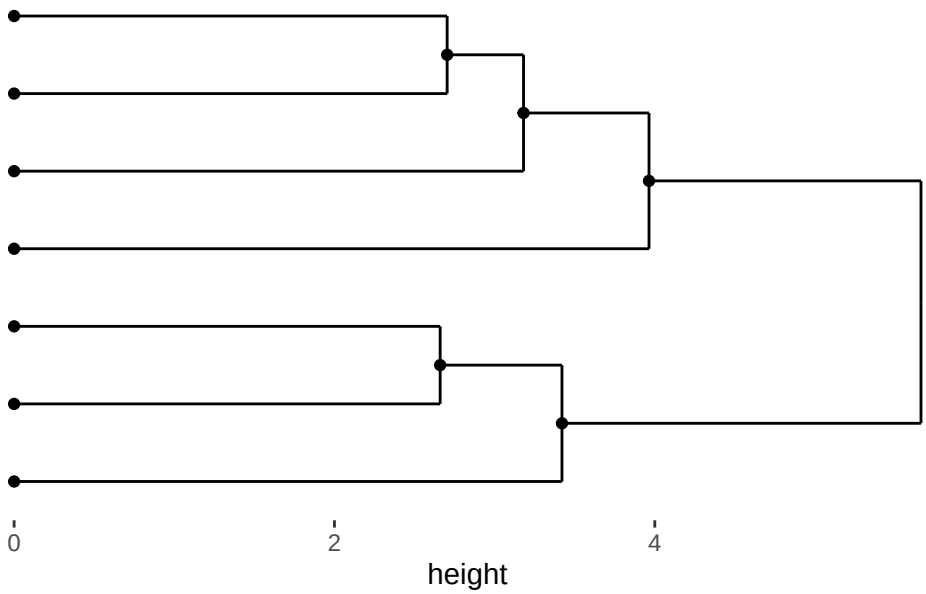
When `align_dendro()` is added to the layout, it performs following actions:

1. reorder the observations.
2. set the active plot to the dendrogram.

The active plot refers to the plot that subsequent ggplot2 components will target. In this case, the active plot is the dendrogram, and any new layers added will be applied to it. For instance, we can add additional layers to visualize the dendrogram's structure or data. The default data underlying the `ggplot` object of `align_dendro()` consists of the dendrogram node data. It is also possible to use the dendrogram's edge data for customization, which I will introduce in Section 5.4.

```
stack_discreteh(small_mat) +                                    ①
    align_dendro() +                                            ②
    geom_point()                                                ③
```

① initialize a horizontal stack layout.
② reorder the observations based on the hierarchical clustering, add a dendrogram tree, and set the active plot to this plot.
③ add a point layer to the dendrogram



The `active` argument controls whether a plot should be set as the active plot. It accepts an `active()` object with the `use` argument to specify if the plot should be active when added.

```
stack_discreteh(small_mat) +                                    ①
    align_dendro(active = active(use = FALSE)) +                ②
    geom_point()                                                ③
#> Error in `chain_layout_add()`:
#> ! Cannot add `geom_point()` to the horizontal `stack_discrete()`
#> i No active plot component
#> i Did you forget to initialize a <ggplot> object with `ggalign()` or
#>   `ggfree()`?
```

① initialize a horizontal stack layout.
② reorder the observations based on the hierarchical clustering, add a dendrogram tree, but don't set the active plot to this plot.
③ try to add a point layer to the dendrogram, should fail due to no active plot

Usually, you don't need to set this manually, as the active context is automatically applied only for functions that add plot areas. You can inspect whether a `align_*` function will add a plot by print it:

```
align_dendro()
#> <Class: AlignDendro AlignHclust Align AlignProto>
```

```
#>      plot: yes
#>   reorder: yes
#>     split: no
```

You might find it confusing that we mentioned `align_dendro()` will split observations into groups, while the print output shows `split = "no"`. This happens because we haven't specified the `k`/`h` argument in `align_dendro()`.

```
align_dendro(k = 3L)
#> <Class: AlignDendro AlignHclust Align AlignProto>
#>      plot: yes
#>   reorder: yes
#>     split: yes
```

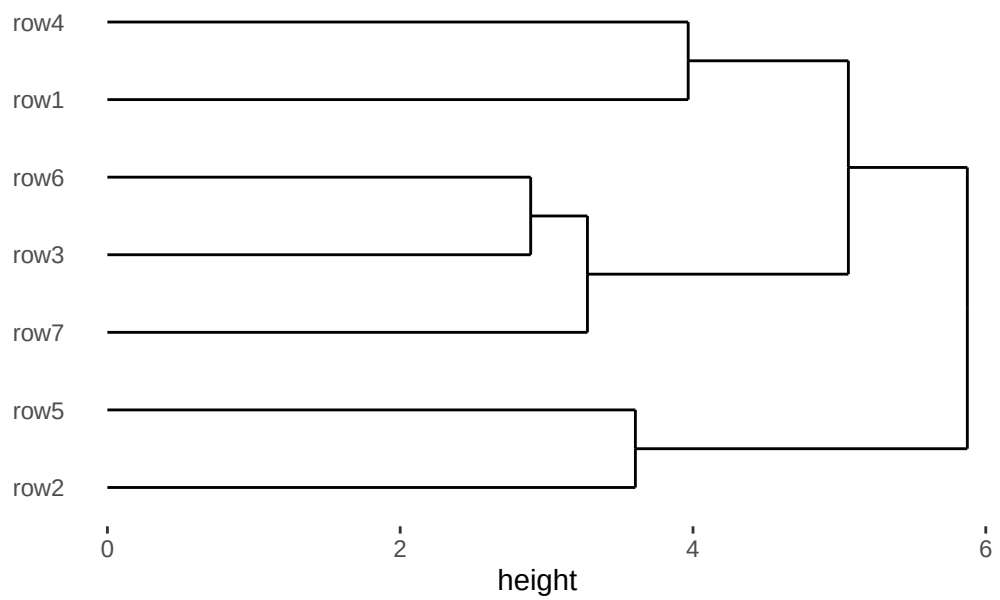
You don't need to explicitly provide `data` to `align_dendro()`. By default, it inherits data from the layout. However, you can always provide another data source, but note that this package uses the concept of `number of observations` (`NROW()`). When aligning the observations, you must ensure the number of observations is consistent across all plots.

```
set.seed(123)
stack_discreteh(small_mat) +                                          ①
    align_dendro(data = matrix(rnorm(56), nrow = 8)) +                ②
    theme(axis.text.y = element_text())                               ③
#> Error in interact_layout(..., self = self): object 'layout_name' not found
```

① initialize a horizontal stack layout.
② reorder the observations based on hierarchical clustering, add a dendrogram tree, and set the active plot to this one, using self-provided data. This should fail because the number of observations is inconsistent.
③ try to add y-axis text to the dendrogram.

```
set.seed(123)
stack_discreteh(small_mat) +                                          ①
    align_dendro(data = matrix(rnorm(70), nrow = 7)) +                ②
    theme(axis.text.y = element_text())                               ③
```

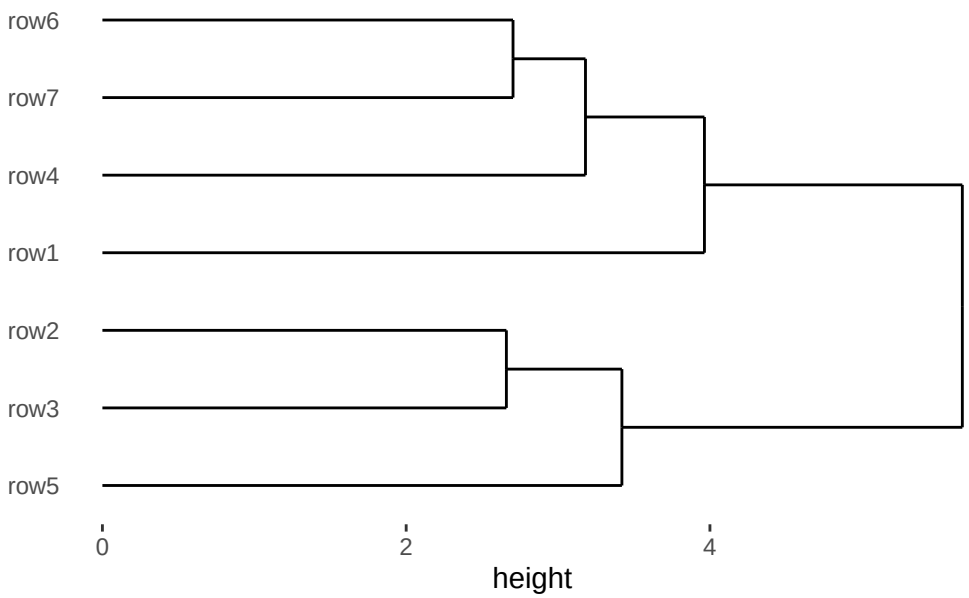
① initialize a horizontal stack layout.
② reorder the observations based on the hierarchical clustering, add a dendrogram tree, and set the active plot to this plot, using self-provided data
③ add y-axis text to the dendrogram.



Alternatively, you can provide a function (or purrr-lambda) that will be applied to the layout's matrix. For layouts that align observations, a matrix is always required, so the data input must be in matrix form.

```
set.seed(123)
stack_discreteh(small_mat) +                                          ①
    align_dendro(data = ~ .x[sample(nrow(.x)), ]) +                   ②
    theme(axis.text.y = element_text())                               ③
```

① initialize a horizontal stack layout.
② reorder the observations based on the hierarchical clustering, add a dendrogram tree, and set the active plot to this plot, using self-provided data function
③ add y-axis text to the dendrogram.



Without adding another plot, it's difficult to appreciate the benefits. Let's now explore how to incorporate a plot.

2.3 Plot initialize

There are two primary functions for adding plots:

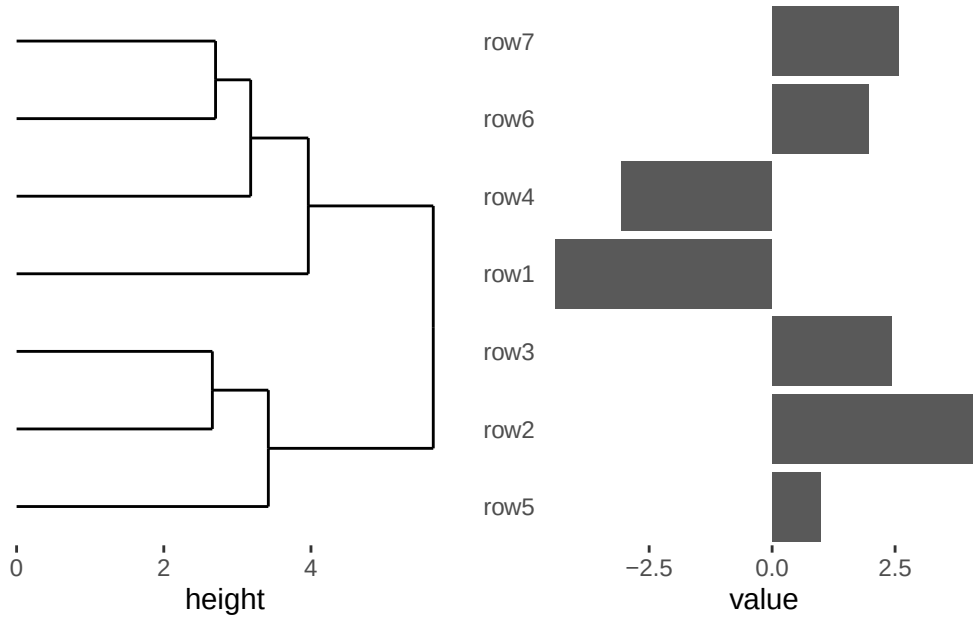
- `ggalign()`: Initialize a ggplot object and align the axes.
- `ggfree()`: Initialize a ggplot object without aligning the axes.

Both functions initialize a `ggplot` object and, by default, set the `active` plot when added to the layout.

```
stack_discreteh(small_mat) +                                              ①
    align_dendro() +                                                      ②
    ggalign(data = rowSums) +                                             ③
    geom_bar(aes(value, .discrete_y), stat = "identity") +                ④
    theme(axis.text.y = element_text())                                   ⑤
```

① initialize a horizontal stack layout.
② reorder the observations based on the hierarchical clustering, add a dendrogram tree, and set the active plot to this plot.

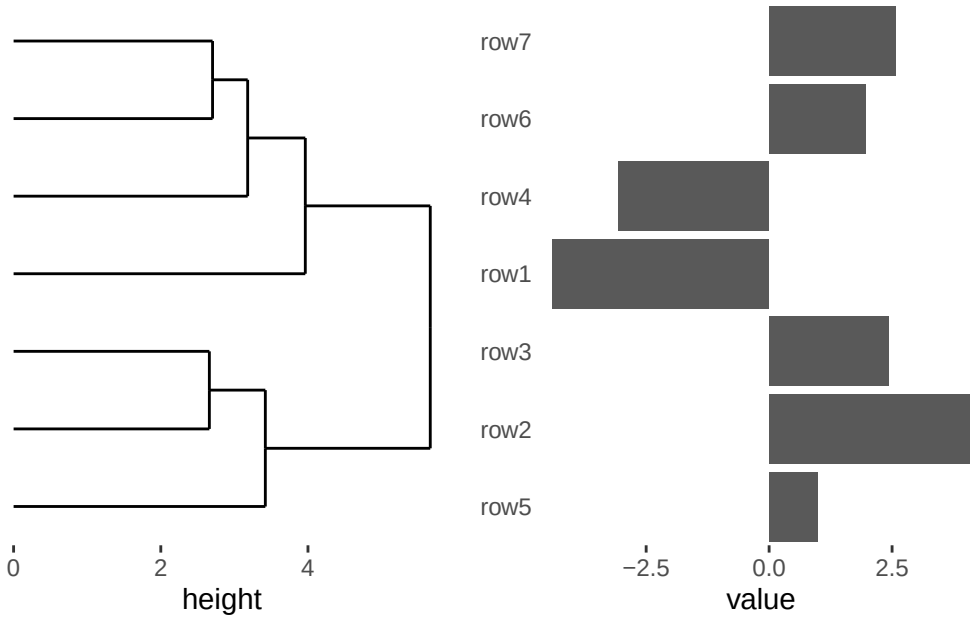
③ initialize a ggplot object, and set the active plot to this plot, using self-provided data function
④ add a bar to the plot
⑤ add y-axis text



You can build the plot separately and then add it to the layout:

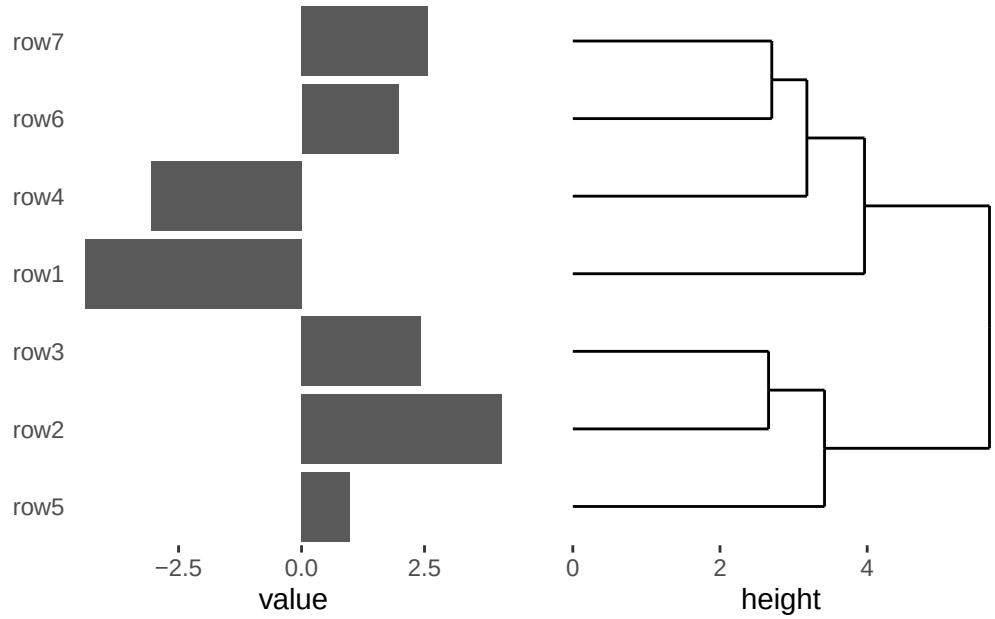
```
my_bar <- ggalign(data = rowSums) +                                    ①
    geom_bar(aes(value, .discrete_y), stat = "identity") +
    theme(axis.text.y = element_text())
stack_discreteh(small_mat) +                                           ②
    align_dendro() +                                                   ③
    my_bar                                                             ④
```

① Create the bar plot.
② initialize a horizontal stack layout.
③ reorder the observations based on the hierarchical clustering, add a dendrogram tree, and set the active plot to this plot.
④ Add another bar plot to the layout.



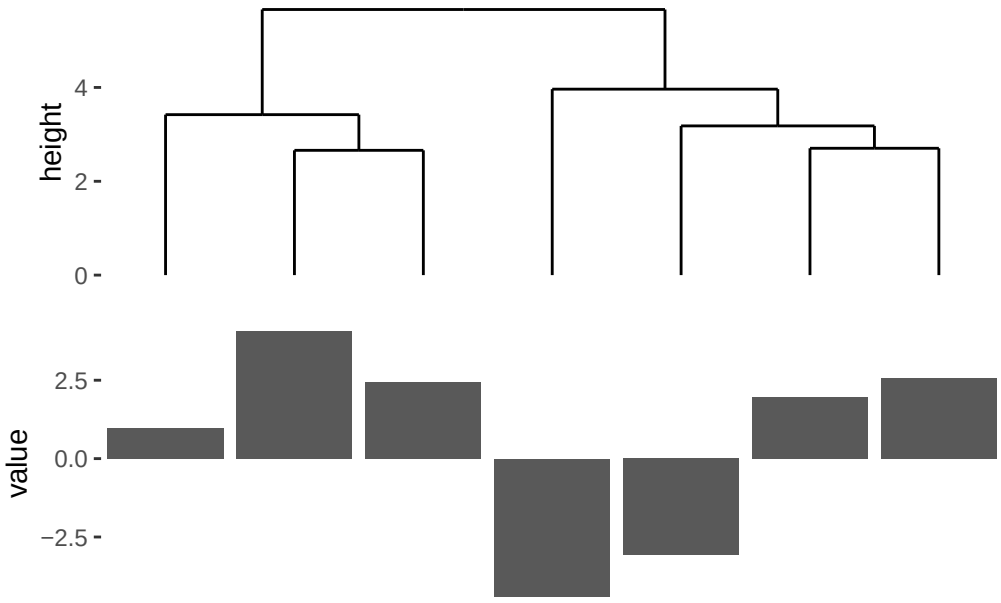
The `active` argument can also control the place of the plot area to be added. It accepts an `active()` object with the `order` argument to specify the order of the plot area.

```
stack_discreteh(small_mat) +
    align_dendro() +
    ggalign(data = rowSums, active = active(order = 1)) +
    geom_bar(aes(value, .discrete_y), stat = "identity") +
    theme(axis.text.y = element_text())
```



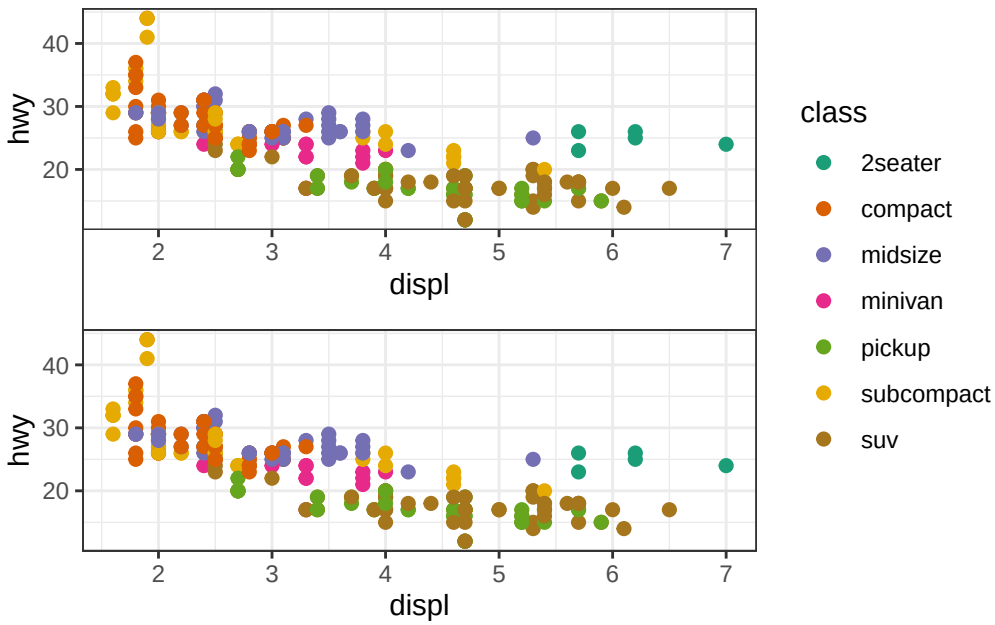
You can also stack plots vertically using `stack_discretev()`:

```
stack_discretev(small_mat) +
    align_dendro() +
    ggalign(data = rowSums) +
    geom_bar(aes(.discrete_x, value), stat = "identity") +
    theme(axis.text.y = element_text())
```



`ggfree()` focuses on layout integration without enforcing strict axis alignment.

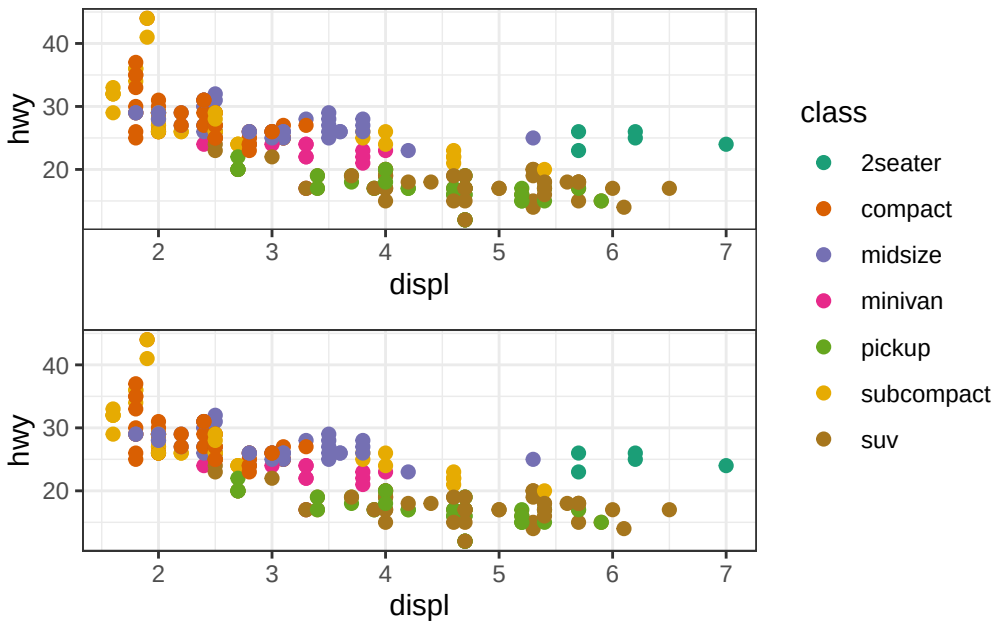
```
stack_discretev() +
    ggfree(mpg, aes(displ, hwy, colour = class)) +
    geom_point(size = 2) +
    ggfree(mpg, aes(displ, hwy, colour = class)) +
    geom_point(size = 2) &
    scale_color_brewer(palette = "Dark2") &
    theme_bw()
```



The `&` operator applies the added element to all plots in the layout, similar to its functionality in the `patchwork` package.

For `stack_continuous()`, only free plots (`ggfree()`) can be added. This layout arranges plots in one row or column without enforcing axis alignment:

```
stack_continuousv(mpg) +
    ggfree(mapping = aes(displ, hwy, colour = class)) +
    geom_point(size = 2) +
    ggfree(mapping = aes(displ, hwy, colour = class)) +
    geom_point(size = 2) &
    scale_color_brewer(palette = "Dark2") &
    theme_bw()
```

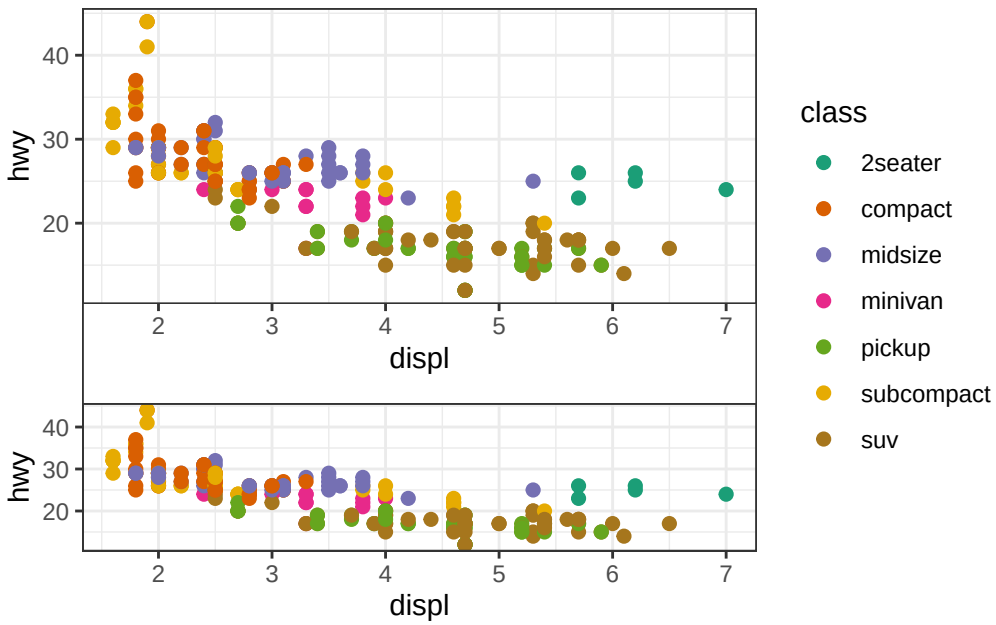


By default, `ggfree()` will also inherit data from the layout and call `fortify_data_frame()` to convert the data to a data frame. So, note that if the layout data is a matrix, it will be converted into a long-formatted data frame.

2.4 Plot Size

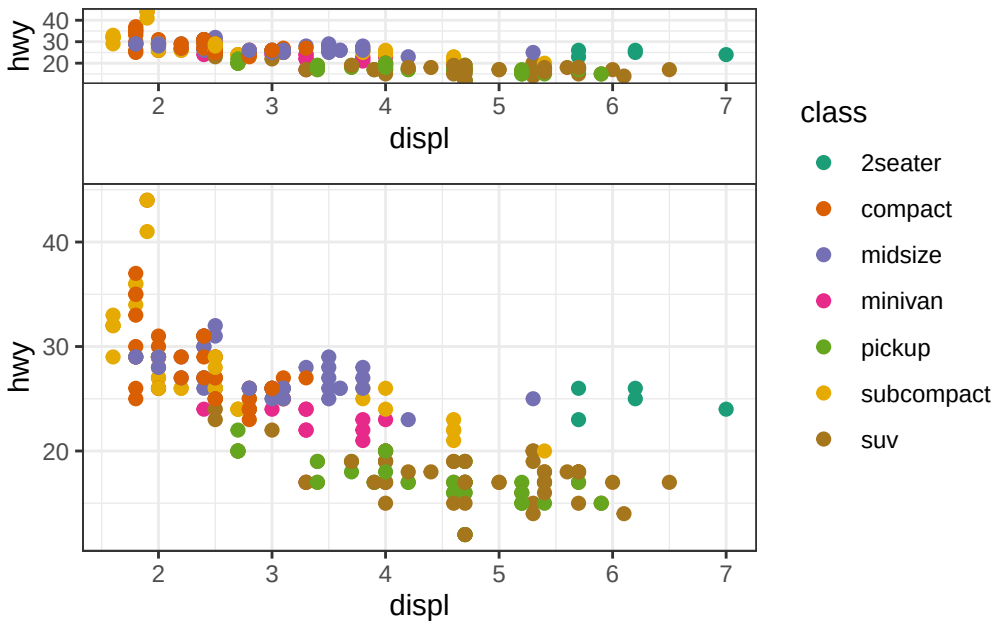
Both `ggalign()` and `ggfree()` functions have a `size` argument to control the relative `width` (for horizontal stack layout) or `height` (for vertical stack layout) of the plot's panel area.

```
stack_continuousv(mpg) +
    ggfree(mapping = aes(displ, hwy, colour = class), size = 2) +
    geom_point(size = 2) +
    ggfree(mapping = aes(displ, hwy, colour = class), size = 1) +
    geom_point(size = 2) &
    scale_color_brewer(palette = "Dark2") &
    theme_bw()
```



Alternatively, you can define an absolute size by using a `unit()` object:

```
stack_continuousv(mpg) +
    ggfree(mapping = aes(displ, hwy, colour = class), size = unit(1, "cm")) +
    geom_point(size = 2) +
    ggfree(mapping = aes(displ, hwy, colour = class)) +
    geom_point(size = 2) &
    scale_color_brewer(palette = "Dark2") &
    theme_bw()
```



2.5 active plot

As mentioned earlier, the active plot refers to the plot that subsequent ggplot2 components will target. The package provide two functions to work with active plot for `stack_layout`.

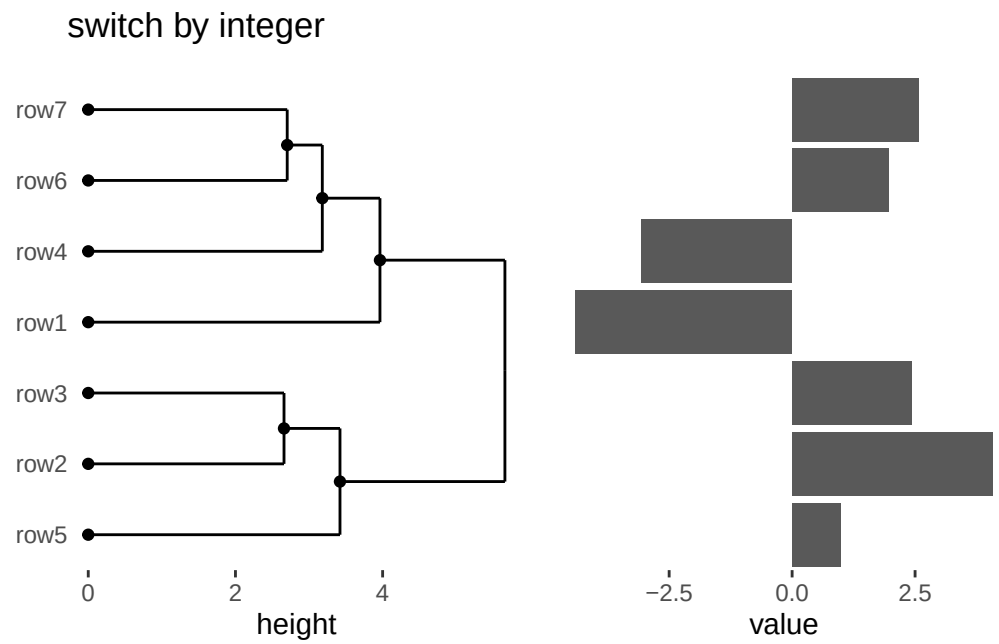
- `stack_switch()`: switch the active context
- `stack_active()`: An alias for `stack_switch()`, which sets `what = NULL`

The `stack_switch()` function accepts the `what` argument, which can either be the index of the plot added (based on its adding order) or the plot name specified via the `active()` object using the `name` argument.

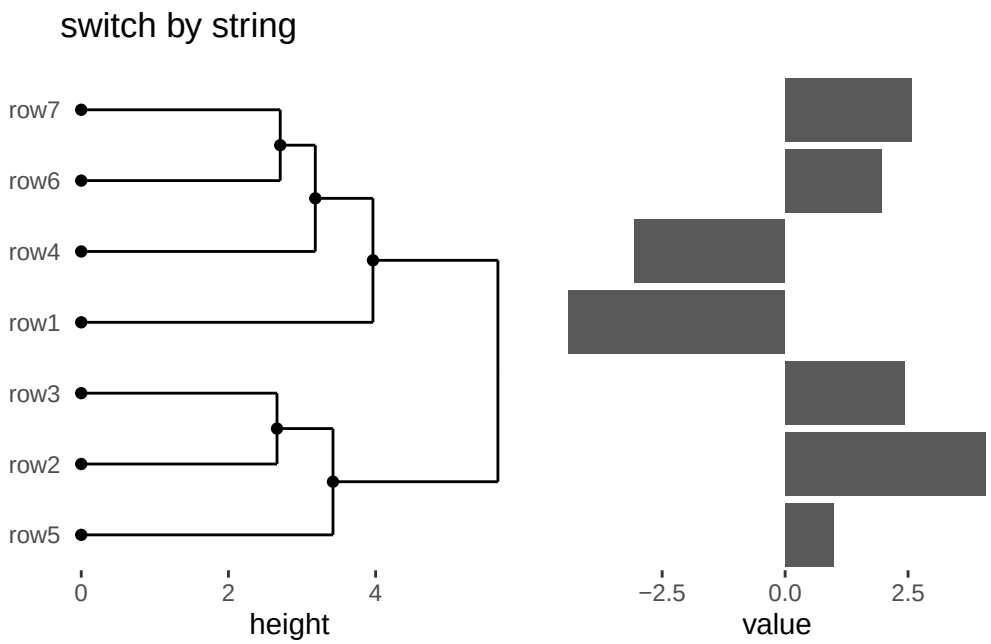
Note that the `what` argument must be explicitly named, as it is placed second in the function signature. This is because, in most cases, we don't need to switch the active plot, manually—adjusting the order of plot additions typically suffices.

```
stack_alignh(small_mat) +
    align_dendro() +
    ggalign(data = rowSums) +
    geom_bar(aes(value, .discrete_y), stat = "identity") +
    stack_switch(what = 1) +
    geom_point() +
```

```
    theme(axis.text.y = element_text()) +
    layout_title(title = "switch by integer")
```




```
stack_alignh(small_mat) +
    align_dendro(active = active(name = "tree")) +
    ggalign(data = rowSums) +
    geom_bar(aes(value, .discrete_y), stat = "identity") +
    stack_switch(what = "tree") +
    geom_point() +
    theme(axis.text.y = element_text()) +
    layout_title(title = "switch by string")
```



In the example, we use `layout_title()` to insert a title for the entire layout. Alternatively, you can add a title to a single plot with `ggtitle()`.

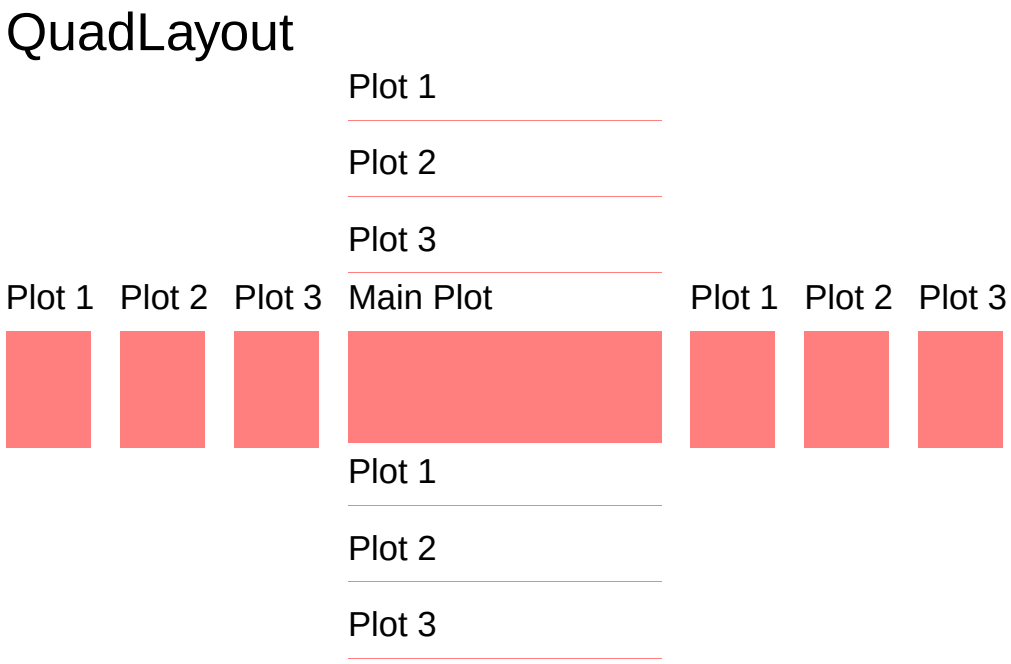
By setting `what = NULL` (or alias `stack_active()`), we remove the active plot. This is particularly useful when the active plot is a nested `Layout` object, as any additions would otherwise be directed to that nested `Layout`. By removing the active plot, you can continue adding components to the `StackLayout`. We'll introduce the nested layout of `StackLayout` in Chapter 8.

In the next chapter, we will dive into the `HeatmapLayout`, which can take the `StackLayout` as input. Heatmap layouts offer additional features for aligning observations in both directions. Let's move ahead and explore how heatmaps can be seamlessly integrated into your layout workflows.

3 heatmap layout

The `heatmap_layout()` function provides a powerful way to create customizable heatmaps in R using `ggplot2`. This chapter will guide you through its usage.

`heatmap_layout()` is a specialized version of `quad_discrete()`, which itself is a specific variant of `QuadLayout` (`quad_layout()`) designed to align discrete variables both horizontally and vertically. We introduce `heatmap_layout()` directly, as it is more familiar to many users, especially those experienced with popular heatmap packages like `pheatmap` and `ComplexHeatmap`.



`heatmap_layout()` simplifies the creation of heatmap plots by integrating essential elements for a standard heatmap layout, ensuring that the appropriate data mapping and visualization layers are automatically applied. `ggheatmap()` is an alias for `heatmap_layout()`.

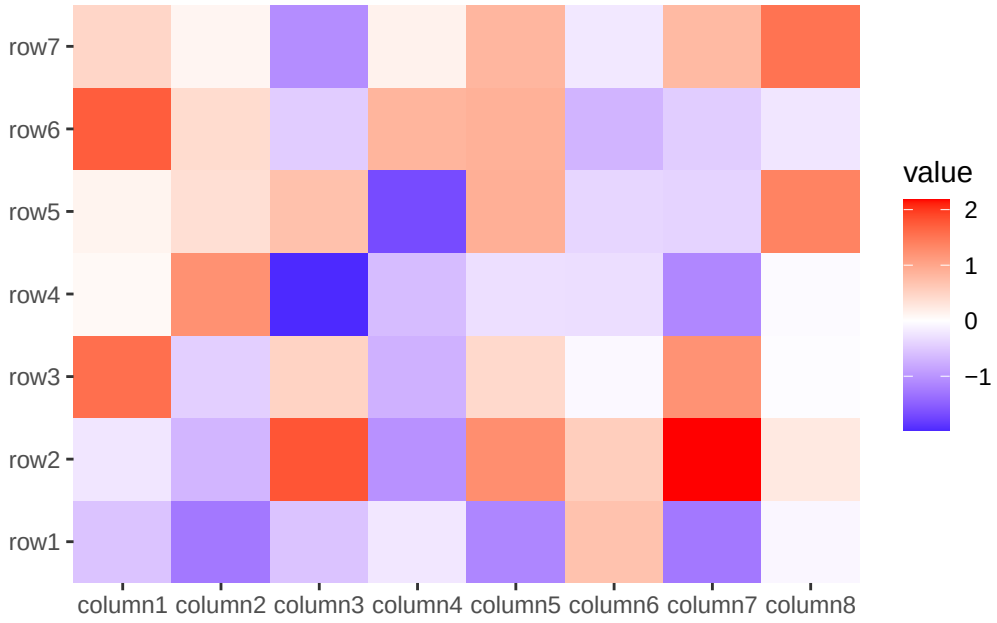
```
library(ggalign)
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
```

```
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

3.1 input data

As mentioned in Section 1.3, we typically require a matrix for the `Layout` which need align discrete variables. Internally, `fortify_matrix()` will be used to process the data. You can provide a numeric or character vector, a data frame, or any other data type that can be converted into a matrix using `as.matrix()`.

```
ggheatmap(small_mat)
#> > heatmap built with `geom_tile()`
```



3.2 Main plot (heatmap body)

The `ggheatmap()`/`quad_layout()` functions arrange plots in the Quad-Side layout of the main plot. When the layout is initialized, a `ggplot` object is automatically created for the main plot.

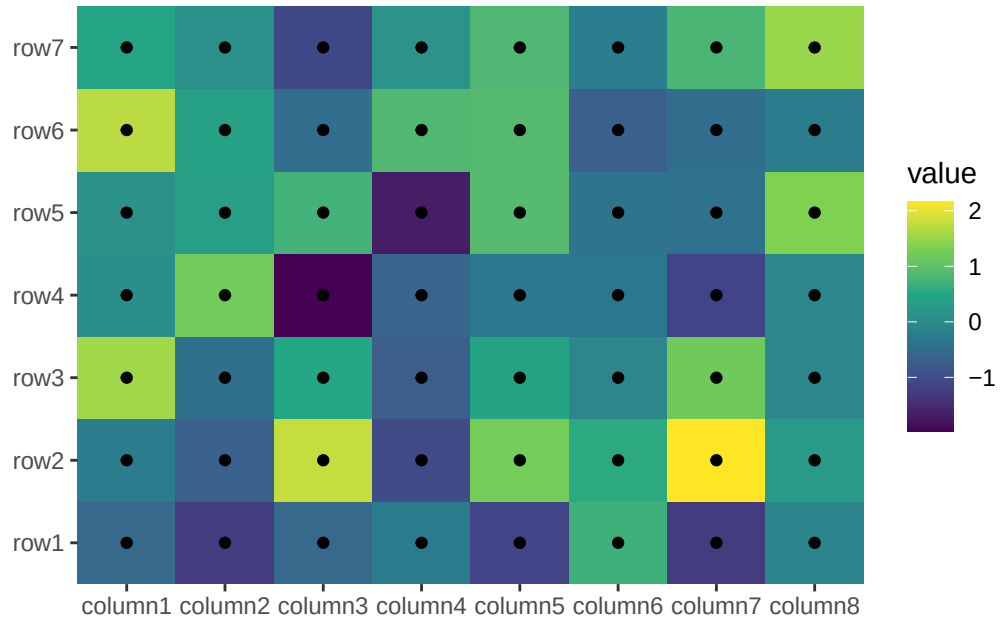
For `ggheatmap()`, the matrix input will be converted into a long-format data frame when drawing. The data in the underlying `ggplot` object includes the following columns:

- `.xpanel` and `.ypanel`: the column and row panel
- `.x` and `.y`: the `x` and `y` coordinates
- `.row_names` and `.column_names`: A factor of the row and column names of the original matrix (only applicable when names exist).
- `.row_index` and `.column_index`: the row and column index of the original matrix.
- `value`: the actual matrix value.

The default mapping will use `aes(.data$.x, .data$.y)`, but can be customized using `mapping` argument.

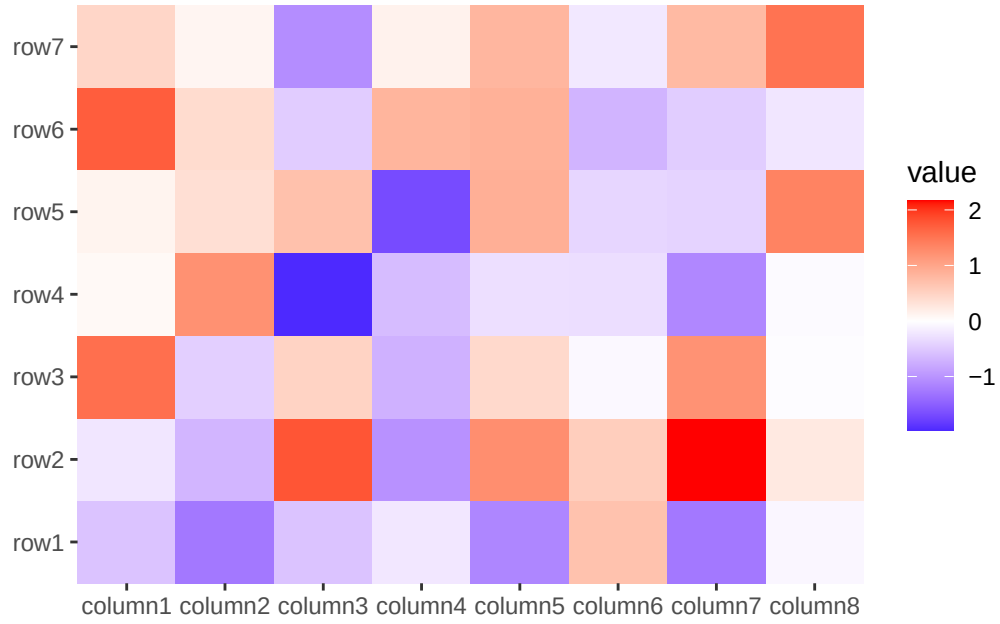
By default, the main plot is regarded as the active plot, meaning you can add ggplot2 elements directly to the main plot.

```
ggheatmap(small_mat) +
    geom_point() +
    scale_fill_viridis_c()
#> > heatmap built with `geom_tile()`
```

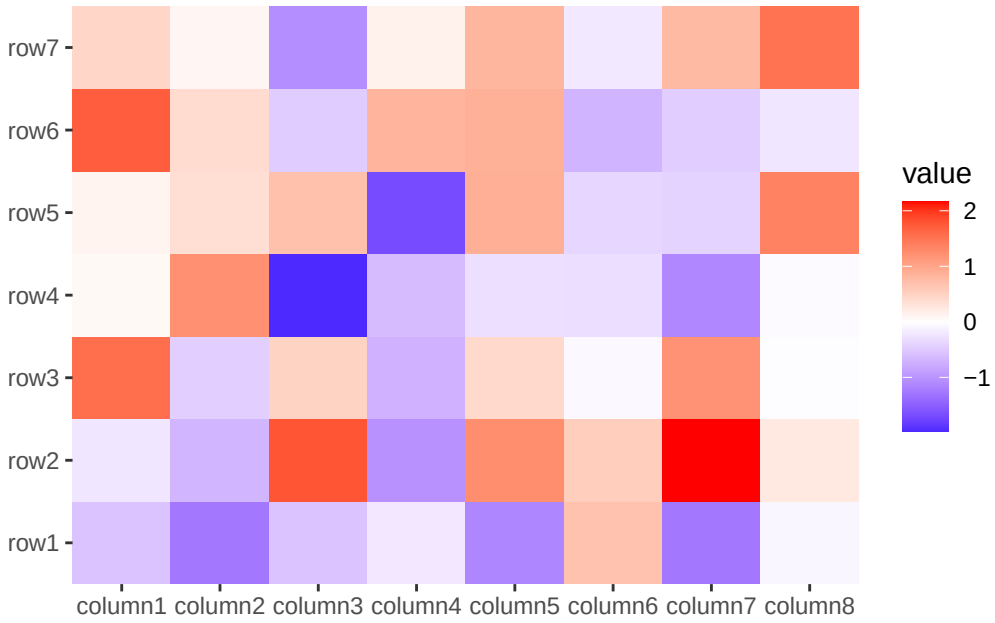


By default, `ggheatmap()` adds a heatmap layer. If the matrix has more than 20,000 cells (`nrow * ncol > 20000`), it uses `geom_raster()` for performance efficiency; for smaller matrices, `geom_tile()` is used. You can explicitly choose the layer by providing a single string (`"raster"` or `"tile"`) in the `filling` argument.

```
ggheatmap(small_mat, filling = "raster")
```

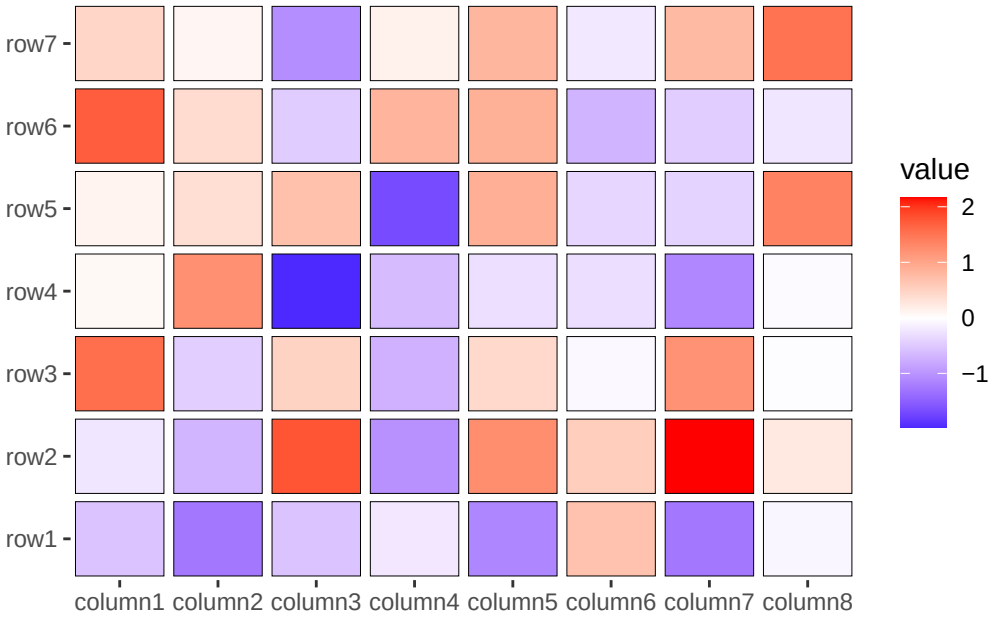



```
ggheatmap(small_mat, filling = "tile")
```



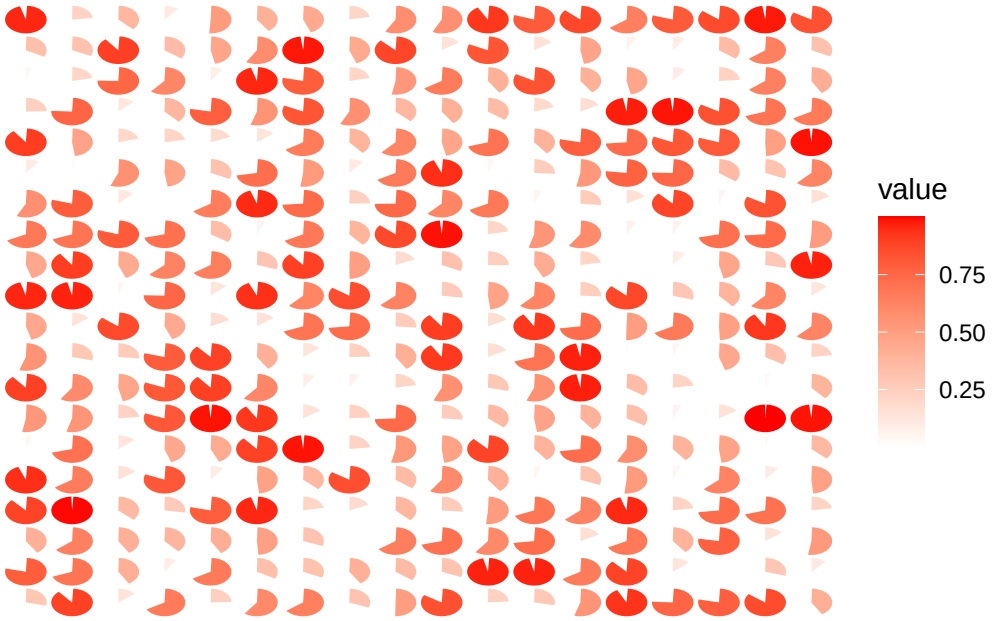
Note, the filling layer will always use `mapping` of `aes(.data$.x, .data$.y)`, if you want to customize filling, you can set `filling = NULL`, which will remove the filling layer and allow you to add custom filling geoms.

```
ggheatmap(small_mat, filling = NULL) +
    geom_tile(aes(fill = value), color = "black", width = 0.9, height = 0.9)
```



A heatmap pie charts can be easily drawn:

```
set.seed(123)
ggheatmap(matrix(runif(360L), nrow = 20L), filling = NULL) +
    geom_pie(aes(angle = value * 360, fill = value))
```

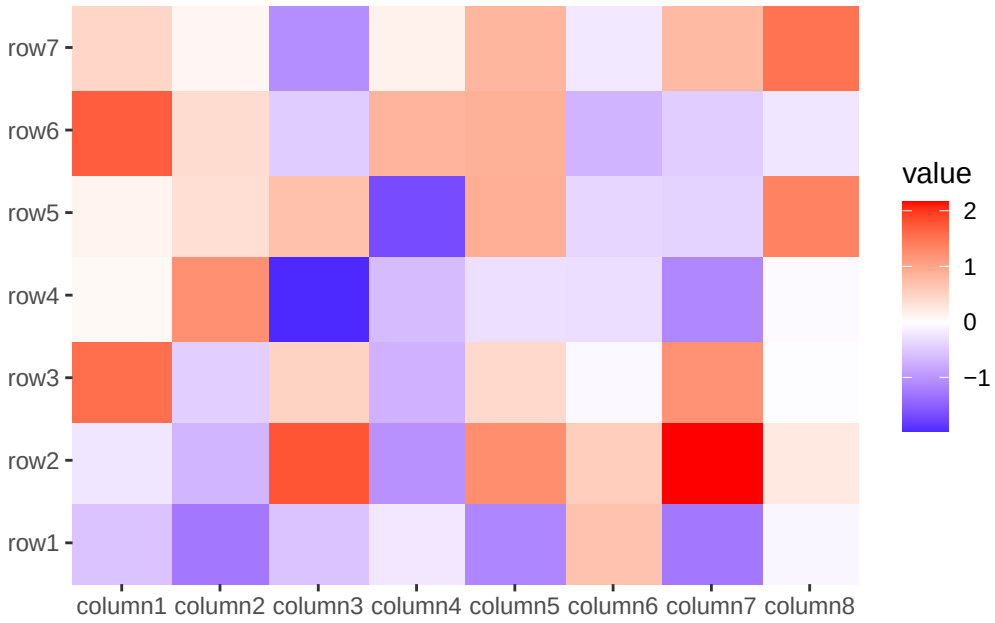


For more complex customizations of pie charts, you can try using `ggforce::geom_arc_bar()` instead.

3.3 rasterization

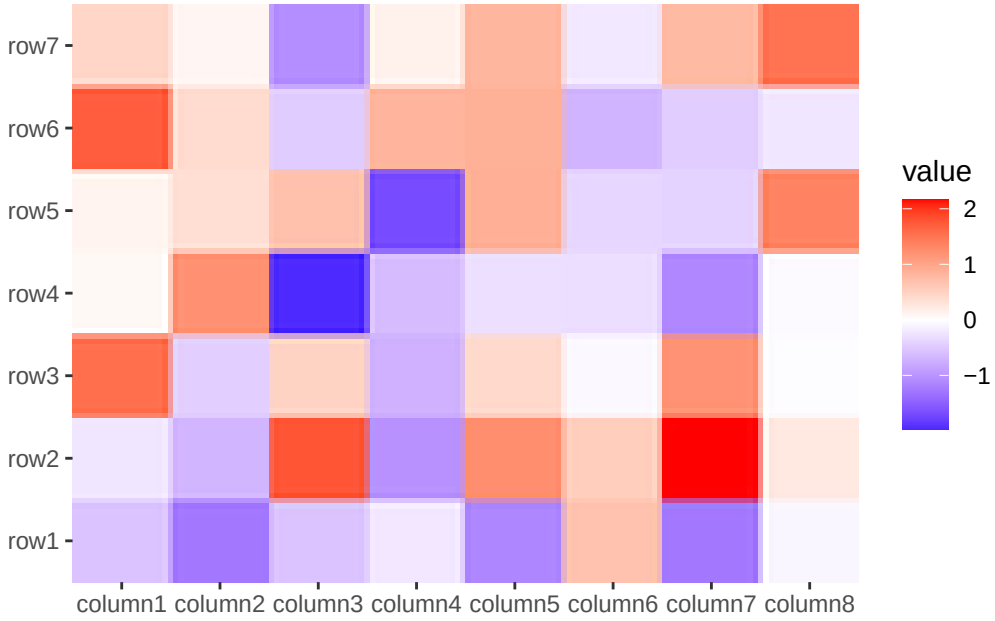
When working with large heatmaps, it's often beneficial to rasterize the heatmap body layer. You can achieve this by using the `raster_magick()` function. The `res` argument controls the resolution of the raster image. By default, the `res` argument matches the resolution of the current device, but specifying a different value can help reduce the resolution of the rasterized heatmap body.

```
ggheatmap(small_mat, aes(.x, .y), filling = NULL) +
    raster_magick(geom_tile(aes(fill = value)), res = 50)
```



By leveraging `raster_magick()`, you can also perform image post-processing using the `magick` package. This allows for custom image resizing with filters.

```
ggheatmap(small_mat, filling = NULL) +
    # Use `magick::filter_types()` to check available `filter` arguments
    raster_magick(geom_raster(aes(fill = value)),
        magick = function(image) {
            magick::image_resize(image,
                # we resize to the 50% of width
                geometry = "50%x", filter = "Lanczos"
            )
        }
    )
```

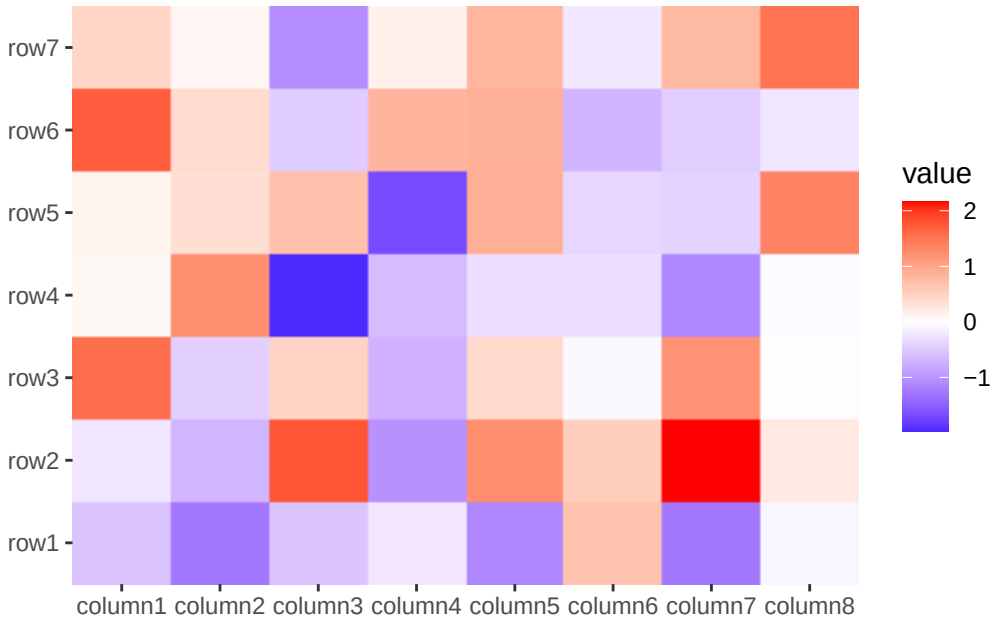


Note: When using `magick::image_resize()`, you should specify the `geometry` argument to resize the image. If only the `filter` is specified, it will only distort the image data (though subtle). For more information on image resizing, refer to ImageMagick's resize documentation.

You can also rasterize all plots in the layout directly with `raster_magick()`. This method is defined for both `ggheatmap()`/`quad_layout()` and `stack_layout()` objects.

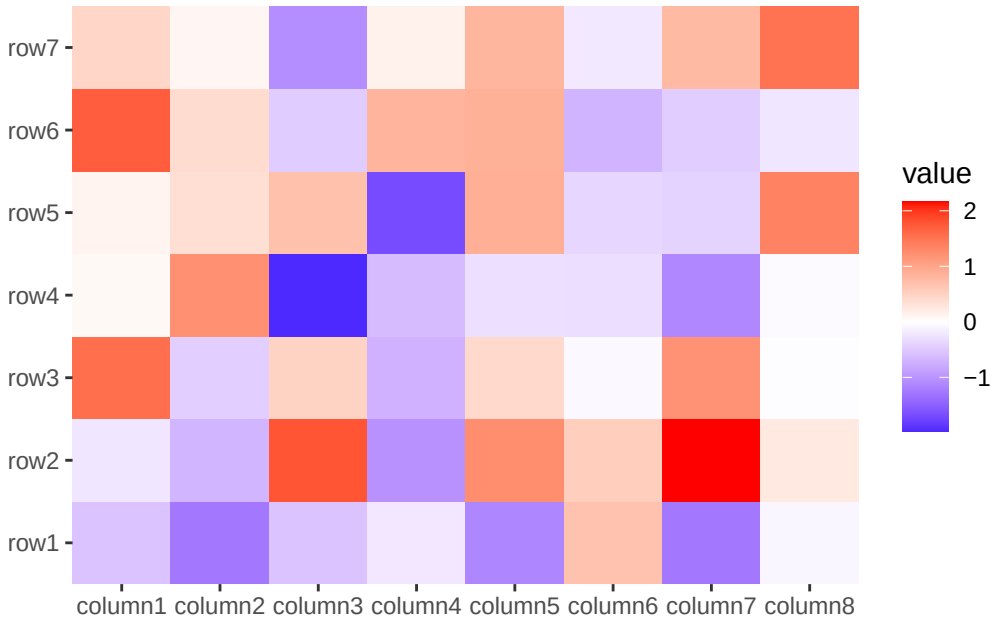
Additionally, You can use external packages like ggrastr or ggfx to rasterize the heatmap body.

```
ggheatmap(small_mat, filling = FALSE) +
    ggrastr::rasterise(geom_tile(aes(fill = value)), dev = "ragg")
```



Likewise, you can also rasterize all plots in the layout directly with `ggrastr::rasterise()` for both `ggheatmap()`/`quad_layout()` and `stack_layout()`.

```
ggrastr::rasterise(ggheatmap(small_mat), dev = "ragg")
#> > heatmap built with `geom_tile()`
```



Furthermore, ggfx offers many image filters that can be applied to ggplot2 layers. See the package for the details.

3.4 annotations

In `ggheatmap()`/`quad_layout()`, annotations are handled by a `stack_layout()` object and can be positioned at the top, left, bottom, or right of the main plot (heatmap body). `quad_layout()` can align discrete or continuous variables either horizontally or vertically. Since the annotation handling is the same for both `ggheatmap()` and `quad_layout()`, we introduce the annotation functionality for both together.

The annotations will always follow the alignment of the `ggheatmap()`/`quad_layout()` in the current direction. For horizontal alignment of discrete variables, `stack_discreteh()` will be used for left and right annotations, while `stack_continuoush()` will be used for continuous variables. The same logic applies to vertical alignment—`stack_discretev()` or `stack_continuousv()` will be used for top and bottom annotations, depending on whether the variables being aligned are discrete or continuous.

By default, `ggheatmap()`/`quad_layout()` do not activate an annotation, You can use `quad_anno()` to activate an annotation, directing all subsequent additions to the specified annotation position. The `quad_anno()` function has the following aliases:

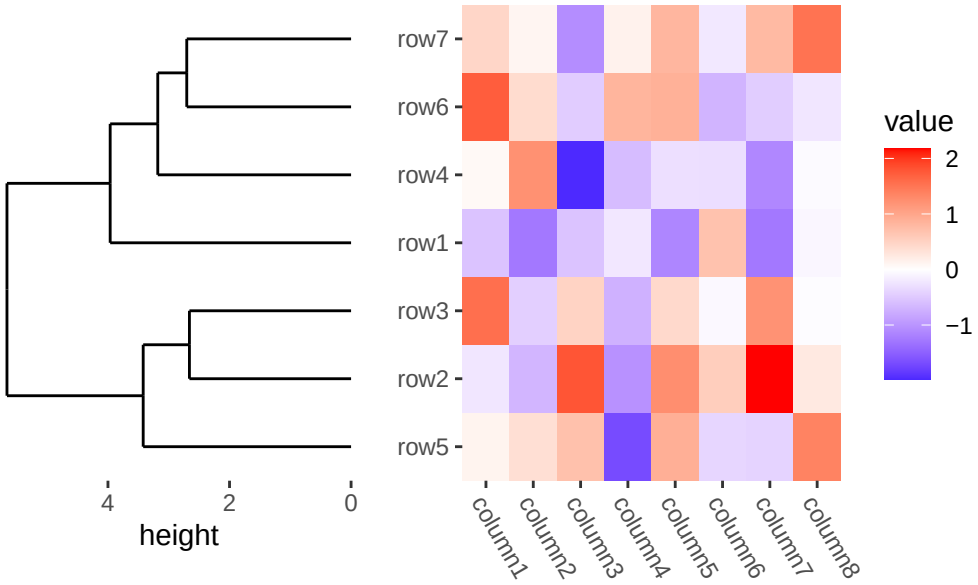
- `anno_top`: A special case of `quad_anno()` with `position = "top"`.

- `anno_left`: A special case of `quad_anno()` with `position = "left"`.
- `anno_bottom`: A special case of `quad_anno()` with `position = "bottom"`.
- `anno_right`: A special case of `quad_anno()` with `position = "right"`.

When `quad_anno()` is added to a `ggheatmap()`/`quad_layout()`, it will try to create a new `stack_layout()`. For top and bottom annotations, `stack_discretev()` or `stack_continuousv()` will be used; for left and right annotations, `stack_discreteh()` or `stack_continuoush()` will be applied.

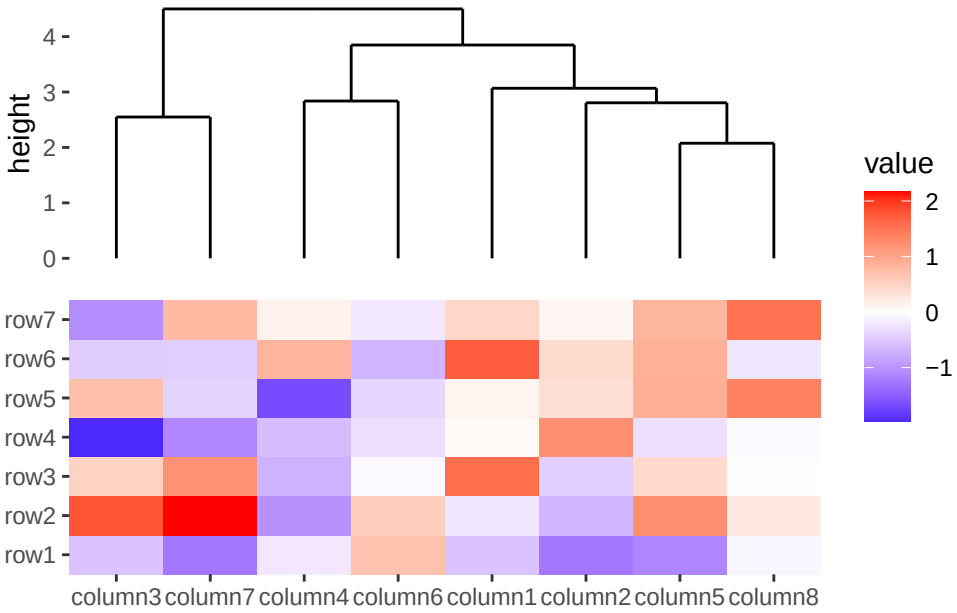
Additionally, `quad_anno()` will set the active context to the annotation. This means that subsequent additions will be directed to the annotation rather than the main plot. We use the term `active context` in contrast to `active plot` (as discussed in Section 2.2), since the annotation is a `Layout` object but not a single plot.

```
ggheatmap(small_mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_left() +
    align_dendro()
#> > heatmap built with `geom_tile()`
```



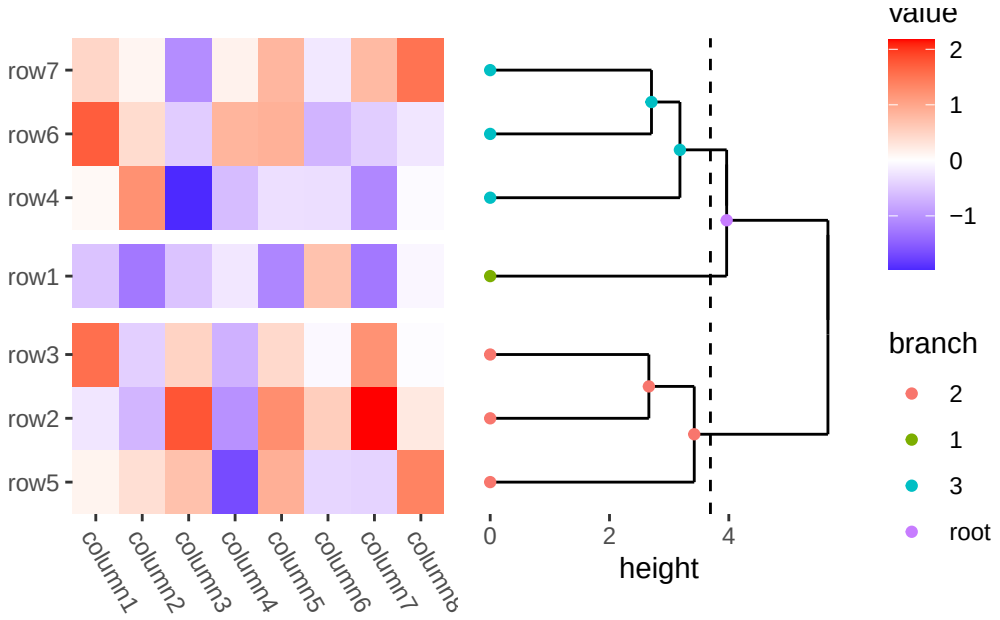
By default, the annotation `stack_layout()` will try to inherit data from `ggheatmap()`/`quad_layout()`. If we need align discrete variables vertically, this means the data from `ggheatmap()`/`quad_layout()` should be a matrix, the column annotations will also require a matrix and the matrix from `ggheatmap()`/`quad_layout()` will be transposed for use in the column annotations.

```
ggheatmap(small_mat) +
    # we set the active context to the top annotation
    anno_top() +
    align_dendro()
#> > heatmap built with `geom_tile()`
```



You can further customize the layout design or add new plots in the annotation stack, as described in Chapter 2.

```
ggheatmap(small_mat) +
    # in the heatmap body, we set the axis text theme
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    # we set the active context to the right annotation
    anno_right() +
    # in the right annotation, we add a dendrogram
    align_dendro(k = 3L) +
    # in the dendrogram, we add a point layer
    geom_point(aes(color = branch))
#> > heatmap built with `geom_tile()`
```



In this example:

- `anno_right()` initialize the right annotation stack, and change the active context to the right annotation of the heatmap.
- `align_dendro(k = 3L)` adds a dendrogram to the annotation and sets itself as the active plot in the annotation stack.
- `geom_point(aes(color = branch))` is then added to this active plot within the annotation stack, here, it means the `align_dendro()` plot.

`ggheatmap()` aligns discrete variable both horizontally and vertically, so it's safe to always use `quad_anno()` directly, as all annotations require a matrix, and the layout data is also a matrix. However, for `quad_layout(xlim = NULL)` and `quad_layout(ylim = NULL)` (which I'll discuss in more detail in a Chapter 7), which only align discrete variable in one direction, the data in the layout may not fit the data for the annotation.

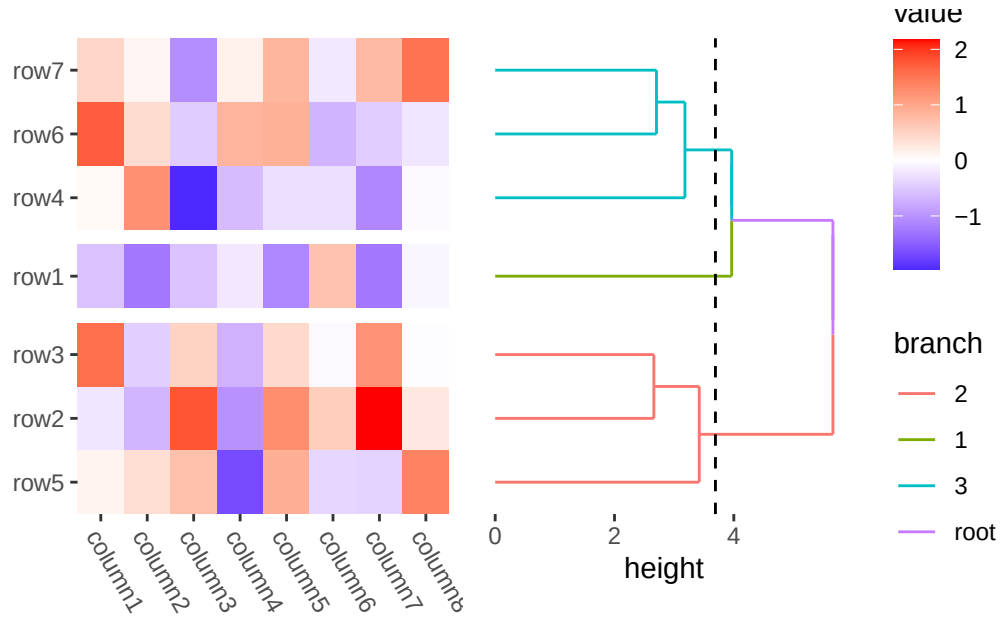
```
- `quad_layout(xlim = NULL)`: aligning discrete variable in horizontal
direction, for column annotations, we ll need a data frame for
`stack_continuous()`.
- `quad_layout(ylim = NULL)`: aligning discrete variable in vertical
direction, for row annotations, we ll need a data frame for
`stack_continuous()`.
```

In both cases, `quad_anno()` won't initialize the annotation by default, instead, you must provide the annotation manually.

3.5 Adding stack layout

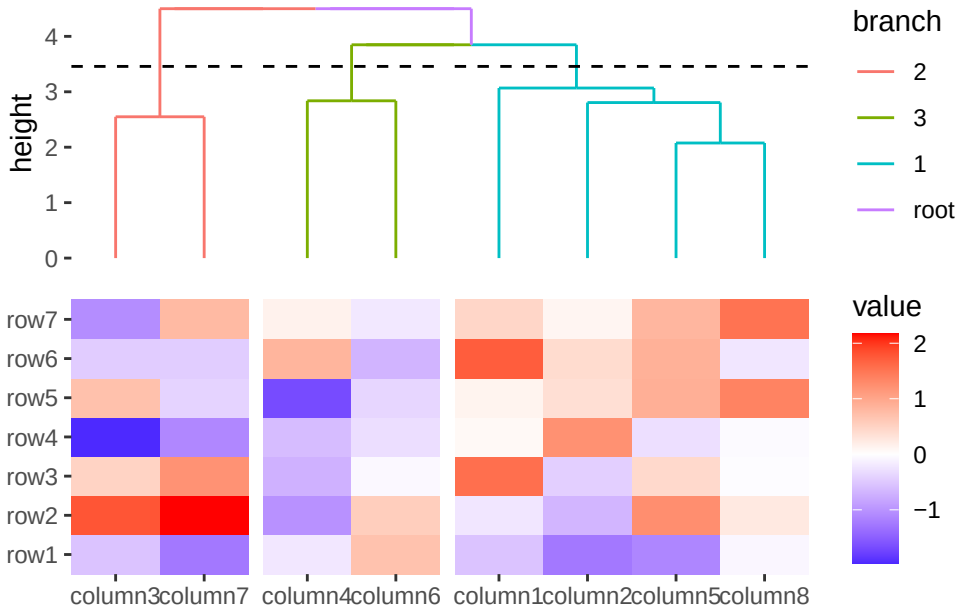
To add a `stack_layout()` to the `ggheatmap()`, we must prevent the automatic creation of annotations by `quad_anno()` by setting `initialize = FALSE`.

```
my_stack <- stack_discreteh(small_mat) +
    align_dendro(aes(color = branch), k = 3L)
ggheatmap(small_mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(initialize = FALSE) +
    my_stack
#> > heatmap built with `geom_tile()`
```



Note when aligning the discrete variable, you must ensure the `number of observations` is consistent in the direction. So for column annotations, you need transpose the data manually.

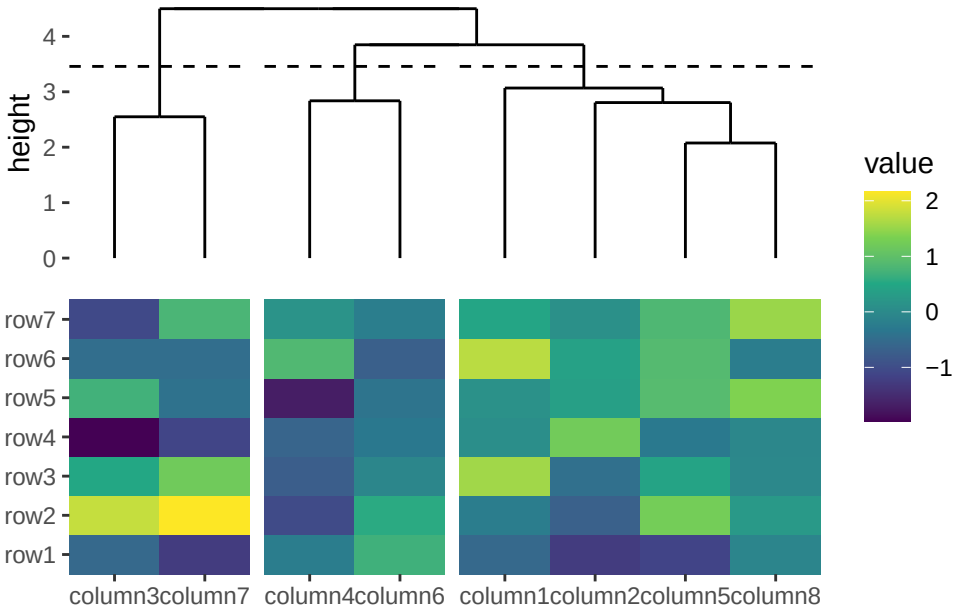
```
my_stack <- stack_discretev(t(small_mat)) +
    align_dendro(aes(color = branch), k = 3L)
ggheatmap(small_mat) +
    anno_top(initialize = FALSE) +
    my_stack
#> > heatmap built with `geom_tile()`
```



3.6 `quad_active()`

To remove the active context and redirect additions back to the heatmap body, you can use `quad_active()`.

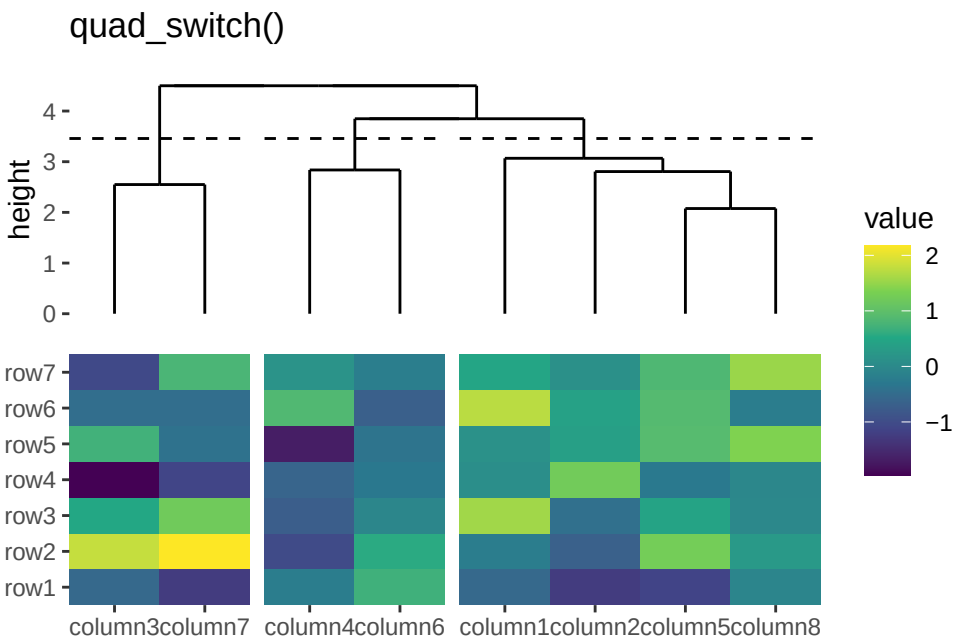
```
ggheatmap(small_mat) +
    # we set the active context to the top annotation
    anno_top() +
    # we split the observations into 3 groups by hierarchical clustering
    align_dendro(k = 3L) +
    # remove any active annotation
    quad_active() +
    # set fill color scale for the heatmap body
    scale_fill_viridis_c()
#> > heatmap built with `geom_tile()`
```



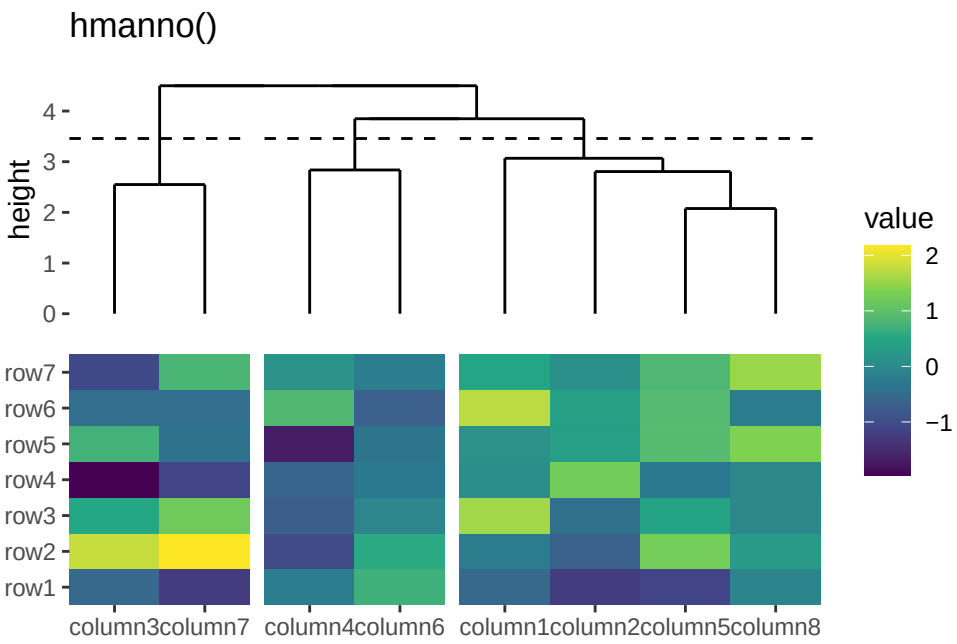
3.7 `quad_switch()/hmanno()`

We also provide `quad_switch()/hmanno()` (heatmap annotation) which integrates `quad_active()` and `quad_anno()` into one function for ease of use. Feel free to use any of these functions to streamline your annotation process.

```
ggheatmap(small_mat) +
    # we set the active context to the top annotation
    quad_switch("t") +
    # we split the observations into 3 groups by hierarchical clustering
    align_dendro(k = 3L) +
    # remove any active annotation
    quad_switch() +
    # set fill color scale for the heatmap body
    scale_fill_viridis_c() +
    layout_title("quad_switch()")
#> > heatmap built with `geom_tile()`
```




```
ggheatmap(small_mat) +
    # we set the active context to the top annotation
    hmanno("t") +
    # we split the observations into 3 groups by hierarchical clustering
    align_dendro(k = 3L) +
    # remove any active annotation
    hmanno() +
    # set fill color scale for the heatmap body
    scale_fill_viridis_c()+
    layout_title("hmanno()")
#> > heatmap built with `geom_tile()`
```

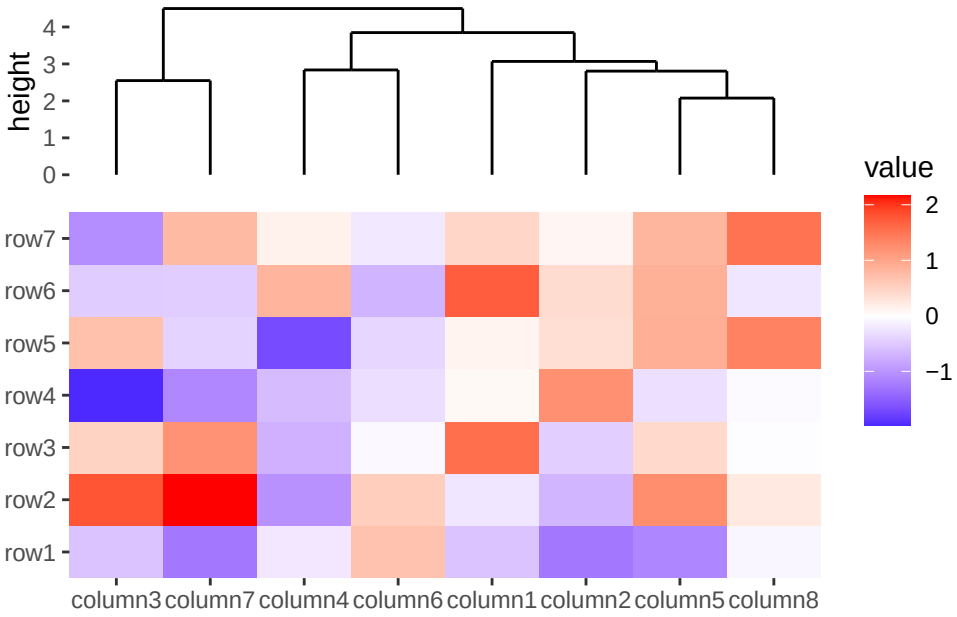


3.8 Plot Size

3.8.1 Heatmap Body Size

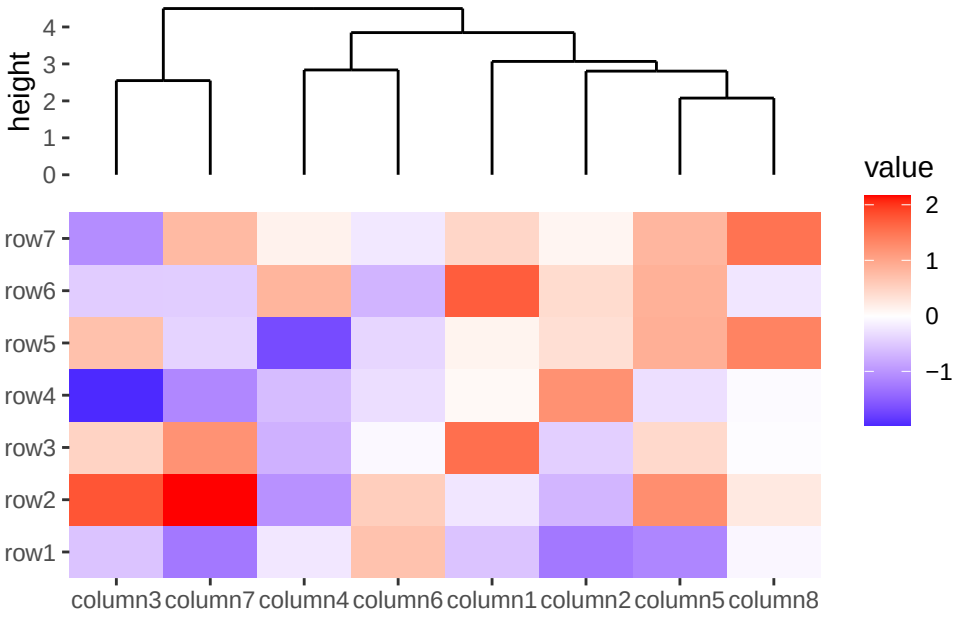
You can specify the relative sizes of the heatmap body using the `width` and `height` arguments in the `ggheatmap()` function.

```
ggheatmap(small_mat, height = 2) +
    anno_top() +
    align_dendro()
#> > heatmap built with `geom_tile()`
```



Alternatively, the `quad_active()` function allows you to control the heatmap body sizes.

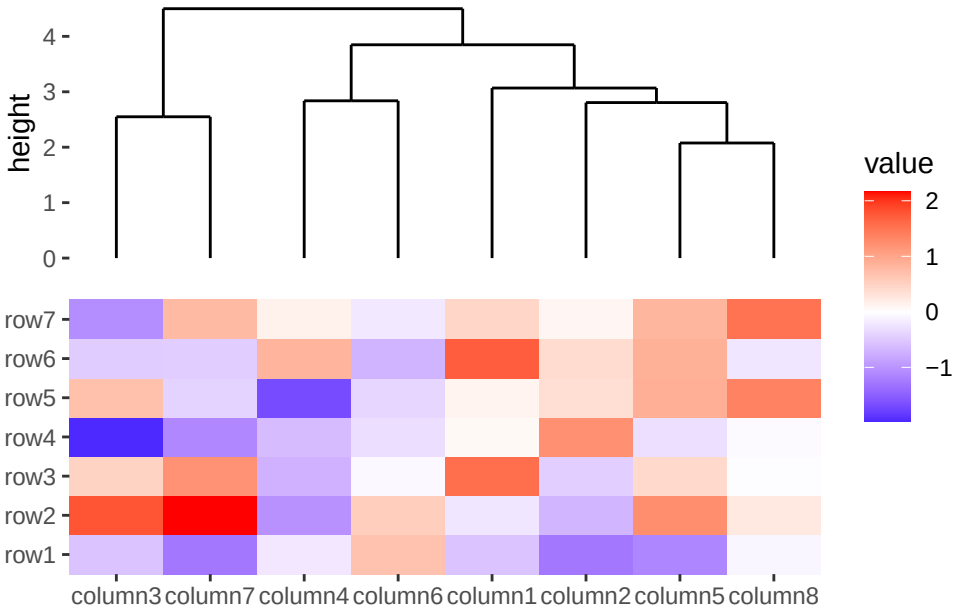
```
ggheatmap(small_mat) +
    quad_active(height = 2) +
    anno_top() +
    align_dendro()
#> > heatmap built with `geom_tile()`
```



3.8.2 Annotation Stack Size

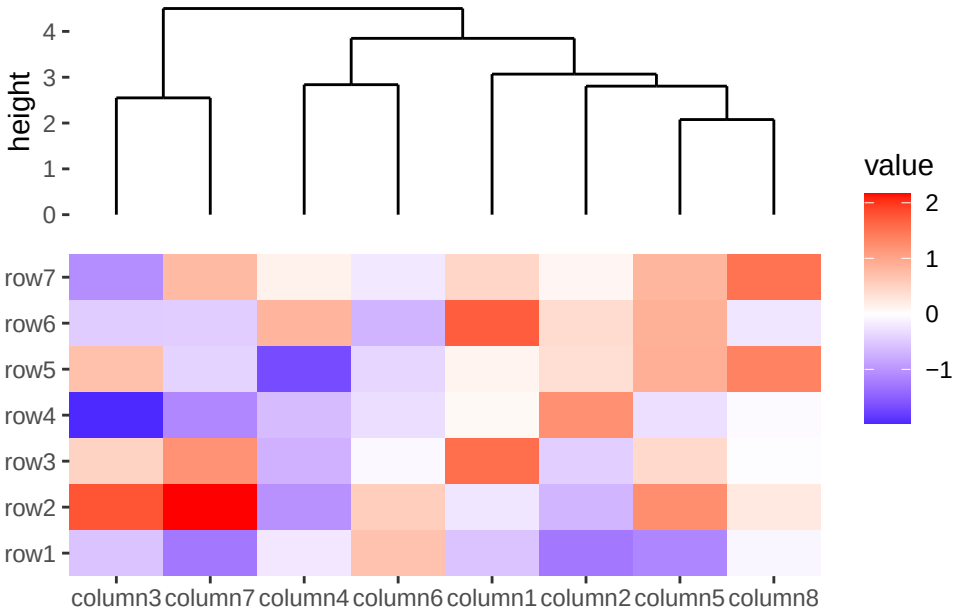
The `quad_anno()` function allows you to control the total annotation stack size. The `size` argument controls the relative width (for left and right annotations) or height (for top and bottom annotations) of the whole annotation stack.

```
ggheatmap(small_mat) +
    anno_top(size = 1) +
    align_dendro()
#> > heatmap built with `geom_tile()`
```



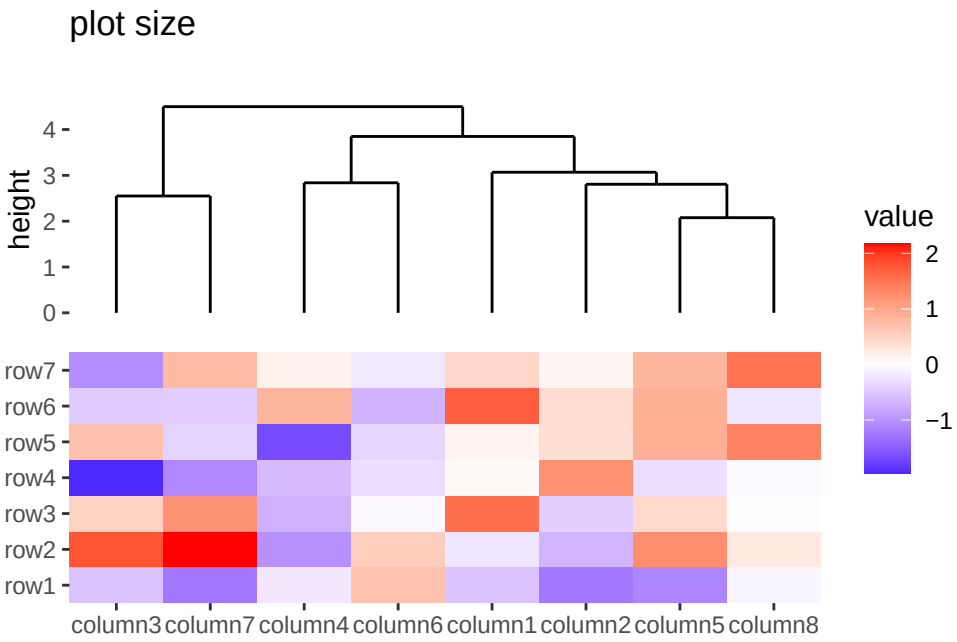
You can also specify it as an absolute size using `unit()`:

```
ggheatmap(small_mat) +
    anno_top(size = unit(30, "mm")) +
    align_dendro()
#> > heatmap built with `geom_tile()`
```

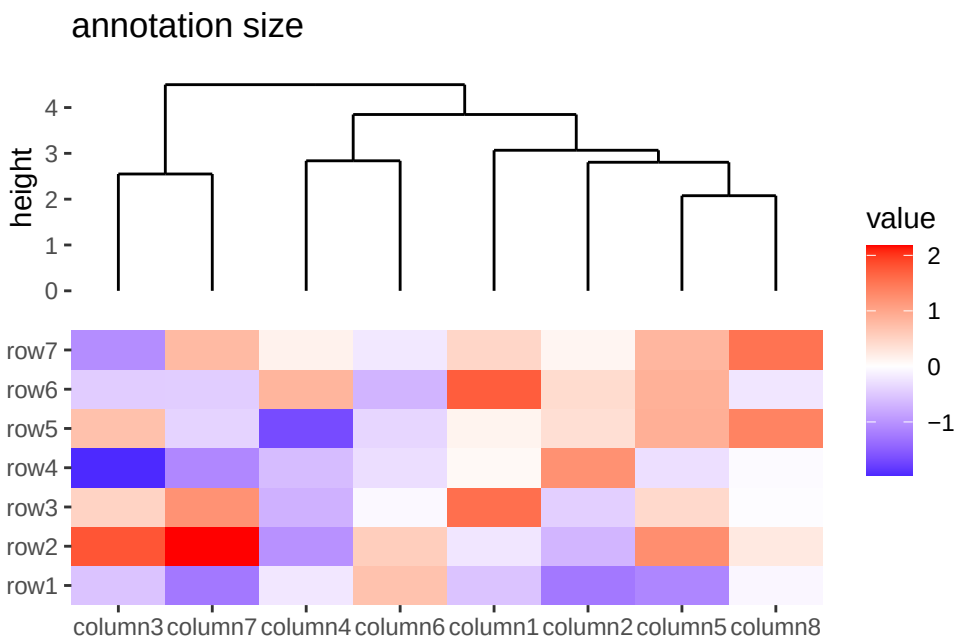


Note that the size of an individual plot (Section 2.4) does not affect the total annotation stack size. You must adjust the annotation size using the method described above.

```
ggheatmap(small_mat) +
    anno_top() +
    align_dendro(size = unit(30, "mm")) +
    layout_title("plot size")
#> > heatmap built with `geom_tile()`
```




```
ggheatmap(small_mat) +
    anno_top(size = unit(30, "mm")) +
    align_dendro() +
    layout_title("annotation size")
#> > heatmap built with `geom_tile()`
```



In this chapter, we explored the usage of heatmap layout. These features provide a strong foundation for visualizing matrix-based data in a structured way. However, as your visualization needs grow more complex, the ability to further customize and fine-tune the layout becomes essential.

In the next chapter, we will dive into the Layout Customize functionalities, where you can gain full control over your plot's layout.

4 Layout customize

For layouts that can align observations, the package provides a suite of `align_*` functions designed to give you precise control over the observations. These functions allow you to reorder observations or partition them into multiple groups.

Currently, there are four key `align_*` functions available for layout customization:

- **`align_group`**: Group and align plots based on categorical factors.
- **`align_kmeans`**: Group observations by k-means clustering results.
- **`align_order`**: Reorder layout observations based on statistical weights or allows for manual reordering based on user-defined ordering index.
- **`align_reorder`**: Reorder observations using an arbitrary statistical function.
- **`align_hclust`**: Reorder or group observations based on hierarchical clustering.

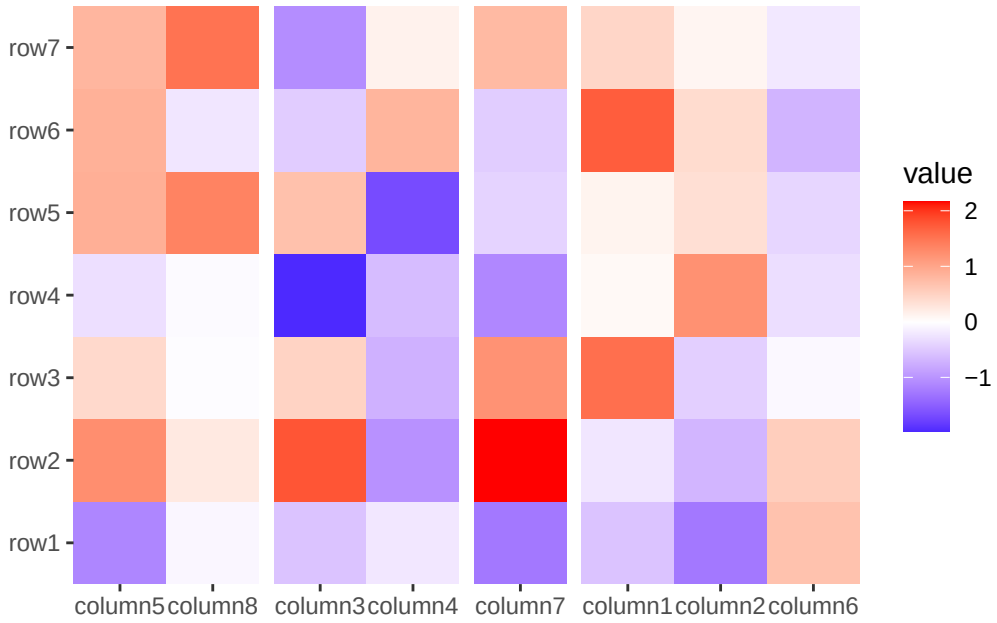
Note that these functions do not add plot areas and set the active context, meaning you cannot incorporate `ggplot2` elements directly into these objects. You can inspect the behavior of any `align_*` function by printing it.

```
library(ggalign)
#> Loading required package: ggplot2
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

4.1 `align_group()`

The `align_group()` function allows you to split the observations into groups.

```
set.seed(1234)
ggheatmap(small_mat) +
    anno_top() +
    align_group(sample(letters[1:4], ncol(small_mat), replace = TRUE))
#> > heatmap built with `geom_tile()`
```



Note that all `align_*` functions which split observations into groups must not break the previous established groups. This means the new groups must nest in the old groups, usually they cannot be used if groups already exist.

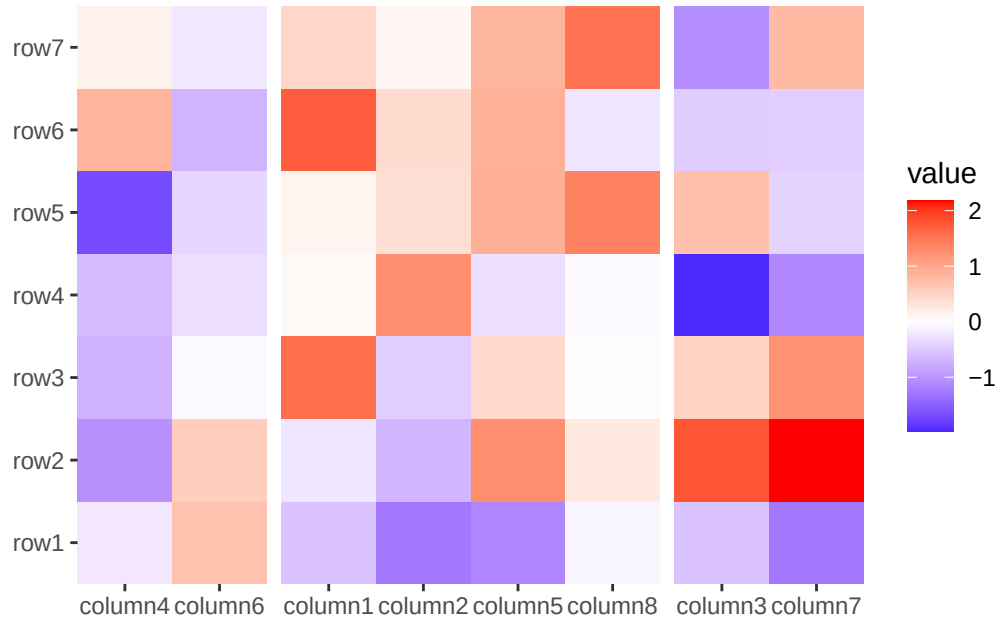
```
set.seed(1234)
ggheatmap(small_mat) +
    anno_top() +
    align_group(sample(letters[1:4], ncol(small_mat), replace = TRUE)) +
    align_group(sample(letters[1:5], ncol(small_mat), replace = TRUE))
#> Error in `setup_design()`:
#> ! `align_group()` disrupt the previously established panel groups of the
#>   top annotation `stack_discrete()`
```

4.2 `align_kmeans()`

The `align_kmeans()` function split the observations into groups based on k-means clustering.

```
set.seed(1234)
ggheatmap(small_mat) +
    anno_top() +
```

```
    align_kmeans(3L)
#> > heatmap built with `geom_tile()`
```

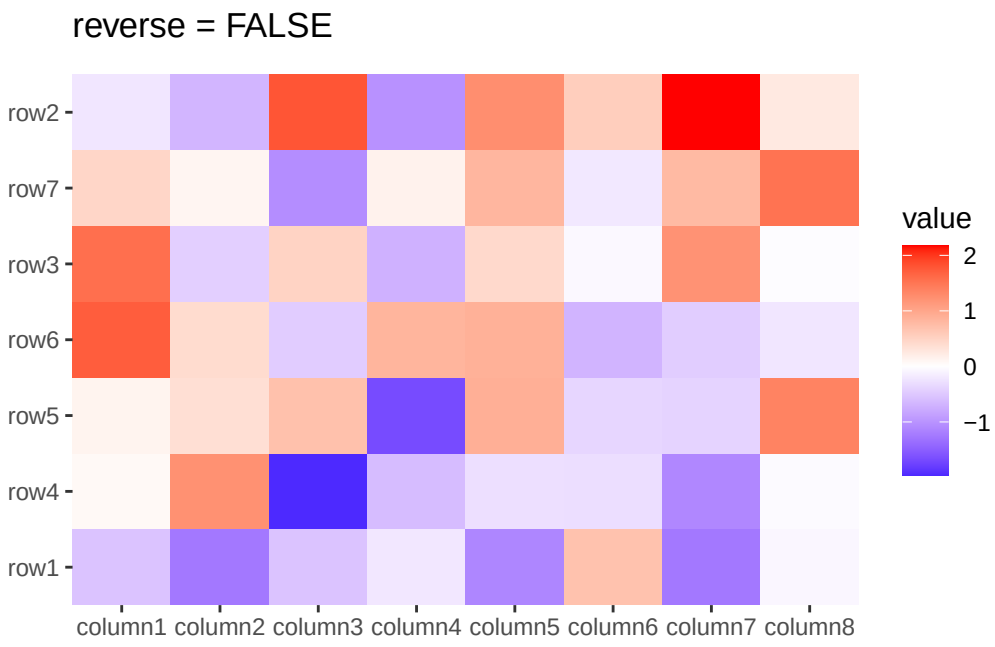


4.3 `align_order()`

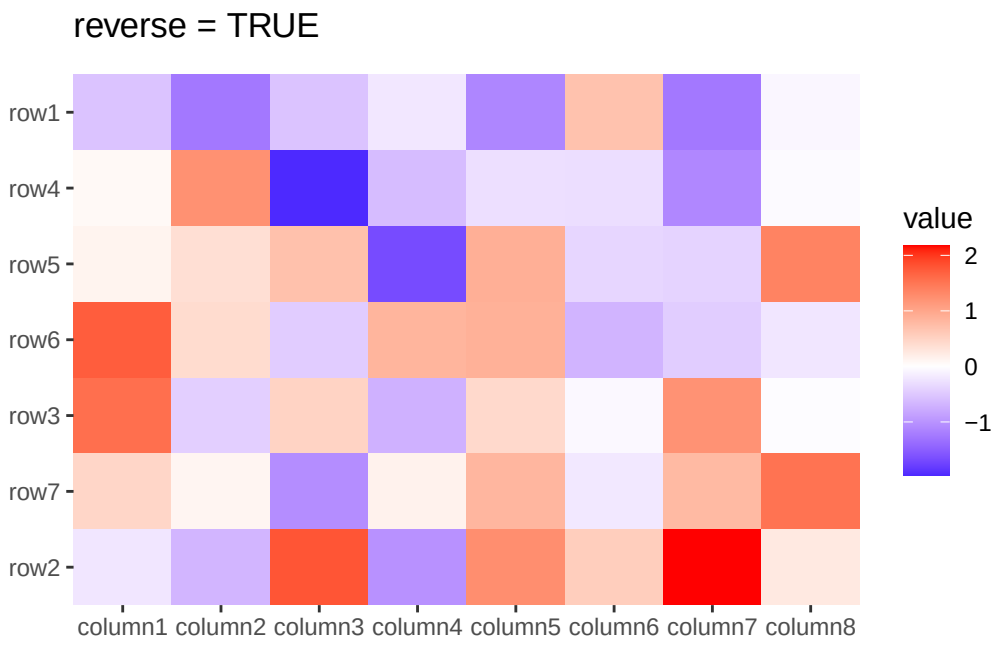
The `align_order()` function reorder the observations based on the summary weights.

In this example, we order the rows based on their means. By default, the ordering is in ascending order according to the summary weights. You can reverse the order by setting `reverse = TRUE`.

```
ggheatmap(small_mat) +
    anno_left() +
    align_order(rowMeans) +
    layout_title(title = "reverse = FALSE")
#> > heatmap built with `geom_tile()`
```



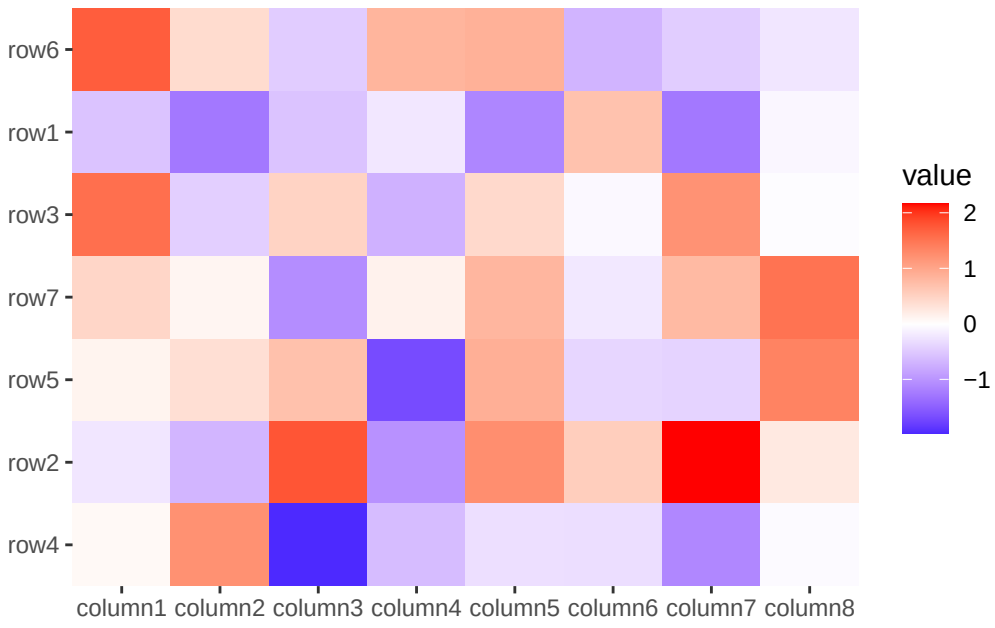

```
ggheatmap(small_mat) +
    anno_left() +
    align_order(rowMeans, reverse = TRUE) +
    layout_title(title = "reverse = TRUE")
#> > heatmap built with `geom_tile()`
```



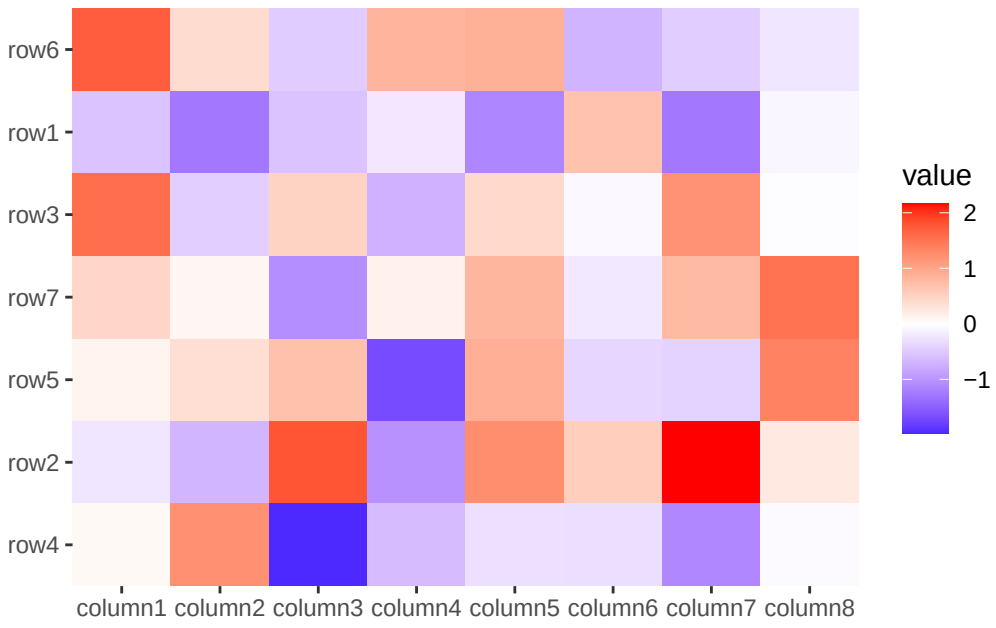
Additionally, you can provide the ordering integer index or character index directly:

```
set.seed(1234)
my_order <- sample(nrow(small_mat))
print(rownames(small_mat)[my_order])
#> [1] "row4" "row2" "row5" "row7" "row3" "row1" "row6"
```

```
ggheatmap(small_mat) +
    anno_left() +
    align_order(my_order)
#> > heatmap built with `geom_tile()`
```



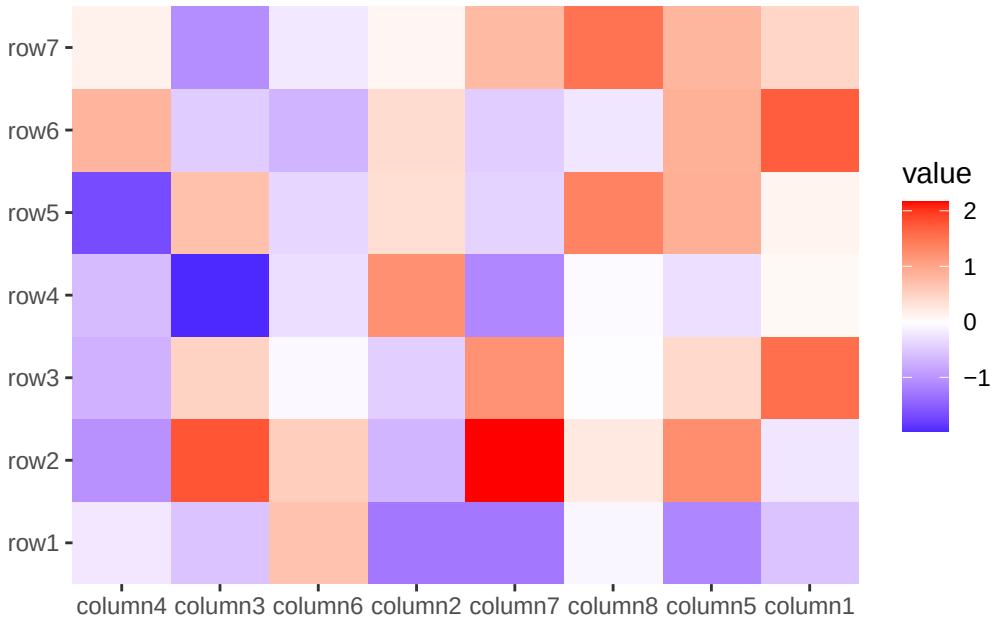

```
ggheatmap(small_mat) +
    anno_left() +
    align_order(rownames(small_mat)[my_order])
#> > heatmap built with `geom_tile()`
```



Some `align_*` functions also accept a `data` argument. It's important to note that all `align_*` functions treat rows as the observations. This means `NROW(data)` must match the `number of observations` along the axis used for alignment. The `data` argument can also accept a function (supporting purrr-like lambda syntax), which will be applied to the layout matrix.

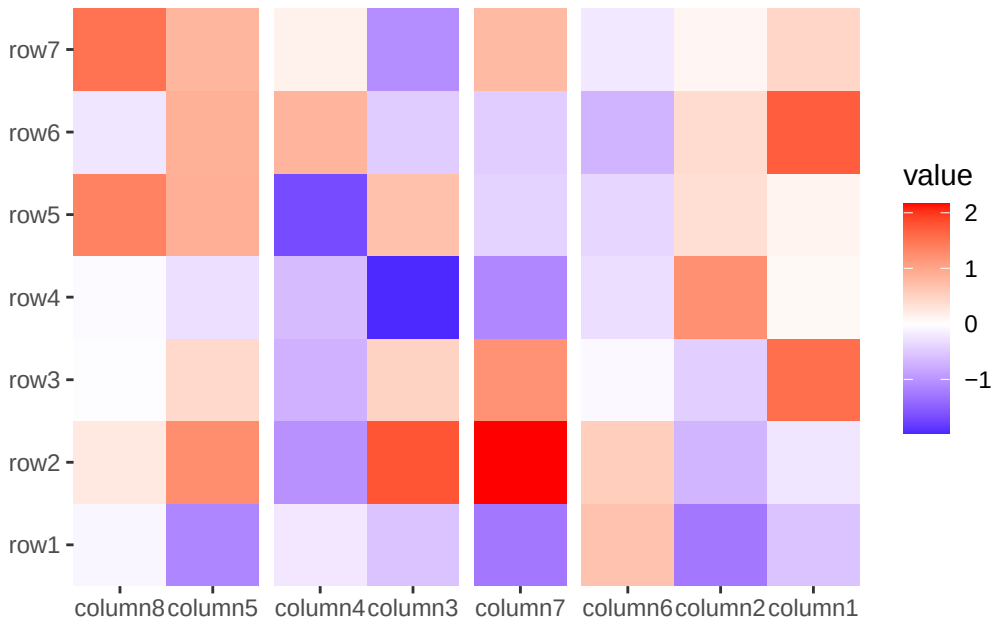
As mentioned in Section 3.4, for top and bottom annotations, the data matrix of `quad_layout()`/`ggheatmap()` is transposed to create the annotation `stack_layout()`. Therefore, you can use `rowMeans()` to calculate the mean value across all columns.

```
ggheatmap(small_mat) +
    anno_top() +
    align_order(rowMeans)
#> > heatmap built with `geom_tile()`
```



Some `align_*` functions that reorder observations include an argument called `strict`. This argument is especially useful when previous groups have already been established. If previous groups have been created and `strict = FALSE`, the function will reorder the observations within each group.

```
set.seed(1234)
ggheatmap(small_mat) +
    anno_top() +
    align_group(sample(letters[1:4], ncol(small_mat), replace = TRUE))+
    align_order(rowMeans, strict = FALSE)
#> > heatmap built with `geom_tile()`
```



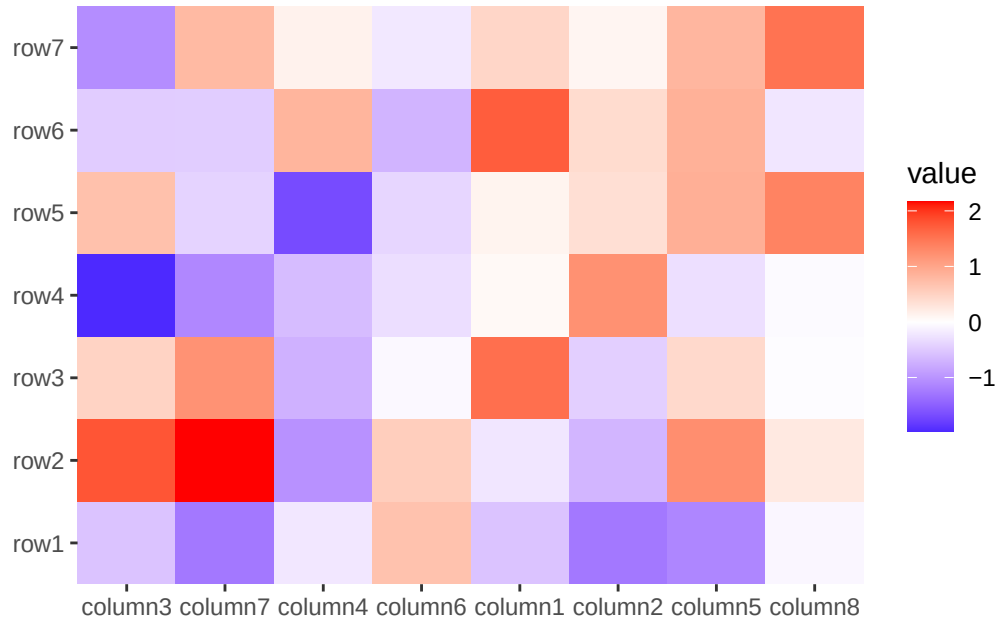
Note that we always prevent reordering the observations into two different orderings. If you want to apply two different orderings, you should use `cross_layout()` instead, which I'll introduce in a later chapter:

```
set.seed(1234)
another_order <- sample(ncol(small_mat))
ggheatmap(small_mat) +
    anno_top() +
    align_order(rowMeans) +
    align_order(another_order)
#> Error in `setup_design()`:
#> ! `align_order()` disrupt the previously established ordering index of
#>   the top annotation `stack_discrete()`
```

4.4 `align_hclust()`

The `align_hclust()` function is designed to reorder observations and group them based on hierarchical clustering. Unlike `align_dendro()`, `align_hclust()` does not add a dendrogram tree to the plot. All the arguments intruduced here can also be used by `align_dendro()`.

```
ggheatmap(small_mat) +
    anno_top() +
    align_hclust()
#> > heatmap built with `geom_tile()`
```

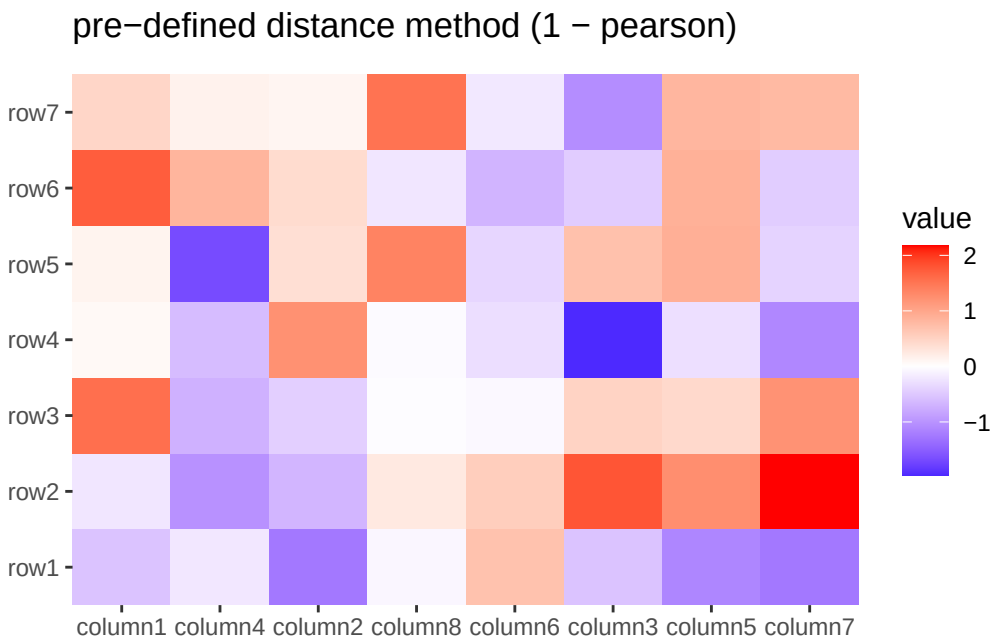


Hierarchical clustering is performed in two steps: calculate the distance matrix and apply clustering. You can use the `distance` and `method` argument to control the builind process.

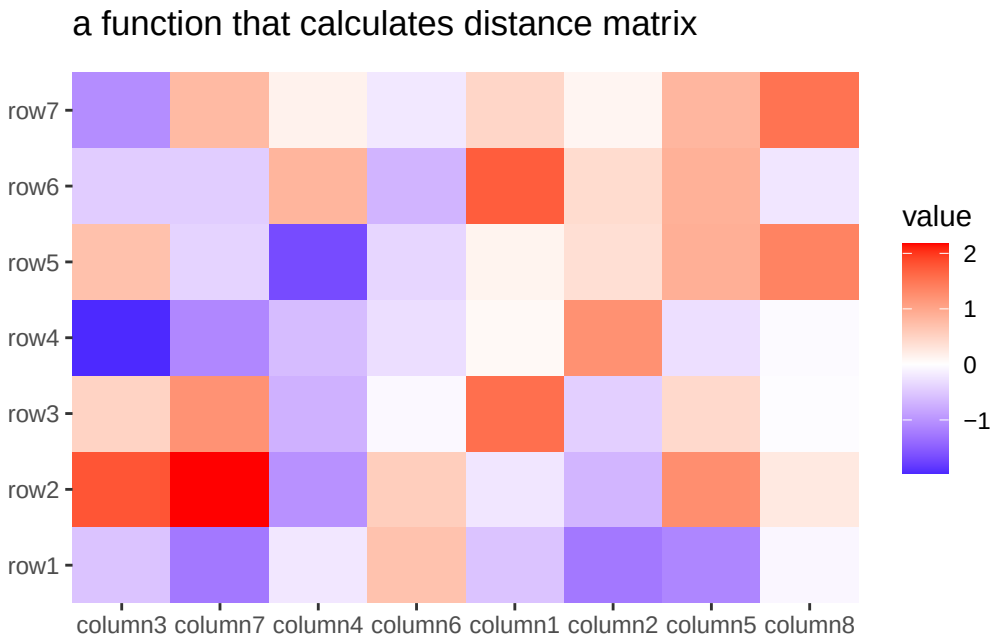
There are two ways to specify `distance` metric for clustering:

- specify `distance` as a pre-defined option. The valid values are the supported methods in `dist()` function and coorelation coefficient `"pearson"`, `"spearman"` and `"kendall"`. The correlation distance is defined as `1 - cor(x, y, method = distance)`.
- a self-defined function which calculates distance from a matrix.

```
ggheatmap(small_mat) +
    anno_top() +
    align_hclust(distance = "pearson") +
    layout_title("pre-defined distance method (1 - pearson)")
#> > heatmap built with `geom_tile()`
```

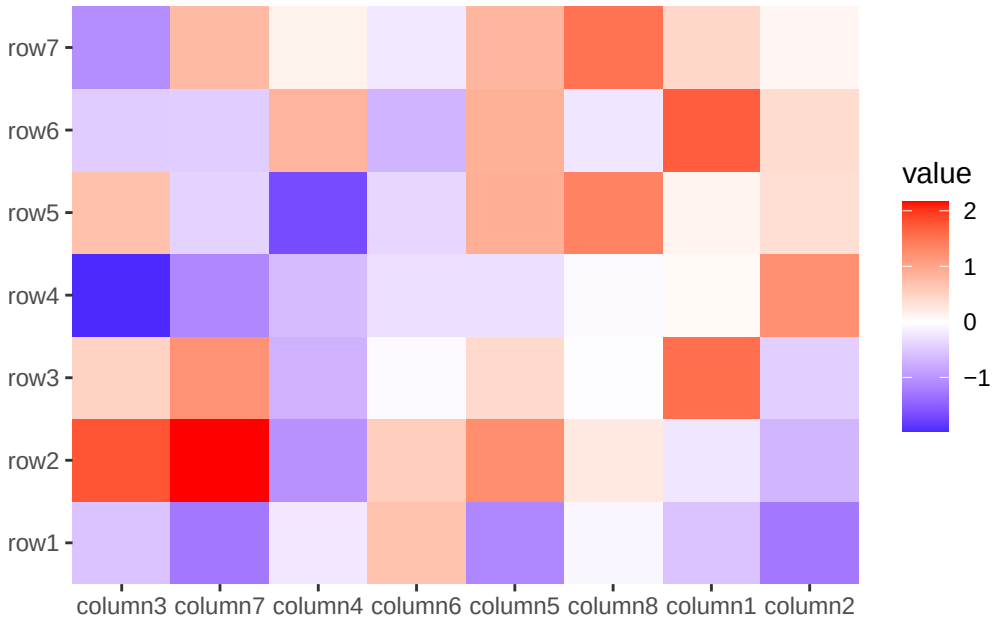



```
ggheatmap(small_mat) +
    anno_top() +
    align_hclust(distance = function(m) dist(m)) +
    layout_title("a function that calculates distance matrix")
#> > heatmap built with `geom_tile()`
```



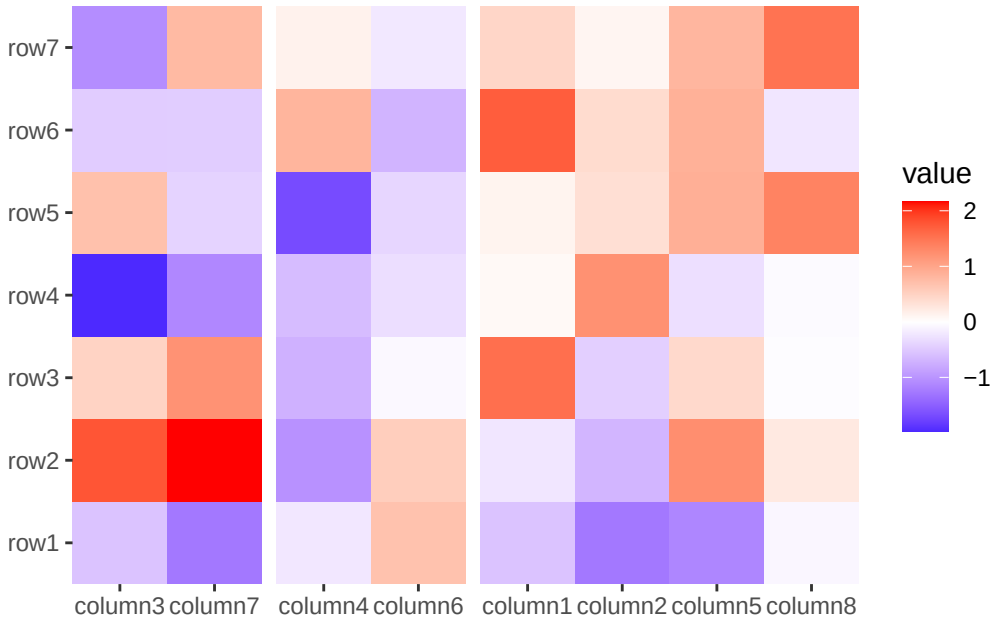
Method to perform hierarchical clustering can be specified by `method`. Possible methods are those supported in `hclust()` function. And you can also provide a self-defined function, which accepts the `distance` object and return a `hclust` object.

```
ggheatmap(small_mat) +
    anno_top() +
    align_hclust(method = "ward.D2")
#> > heatmap built with `geom_tile()`
```



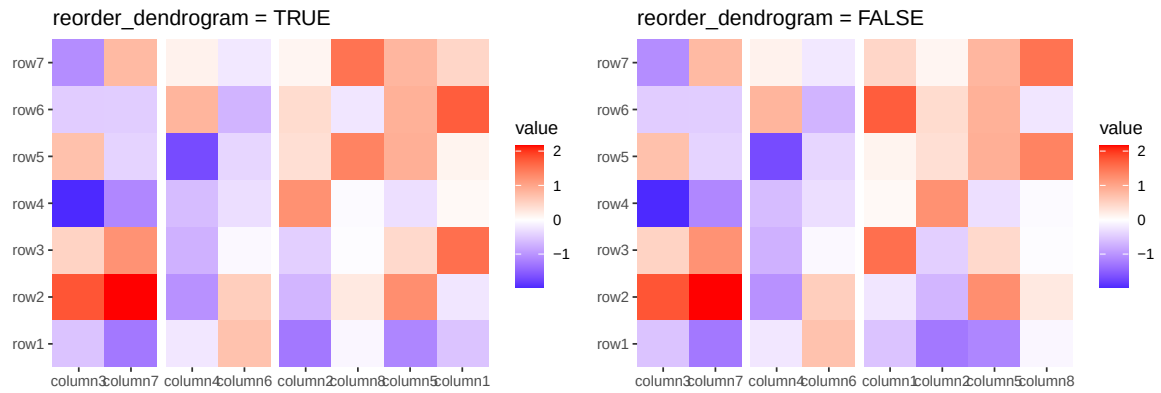
You can specify `k` or `h` to split observations into groups, which work similarly to `cutree()`:

```
ggheatmap(small_mat) +
    anno_top() +
    align_hclust(k = 3L)
#> > heatmap built with `geom_tile()`
```



You can reorder the dendrogram based on the mean values of the observations by setting `reorder_dendrogram = TRUE`.

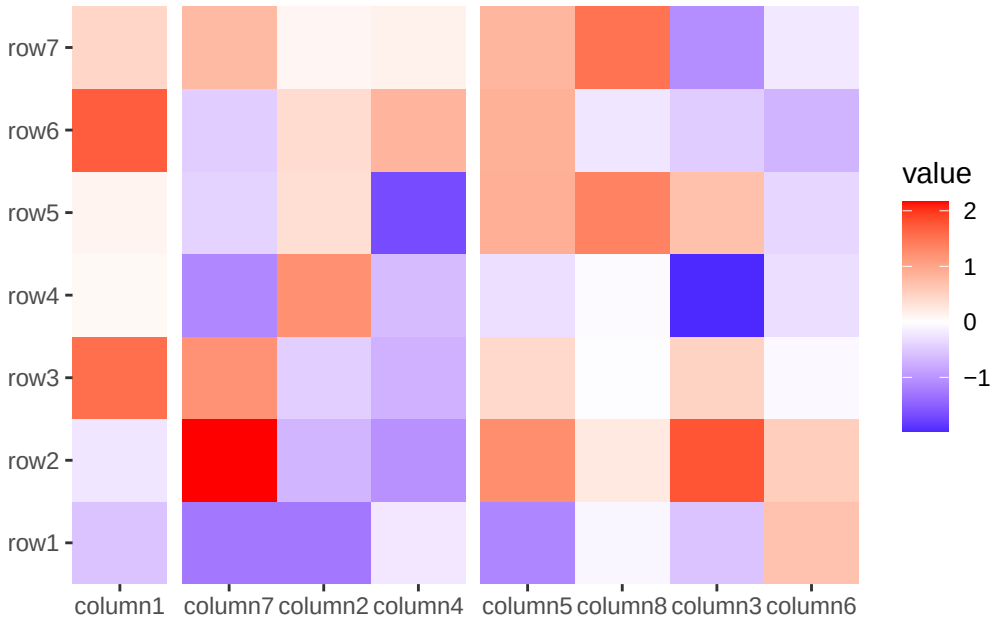
```
h1 <- ggheatmap(small_mat) +
    ggtitle("reorder_dendrogram = TRUE") +
    anno_top() +
    align_hclust(k = 3, reorder_dendrogram = TRUE)
h2 <- ggheatmap(small_mat) +
    ggtitle("reorder_dendrogram = FALSE") +
    anno_top() +
    align_hclust(k = 3)
align_plots(h1, h2)
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```



In this example, we use `align_plots()` to arrange the layouts, which functions similarly to `cowplot::align_plots()` and `patchwork::wrap_plots()`. However, unlike those, `align_plots()` can be directly used with `quad_layout()` and `stack_layout()`, ensuring proper alignment by plot panel. Additionally, `align_plots()` can align `pheatmap` and `ComplexHeatmap` objects, though they won't align by panel area in the same way as ggplot2 plots.

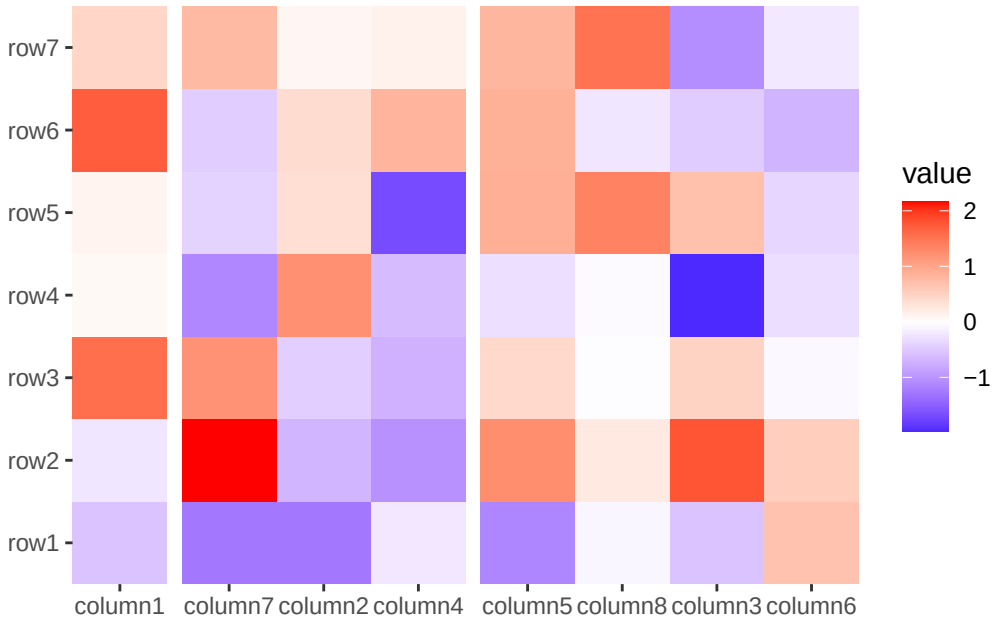
`align_hclust()` can also perform clustering between groups, meaning it can be used even if there are existing groups present in the layout, in this way, you cannot specify `k` or `h`:

```
set.seed(3L)
column_groups <- sample(letters[1:3], ncol(small_mat), replace = TRUE)
ggheatmap(small_mat) +
    anno_top() +
    align_group(column_groups) +
    align_hclust()
#> > heatmap built with `geom_tile()`
```



You can reorder the groups by setting `reorder_group = TRUE`, which reorders the hierarchical clusters based on the group tree:

```
ggheatmap(small_mat) +
    anno_top() +
    align_group(column_groups) +
    align_hclust(reorder_group = TRUE)
#> > heatmap built with `geom_tile()`
```



If you specify `k` or `h`, this will always turn off sub-clustering. The same principle applies to `align_hclust()`, where new groups must be nested within the previously established groups.

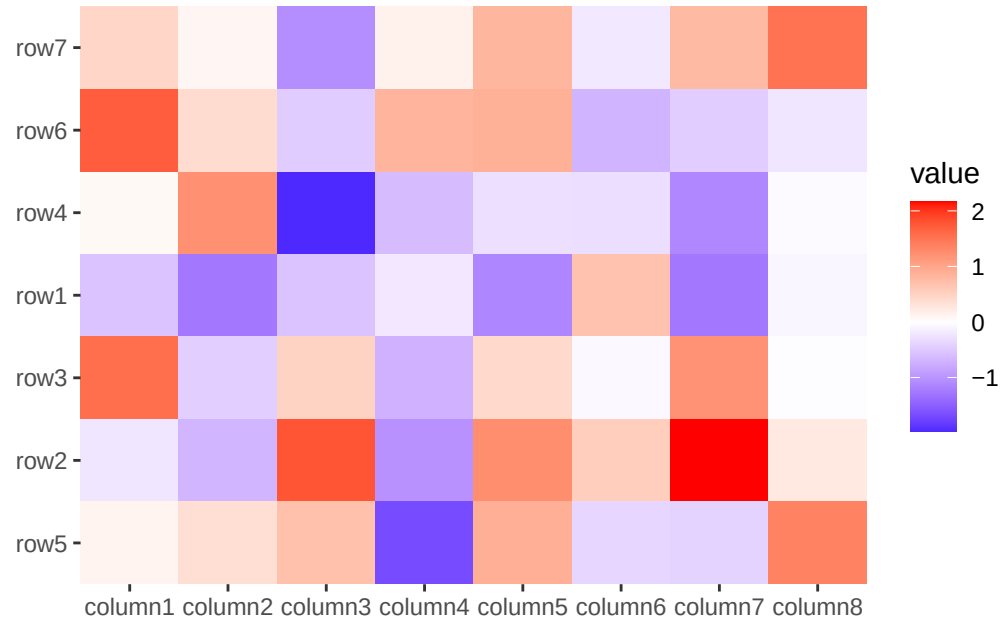
```
ggheatmap(small_mat) +
    anno_top() +
    align_group(column_groups) +
    align_hclust(k = 2L)
#> Error in `setup_design()`:
#> ! `align_hclust()` disrupt the previously established panel groups of
#>   the top annotation `stack_discrete()`
```

4.5 `align_reorder()`

The `align_reorder()` function enables the reordering of observations based on a specified statistical function. This function accepts a data argument and computes a statistic that determines the new ordering of the observations. The resulting order is extracted using the `order2()` function.

Foe example, you can also use hierarchical clustering to reorder the observations like this:

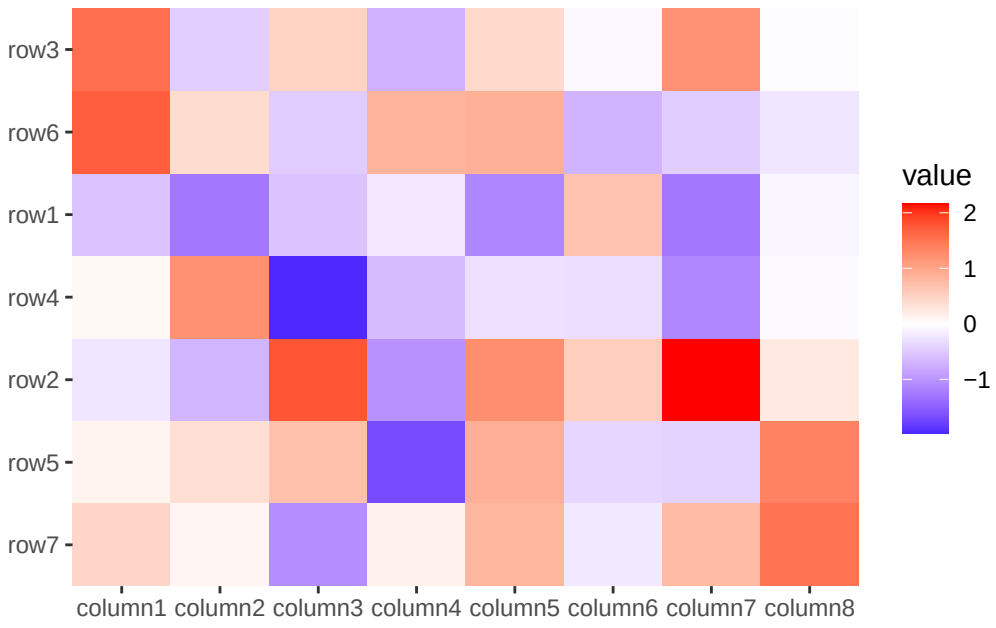
```
ggheatmap(small_mat) +
    anno_left() +
    align_reorder(hclust2)
#> > heatmap built with `geom_tile()`
```



Here, `hclust2()` is a special function used by `align_hclust()` to calculate the distance matrix and perform hierarchical clustering.

In addition to hierarchical clustering, the `align_reorder()` function can also handle objects from the seriation package. For example, you can use the `seriate()` function with a method like `"BEA_TSP"` to reorder the observations based on a specific seriation algorithm:

```
ggheatmap(small_mat) +
    anno_left() +
    align_reorder(seriation::seriate, method = "BEA_TSP", data = abs)
#> > heatmap built with `geom_tile()`
```



This approach gives you the flexibility to apply different statistical or algorithmic methods for reordering observations, which can be especially useful for exploring complex patterns in data.

With the `align_*` functions in place, we've covered how to reorder and group observations within a layout. Now, having set the stage for proper observation alignment, we can move on to the next essential step: `plot initialize`. In the following chapter, we'll dive deeper into how to set up your plots within the layout.

5 Plot initialize

There are following primary functions for adding plots:

- `ggalign()`: Create a ggplot object and aligns the axes.
- `ggfree()`: Create a ggplot object without alignment.
- `align_dendro()`: Create a ggplot object of dendrogram tree, and align the observation. In addition, it can reorder and group the observations.

All these functions will set the active plot when added to the layout.

Both `ggmark()` and `align_dendro()` can only for discrete variables.

```
library(ggalign)
#> Loading required package: ggplot2
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

5.1 `ggalign()`

`ggalign` is the package name but it's also a function in the package. `ggalign()` is similar to `ggplot` in that it initializes a `ggplot` data and `mapping`. `ggalign()` allowing you to provide data in various formats, including matrices, data frames, or simple vectors. By default, it will inherit from the layout. If a function, it will apply with the layout data.

The underlying plot data will be created using `fortify_data_frame()`, which, By default, calls `ggplot2::fortify()` to build the data frame. Additional methods have been added for atomic vector and matrix. For atomic vector, it will convert it to a data frame with following columns:

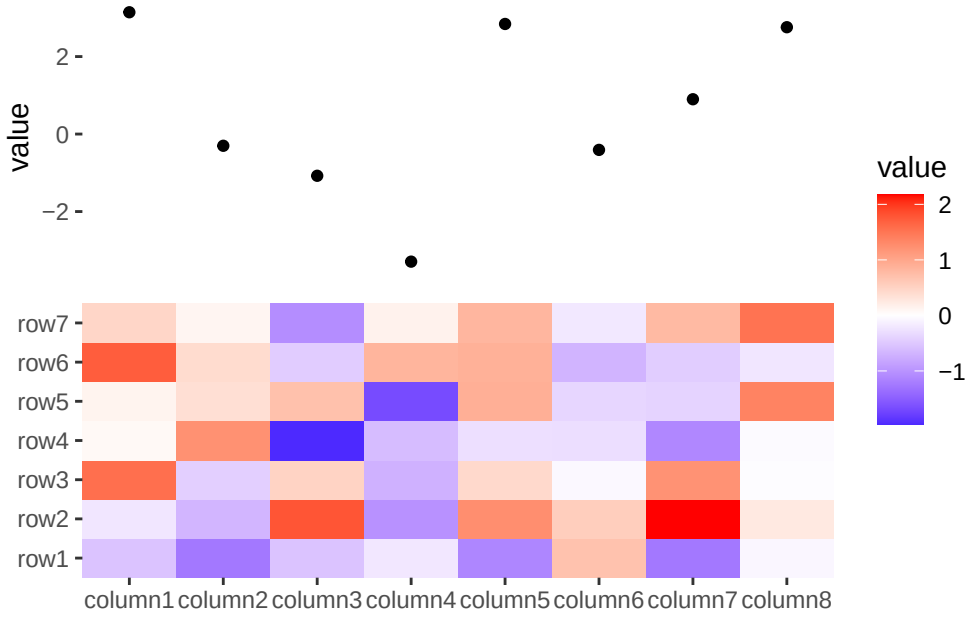
- `.names`: the names for the vector (only applicable if names exist).
- `value`: the actual value of the vector.

When `data` is a matrix, it will automatically be transformed into a long-form data frame, where each row represents a unique combination of matrix indices and their corresponding values. The resulting data frame will contain the following columns:

- `.row_names` and `.row_index`: the row names (only applicable when names exist) and an integer representing the row index of the original matrix.
- `.column_names` and `.column_index`: the column names (only applicable when names exist) and column index of the original matrix.
- `value`: the actual value.

When alignning continuous variables, `ggalign()` will apply the `limits` set by the layout when drawing.

```
ggheatmap(small_mat) +
    anno_top() +
    ggalign(data = rowSums) +
    geom_point(aes(y = value))
#> > heatmap built with `geom_tile()`
```



When aligning discrete variables, `ggalign()` always applies a default mapping for the axis of the data index in the layout. Specifically, This mapping is `aes(y = .data$.y)` for horizontal stack (including left and right annotation) and `aes(x = .data$.x)` for vertical stack (including top and bottom annotation).

The following columns will be added to the data frame to align discrete variables:

- `.panel`: The panel for the aligned axis. Refers to the `x-axis` for vertical `stack_layout()` (including top and bottom annotations), and the `y-axis` for horizontal `stack_layout()` (including left and right annotations).

- `.names` ([`vec_names()`][vctrs::vec_names]) and `.index` ([`vec_size()`][vctrs::vec_size()]/[`NROW()`]): Character names (if available) and the integer index of the original data.
- `.x`/`.y` and `.discrete_x`/`.discrete_y`: Integer indices for `x`/`y` coordinates, and a factor of the data labels (only applicable when names exist).

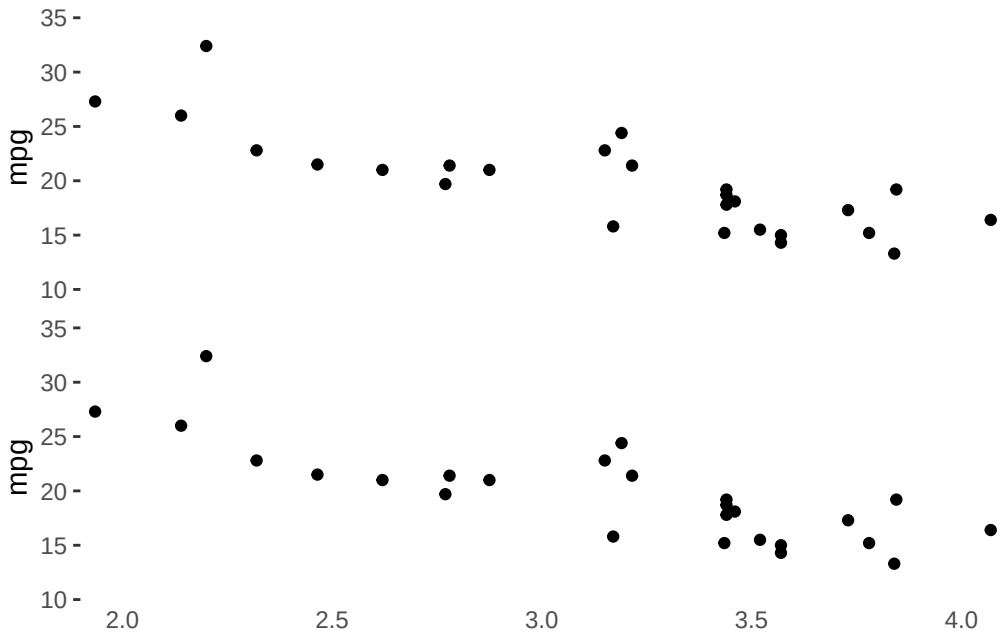
  It is recommended to use `.x`/`.y`, or `.discrete_x`/`.discrete_y` as the `x`/`y` mapping.

When aligning discrete variables, almost all functions that add plots will generate data containing two key columns:

- `.panel`: used to create ggplot2 facets.
- `.index`: serves to match the data. It is useful for aligning observations or linking different data sources. You can use `.index` to merge data and create a new data frame, using method provided in Section 11.2.

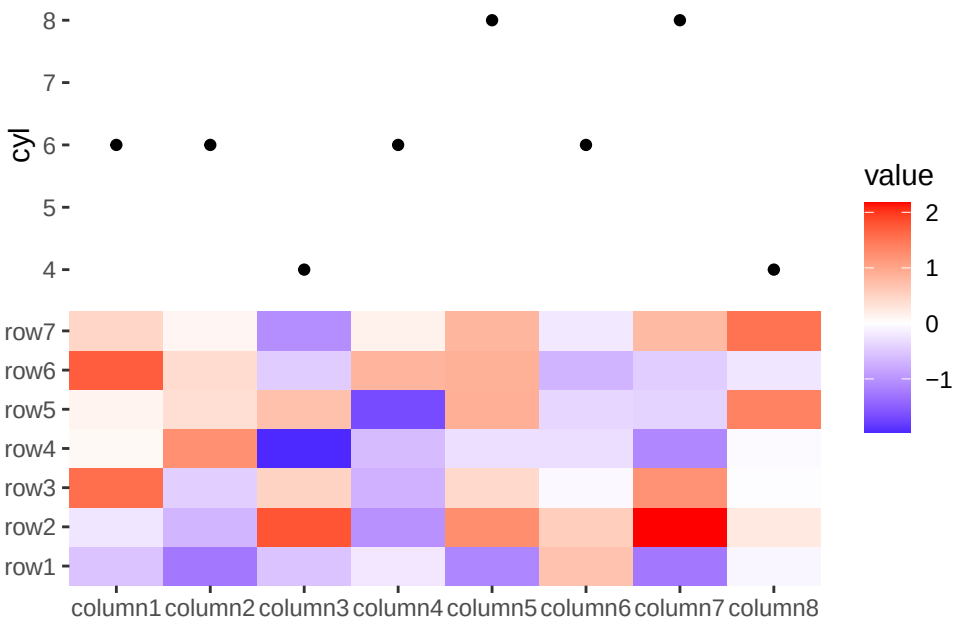
Additionally, if names exist, the `.names` column will also be created.

```
stack_continuous("v", mtcars, limits = continuous_limits(c(2, 4))) +
    ggalign(mapping = aes(wt, mpg)) +
    geom_point() +
    ggalign(mapping = aes(wt, mpg)) +
    geom_point() +
    theme(axis.text.x = element_text())
```



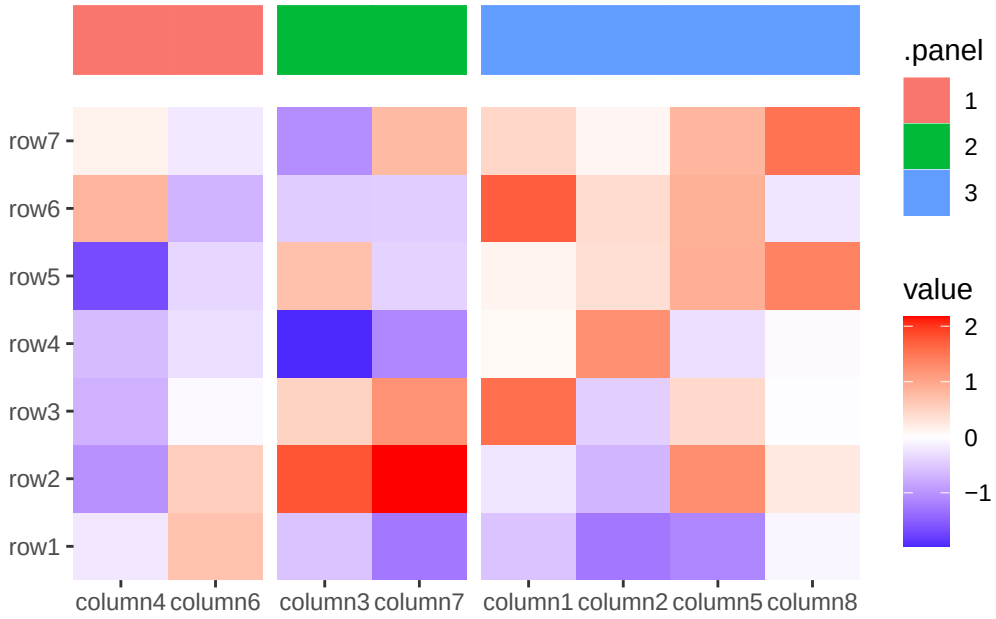
When aligning discrete variables, ensure that the number of rows in the data matches the number of observations along the axis used for alignment:

```
my_df <- mtcars[seq_len(ncol(small_mat)), ]
ggheatmap(small_mat) +
    anno_top() +
    ggalign(data = my_df) +
    geom_point(aes(y = cyl))
#> > heatmap built with `geom_tile()`
```



If `data = NULL`, the data in the underlying `ggplot` object only contains following columns: `.panel`, `.index`, `.names`, `.x`/`.y`, `.discrete_x`/`.discrete_y`. You can use it to integrate additional elements, such as block annotation or customized panel title, into your layout.

```
ggheatmap(small_mat) +
    anno_top(size = unit(1, "cm")) +
    align_kmeans(centers = 3L) +
    ggalign(data = NULL) +
    geom_tile(aes(y = 1L, fill = .panel, color = .panel)) +
    theme_no_axes("y")
#> > heatmap built with `geom_tile()`
```



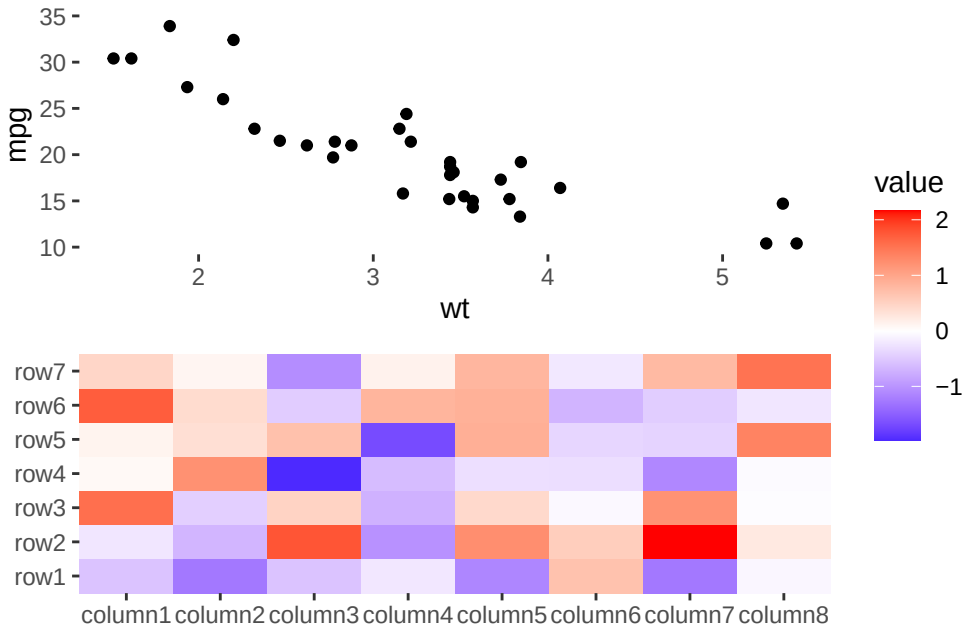
The function `theme_no_axes()` can be used to quickly remove axis text and titles from the plot.

5.2 `ggfree()`

The `ggfree()` function allows you to incorporate a ggplot object into your layout. Unlike `ggalign()`, which aligns every axis value precisely, `ggfree()` focuses on layout integration without enforcing strict axis alignment.

Internally, the function also uses `fortify_data_frame()` to transform the input into a data frame.

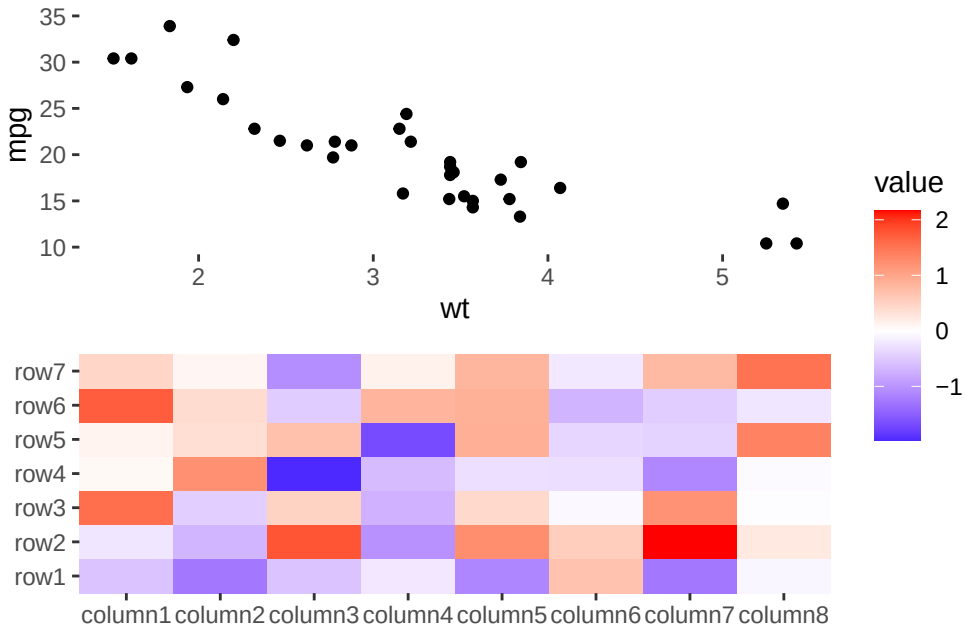
```
ggheatmap(small_mat) +
    anno_top() +
    ggfree(mtcars, aes(wt, mpg)) +
    geom_point()
#> > heatmap built with `geom_tile()`
```



Since `ggfree()` may use axes that are not aligned with the primary plot's axes, the axis titles will not be removed automatically. If you want to remove the axis titles, you must do so manually.

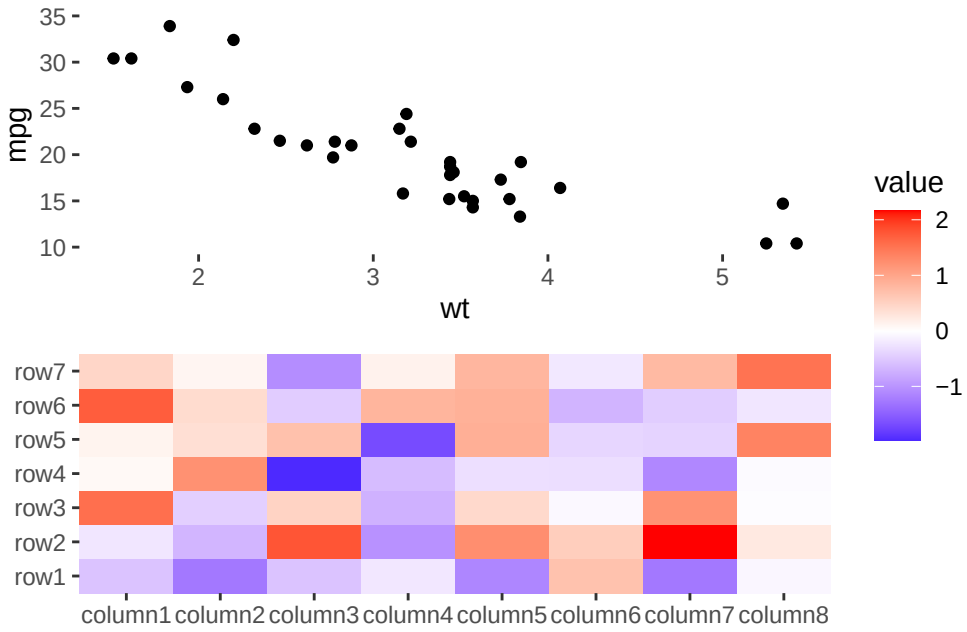
Alternatively, you can directly input the ggplot object.

```
ggheatmap(small_mat) +
    anno_top() +
    ggfree(ggplot(mtcars, aes(wt, mpg))) +
    geom_point()
#> > heatmap built with `geom_tile()`
```



You can also add the `ggplot` object directly without using `ggfree()`. However, doing so will limit control over the plot (like plot area `size`, and `active` components):

```
ggheatmap(small_mat) +
    anno_top() +
    ggplot(mtcars, aes(wt, mpg)) +
    geom_point()
#> > heatmap built with `geom_tile()`
```



5.2.1 Cross panel sumamry

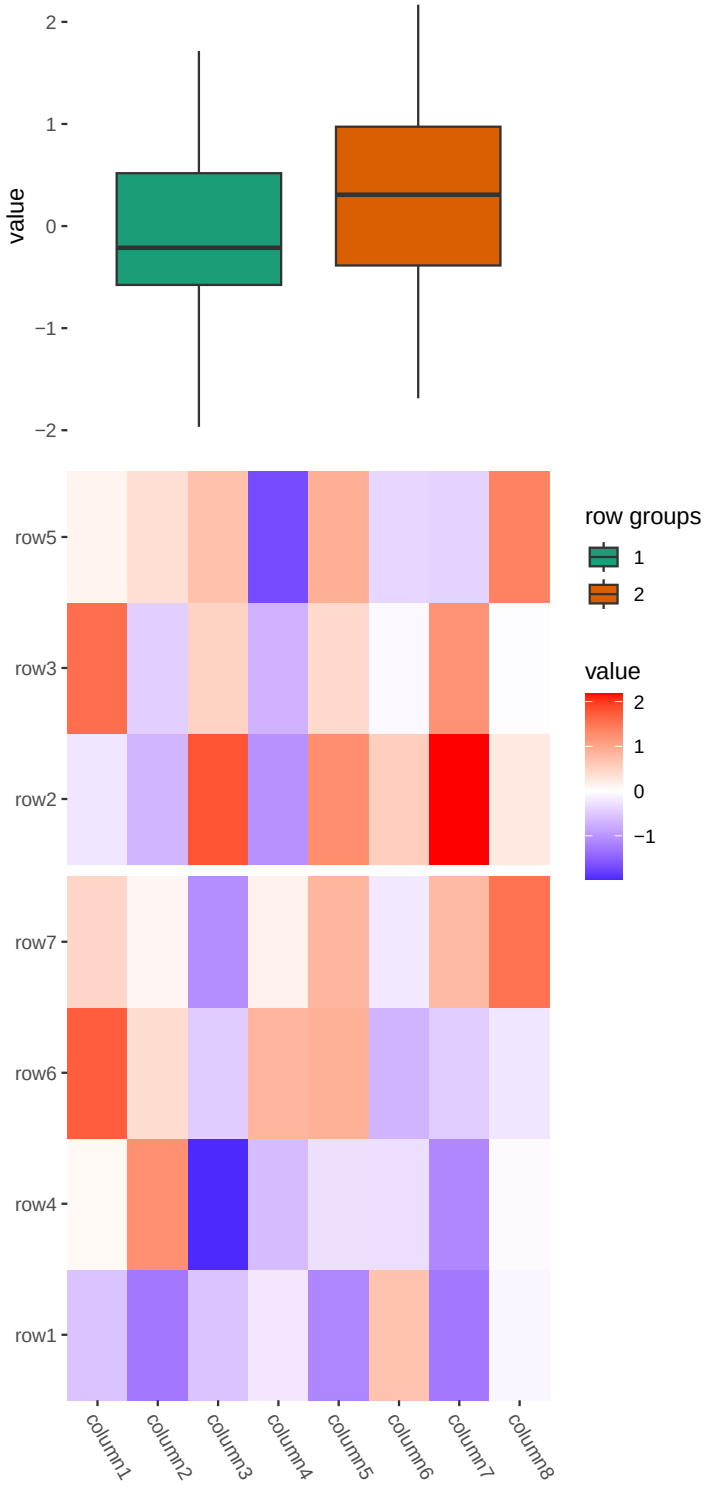
When used in `quad_layout()`/`ggheatmap()`, if the data is inherited from the `quad_layout()` and the other direction aligns discrete variables, following columns will be added:

- `.extra_panel`: Provides the panel information for the column (left or right annotation) or row (top or bottom annotation).
- `.extra_index`: The index information for the column (left or right annotation) or row (top or bottom annotation).

This is useful if you want to create summary plot using another axis panel groups.

```
set.seed(1234)
ggheatmap(small_mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +

    # in the right annotation
    anno_right() +
    align_kmeans(2) +

    # in the top annotation
    anno_top(size = 0.5) +
    ggfree() +
```

```
    geom_boxplot(aes(.extra_panel, value, fill = .extra_panel)) +
    scale_fill_brewer(palette = "Dark2", name = "row groups") +
    theme_no_axes("x")
#> > heatmap built with `geom_tile()`
```

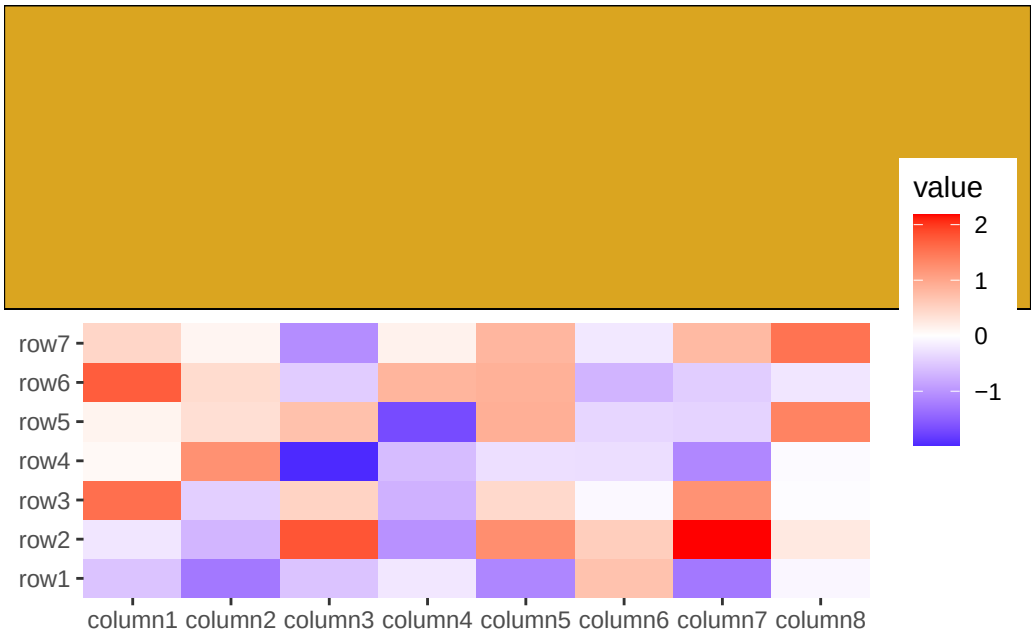

value
2
1
0
−1
−2
row5
row3
row2
row7
row6
row4
row1
column1
column2
column3
column4
column5
column6
column7
column8
row groups
1
2
value
2
1
0
−1

This approach replicates the functionality of ComplexHeatmap::anno_summary(), but is versatile enough to be used with any heatmap, not just single-column or single-row heatmaps.

5.3 `ggwrap()` and `inset()`

The `ggwrap()` function allows you to wrap objects that can be converted into a grob, turning them into a `ggplot` for plotting. Further you can still add ggplot elements like title, subtitle, tag, caption, and geoms using the same approach as with normal ggplots (using `ggtitle()`, `labs()`, `geom_*()`) as well as styling using `theme()`. This enables you to pass these wrapped objects into `ggfree()`.

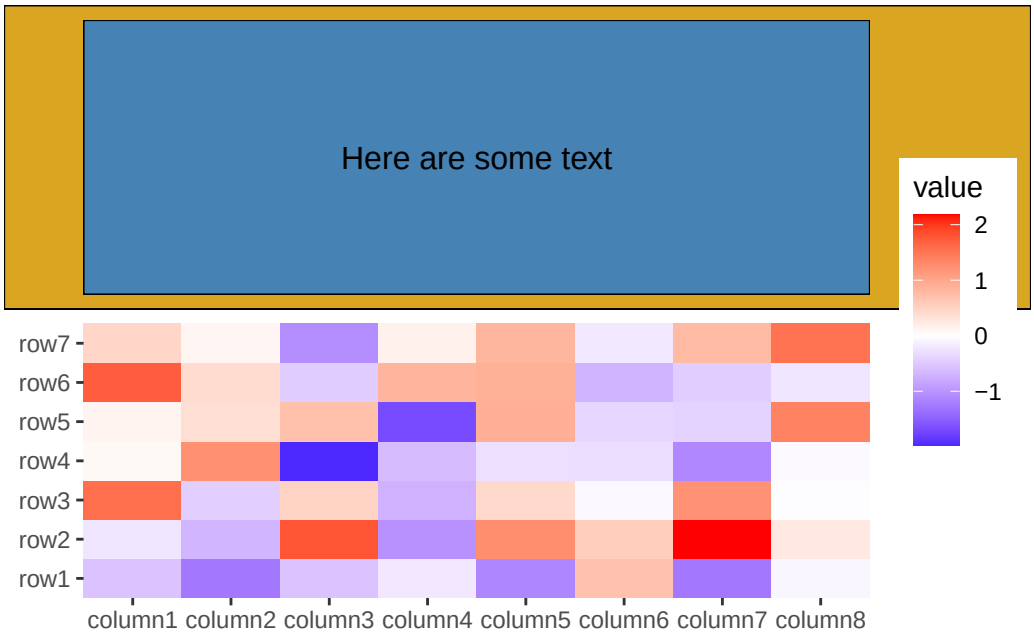
```
library(grid)
ggheatmap(small_mat) +
    anno_top() +
    # `ggwrap()` will create a `ggplot` object, we use `ggfree` to add it into the layout
    ggfree(data = ggwrap(rectGrob(gp = gpar(fill = "goldenrod")), align = "full"))
#> > heatmap built with `geom_tile()`
```



You can also integrate base plots, `pheatmap`, `ComplexHeatmap`, e.g.

Additionally, you can add any graphics as a inset to a ggplot using the `inset()` function. Like `ggwrap()`, `inset()` can accept any object that can be converted to a grob.

```
ggheatmap(small_mat) +
    anno_top() +
    ggfree(data = ggwrap(rectGrob(gp = gpar(fill = "goldenrod")), align = "full")) +
    # we can then add any inset grobs (the same as ggwrap, it can take any objects
    # which can be converted to a `grob`)
    inset(rectGrob(gp = gpar(fill = "steelblue")), align = "panel") +
    inset(textGrob("Here are some text", gp = gpar(color = "black")),
        align = "panel"
    )
#> > heatmap built with `geom_tile()`
```



5.4 `align_dendro()`

`align_dendro()` is an extension of `align_hclust()` that adds a dendrogram to the layout. All functions of `align_hclust()` introduced in Section 4.4 can be used with `align_dendro()`. Here, we focus on the plot-related function.

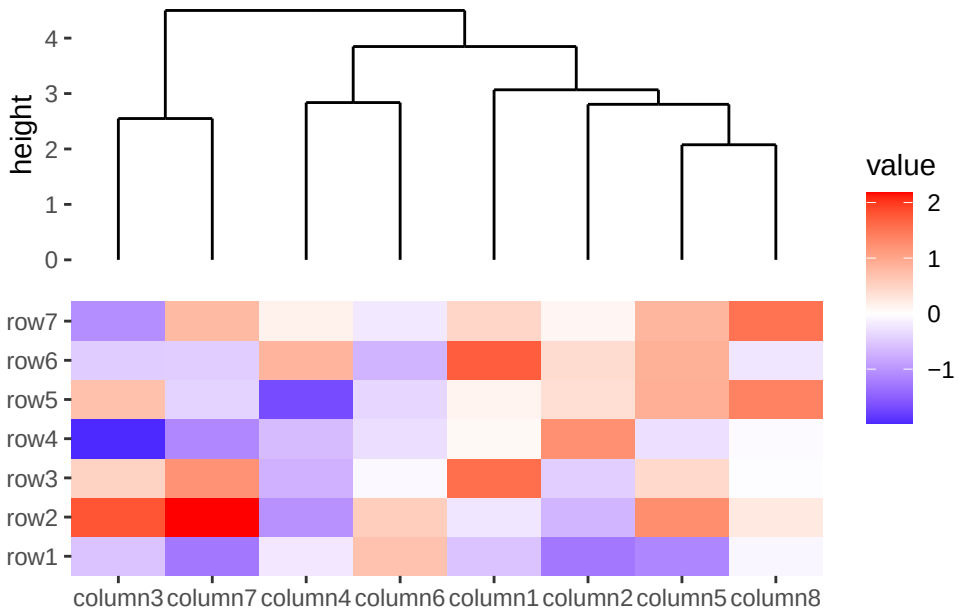
`align_dendro()` will initialize a ggplot object, the data underlying the ggplot object contains the dendrogram `node` data with dendrogram `edge` data attached in a special attribute.

dendrogram `node` and `edge` contains following columns:

- `.panel`: Tree branch groups, used to create ggplot2 facet.
- `.names` and `.index`: a character names (only applicable when names exists) and an integer index of the original data.
- `label`: node label text
- `x` and `y`: x-axis and y-axis coordinates for current node or the start node of the current edge.
- `xend` and `yend`: the x-axis and y-axis coordinates of the terminal node for current edge.
- `branch`: which branch current node or edge is. You can use this column to color different groups.
- `leaf`: A logical value indicates whether current node is a leaf.

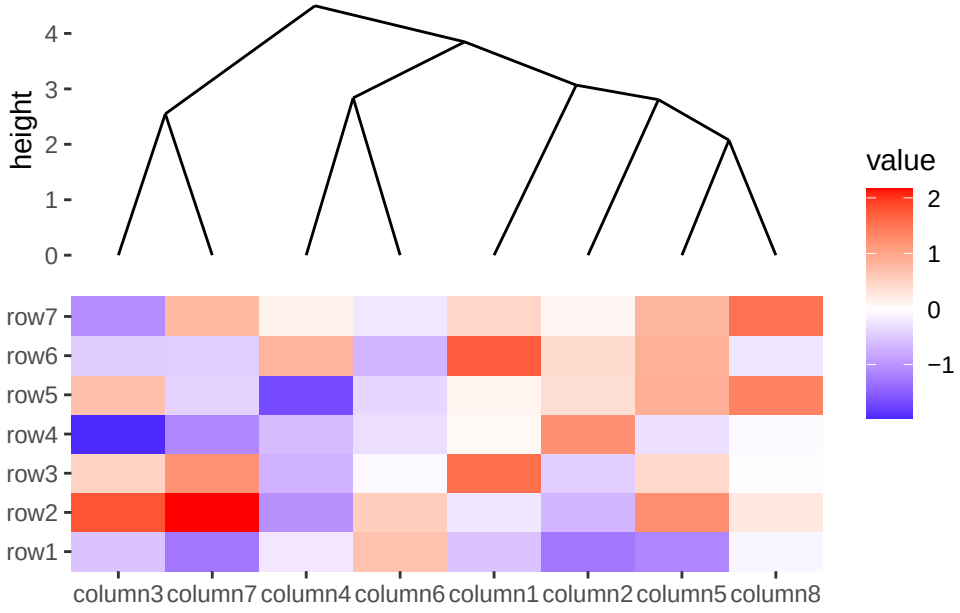
By default, `plot_dendrogram` is set to `TRUE`, meaning a `geom_segment()` layer will be added using the dendrogram edge data when drawing. Note that this layer is always added to the first.

```
ggheatmap(small_mat) +
    anno_top() +
    align_dendro()
#> > heatmap built with `geom_tile()`
```



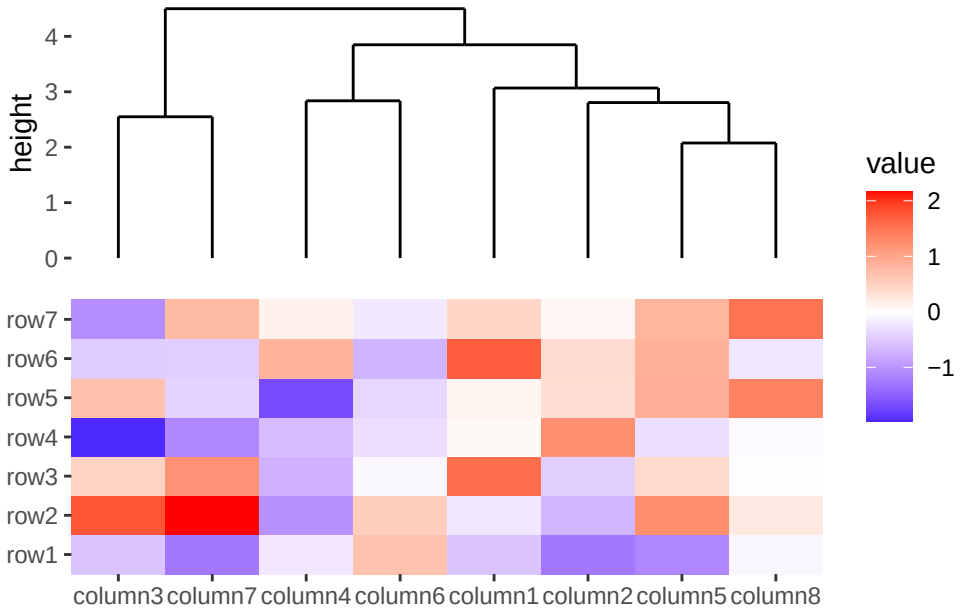
You can choose between two dendrogram types: `"rectangle"` (default) and `"triangle"`. However, if there are any groups in the stack, `"rectangle"` will be used.

```
ggheatmap(small_mat) +
    anno_top() +
    align_dendro(type = "triangle")
#> > heatmap built with `geom_tile()`
```



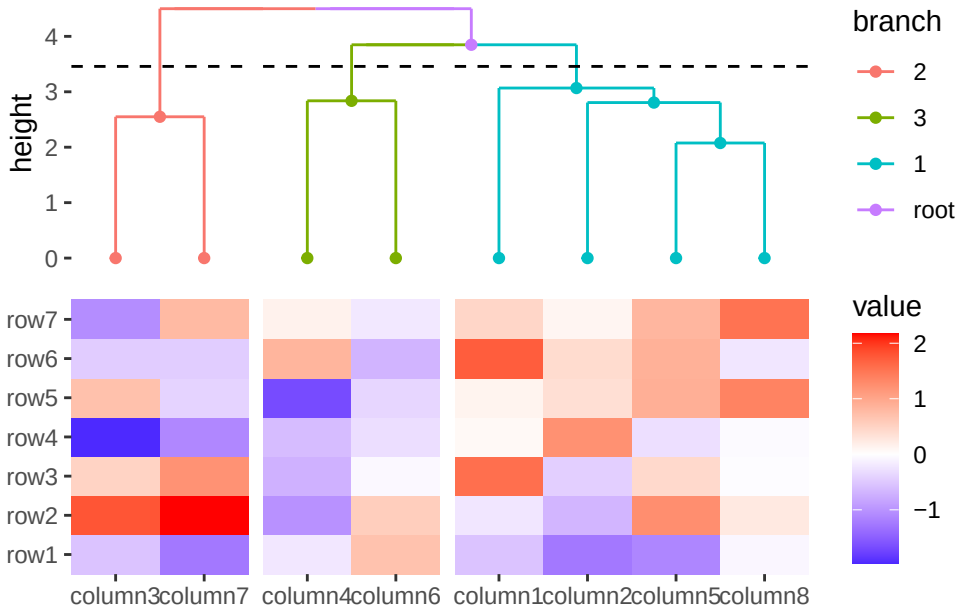
You can also manually add the dendrogram tree using the edge data by setting `plot_dendrogram = FALSE`. In this case, you can access the dendrogram `edge` data with `ggalign_attr()`. The `edge` data is stored in the edge field of `ggalign_attr()`:

```
ggheatmap(small_mat) +
    anno_top() +
    align_dendro(plot_dendrogram = FALSE) +
    geom_segment(
        aes(x = .data$x, y = .data$y, xend = .data$xend, yend = .data$yend),
        data = function(x) ggalign_attr(x, "edge")
    )
#> > heatmap built with `geom_tile()`
```



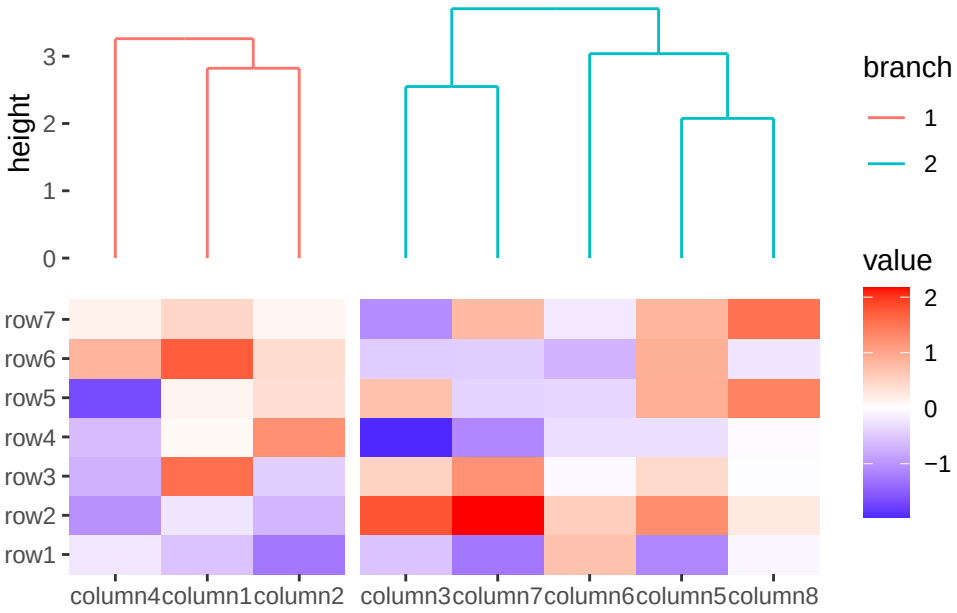
When there are multiple groups, a `branch` column will be available. This can be used to color the nodes or edges based on the group source.

```
ggheatmap(small_mat) +
    anno_top() +
    align_dendro(aes(color = branch), k = 3) +
    geom_point(aes(color = branch))
#> > heatmap built with `geom_tile()`
```



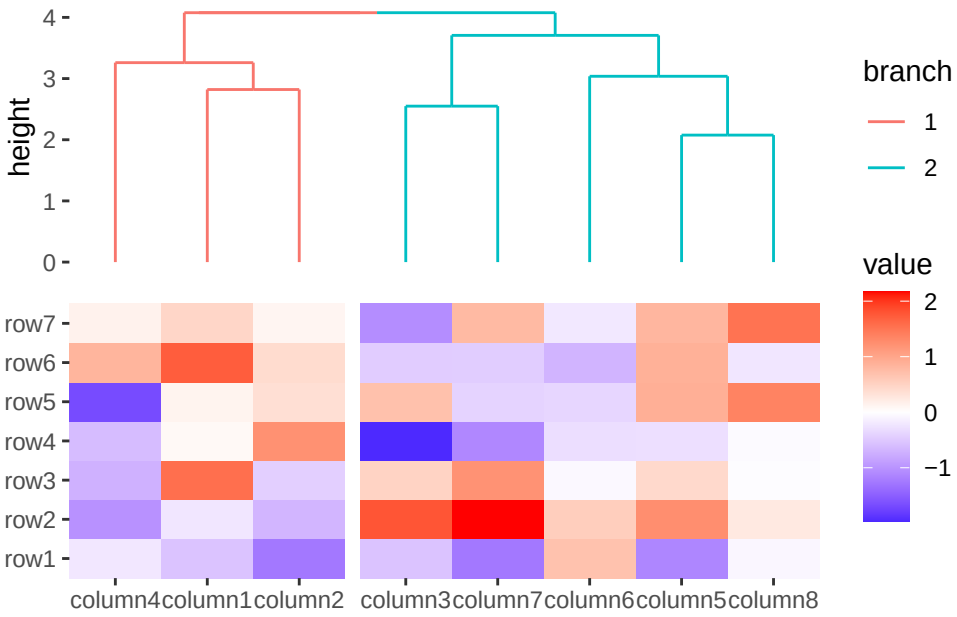
`align_dendro()` will draw dendrogram tree in each group when previous group exists.

```
set.seed(1234)
ggheatmap(small_mat) +
    anno_top() +
    align_kmeans(2) +
    align_dendro(aes(color = branch))
#> > heatmap built with `geom_tile()`
```



You can merge the sub-tree by settting `merge_dendrogram = TRUE`.

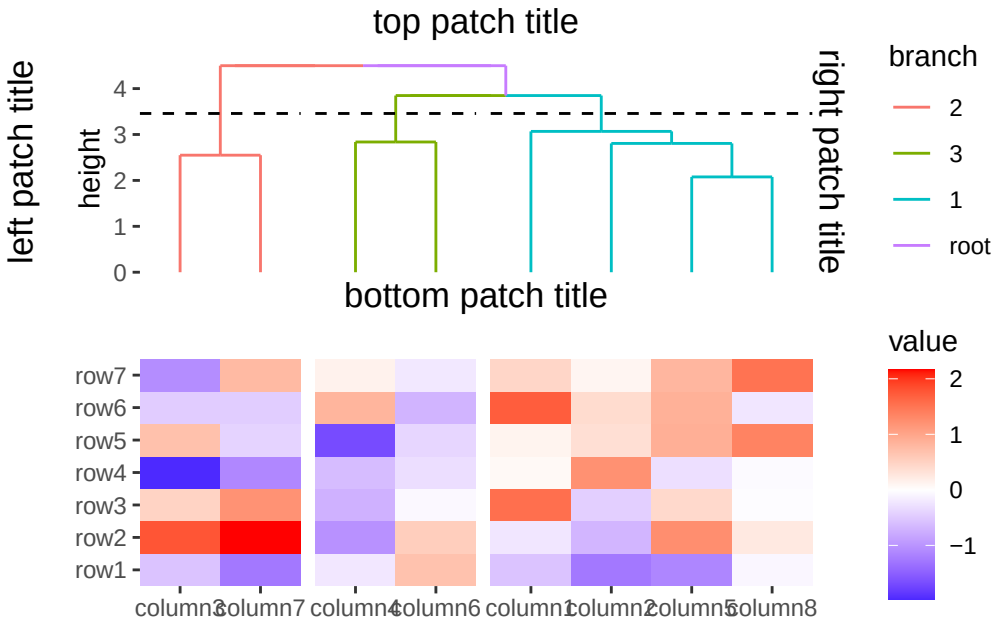
```
ggheatmap(small_mat) +
    anno_top() +
    align_kmeans(2) +
    align_dendro(aes(color = branch), merge_dendrogram = TRUE)
#> > heatmap built with `geom_tile()`
```



5.5 Plot titles

`ggplot2` only allow add titles in the top or add caption in the bottom. we extends this capability, allowing you to place titles around any border of the plot using the `patch_titles()` function.

```
ggheatmap(small_mat) +
    anno_top() +
    align_dendro(aes(color = branch), k = 3) +
    patch_titles(
        top = "top patch title",
        left = "left patch title",
        bottom = "bottom patch title",
        right = "right patch title"
    )
#> > heatmap built with `geom_tile()`
```

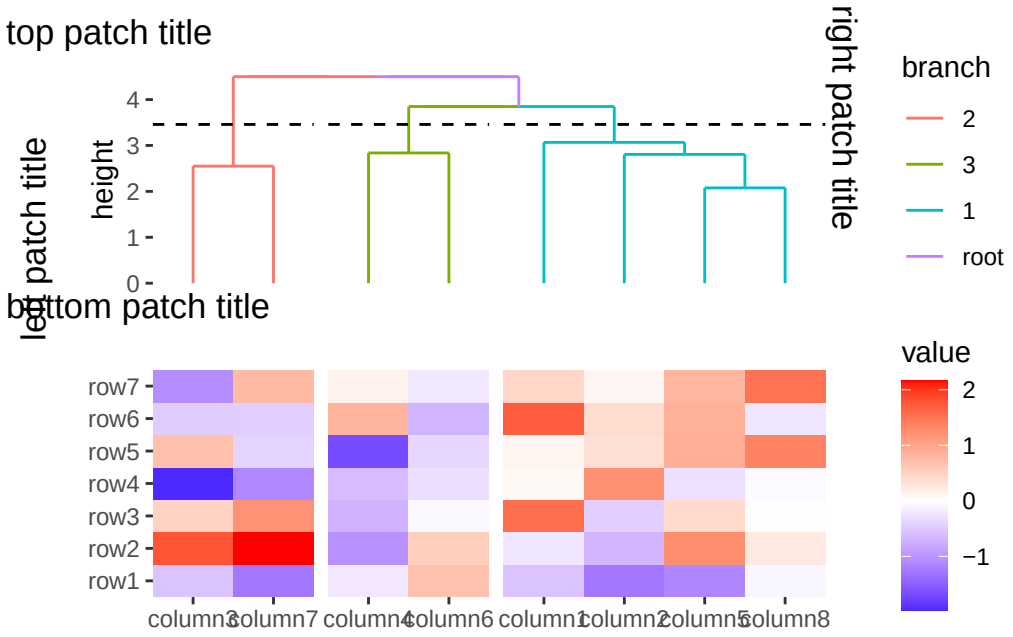


The appearance and alignment of these patch titles can be customized using `ggplot2::theme()`:

- `plot.patch_title`/`plot.patch_title.*`: Controls the text appearance of patch titles. By default, `plot.patch_title` inherit from `plot.title`, and settings for each border will inherit from `plot.patch_title`, with the exception of the `angle` property, which is not inherited.
- `plot.patch_title.position`/`plot.patch_title.position.*`: Determines the alignment of the patch titles. By default, `plot.patch_title.position` inherit from `plot.title.position`, and settings for each border will inherit from `plot.patch_title`. The value `"panel"` aligns the patch titles with the plot panels. Setting this to `"plot"` aligns the patch title with the entire plot (excluding margins and plot tags).

```
ggheatmap(small_mat) +
    anno_top() +
    align_dendro(aes(color = branch), k = 3) +
    patch_titles(
        top = "top patch title",
        left = "left patch title",
        bottom = "bottom patch title",
        right = "right patch title"
    ) +
    theme(
        plot.patch_title.position = "plot",
```

```
        plot.patch_title = element_text(hjust = 0)
    )
#> > heatmap built with `geom_tile()`
```



Now that you know the general approach to adding a plot, it would be useful to explore how to add annotation plots for specific observations. Let's move on to the next chapter.

6 Annotate observations

```
library(ggalign)
#> Loading required package: ggplot2
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

To add an annotation plot for specific observations, we must first know how to select the observations to be linked.

6.1 Links

The `pair_links()` function is used to define pairs of connected observations. In the formula, the left side (before the `~`) represents `hand1`—the observations on the left (for a horizontal stack layout) or top (for a vertical stack layout). The right side (after the `~`) represents `hand2`—the observations on the right (for horizontal stack) or bottom (for vertical stack).

These defined pairs will either be linked together, or each group in the pair will be linked separately within the same plot area.

Both sides of the formula can be specified using integer or character indices of the original data (before reordering).

```
pair_links(1:2 ~ c("c", "d"), c("a", "b") ~ 3:4)
#> <ggalign_pair_links>
#> A total of 2 pairs of link groups
#>
#>             hand1 ~ hand2
#>   1:          1:2 ~ c("c", "d")
#>   2:  c("a", "b") ~ 3:4
#>
#> A total of 4 link groups
```

The print method showed various informations:

- The object class and the number of paired groups.
- The specific groups in each pair.
- The total number of groups (rather than the number of paired groups). For example, in this case, there are 4 groups in total since each pair consists of 2 groups.

If only the left-hand side of the formula exists, you can input it directly.

```
pair_links(1:2, c("a", "b"))
#> <ggalign_pair_links>
#> A total of 2 pairs of link groups
#>
#>             hand1 ~ hand2
#>   1:          1:2 ~
#>   2:  c("a", "b") ~
#>
#> A total of 2 link groups
```

To specify links in the right only, you must use formula:

```
pair_links(~ 1:2, ~ c("a", "b"))
#> <ggalign_pair_links>
#> A total of 2 pairs of link groups
#>
#>       hand1 ~ hand2
#>   1:        ~ 1:2
#>   2:        ~ c("a", "b")
#>
#> A total of 2 link groups
```

For integer indices, wrap them with `I()` to follow ordering from the layout.

```
pair_links(I(1:2))
#> <ggalign_pair_links>
#> A total of 1 pair of link groups
#>
#>        hand1 ~ hand2
#>   1:  I(1:2) ~
#>
#> A total of 1 link group
```

You can wrap the whole formula.

```
pair_links(I(1:2 ~ 3:4))
#> <ggalign_pair_links>
#> A total of 1 pair of link groups
#>
#>        hand1 ~ hand2
#>   1:  I(1:2) ~ I(3:4)
#>
#> A total of 2 link groups
```

`range_link()` function can be used to define a range of observations, which accepts two argument that specify the lower and upper bounds of the range. These bounds should be defined as a single integer or character.

```
pair_links(range_link(1, "a"))
#> <ggalign_pair_links>
#> A total of 1 pair of link groups
#>
#>                    hand1 ~ hand2
#>   1:  range_link(1, "a") ~
#>
#> A total of 1 link group
```

In this case, the left-hand is defined as the range between the `1st` observation and the observation named `"a"`.

You can also use `waiver()` to inherit values from the opposite group.

```
pair_links(range_link(1, "a") ~ waiver())                                    ①
#> <ggalign_pair_links>
#> A total of 1 pair of link groups
#>
#>                    hand1 ~ hand2
#>   1:  range_link(1, "a") ~ waiver()
#>
#> A total of 2 link groups
```

① inherit values from the left hand

```
pair_links(waiver() ~ range_link(1, "a"))                                    ①
#> <ggalign_pair_links>
#> A total of 1 pair of link groups
#>
#>          hand1 ~ hand2
#>   1:  waiver() ~ range_link(1, "a")
#>
#> A total of 2 link groups
```

① inherit values from the right hand

You can combine any of these into a list.

```
pair_links(list(range_link(1, "a"), waiver()) ~ list(4:5, c("b", "c")))      ①
#> <ggalign_pair_links>
#> A total of 1 pair of link groups
#>
#>                                     hand1 ~ hand2
#>   1:  list(range_link(1, "a"), waiver()) ~ list(4:5, c("b", "c"))
#>
#> A total of 2 link groups
```

In this example, the left side combines the range between the `1st` observation and "a" with the observations 4 and 5, and the observations "b" and "c".

6.2 `ggmark()`

`ggmark()` can be used to add annotation plot for the selected observations. `ggmark` accepts `mark` argument, which should be a `mark_draw()` object to define how to draw the links. Currently, two internal functions `mark_line()`, `mark_tetragon()` can be used to quickly draw line and quadrilateral links used to connect the selected observations and the plot panel.

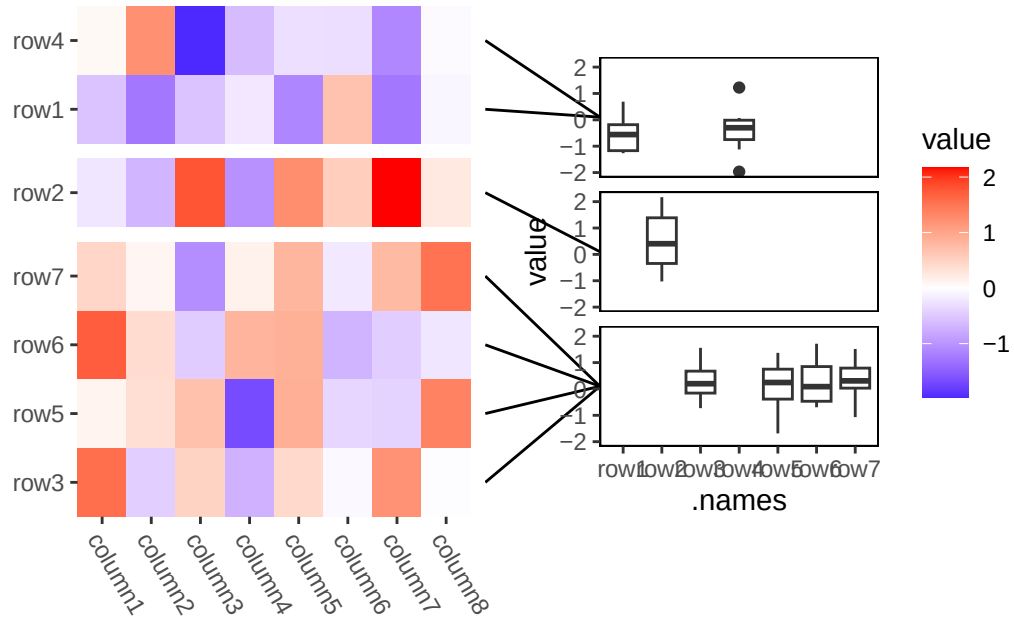
By default, when no manual observations were selected, `ggmark()` will select all observations and split them based on the groups defined in the layout.

The data underlying the ggplot object generated by `ggmark()` is similar to that of `ggalign()` (Section 5.1), but it differs in that it does not include the `.x`, `.y`, and `.discrete_x`/`.discrete_y` columns. Instead, a special column named `.hand` is added, which is a factor with levels `c("left", "right")` for horizontal stack layouts or `c("top", "bottom")` for vertical stack layouts. This column indicates the position of the linked observations.

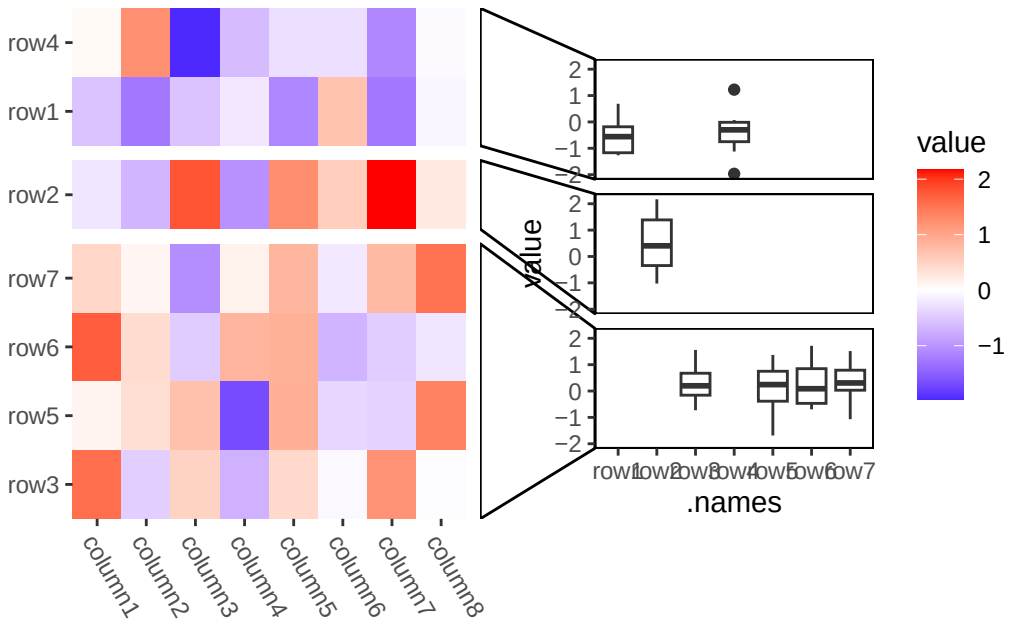
Note: Only data for selected observations are retained.

You can adjust the link size by using the `plot.margin` argument.

```
set.seed(123)
ggheatmap(small_mat) +
    theme(axis.text.x = element_text(hjust = 0, angle = -60)) +
    anno_right() +
    align_kmeans(3L) +
    ggmark(mark_line()) +
    geom_boxplot(aes(.names, value)) +
    theme(plot.margin = margin(l = 0.1, t = 0.1, unit = "npc"))
#> > heatmap built with `geom_tile()`
```

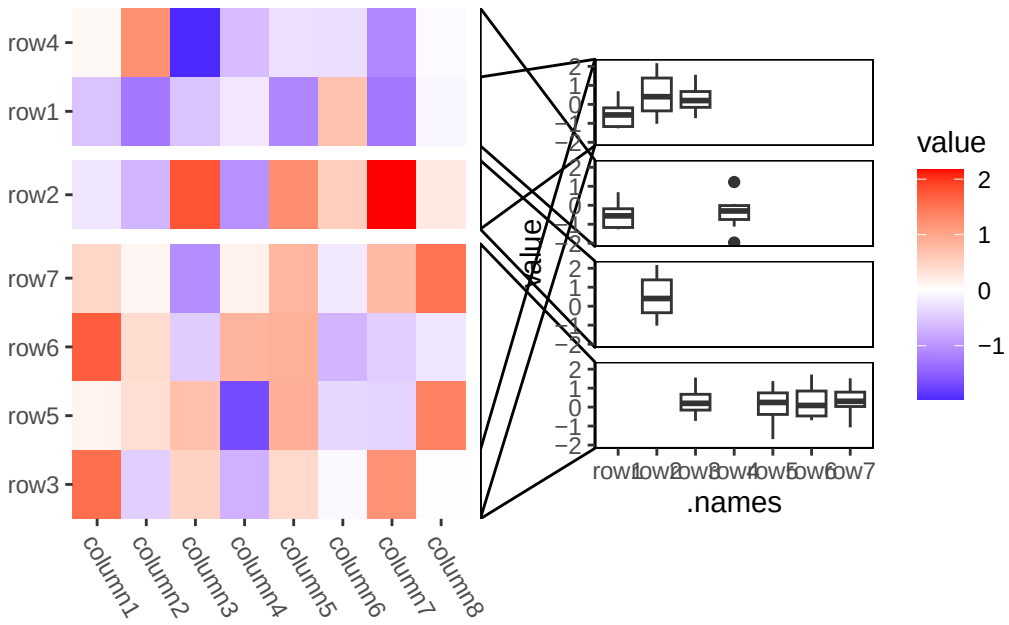



```
set.seed(123)
ggheatmap(small_mat) +
    theme(axis.text.x = element_text(hjust = 0, angle = -60)) +
    anno_right() +
    align_kmeans(3L) +
    ggmark(mark_tetragon()) +
    geom_boxplot(aes(.names, value)) +
    theme(plot.margin = margin(l = 0.1, t = 0.1, unit = "npc"))
#> > heatmap built with `geom_tile()`
```



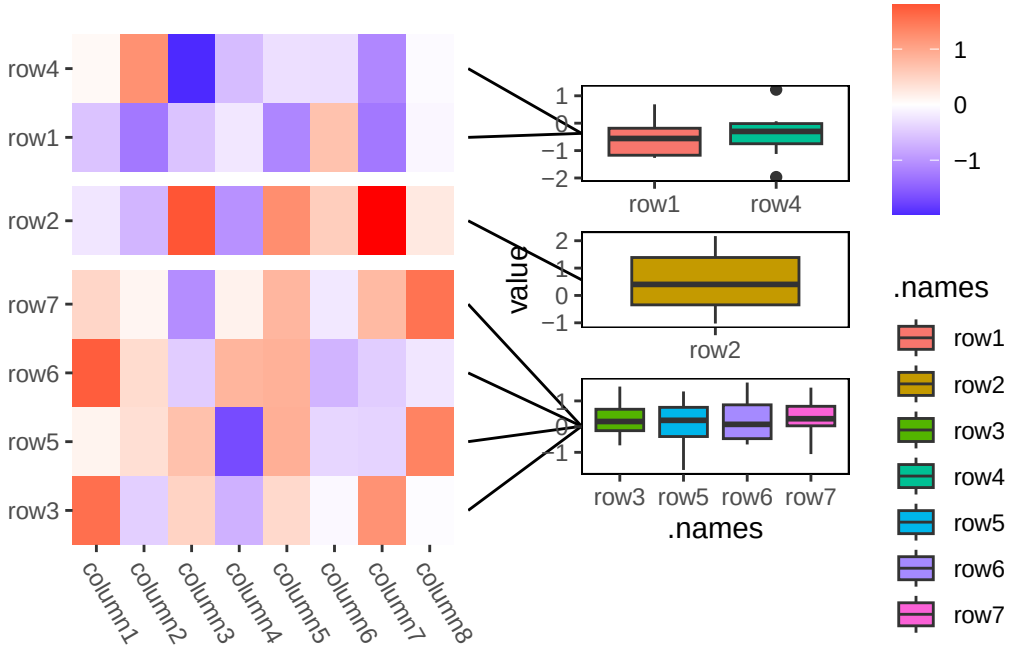
If you manually provide the linked observations, you can use the `group1` and `group2` arguments to control whether the layout panel groups and their ordering should be used to create the annotations.

```
set.seed(123)
ggheatmap(small_mat) +
    theme(axis.text.x = element_text(hjust = 0, angle = -60)) +
    anno_right() +
    align_kmeans(3L) +
    ggmark(mark_tetragon(1:3), group1 = TRUE) +
    geom_boxplot(aes(.names, value)) +
    theme(plot.margin = margin(l = 0.1, t = 0.1, unit = "npc"))
#> > heatmap built with `geom_tile()`
```



By default, `ggmark()` uses `facet_wrap` to define the facet, and you can use it to control the facet apearance (just ignore the `facets` argument). We prefer `facet_wrap()` here because it offers flexibility in positioning the strip on any side of the panel, and typically, we only want to a single dimension to create the annotate the selected observations. However, you can still use `facet_grid()` to create a two-dimensional plot. Note that for horizontal stack layouts, the row facets, or for vertical stack layouts, the column facets will always be overwritten.

```
set.seed(123)
ggheatmap(small_mat) +
    theme(axis.text.x = element_text(hjust = 0, angle = -60)) +
    anno_right() +
    align_kmeans(3L) +
    ggmark(mark_line()) +
    geom_boxplot(aes(.names, value, fill = .names)) +
    facet_wrap(vars(), scales = "free", strip.position = "right") +
    theme(plot.margin = margin(l = 0.1, t = 0.1, unit = "npc"))
#> > heatmap built with `geom_tile()`
```

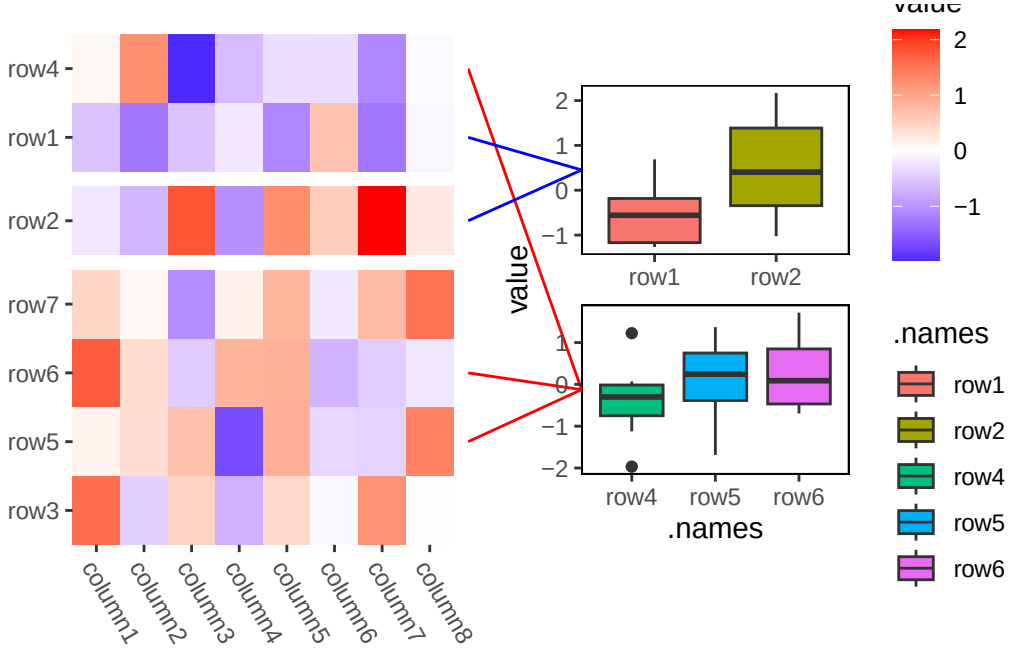


You can further customize the appearance of link lines and quadrilaterals using the element argument in `mark_line()`/`mark_tetragon()` function:

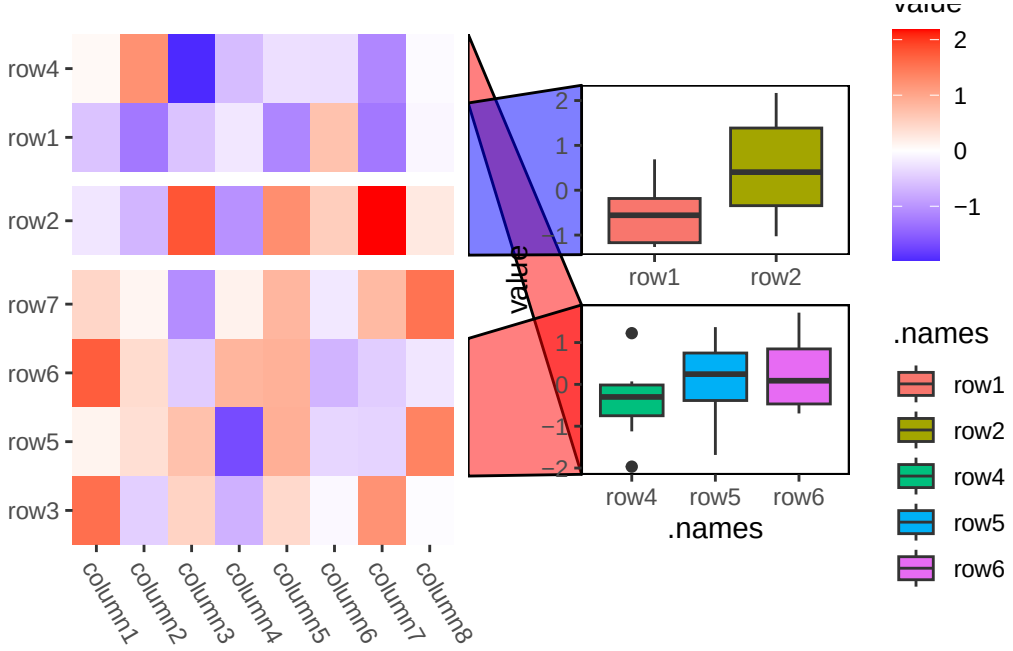
- Link lines can be customized using the `element_line()`.
- Link ranges can be customized using the `element_polygon()`.

By default, vectorized fields in `element_line()` and `element_polygon()` will be recycled to match the total number of groups.

```
set.seed(123)
ggheatmap(small_mat) +
    theme(axis.text.x = element_text(hjust = 0, angle = -60)) +
    anno_right() +
    align_kmeans(3L) +
    ggmark(
        mark_line(4:6, 1:2,
            .element =  element_line(color = c("red", "blue"))
        )
    ) +
    geom_boxplot(aes(.names, value, fill = .names)) +
    facet_wrap(vars(), scales = "free", strip.position = "right") +
    theme(plot.margin = margin(l = 0.1, t = 0.1, unit = "npc"))
#> > heatmap built with `geom_tile()`
```

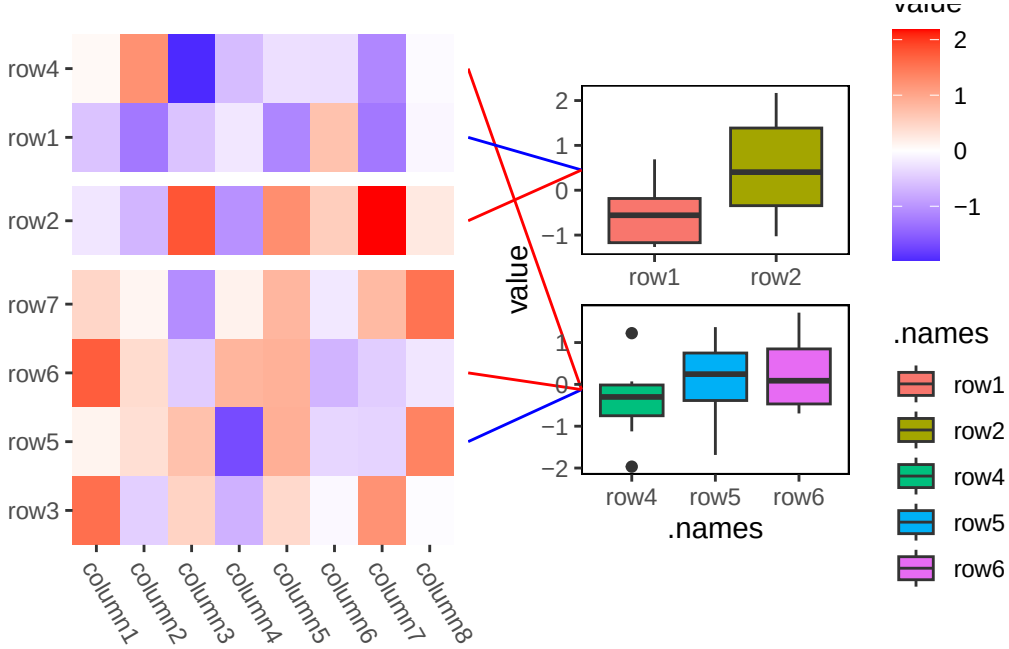



```
set.seed(123)
ggheatmap(small_mat) +
    theme(axis.text.x = element_text(hjust = 0, angle = -60)) +
    anno_right() +
    align_kmeans(3L) +
    ggmark(
        mark_tetragon(4:6, 1:2,
            .element =  element_polygon(fill = c("red", "blue"), alpha = 0.5)
        )
    ) +
    geom_boxplot(aes(.names, value, fill = .names)) +
    facet_wrap(vars(), scales = "free", strip.position = "right") +
    theme(plot.margin = margin(l = 0.1, t = 0.1, unit = "npc"))
#> > heatmap built with `geom_tile()`
```



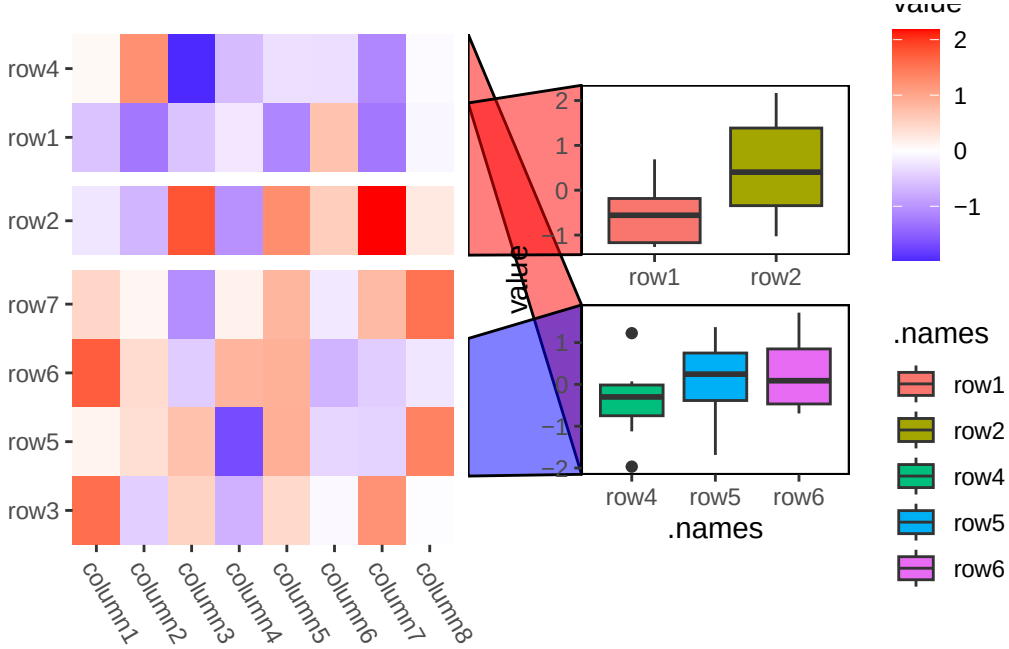
You can wrap the `element` with `I()` to recycle it to match the drawing groups. The drawing groups typically correspond to the number of observations for `element_line()`, as each observation will be linked with the plot panel.

```
set.seed(123)
ggheatmap(small_mat) +
    theme(axis.text.x = element_text(hjust = 0, angle = -60)) +
    anno_right() +
    align_kmeans(3L) +
    ggmark(
        mark_line(4:6, 1:2,
            .element =  I(element_line(color = c("red", "blue")))
        )
    ) +
    geom_boxplot(aes(.names, value, fill = .names)) +
    facet_wrap(vars(), scales = "free", strip.position = "right") +
    theme(plot.margin = margin(l = 0.1, t = 0.1, unit = "npc"))
#> > heatmap built with `geom_tile()`
```



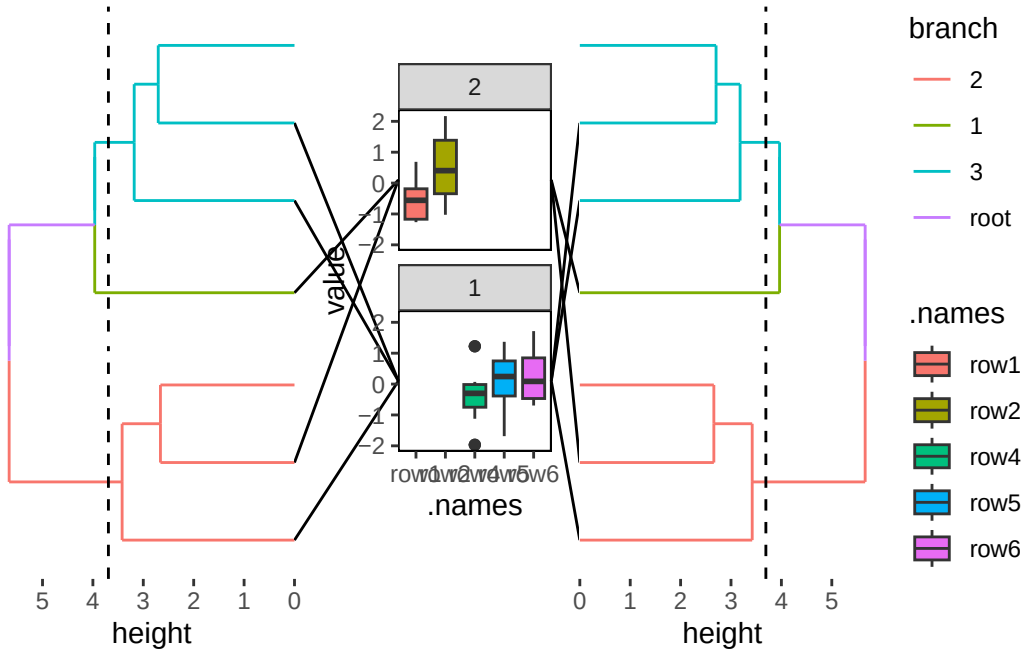
For `element_polygon()`, the drawing groups usually align with the defined groups. However, if the defined group of observations is separated and cannot be linked with a single quadrilateral, the number of drawing groups will be larger than the number of defined groups.

```
set.seed(123)
ggheatmap(small_mat) +
    theme(axis.text.x = element_text(hjust = 0, angle = -60)) +
    anno_right() +
    align_kmeans(3L) +
    ggmark(
        mark_tetragon(4:6, 1:2,
            .element =  I(element_polygon(fill = c("red", "blue"), alpha = 0.5))
        )
    ) +
    geom_boxplot(aes(.names, value, fill = .names)) +
    facet_wrap(vars(), scales = "free", strip.position = "right") +
    theme(plot.margin = margin(l = 0.1, t = 0.1, unit = "npc"))
#> > heatmap built with `geom_tile()`
```



For `stack_layout()`, we usually don't need to specify the observations for hand2, since it should match hand1. This is because all plots in stack_discrete() should maintain the same ordering index. However, specifying hand2 becomes useful in `stack_cross()`, where different orderings are involved.

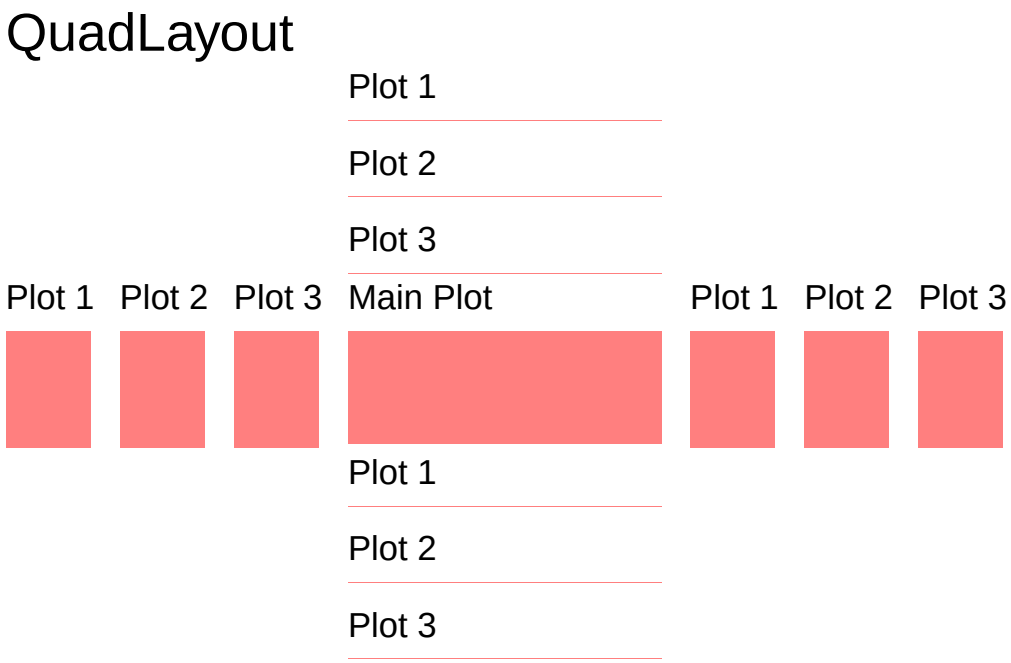
```
stack_discreteh(small_mat) +
    align_dendro(aes(color = branch), k = 3L) +
    scale_x_reverse(expand = expansion()) +
    theme(plot.margin = margin()) +
    ggmark(mark_line(4:6 ~ waiver(), 1:2 ~ waiver())) +
    geom_boxplot(aes(.names, value, fill = .names)) +
    theme(plot.margin = margin(l = 0.1, t = 0.1, r = 0.1, b = 0.1, unit = "npc")) +
    align_dendro(aes(color = branch), k = 3L) +
    scale_x_continuous(expand = expansion()) +
    theme(plot.margin = margin())
```



Now, let's move on to the next chapter, where we will introduce `quad_layout()` in full. While we've already introduced `ggheatmap()`—a specialized version of `quad_layout()`—most of the operations discussed in Chapter 3 can also be applied to `quad_layout()`. In the next section, we'll delve into `quad_layout()` and explore its full functionality.

7 quad-layout

`quad_layout()` arranges plots around the quad-sides of a main plot, aligning both horizontal and vertical axes, and can handle either discrete or continuous variables.




```
library(ggalign)
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

7.1 Introduction

Depending on whether you want to align discrete or continuous variables in the `horizontal` and `vertical` direction, there are four main types of `quad_layout()`:

Alignment of Observations	horizontal	vertical	Data Format
`quad_continuous()`/`ggside()`	continuous	continuous	data frame
`quad_layout(xlim = ...)`	discrete	continuous	matrix
`quad_layout(ylim = ...)`	continuous	discrete	matrix
`quad_discrete()`/`ggheatmap()`	discrete	discrete	matrix

7.2 Annotations

Annotation is typically handled using a `stack_layout()`. Depending on whether you want to align observations in the specified direction, different `stack_layout()` are compatible (Section 3.5). Below is a table outlining the compatibility of various layout types for annotations:

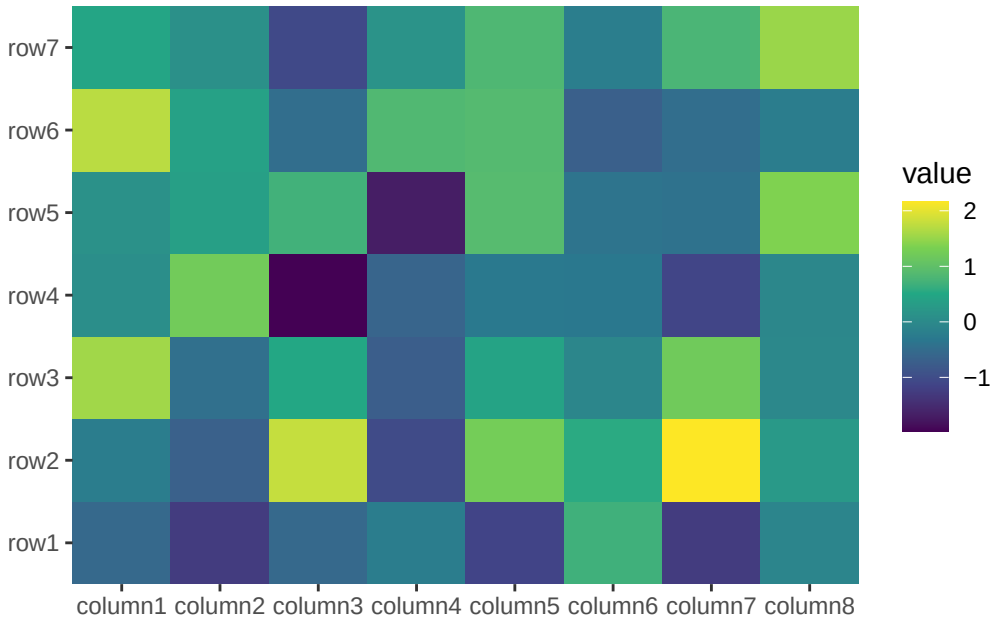
Annotations	left and right	top and bottom
`quad_continuous()`/`ggside()`	`stack_continuous()`	`stack_continuous()`
`quad_layout(xlim = ...)`	`stack_discrete()`	`stack_continuous()`
`quad_layout(ylim = ...)`	`stack_continuous()`	`stack_discrete()`
`quad_discrete()`/`ggheatmap()`	`stack_discrete()`	`stack_discrete()`

7.3 `quad_discrete()`

`quad_discrete()` aligns discrete variables in both horizontal and vertical directions. It serves as the base version of `ggheatmap()`/`heatmap_layout()` and does not automatically add default layers or mappings.

The underlying `ggplot` data of the main plot is the same with `ggheatmap()`/`heatmap_layout()` (Section 3.2), it is recommended to use `.y`, or `.discrete_y` as the `y` mapping and use `.x` or `.discrete_x` as the `x` mapping in the main plot.

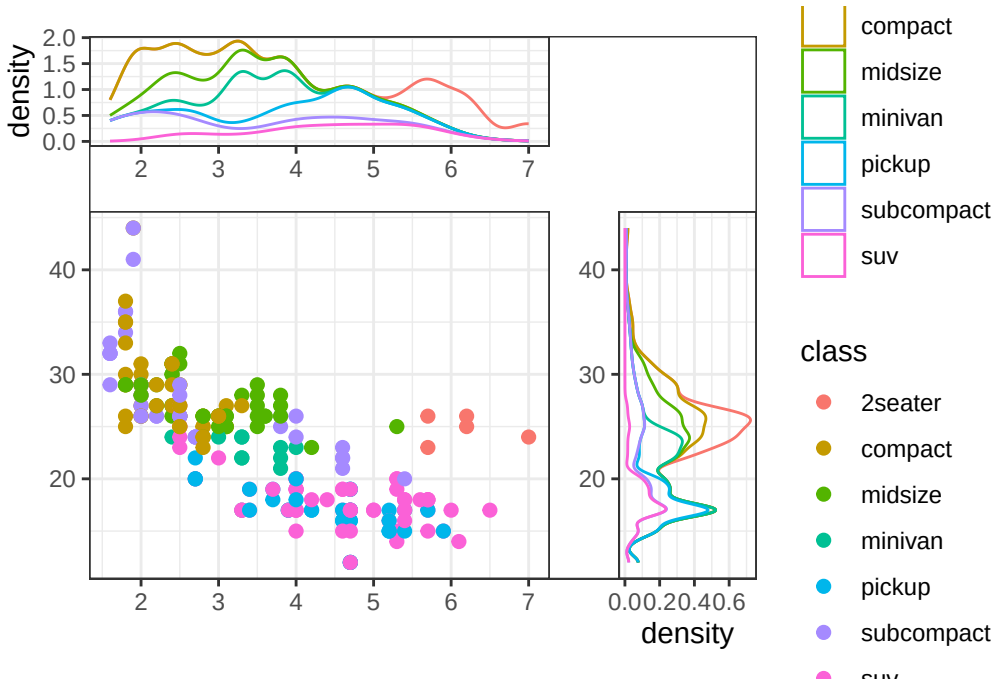
```
quad_discrete(small_mat, aes(.x, .y)) +
    geom_tile(aes(fill = value)) +
    scale_fill_viridis_c()
```



7.4 `quad_continuous()`

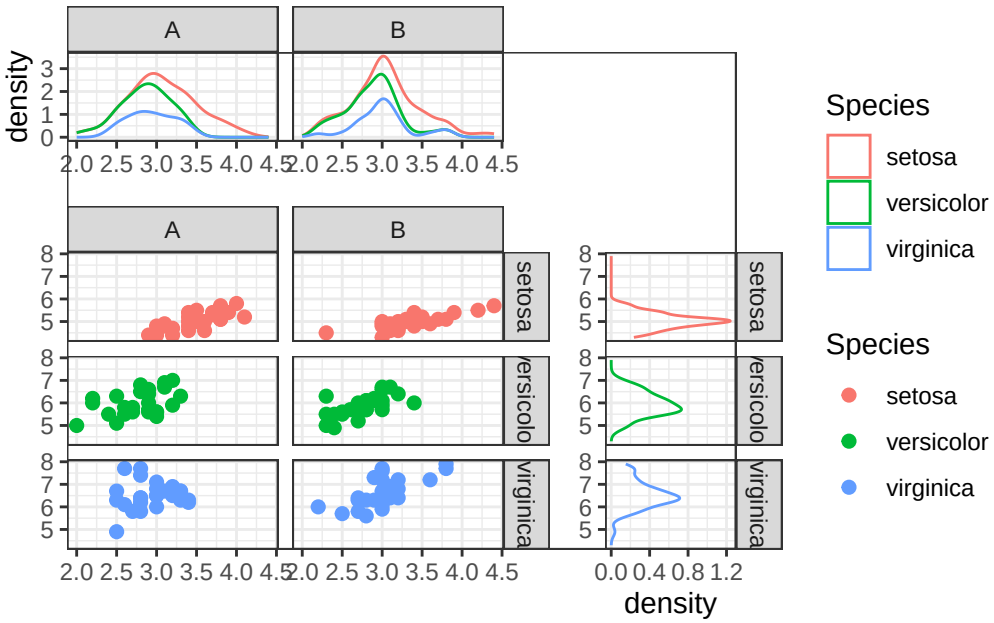
`quad_continuous()` align continuous variables and is functionally equivalent to the ggside package. For convenience, `ggside()` is provided as an alias for `quad_continuous()`. This layout is particularly useful for adding metadata or summary graphics along a continuous axis.

```
ggside(mpg, aes(displ, hwy, colour = class)) +
    geom_point(size = 2) +
    # initialize top annotation
    anno_top(size = 0.3) +
    # add a plot in the top annotation
    ggalign() +
    geom_density(aes(displ, y = after_stat(density), colour = class), position = "stack") +
    # initialize right annotation
    anno_right(size = 0.3) +
    # add a plot in the right annotation
    ggalign() +
    geom_density(aes(x = after_stat(density), hwy, colour = class),
        position = "stack"
    ) &
    theme_bw()
```



`ggside()` allows facetting for the main plot, which should also be applied to the annotations for proper alignment.

```
i2 <- iris
i2$Species2 <- rep(c("A", "B"), 75)
ggside(i2, aes(Sepal.Width, Sepal.Length, color = Species)) +
    geom_point(size = 2) +
    facet_grid(Species ~ Species2) +
    anno_top(size = 0.3) +
    ggalign() +
    geom_density(aes(Sepal.Width, y = after_stat(density), colour = Species),
        position = "stack"
    ) +
    facet_grid(cols = vars(Species2)) +
    anno_right(size = 0.3) +
    ggalign() +
    geom_density(aes(x = after_stat(density), Sepal.Length, colour = Species),
        position = "stack"
    ) +
    facet_grid(rows = vars(Species)) &
    theme_bw()
```



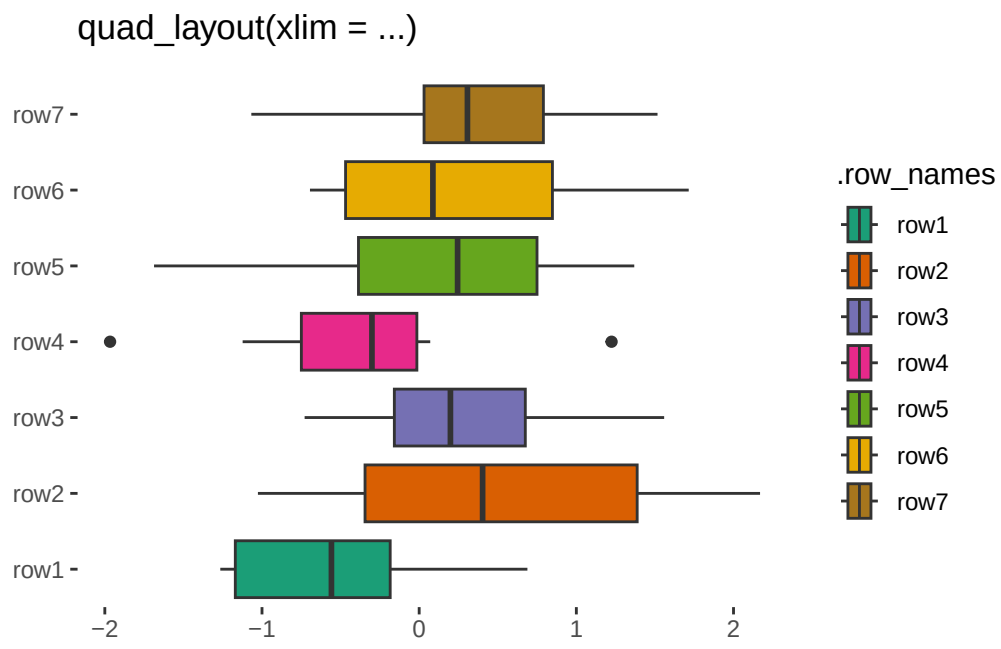
If an annotation contains multiple plots, it can be tedious to add the same element to each one individually. One way to simplify this is by creating an external `stack_layout()` and adding the desired elements using the `&` operator. Then, you can add this `stack_layout()` to the `quad_layout()`. In Chapter 10, I will introduce another more powerful operator that seamlessly combines with the `+` operator, allowing you to add elements to multiple plots at once.

7.5 `quad_layout()`

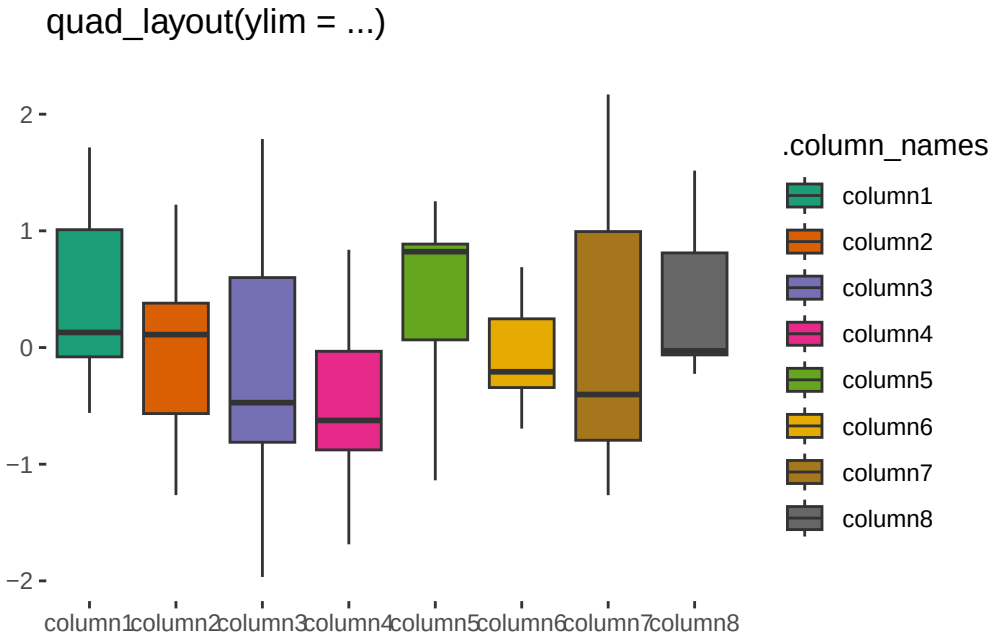
This function arranges plots around the quad-sides of a main plot, aligning both horizontal and vertical axes, and can handle either discrete or continuous variables.

- If `xlim` is provided, a continuous variable will be required and aligned in the vertical direction. Otherwise, a discrete variable will be required and aligned.
- If `ylim` is provided, a continuous variable will be required and aligned in the horizontal direction. Otherwise, a discrete variable will be required and aligned.

```
quad_layout(small_mat, xlim = NULL) +
    geom_boxplot(aes(value, .discrete_y, fill = .row_names)) +
    scale_fill_brewer(palette = "Dark2") +
    layout_title("quad_layout(xlim = ...)")
```




```
quad_layout(small_mat, ylim = NULL) +
    geom_boxplot(aes(.discrete_x, value, fill = .column_names)) +
    scale_fill_brewer(palette = "Dark2") +
    layout_title("quad_layout(ylim = ...)")
```



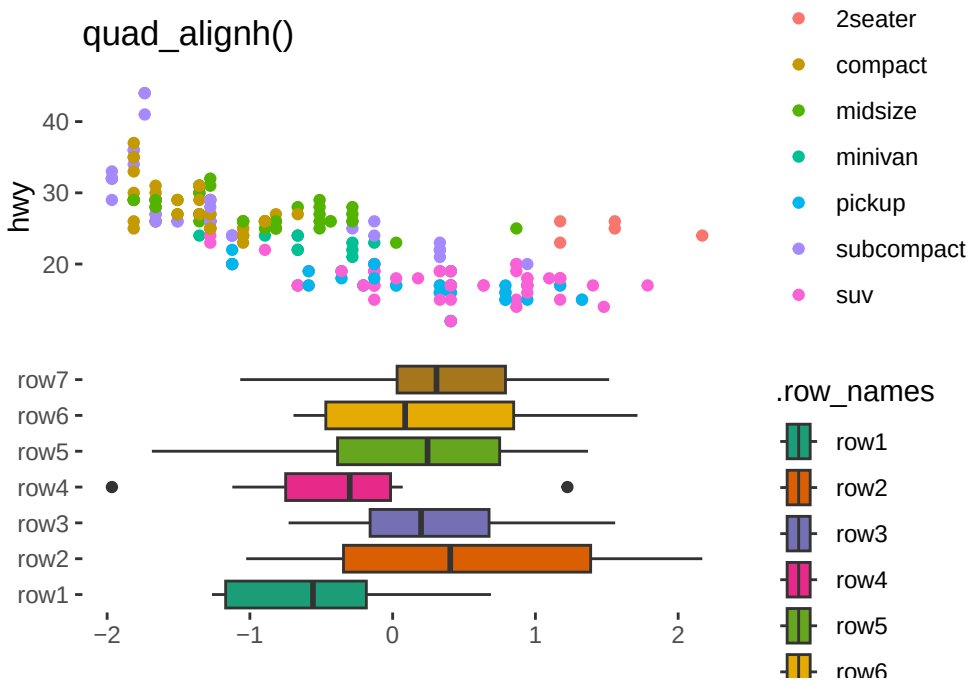
As discussed in Section 3.4, `quad_anno()` will always attempt to initialize a `stack_layout()` with the same alignment as the current direction. For top and bottom annotations in `quad_layout(xlim = ...)`, and left and right annotations in `quad_layout(ylim = NULL)`, `quad_anno()` will not initialize the annotation due to inconsistent data types.

```
quadh <- quad_layout(small_mat, xlim = NULL) +
    anno_top()
#> Warning: `data` in `quad_layout()` is a double matrix, but the top annotation stack need
#> a <data.frame>, won't initialize the top annotation stack
quadv <- quad_layout(small_mat, ylim = NULL) +
    anno_left()
#> Warning: `data` in `quad_layout()` is a double matrix, but the left annotation stack
#> need a <data.frame>, won't initialize the left annotation stack
```

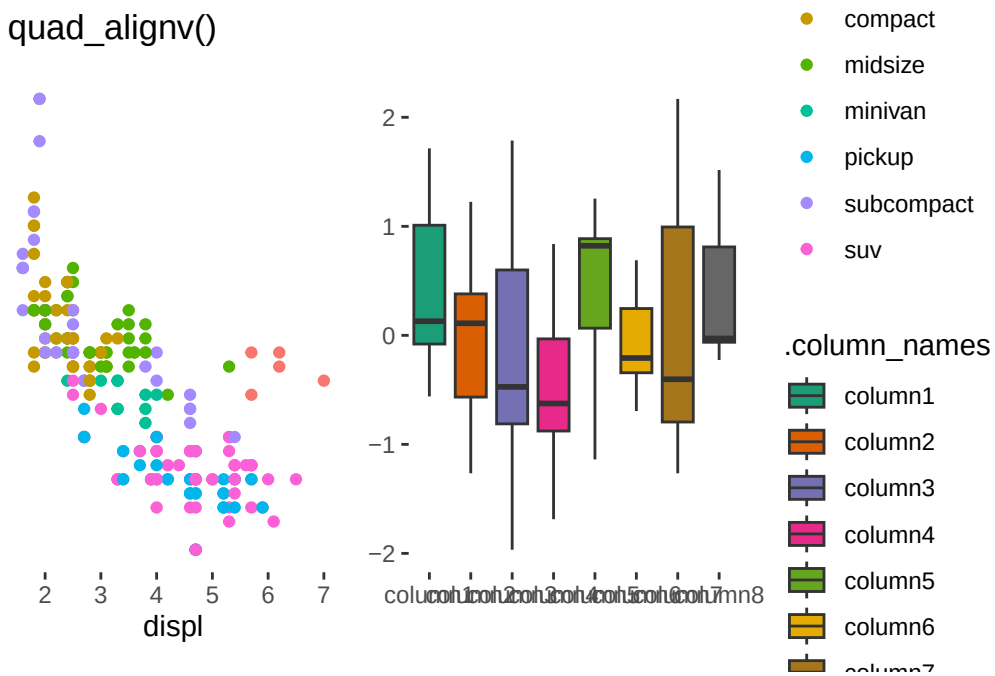
Manual adding of a `stack_layout()` is required in such cases, you can set `initialize = FALSE` to prevent the warning message.

```
quadh <- quad_layout(small_mat, xlim = NULL) +
    anno_top(initialize = FALSE)
quadv <- quad_layout(small_mat, ylim = NULL) +
    anno_left(initialize = FALSE)
```

```
quadh +
    stack_continuous("v", mpg) +
    # add a plot in the top annotation
    ggalign(mapping = aes(displ, hwy, colour = class)) +
    geom_point(aes(displ, hwy, colour = class)) +
    quad_active() +
    geom_boxplot(aes(value, .discrete_y, fill = .row_names)) +
    scale_fill_brewer(palette = "Dark2")+
    layout_title("quad_alignh()")
```

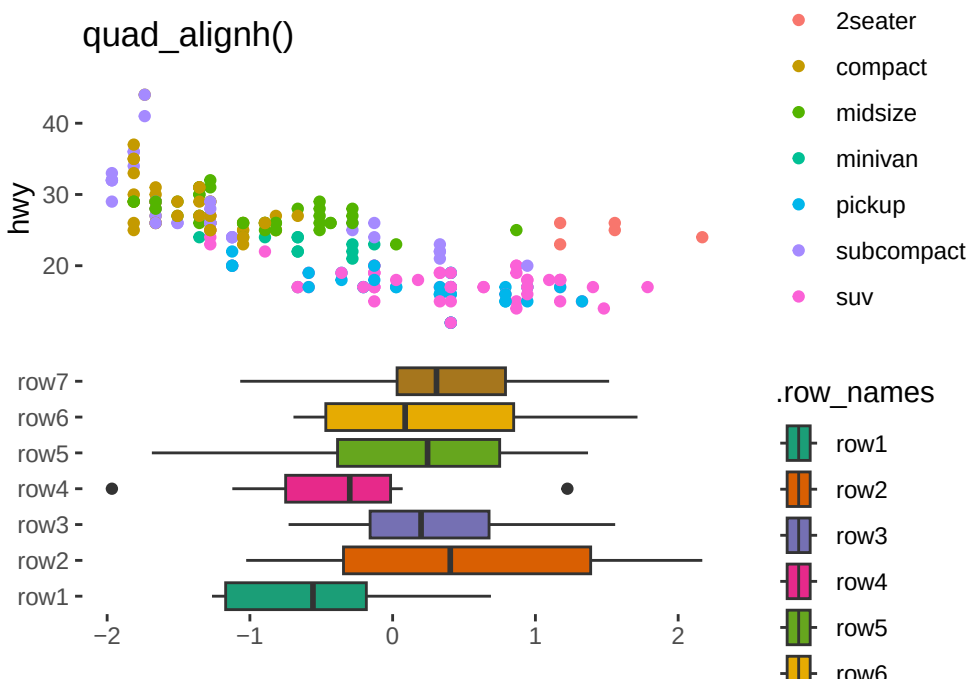



```
quadv +
    stack_continuous("h", mpg) +
    # add a plot in the left annotation
    ggalign(mapping = aes(displ, hwy, colour = class)) +
    geom_point(aes(displ, hwy, colour = class)) +
    quad_active() +
    geom_boxplot(aes(.discrete_x, value, fill = .column_names)) +
    scale_fill_brewer(palette = "Dark2") +
    layout_title("quad_alignv()")
```

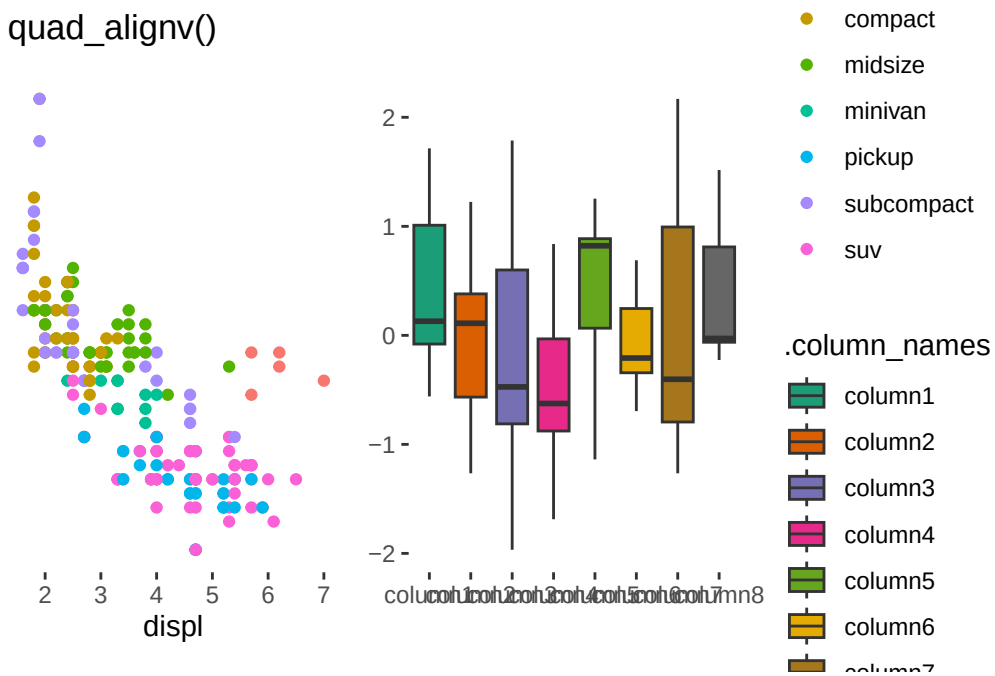


Alternatively, you can set `initialize = TRUE`, which will initialize the annotation stack layout with no data. In this case, you must provide `data` in each plot within the annotation.

```
quad_layout(small_mat, xlim = NULL) +
    geom_boxplot(aes(value, .discrete_y, fill = .row_names)) +
    scale_fill_brewer(palette = "Dark2") +
    anno_top(initialize = TRUE) +
    ggalign(data = mpg, aes(displ, hwy, colour = class)) +
    geom_point(aes(displ, hwy, colour = class))+
    layout_title("quad_alignh()")
```




```
quad_layout(small_mat, ylim = NULL) +
    geom_boxplot(aes(.discrete_x, value, fill = .column_names)) +
    scale_fill_brewer(palette = "Dark2") +
    anno_left(initialize = TRUE) +
    ggalign(data = mpg, aes(displ, hwy, colour = class)) +
    geom_point(aes(displ, hwy, colour = class))+
    layout_title("quad_alignv()")
```



In the next chapter, we will explore even more advanced techniques for combining multiple `quad_layout()`s. These methods will provide you with the tools to manage more complex plot arrangements and make your visualizations even more flexible and powerful.

8 A list of quad_layout()

Similarly, stack_layout() can be added to a quad_layout(), and a quad_layout() can also be added to a stack_layout().

```
library(ggalign)
#> Loading required package: ggplot2
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

> note: when stack_layout() contains a nested quad_layout(), it cannot be used within the annotation of another quad_layout().

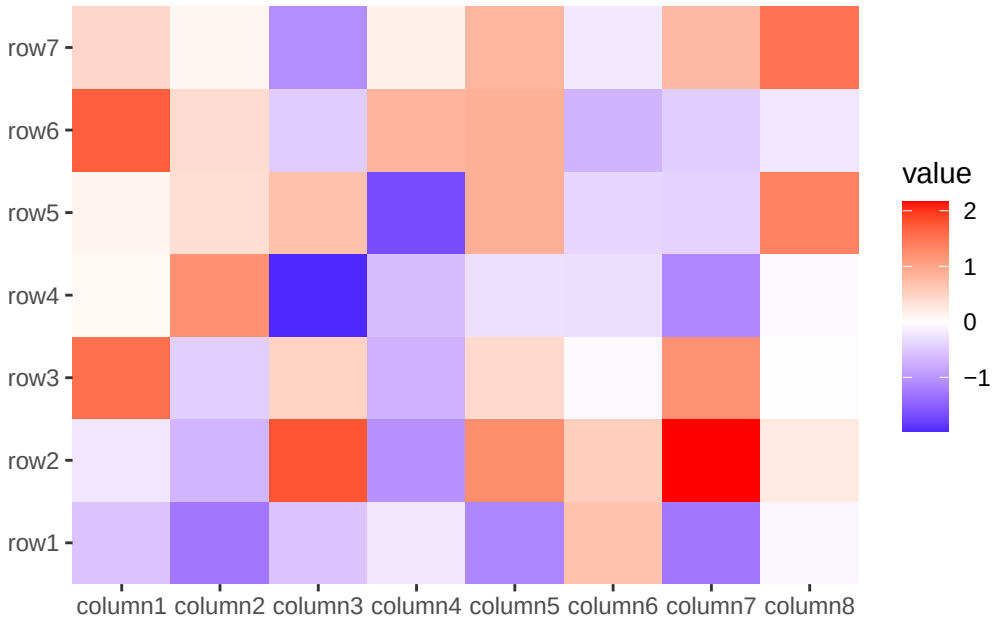
8.1 Add quad_layout() to stack_layout()

Here is a summarized table showing which quad_layout() can be used with each stack_layout():

	stack_discreteh()	stack_discretev()	stack_continuoush()	stack_continuousv()
quad_continuous()/ggside()				
quad_layout(xlim = ...)				
quad_layout(ylim = ...)				
quad_discrete()/ggheatmap()				

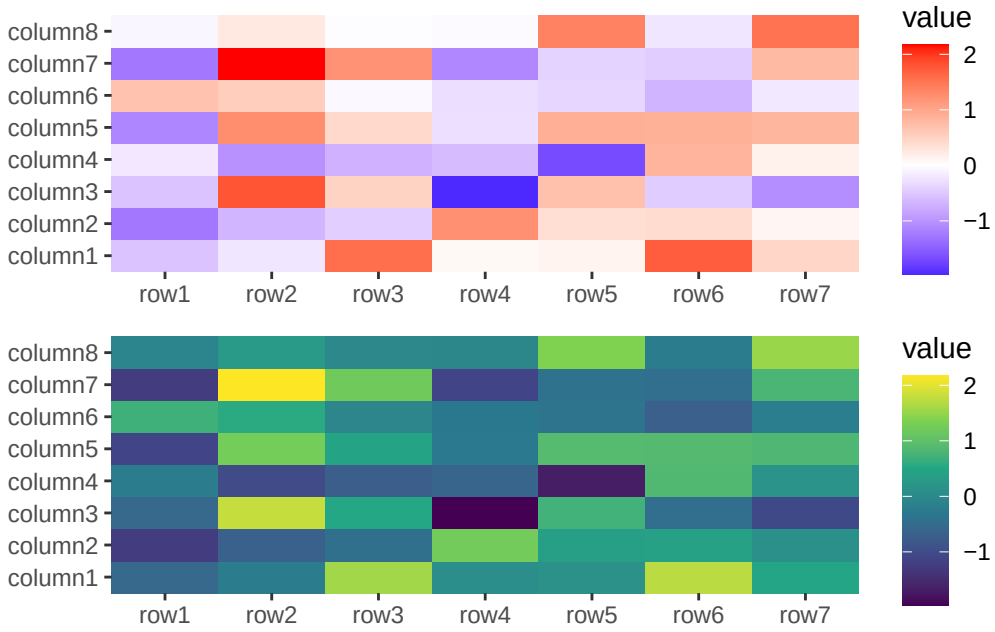
As long as the alignment is consistent across both stack_layout() and quad_layout(), you can directly add quad_layout().

```
stack_discreteh(small_mat) +
    ggheatmap()
#> > heatmap built with `geom_tile()`
```



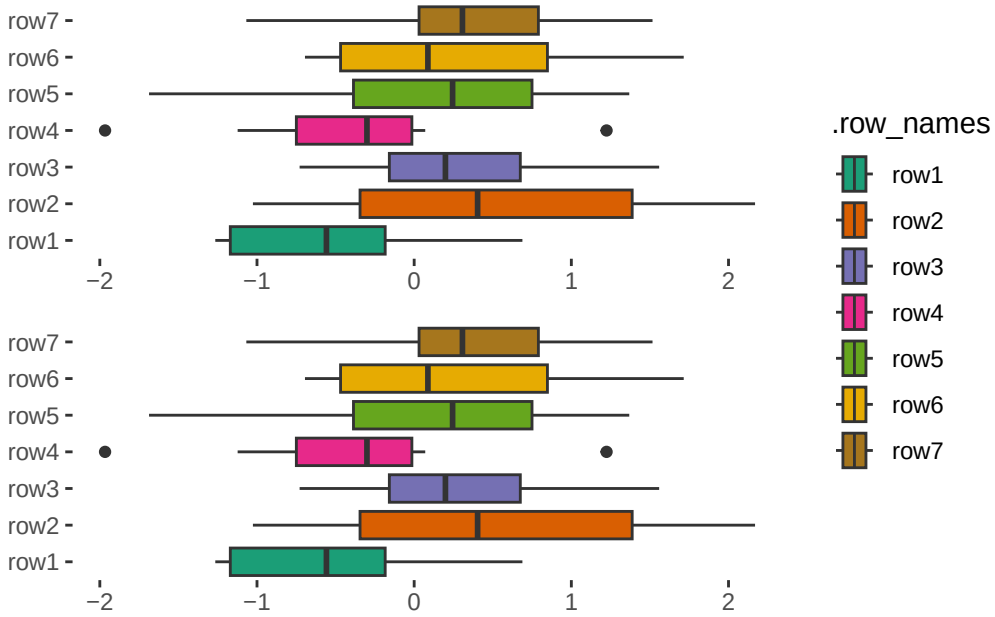
When `ggheatmap()/quad_layout()` is added to a `stack_layout()`, it will also set the active context to itself, which means subsequent addition will be directed to `ggheatmap()/quad_layout()`. One exception is the `ggheatmap()/quad_layout()` itself, which cannot be added to another `quad_layout()`. In this case, they will be added directly to the `stack_layout()`.

```
stack_discretev(small_mat) +
    ggheatmap() +
    ggheatmap() +
    scale_fill_viridis_c()
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```



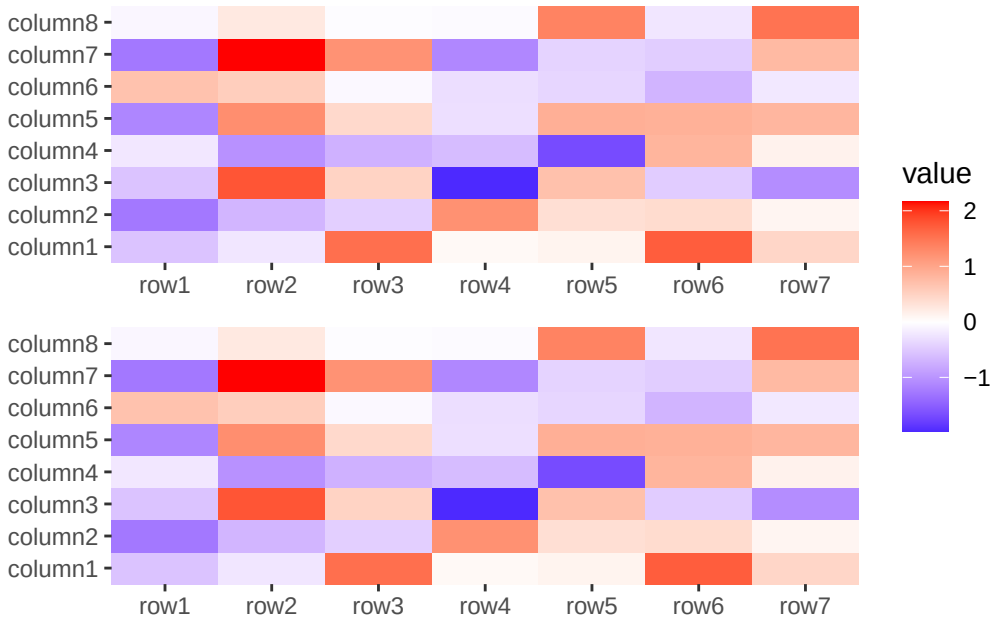
The data of `ggheatmap()`/`quad_layout()` can inherit from the `stack_layout()`, but the data format must match. Otherwise, you will need to manually provide the data.

```
quad_continuousv_plot <- quad_layout(small_mat, xlim = NULL) +
    geom_boxplot(aes(value, .discrete_y, fill = .row_names)) +
    scale_fill_brewer(palette = "Dark2")
# `stack_continuous()` need a data frame
stack_continuousv() +
    quad_continuousv_plot +
    quad_continuousv_plot
```



When `ggheatmap()`/`quad_layout()` is added to a vertical `stack_layout()`, the inherited matrix is transposed before use. This is because the columns of `ggheatmap()`/`quad_layout()` must match the number of observations in `stack_layout()`.

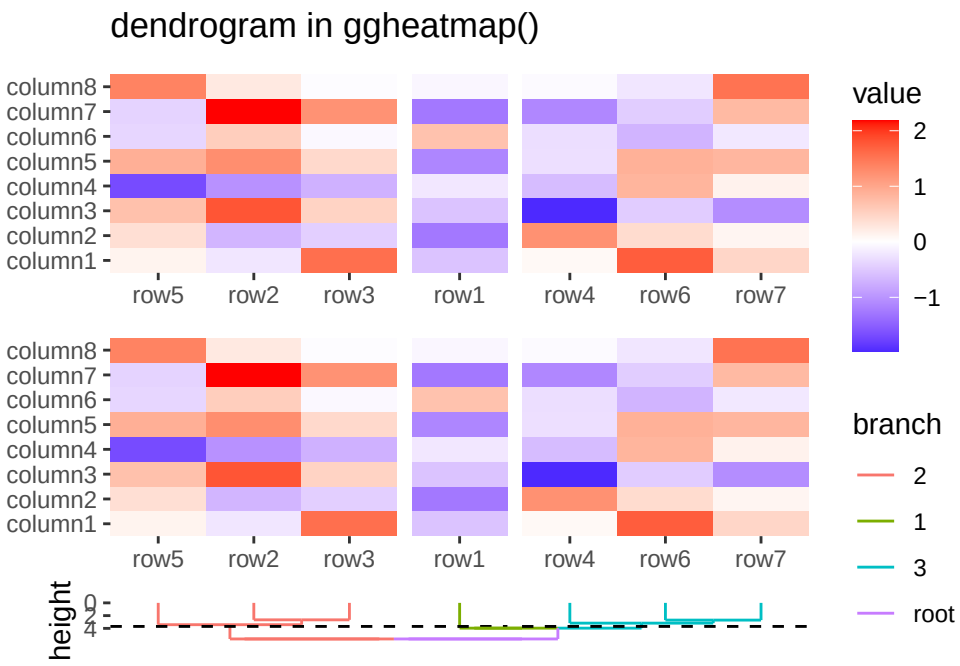
```
stack_discretev(small_mat) +
    ggheatmap() +
    ggheatmap()
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```



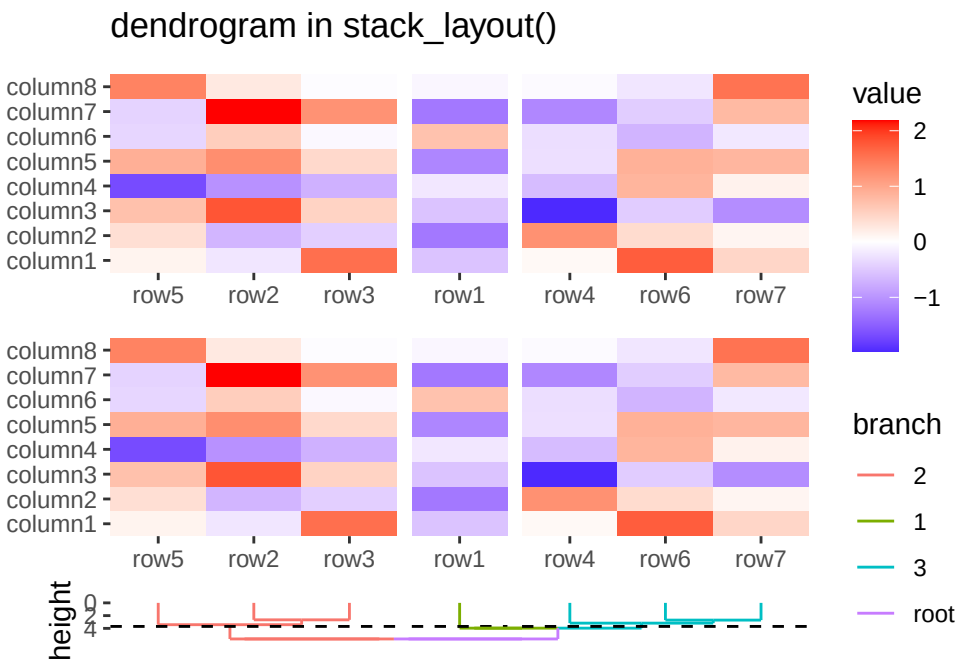
`stack_discrete()` ensures that all plots aligned along the stack have the same ordering index or groups.

We can customize the layout in the `stack_discrete()` directly, or in `quad_layout()`. As introduced in Section 2.5, you can easily switch from the `ggheatmap()`/`quad_layout()` to the `stack_layout()` using `stack_active()`.

```
stack_discretev(small_mat) +
    ggheatmap() +
    ggheatmap() +
    anno_bottom(size = 0.2) +
    align_dendro(aes(color = branch), k = 3)+
    layout_title("dendrogram in ggheatmap()")
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```




```
stack_discretev(small_mat) +
    ggheatmap() +
    ggheatmap() +
    stack_active() +
    align_dendro(aes(color = branch), k = 3, size = 0.2) +
    scale_y_reverse() +
    layout_title("dendrogram in stack_layout()")
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```



When applied to a `stack_layout()`, the orientation of the dendrogram may need to be manually adjusted.

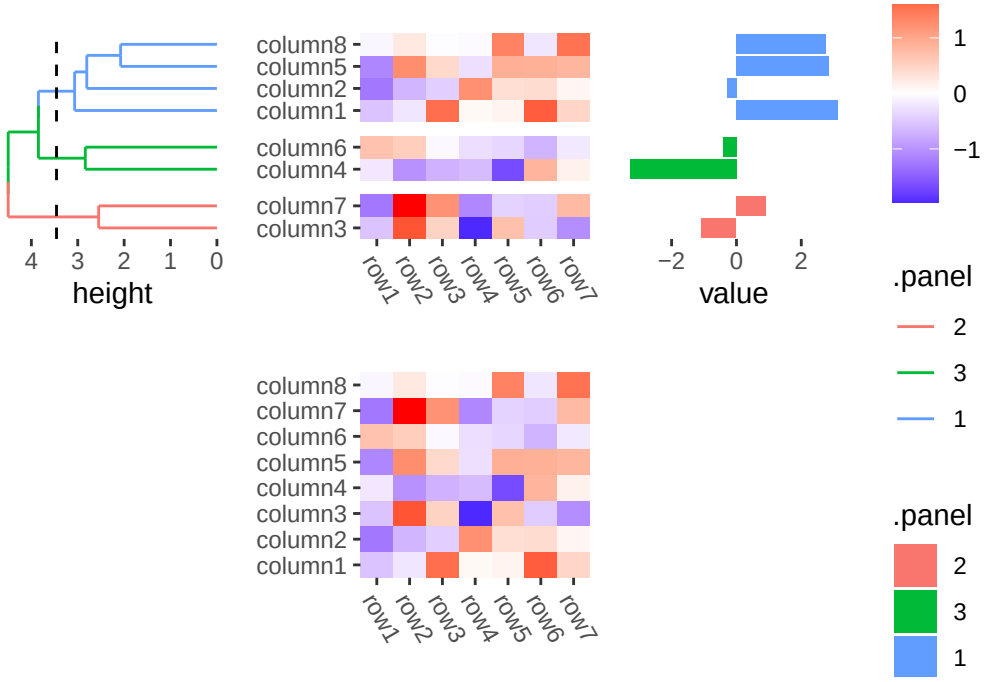
8.2 Control sizes

A numeric or a unit object of length 3 should be provided in `stack_discrete()`/`stack_continuous()` when placing a `quad_layout()`. For vertical `stack_layout()`, this means `quad_layout()` with left or right annotations; for horizontal `stack_layout()`, this means `quad_layout()` with top or bottom annotations. The first size controls the relative `width`/`height` of the left or top annotation, the second controls the relative `width`/`height` of the main plot, and the third controls the relative `width`/`height` of the right or bottom annotation.

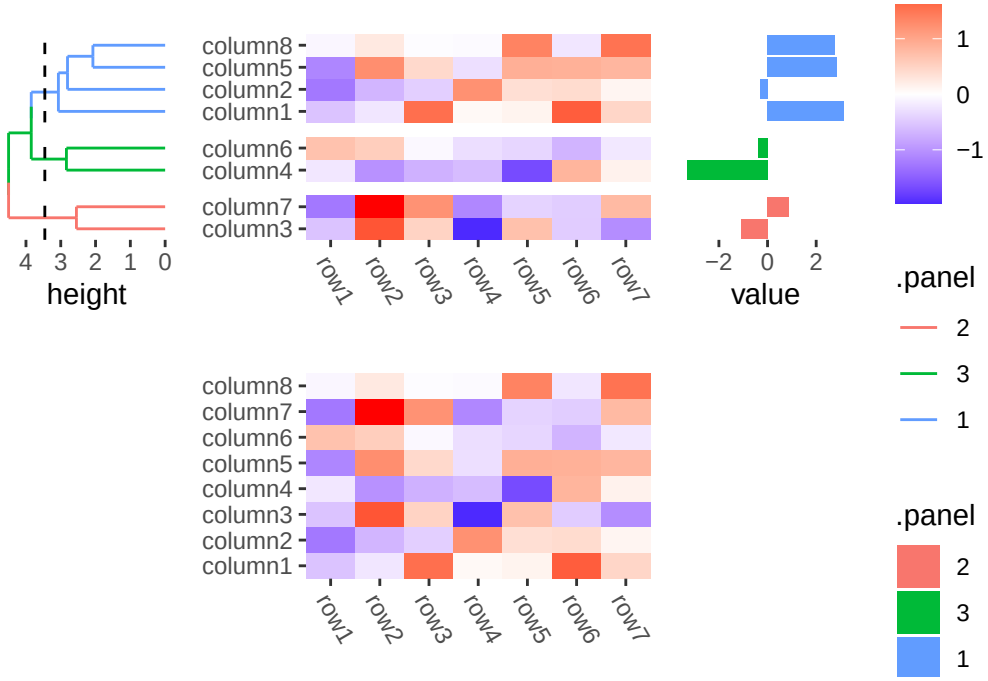
By default the three rows/columns will have equal sizes.

```
stack_discretev(small_mat) +
    ggheatmap() +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_left() +
    align_dendro(aes(color = .panel), k = 3L) +
    anno_right() +
    ggalign(data = rowSums) +
    geom_bar(aes(value, fill = .panel), orientation = "y", stat = "identity") +
```

```
    ggheatmap() +
    theme(axis.text.x = element_text(angle = -60, hjust = 0))
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```

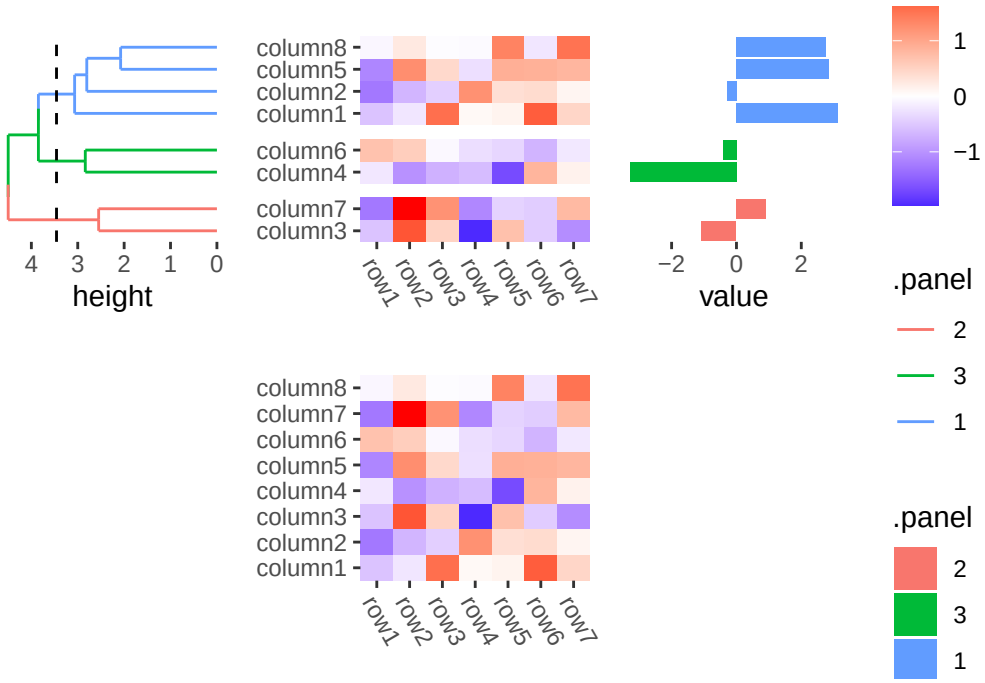



```
heat1 <- ggheatmap(t(small_mat)) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_left() +
    align_dendro(aes(color = .panel), k = 3L) +
    anno_right() +
    ggalign(data = rowSums) +
    geom_bar(aes(value, fill = .panel), orientation = "y", stat = "identity")

stack_discretev(small_mat, sizes = c(1, 2, 1)) +
    heat1 +
    ggheatmap() +
    theme(axis.text.x = element_text(angle = -60, hjust = 0))
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```



In this way, the width/height of main plot specified in `quad_active()` or `quad_layout()`/`ggheatmap()` won't work.

```
stack_discretev(small_mat) +
    ggheatmap(width = unit(2, "null")) + # not work
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_left() +
    align_dendro(aes(color = .panel), k = 3L) +
    anno_right() +
    ggalign(data = rowSums) +
    geom_bar(aes(value, fill = .panel), orientation = "y", stat = "identity") +
    ggheatmap(width = unit(2, "null")) + # not work
    theme(axis.text.x = element_text(angle = -60, hjust = 0))
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```

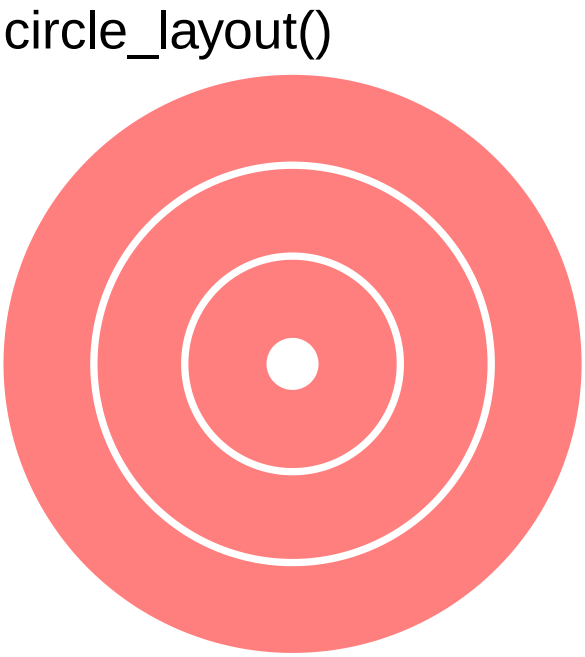


Now that you've learned how to combine `quad_layout()` and `stack_layout()` in various configurations, you're ready to explore a new, exciting way to organize and visualize your data: the circle layout. This layout offers a unique, radial perspective that can be particularly useful for visualizing hierarchical data or creating visually engaging plots.

9 circle layout

`circle_layout()` arranges plots in a circular, each plot will occupy one circle track. Based on whether we want to align the discrete or continuous variables, there are two types of circle layouts:

- `circle_discrete()`: Align discrete variable along the circle.
- `circle_continuous()`: Align continuous variable along the circle.

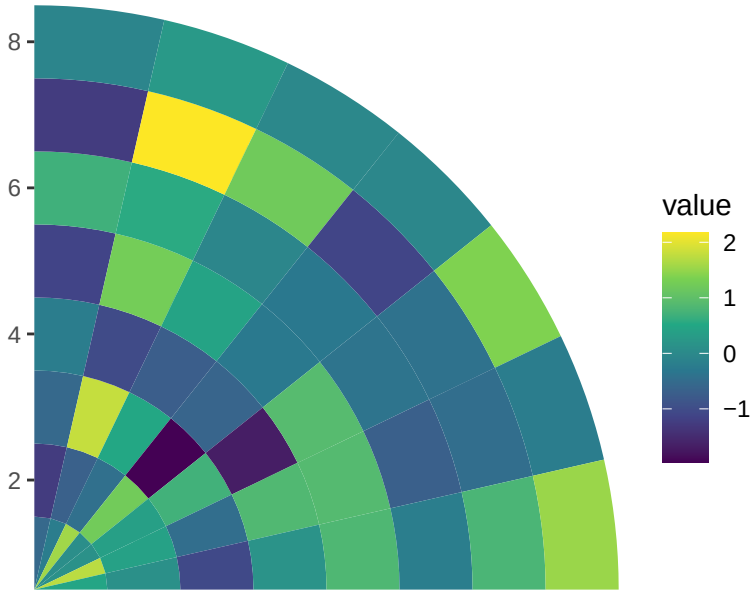



```
library(ggalign)
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

9.1 radial

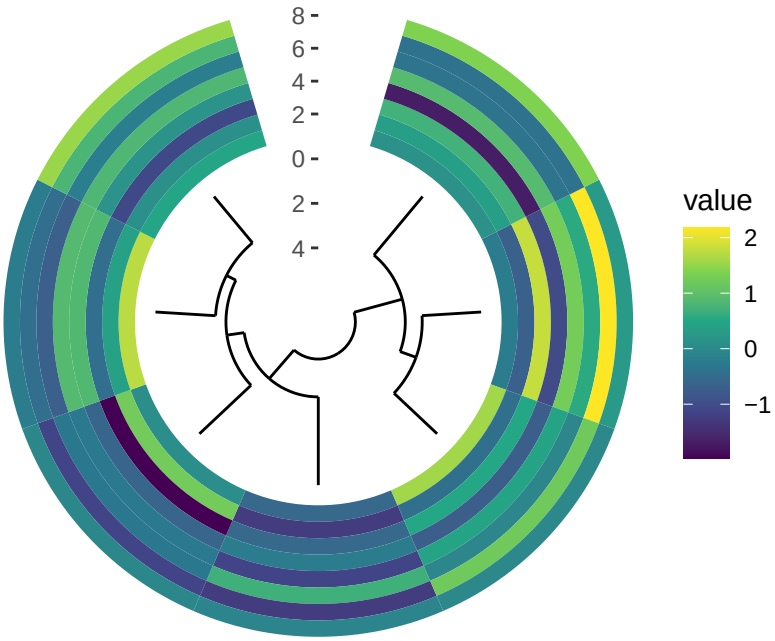
the core argument of `circle_layout()` is `radial`, which should be a `coord_radial()` object that defines the global parameters for `coord_radial()` across all plots in the layout. The parameters `start`, `end`, `direction`, and `expand` will be inherited and applied uniformly to all plots within the layout. The parameters `theta` and `r.axis.inside` will always be ignored and will be set to "x" and `TRUE`, respectively, for all plots.

```
circle_discrete(small_mat, radial = coord_radial(end = pi / 2, expand = FALSE)) +
    ggalign() +
    geom_tile(aes(y = .column_index, fill = value)) +
    scale_fill_viridis_c()
```



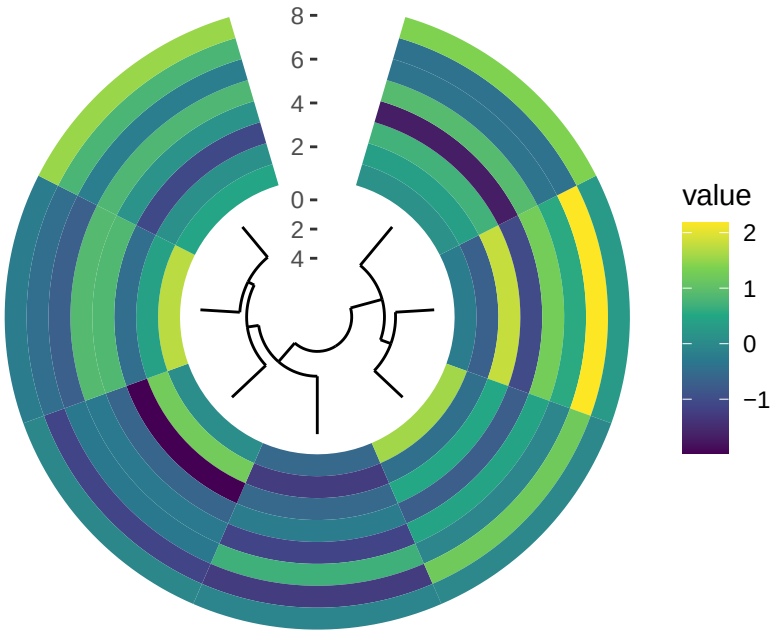
In essence, you can think of `circle_layout()` as a radial version of `stack_vertical()`. When rendered, `circle_layout()` uses `coord_radial()` to arrange each plot along a circular track. The `radial` argument in `circle_layout()` controls the overall inner radius. Plots are added from the outermost to the innermost position.

```
circle_discrete(small_mat, radial = coord_radial(inner.radius = 0.1)) +
    align_dendro() +
    ggalign() +
    geom_tile(aes(y = .column_index, fill = value)) +
    scale_fill_viridis_c()
```



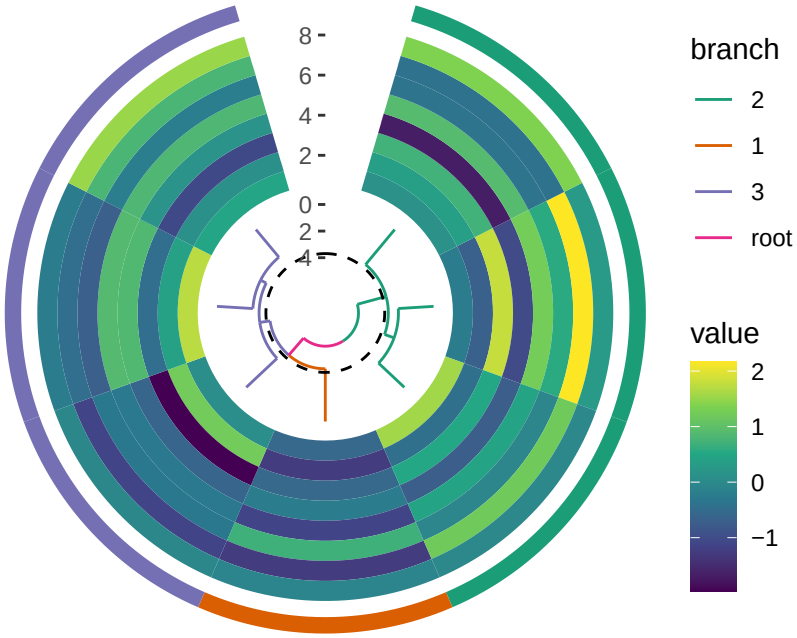
The `size` of each plot within the circle can be adjusted using the `size` argument (Section 2.4). However, it's important to note that `circle_layout()` only supports relative `size` adjustments, meaning all size values are interpreted relative to one another, even for `unit` objects. By default, all plots have a relative size of `1`.

```
circle_discrete(small_mat, radial = coord_radial(inner.radius = 0.1)) +
    align_dendro(size = 0.5) +
    ggalign() +
    geom_tile(aes(y = .column_index, fill = value)) +
    scale_fill_viridis_c()
```



Although `circle_layout()` does not currently support splitting observations into different facets, you can still indicate different groups visually. For instance, you can add a tile to represent each group. If you're using a dendrogram, you can color the branches to indicate different groups.

```
circle_discrete(small_mat, radial = coord_radial(inner.radius = 0.1)) +

    # add a dendrogram
    align_dendro(aes(color = branch), k = 3L, size = 0.5) +
    scale_color_brewer(palette = "Dark2") +

    # add a heatmap
    ggalign() +
    geom_tile(aes(y = .column_index, fill = value)) +
    scale_fill_viridis_c() +

    # add a single tile for each group
    ggalign(NULL, size = 0.1) +
    geom_tile(aes(y = 1L, fill = .panel)) +
    theme_no_axes("y") +
    scale_fill_brewer(palette = "Dark2", guide = "none")
```

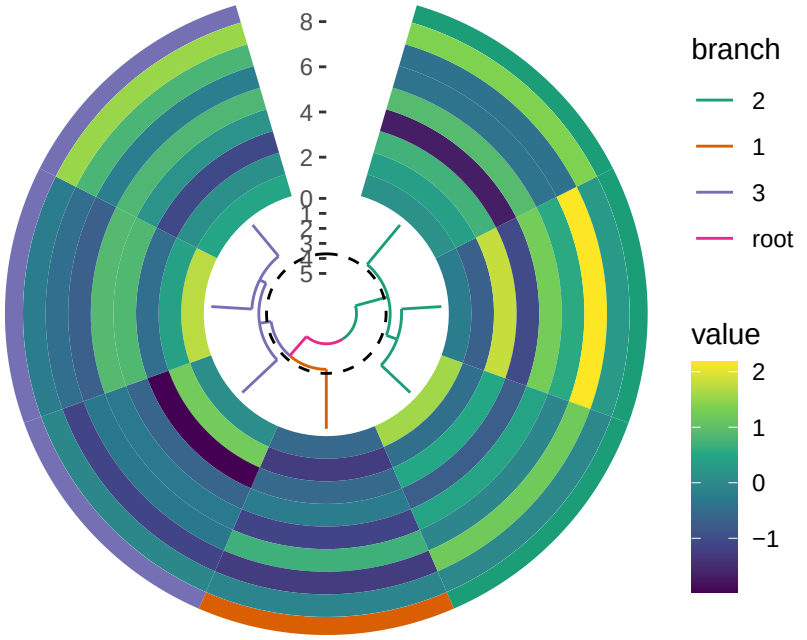


9.2 spacing

The spacing between plot tracks in `circle_layout()` is controlled `panel.spacing.r` parameter. The `panel.spacing.r` parameter sets the spacing between the individual plot panels (tracks) within the circle layout. Increasing this value will add more space between the tracks. Specifically, the `panel.spacing.r` of the outer plot determines the spacing between it and the inner plot. By modifying this value, you can control the overall visual separation between tracks. Note, you should also remove the scale expansion if you remove all spaces.

```
circle_discrete(small_mat, radial = coord_radial(inner.radius = 0.1)) +

    # add a dendrogram
    align_dendro(aes(color = branch), k = 3L, size = 0.5) +
    no_expansion("y") +
    scale_color_brewer(palette = "Dark2") +

    # add a heatmap
    ggalign() +
    geom_tile(aes(y = .column_index, fill = value)) +
    scale_fill_viridis_c() +
    no_expansion("y") +
```

```
    theme(panel.spacing.r = unit(0, "mm")) +

    # add a single tile for each group
    ggalign(NULL, size = 0.1) +
    geom_tile(aes(y = 1L, fill = .panel)) +
    scale_fill_brewer(palette = "Dark2", guide = "none") +
    no_expansion("y") +
    theme(panel.spacing.r = unit(0, "mm"))
```



The `no_expansion()` function is used to remove expansion around specific borders. It accepts a string with one or more of the following values: `"t"` (top), `"l"` (left), `"b"` (bottom), `"r"` (right), `"x"` (both left and right), and `"y"` (both bottom and top).

Now we have explored all the `Layout` defined in the package, next, we will build on these concepts and explore even more advanced strategies for integrating elements across multiple plots or annotations in a layout.

10 Operators

In `ggalign`, operators are used to manage and manipulate the plot elements in various layouts. These operators help you build complex visualizations by adding, or modifying elements across multiple plots in a layout. You may be familiar with the `+` and `&` operators, this section will expand on their usage, as well as introduce the subtraction operator (`-`) and how to apply it in different contexts.

1. Addition Operator (`+`): Adds elements to the active plot in the active layout.
2. Logical AND Operator (`&`): Applies elements to all plots in the layout.
3. Subtraction Operator (`-`): Allows you to add elements or modify them across multiple plots in the layout

```
library(ggalign)
#> Loading required package: ggplot2
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

10.1 Addition operator

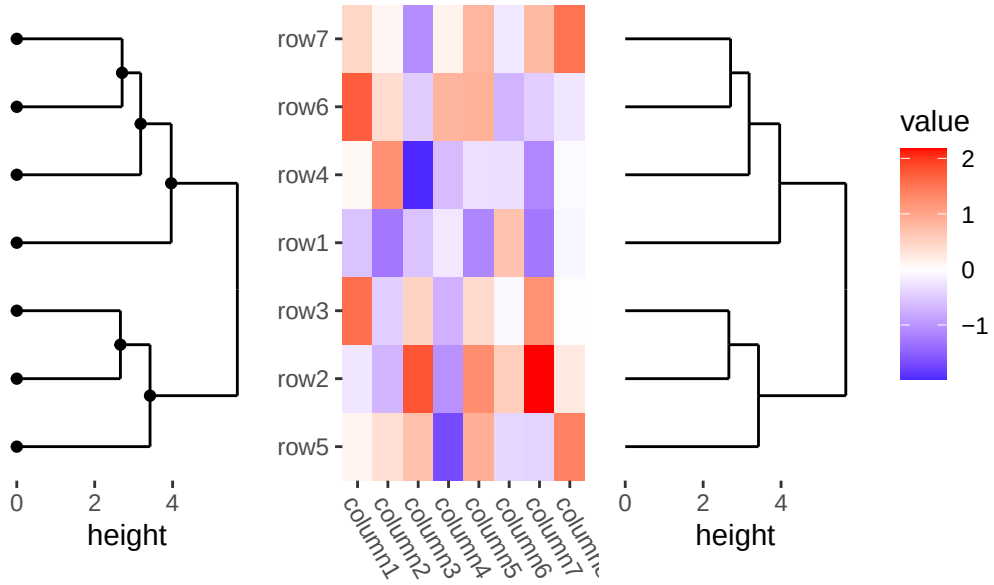
`+`: adds elements to the active plot in the active layout.

The `+` operator is straightforward and should be used as needed.

In `stack_layout()`, a nested layout will only occur if you pass a `quad_layout()` into `stack_layout()` (Chapter 8). If the active context in the `stack_layout()` is `quad_layout()`, this `quad_layout()` is treated as the active layout, and the `+` operator will add elements to it, following the same principles as in `quad_layout()`. Otherwise, the `stack_layout()` itself is treated as the active layout, and the `+` operator will add elements directly to this plot.

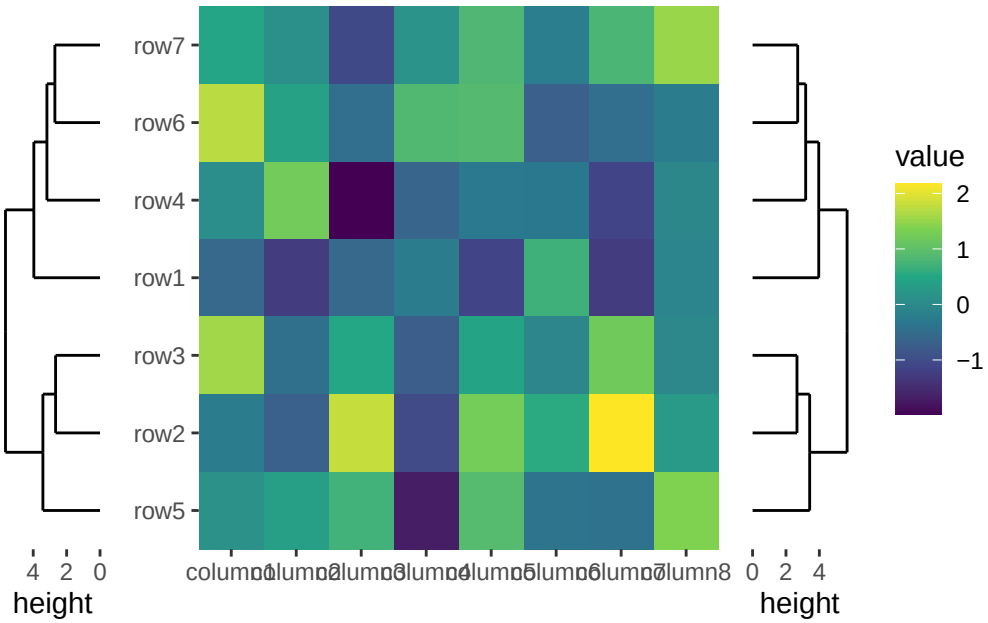
`circle_layout()` works similarly to `stack_layout()`, but it does not support nested layouts. Therefore, the active layout in `circle_layout()` will always be the `circle_layout()` itself.

```
stack_alignh(small_mat) +
    align_dendro() +
    geom_point() +
    ggheatmap() +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right() +
    align_dendro()
#> > heatmap built with `geom_tile()`
```



In `quad_layout()`, four nested layouts are available for annotations: `top`, `left`, `bottom`, and `right`. If no active annotation is set, `quad_layout()` treat itself as the active layout. Since there is only one main plot in the `quad_layout()`, the main plot is always treated as the active plot in this context. Otherwise, the active annotation is treated as the active layout, and the `+` operator will add elements to it, following the same principles as in `stack_layout()`.

```
ggheatmap(small_mat) +
    scale_fill_viridis_c() +
    anno_left(size = 0.2) +
    align_dendro() +
    anno_right(size = 0.2) +
    align_dendro()
#> > heatmap built with `geom_tile()`
```

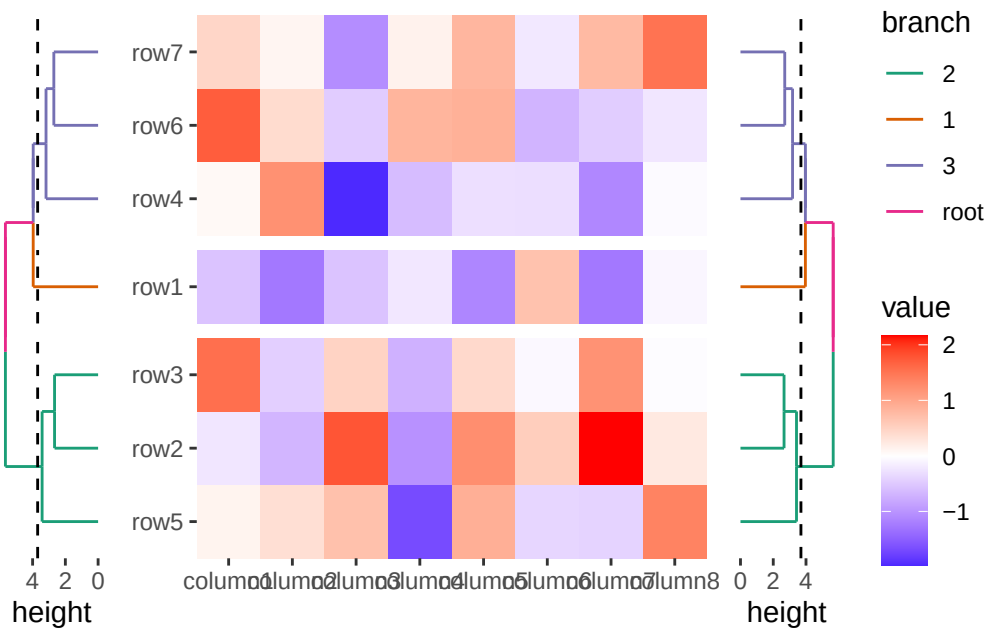


10.2 logical AND operator

`&`: applies elements to all plots in the layout including plots in the nested layout.

The `&` operator works similarly to `patchwork`, applying an element across all plots in a layout. Since `&` has lower precedence than `+`, it's generally best to use it at the end of an expression or you should wrap it in parentheses when needed.

```
# Initialize the heatmap
ggheatmap(small_mat) +
    # initialize the left annotation
    anno_left(size = 0.2) +
    # Add a dendrogram in the left annotation and split the dendrogram into 3 groups
    align_dendro(aes(color = branch), k = 3L) +
    anno_right(size = 0.2) +
    # Add a dendrogram in the right annotation and split the dendrogram into 3 groups
    align_dendro(aes(color = branch), k = 3L) &
    # Set color scale for all plots
    scale_color_brewer(palette = "Dark2")
#> > heatmap built with `geom_tile()`
```



10.3 Subtraction operator

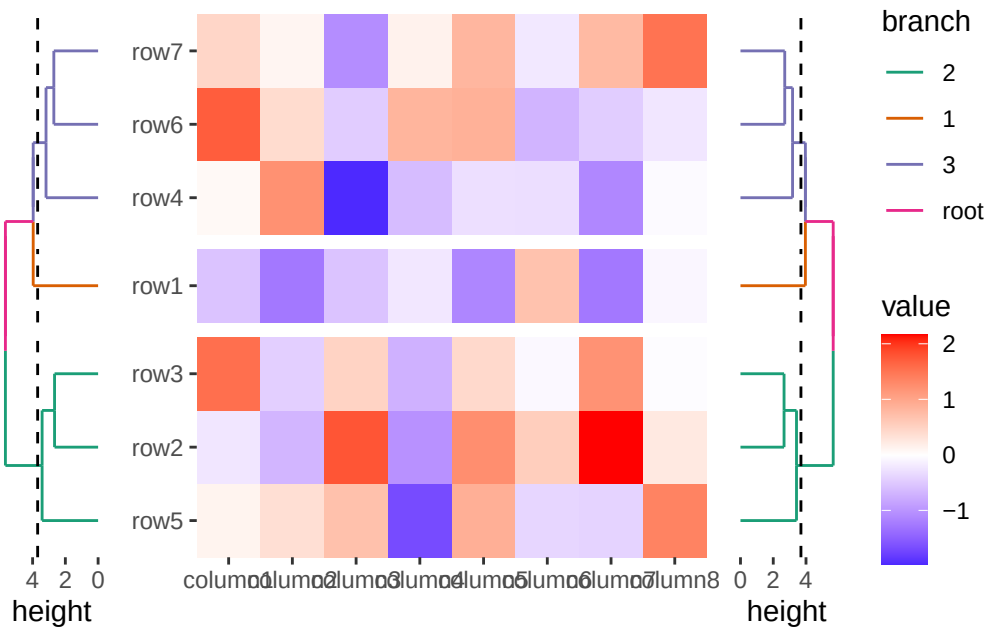
The - operator is more powerful than the & operator, enabling flexible addition of elements to multiple plots. While its use might initially seem unintuitive, the reason behind this is that - shares the same precedence group as +, which allows it to seamlessly combine with +.

10.3.1 `quad_layout()`

For `ggheatmap()`/`quad_layout()`, if the active context is the `ggheatmap()`/`quad_layout()` itself (no active annotation), the - operator behaves similarly to &. It applies the specified elements to all plots within the layout.

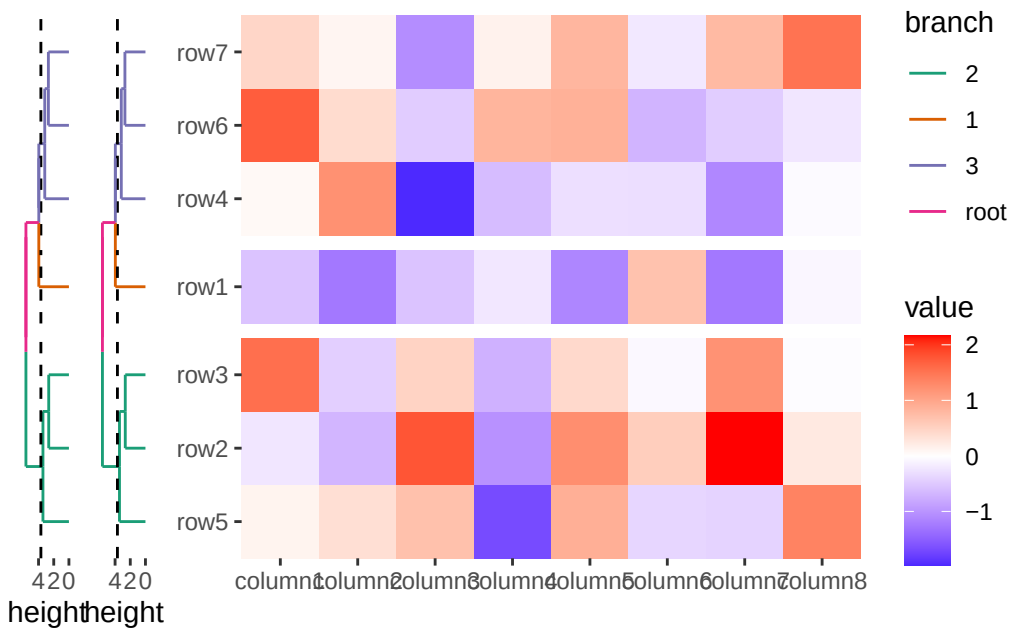
```
# Initialize the heatmap
ggheatmap(small_mat) +
    # initialize the left annotation
    anno_left(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) +
    anno_right(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) +
    # Remove any active annotation
    quad_active() -
```

```
    # Set color scale for all plots, since the active layout is the `ggheatmap()`/`quad_layou
    scale_color_brewer(palette = "Dark2")
#> > heatmap built with `geom_tile()`
```



If the active layout is an annotation stack, the - operator will only add the elements to all plots in the active annotation stack:

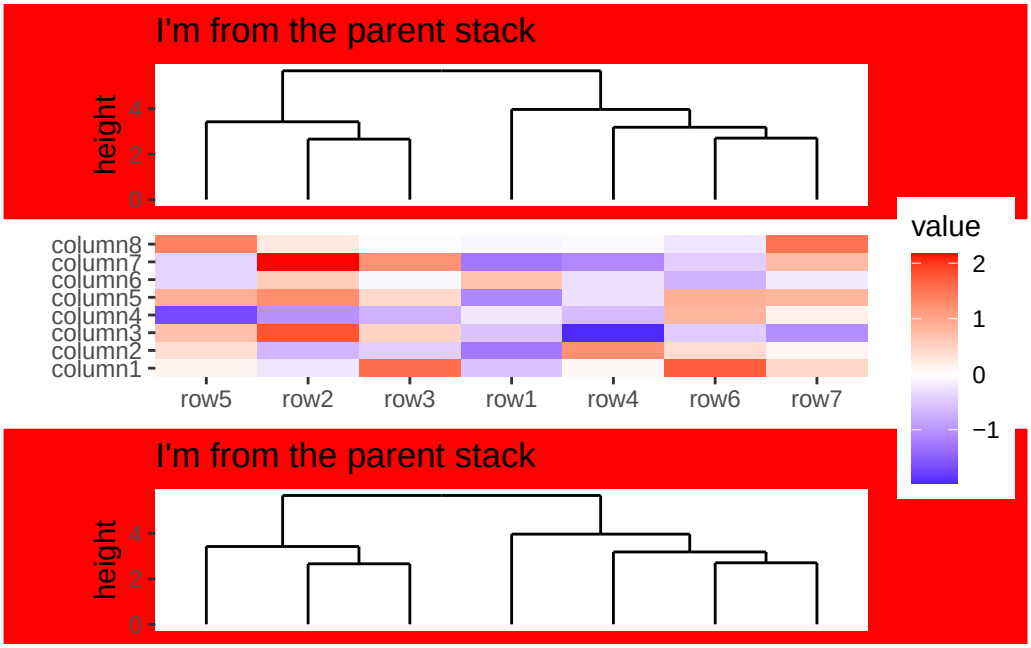
```
ggheatmap(small_mat) +
    # initialize the left annotation
    anno_left(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) +
    align_dendro(aes(color = branch), k = 3L) -
    # Modify the the color scales of all plots in the left annotation
    scale_color_brewer(palette = "Dark2")
#> > heatmap built with `geom_tile()`
```



10.3.2 `stack_layout()`

For `stack_layout()`, if the active layout is the `stack_layout()` itself, `-` applies the elements to all plots in the layout except the nested `ggheatmap()`/`quad_layout()`.

```
stack_alignv(small_mat) +
    align_dendro() +
    ggtitle("I'm from the parent stack") +
    ggheatmap() +
    # remove any active context
    stack_active() +
    align_dendro() +
    ggtitle("I'm from the parent stack") -
    # Modify the the color scales of all plots in the stack layout except the heatmap layout
    scale_color_brewer(palette = "Dark2") -
    # set the background of all plots in the stack layout except the heatmap layout
    theme(plot.background = element_rect(fill = "red"))
#> > heatmap built with `geom_tile()`
```



When the active layout is the nested `ggheatmap()`/`quad_layout()`, the `-` operator applies the elements to this nested layout, following the same principles as in the Section 10.3.1.

Want apply elements for plots in both `stack_layout()` and the nested `ggheatmap()`/`quad_layout()` at the same time? refer to the following section.

10.4 `with_quad()`

The `with_quad()` function adjusts the context in which elements are applied in `ggheatmap()`/`quad_layout()`. It allows you to control how objects such as themes, scales, and other plot elements are applied to specific annotation stacks or the main plot, without changing the currently active context.

This function accepts three arguments:

1. **x**: An object which can be added to the plot.
2. **position**: A string containing one or more of `"t"`, `"l"`, `"b"`, and `"r"` specifies the context for applying `x`.
3. **main**: A single boolean value indicates whether `x` should also apply to the main plot within `ggheatmap()`/`quad_layout()`. Only used when `position` is not `NULL`.

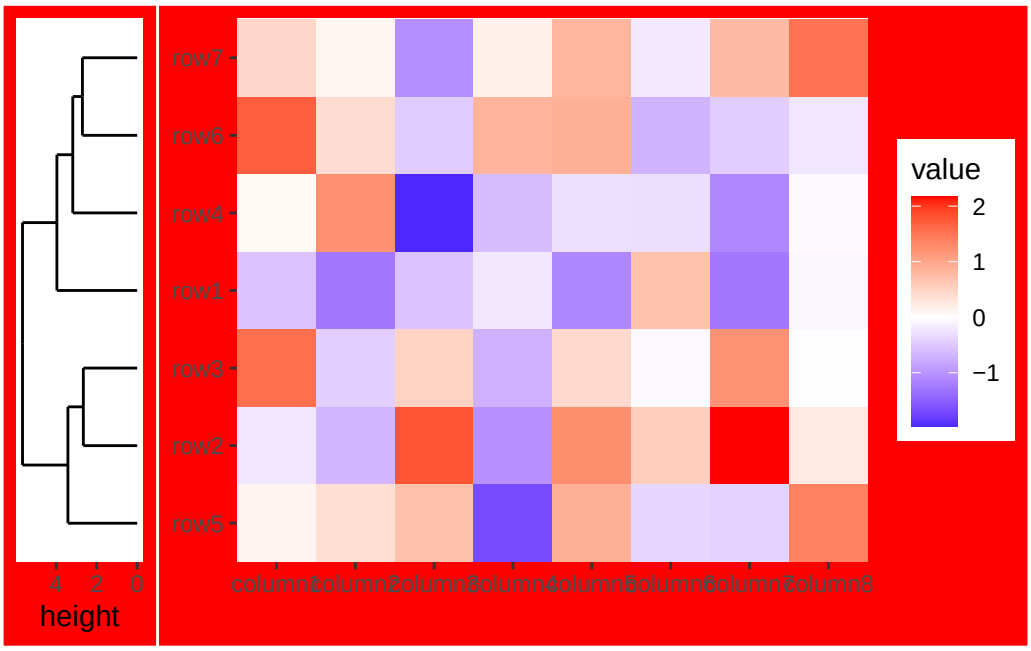
10.4.1 `quad_layout()`

Default Behavior by wrapping object with `with_quad()`:

- When `ggheatmap()`/`quad_layout()` has no active annotation stack, objects added via `+` or `-` operate normally without `with_quad()`.
- When the active annotation stack is set, `with_quad()` ensures the applied object also modifies:
  - The main plot (by default).
  - Opposite annotation stacks when using `-`.

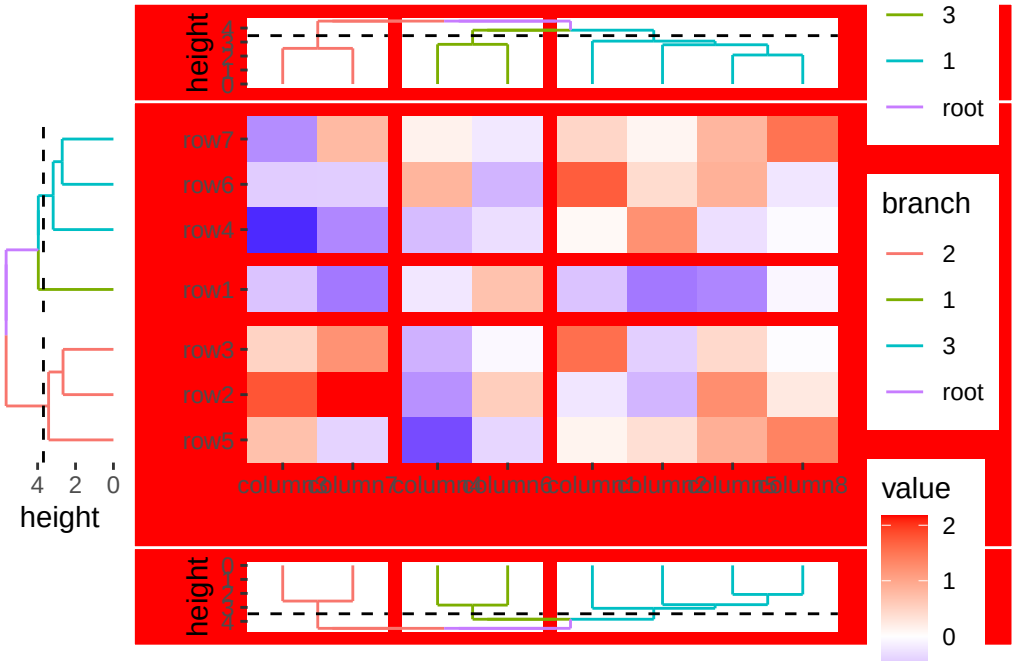
By wrapping object with `with_quad()`, the `+` operator will apply the object not only to the active plot in the annotation stack, but also to the main plot unless specified by `main` argument otherwise.

```
ggheatmap(small_mat) +
    # initialize the left annotation
    anno_left(size = 0.2) +
    align_dendro() +
    # apply the object not only to the active plot in the annotation stack, but
    # also to the main plot
    with_quad(theme(plot.background = element_rect(fill = "red")))
#> > heatmap built with `geom_tile()`
```



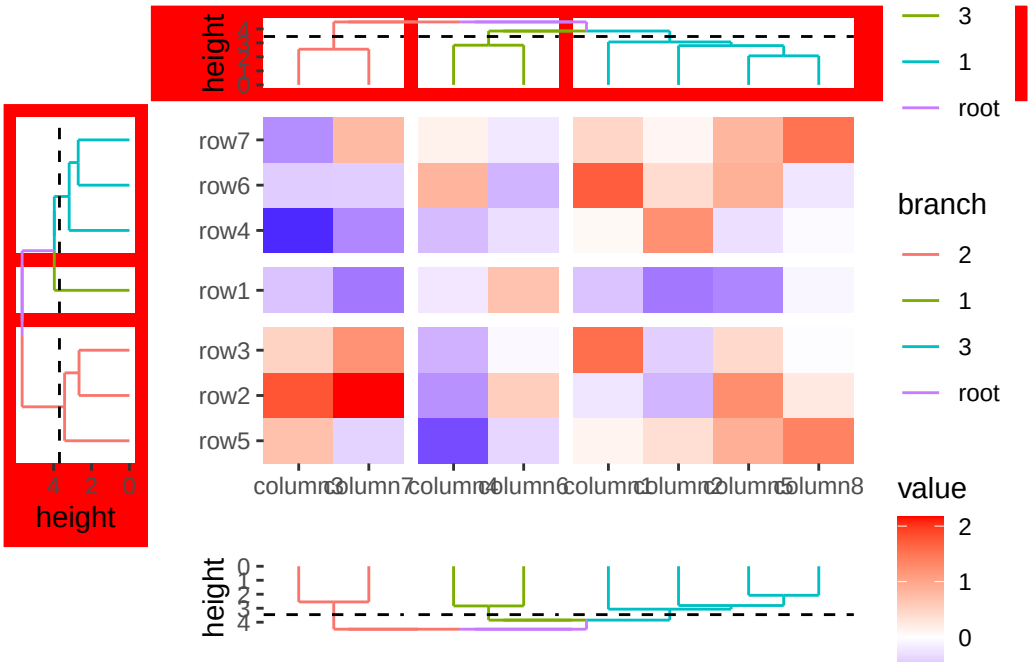
By wrapping object with `with_quad()`, the `-` operator will apply the object not only to that annotation stack but also to the opposite one (i.e., bottom if top is active, and vice versa). In these cases, the object will also be applied to the main plot by default unless specified by `main` argument otherwise.

```
ggheatmap(small_mat) +
    # initialize the left annotation
    anno_left(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) +
    # Change the active layout to the left annotation
    anno_top(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) +
    anno_bottom(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) -
    # Modify the theme of all plots in the bottom and the opposite annotation
    # in this way, the `main` argument by default would be `TRUE`
    with_quad(theme(plot.background = element_rect(fill = "red")))
#> > heatmap built with `geom_tile()`
```



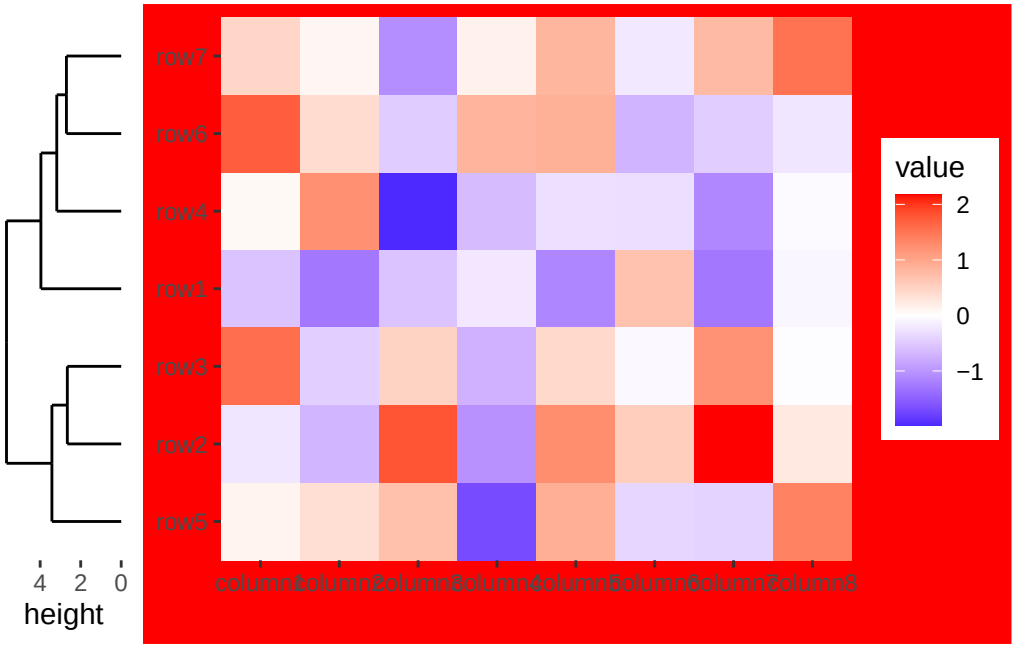
The `position` argument can be a string containing one or more of `"t"`, `"l"`, `"b"`, and `"r"`, indicating which annotation stack should be used as the context. When the `position` argument is manually set, the default value of the `main` argument will be `FALSE`.

```
ggheatmap(small_mat) +
    # initialize the left annotation
    anno_left(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) +
    # initialize the top annotation
    anno_top(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) +
    # initialize the bottom annotation
    anno_bottom(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) -
    # Modify the background of all plots in the left and top annotation
    with_quad(theme(plot.background = element_rect(fill = "red")), "tl")
#> > heatmap built with `geom_tile()`
```

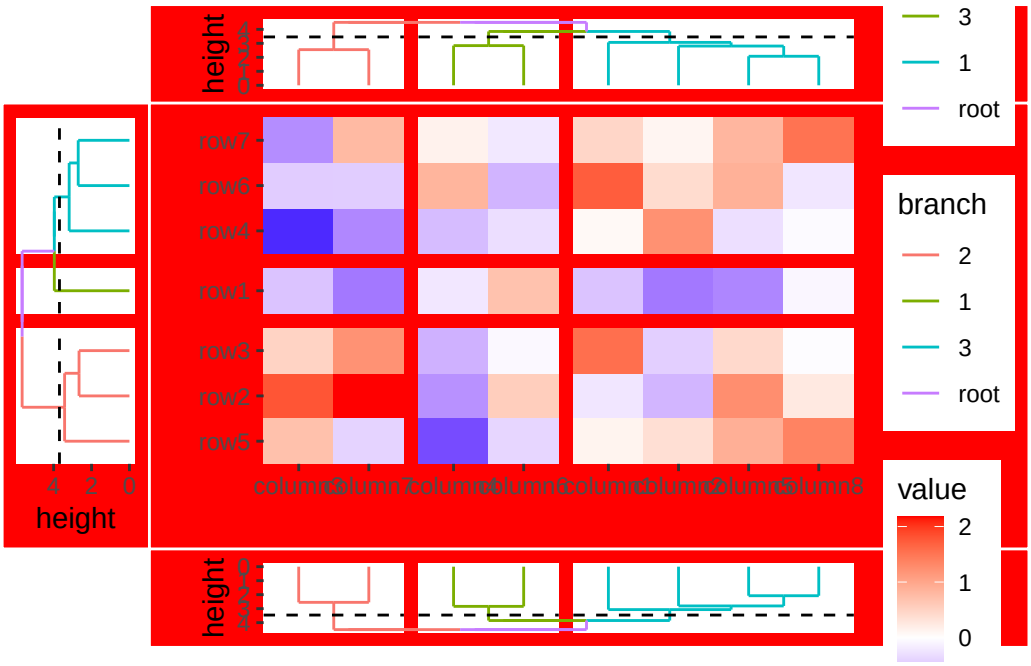


Setting `position` to `NULL` change the context to the `ggheatmap()`/`quad_layout()` itself.

```
ggheatmap(small_mat) +
    # initialize the left annotation
    anno_left(size = 0.2) +
    align_dendro() +
    # we apply the theme to the main plot only
    with_quad(theme(plot.background = element_rect(fill = "red")), NULL)
#> > heatmap built with `geom_tile()`
```




```
ggheatmap(small_mat) +
    # initialize the left annotation
    anno_left(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) +
    # initialize the top annotation
    anno_top(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) +
    # initialize the bottom annotation
    anno_bottom(size = 0.2) +
    align_dendro(aes(color = branch), k = 3L) -
    # Modify the background of all plots
    with_quad(theme(plot.background = element_rect(fill = "red")), NULL)
#> > heatmap built with `geom_tile()`
```

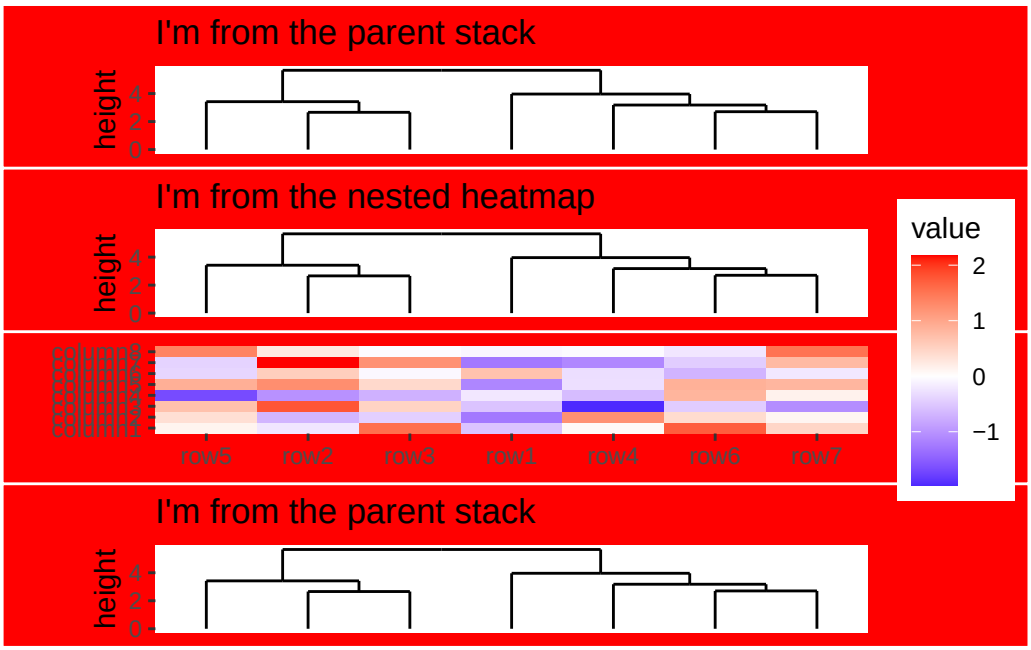


10.4.2 `stack_layout()`

When the active layout is the `stack_layout()` itself, by default, by wrapping object with `with_quad()`, `-` operator will apply changes to all plots along the `stack_layout()`, which means if the stack layout is in horizontal, `-` operator will also add the element to the left and right annotation, if the stack layout is in vertical, `-` operator will also add element to the top and bottom annotation. In these cases, the object will also be applied to the main plot by default unless specified by `main` argument otherwise.

```
stack_alignv(small_mat) +
    align_dendro() +
    ggtitle("I'm from the parent stack") +
    ggheatmap() +
    anno_top() +
    align_dendro() +
    ggtitle("I'm from the nested heatmap") +
    # remove any active context
    stack_active() +
    align_dendro() +
    ggtitle("I'm from the parent stack") -
    # Modify the the color scales of all plots in the stack layout except the heatmap layout
    scale_color_brewer(palette = "Dark2") -
```

```
    # set the background of all plots in the stack layout (including plots in the heatmap lay
    with_quad(theme(plot.background = element_rect(fill = "red")))
#> > heatmap built with `geom_tile()`
```



`+` operator won't do anything special when the active layout is the `stack_layout()` itself.

When the active layout is the nested `ggheatmap()`/`quad_layout()`, the `+`/`-` operator applies the elements to this nested layout, following the same principles as for `ggheatmap()`/`quad_layout()`.

11 Schemes

Schemes control the actions of plots within the layout and can be applied either globally to the layout or individually to specific plots.

- To apply a scheme to a single plot, use the `+` operator.
- To set a scheme at the layout level, use the `-` operator. Scheme set at the layout level will be inherited by all plots when rendering the layout.

  scheme inherit properties from parent layout hierarchically.

The package currently provides three schemes, each prefixed with `scheme_`:

- `scheme_theme`: Sets the default theme for the plot.
- `scheme_data`: Transforms the plot data. Many functions in this package require a specific data format to align observations, `scheme_data()` helps reformat data frames as needed.
- `scheme_align`: Defines alignment specifications for plots within the layout.

```
library(ggalign)
#> Loading required package: ggplot2
```

```
set.seed(123)
small_mat <- matrix(rnorm(81), nrow = 9)
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

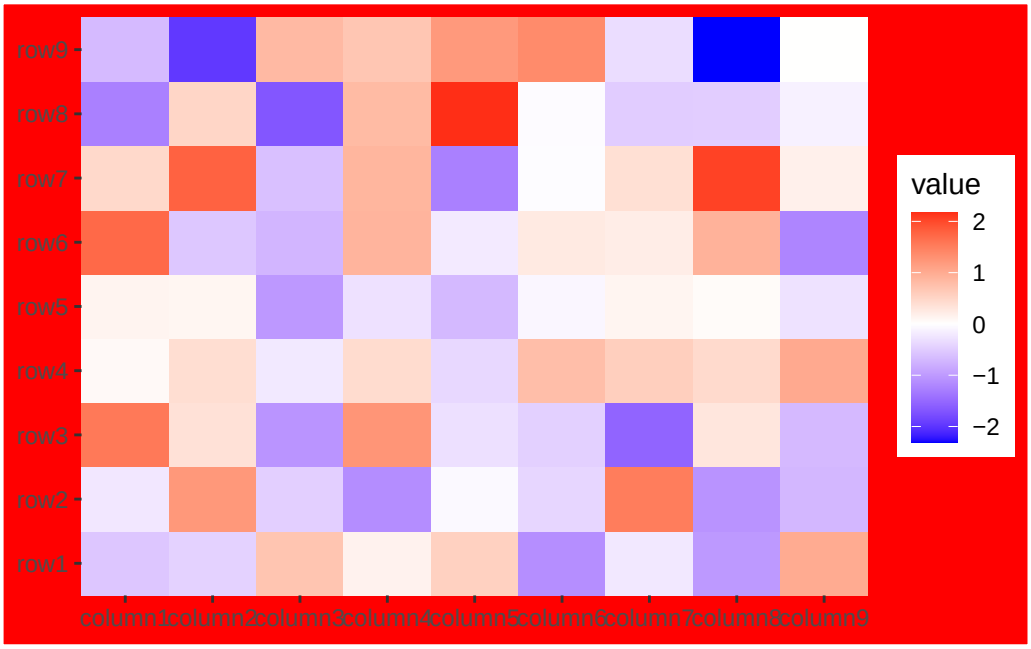
11.1 `scheme_theme()`

The `scheme_theme()` function extends `theme()` to set a default theme for plots, allowing you to input `theme()` elements directly or add the theme elements.

To set a scheme for a single plot, simply use the `+` operator:

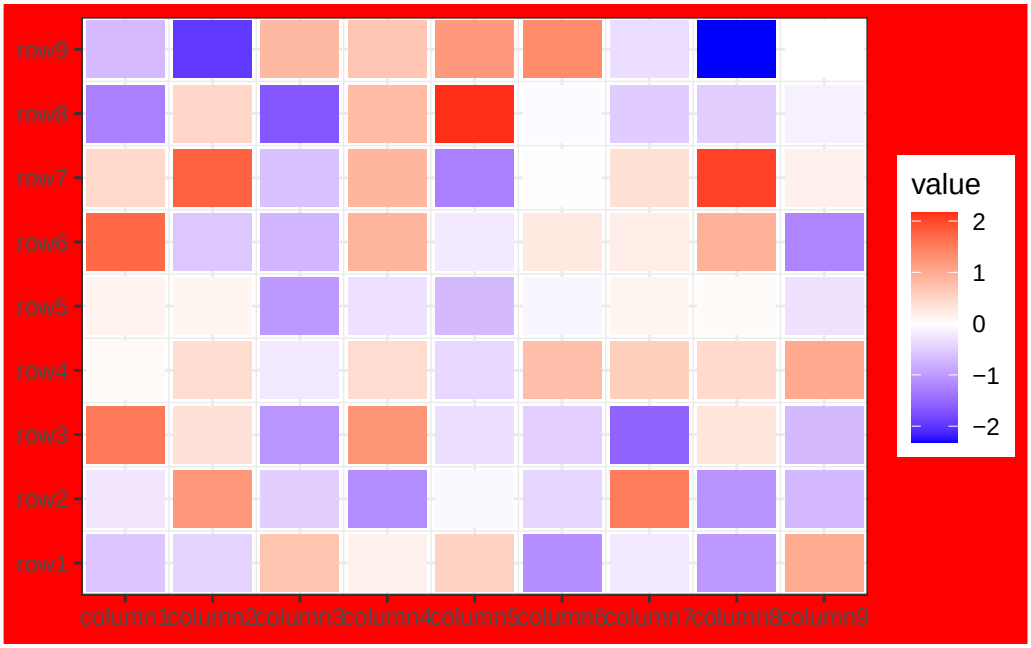
```
ggheatmap(small_mat) +                                                    ①
    scheme_theme(plot.background = element_rect(fill = "red"))            ②
#> > heatmap built with `geom_tile()`
```

① initialize a heatmap layout
② set the default theme, change the plot background for the main plot



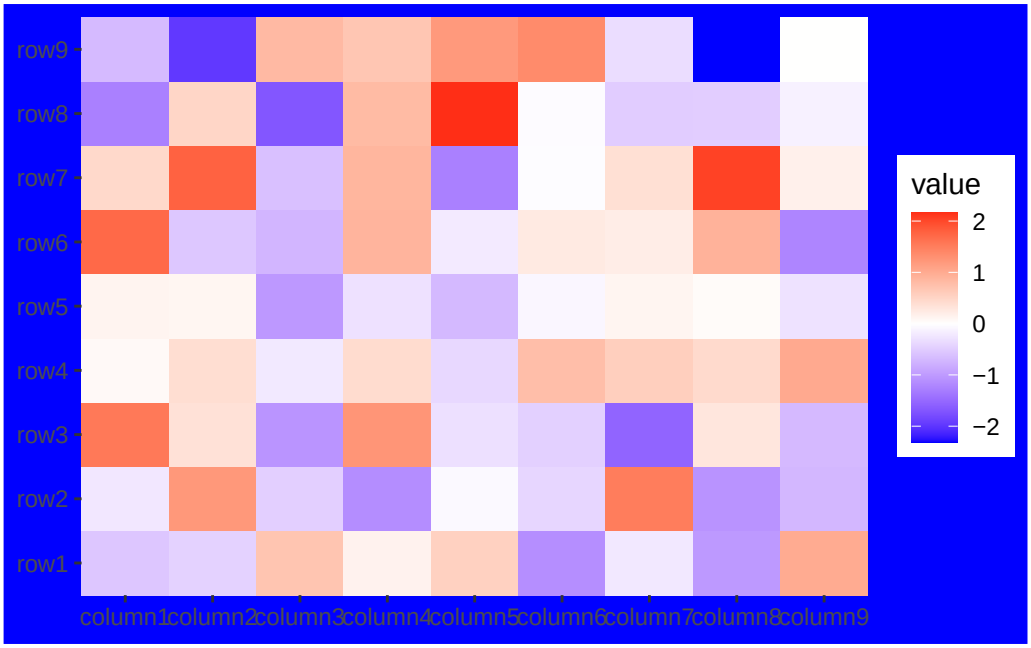
You can use a `theme()` object directly in `scheme_theme()`.

```
ggheatmap(small_mat, filling = FALSE) +
    geom_tile(aes(fill = value), width = 0.9, height = 0.9) +
    scheme_theme(theme_bw(), plot.background = element_rect(fill = "red"))
```



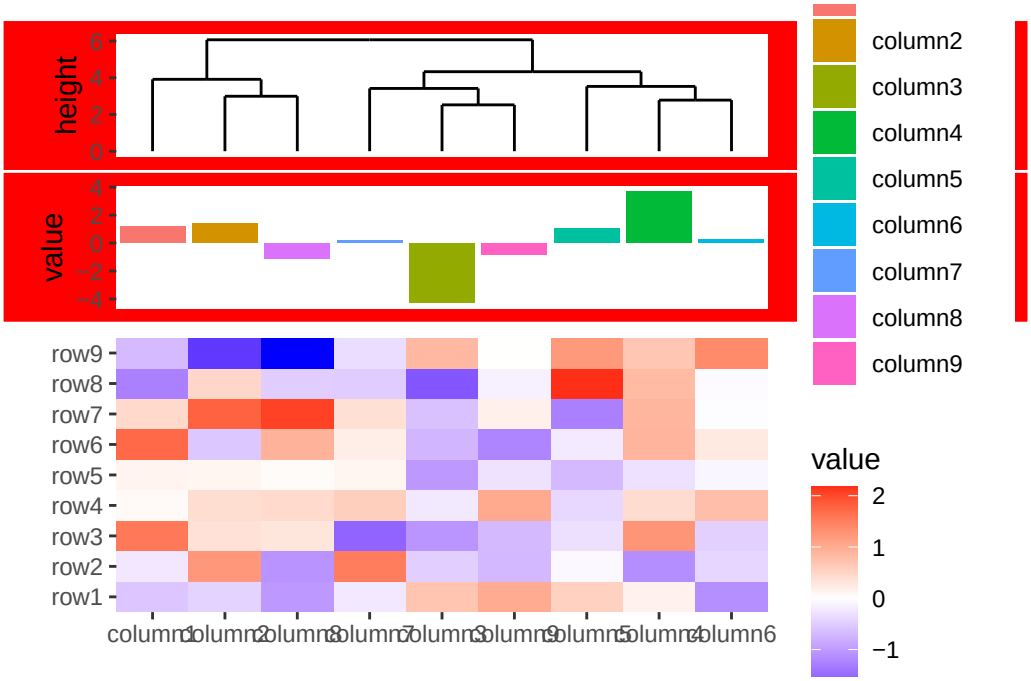
Note that `scheme_theme()` serves as the default theme and will always be overridden by any `theme()` settings applied directly to the plot. The default theme (`scheme_theme()`) is applied first, followed by any specific `theme()` settings, even if `theme()` is added before `scheme_theme()`.

```
ggheatmap(small_mat) +
    # change the plot theme of the heatmap body
    theme(plot.background = element_rect(fill = "blue")) +
    # change the default theme of the heatmap body
    scheme_theme(plot.background = element_rect(fill = "red"))
#> > heatmap built with `geom_tile()`
```



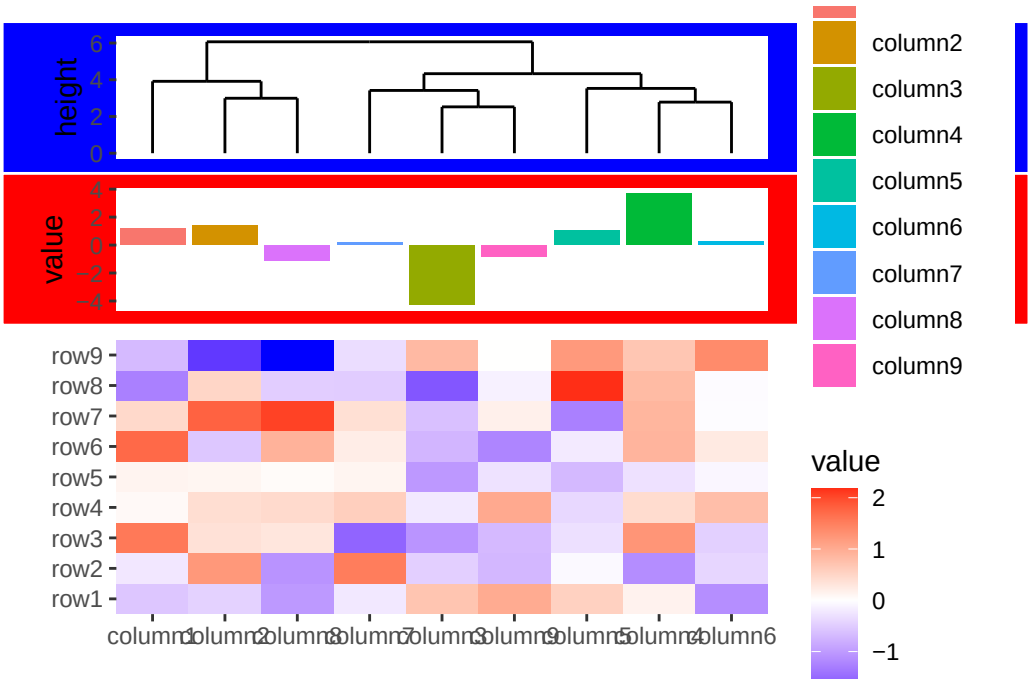
By using the - operator with schemes, we apply the scheme directly to the active layout.

```
ggheatmap(small_mat) +
    # Change the active layout to the top annotation
    anno_top() +
    # add a dendrogram to the top annotation
    align_dendro() +
    # add a bar plot to the top annotation
    ggalign(aes(.discrete_x, value, fill = factor(.names)), data = rowSums) +
    geom_bar(stat = "identity") -
    # Change the default theme of the top annotation
    # All plots in the top annotation will inherit this default theme
    scheme_theme(plot.background = element_rect(fill = "red"))
#> > heatmap built with `geom_tile()`
```



Unlike individual ggplot2 elements, which will be added directly to each plot by `-` operator, **layout-level schemes** set by `-` operator are **inherited** by all plots in the layout when `rendered`. Any plot-specific schemes will override these layout-level schemes, regardless of the order in which they are added.

```
ggheatmap(small_mat) +
    # Change the active layout to the top annotation
    anno_top() +
    # add a dendrogram to the top annotation
    align_dendro() +
    # change the scheme_theme for the dendrogram plot
    scheme_theme(plot.background = element_rect(fill = "blue")) +
    # add a bar plot to the top annotation
    ggalign(aes(.discrete_x, value, fill = factor(.names)), data = rowSums) +
    geom_bar(stat = "identity") -
    # Change the default theme of the top annotation
    # All plots in the top annotation will inherit this default theme
    # But the plot-specific options will override these
    scheme_theme(plot.background = element_rect(fill = "red"))
#> > heatmap built with `geom_tile()`
```



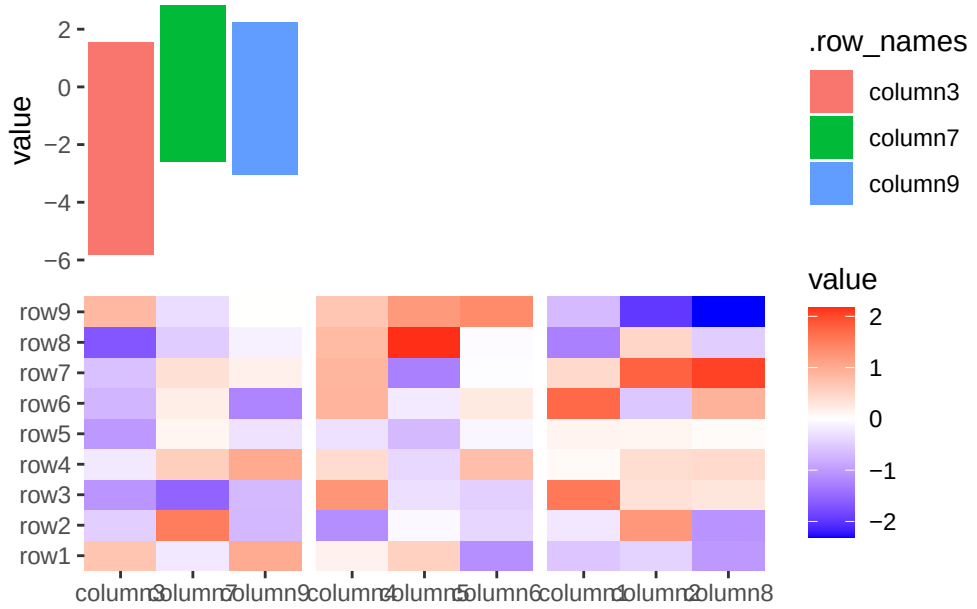
11.2 `scheme_data()`

`ggalign()` requires the specific data format for its operations. If you need to transform or filter data for individual `geoms`, you can use the `data` argument within each `geom`. However, if you have multiple `geoms` and want a consistent transformation applied across all, you can utilize the `scheme_data()` function. This allows you to transform the default data for the entire plot.

The `scheme_data()` accepts a function that takes a data frame as input and returns a modified data frame. By default, `scheme_data()` will attempt to inherit from the parent layout if the data is inherited from it. However, there is one exception: `align_dendro()` will not inherit `scheme_data()` transformations by default.

```
set.seed(1234L)
ggheatmap(small_mat) +
    anno_top() +
    align_kmeans(3L) +
    # we add a bar plot
    ggalign() +
    # we subest the plot data
    scheme_data(~ subset(.x, .panel == 1L)) +
```

```
    geom_bar(aes(y = value, fill = .row_names), stat = "identity")
#> > heatmap built with `geom_tile()`
```



11.3 `scheme_align()`

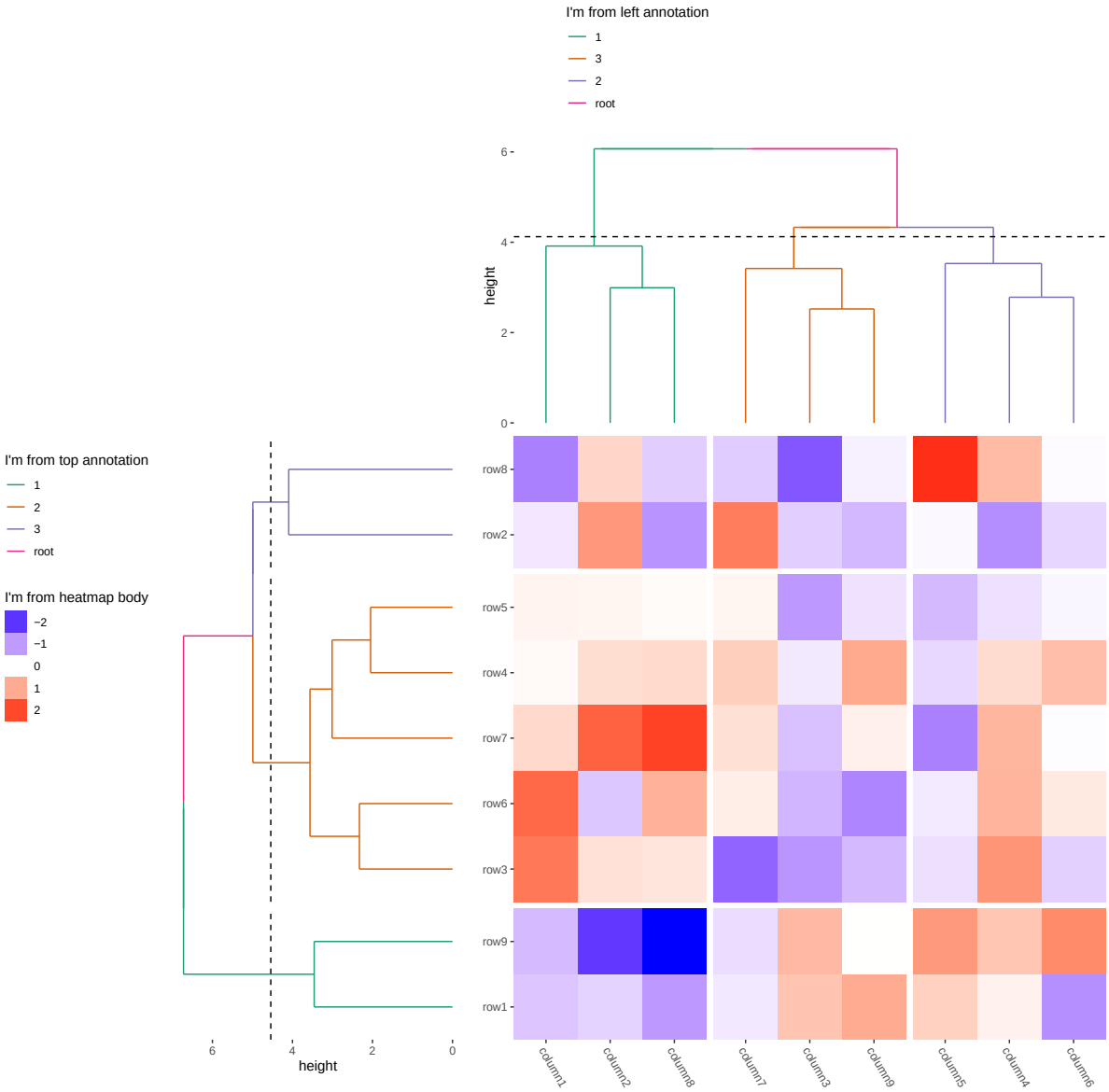
The `scheme_align()` function controls the align specifications for plots.

11.3.1 guides

By default, `ggheatmap()` will collect all guide legends on the side from which they originate.

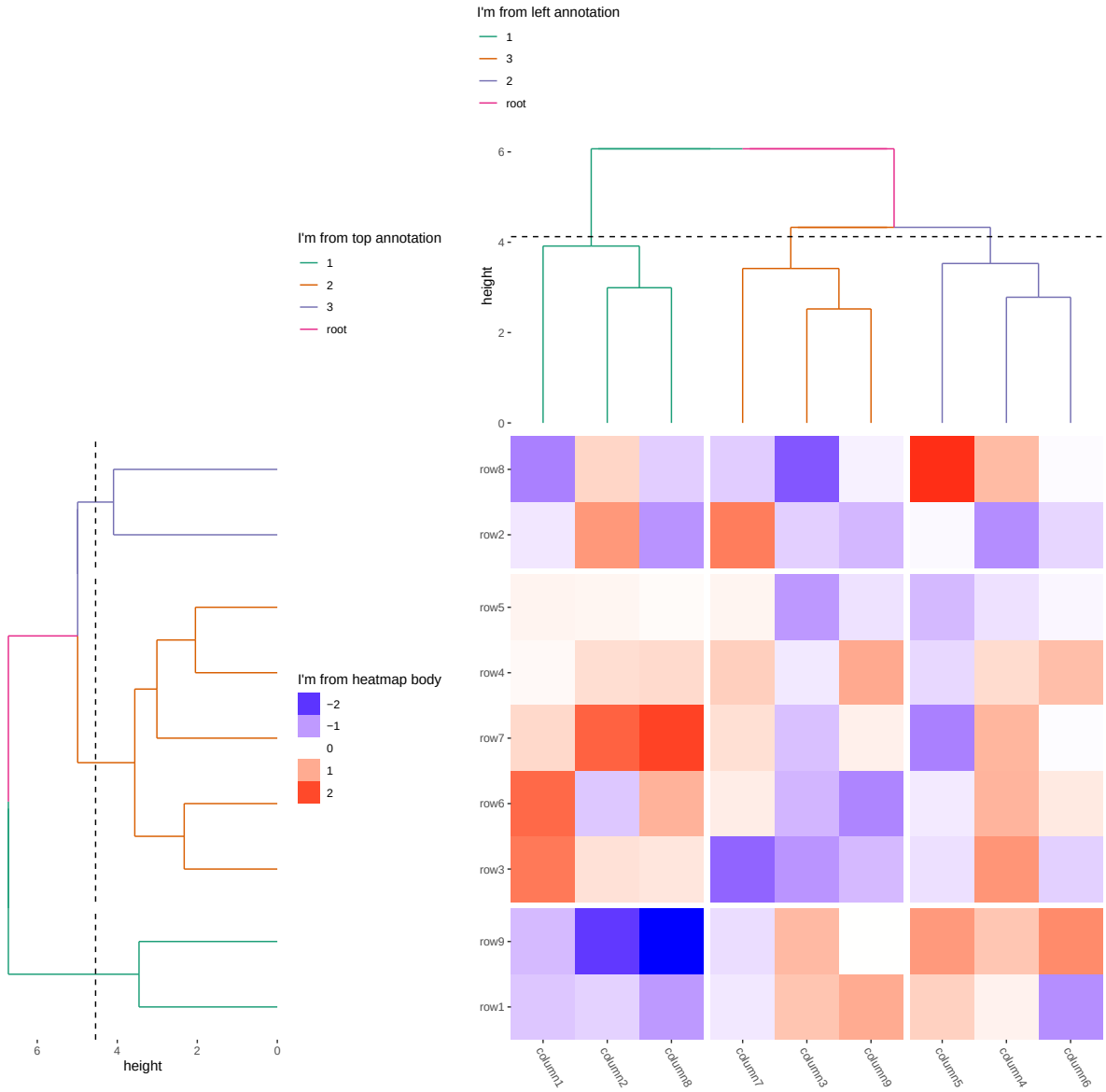
```
heatmap_collect_all_guides <- ggheatmap(small_mat, width = 2, height = 2L) +
    # we set the legend to the left side
    scale_fill_gradient2(
        low = "blue", high = "red",
        name = "I'm from heatmap body",
        guide = guide_legend(position = "left")
    ) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    # we add a top annotation
```

```
    anno_top() +
    # in the top annotation, we add a dendrogram
    align_dendro(aes(color = branch), k = 3L) +
    # we set the legends of the dendrogram to the left side
    scale_color_brewer(
        name = "I'm from top annotation", palette = "Dark2",
        guide = guide_legend(position = "left")
    ) +
    # we add a left annotation
    anno_left() +
    align_dendro(aes(color = branch), k = 3L) +
    # we set the legends of the dendrogram to the top side
    scale_color_brewer(
        name = "I'm from left annotation", palette = "Dark2",
        guide = guide_legend(position = "top", direction = "vertical")
    ) &
    # we remove all margins for all plots
    theme(plot.margin = margin())
heatmap_collect_all_guides
#> > heatmap built with `geom_tile()`
```



The guides argument schemes which side of guide legends should be gathered. In the following example, we'll collect the guide legends only on the top (`t`) sides:

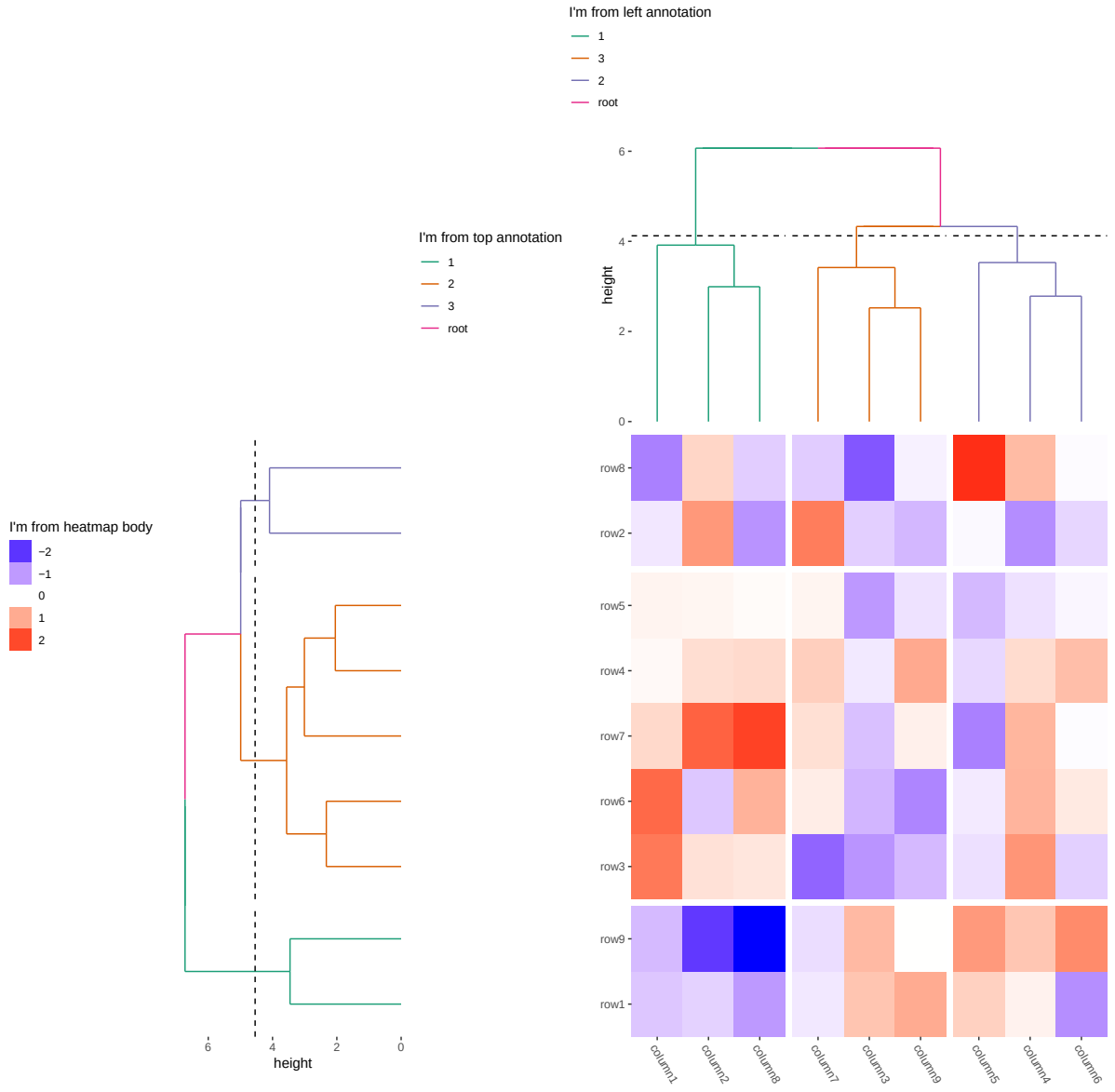
```
heatmap_collect_all_guides -
    # we set global `guides` argument for `the heatmap layout`
    # we only collect guides in the top side
    with_quad(scheme_align(guides = "t"), NULL)
#> > heatmap built with `geom_tile()`
```



You can also apply the `scheme_align()` function directly to specific plots:

```
heatmap_collect_all_guides -
    # we set global `guides` argument for the heatmap layout
    # we only collect guides in the top side
    with_quad(scheme_align(guides = "t"), NULL) +
    # `+` apply it to the active plot
    # for the heatmap body, we collect guide in the left side
    with_quad(scheme_align(guides = "l"), NULL)
```

```
#> > heatmap built with `geom_tile()`
```



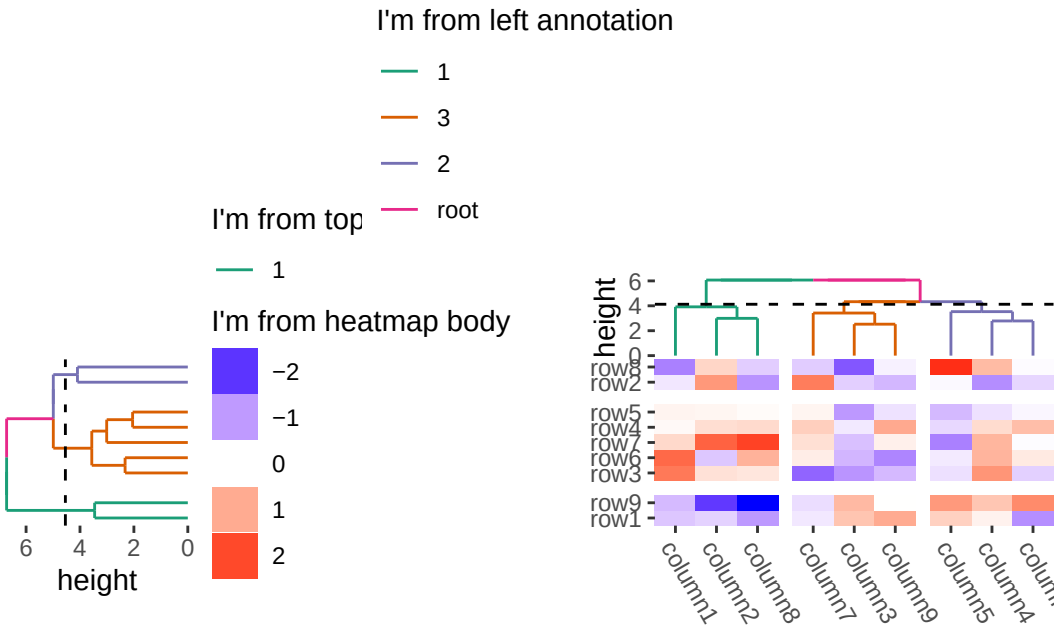
Note: The legend on the left side of the heatmap body is collected and positioned on the left side at the layout level.

If you're annoyed by the large space between the left annotation and the heatmap body, don't worry! This issue will be addressed in Section 11.3.2.

Now, Let's dive deeper into the guide collection process.

In the last example, we set the `guides` argument for the heatmap body. But what happens when we set the `guides` for the dendrogram in the top annotation?

```
heatmap_collect_all_guides -
    # we set global `guides` argument for `the heatmap layout`
    # we only collect guides in the top side in the heatmap layout
    with_quad(scheme_align(guides = "t"), NULL) +
    # `+` apply it to the active plot
    # for the dendrogram in the top annotation, we collect guide in the left side
    with_quad(scheme_align(guides = "l"), "t")
#> > heatmap built with `geom_tile()`
```



Nothing seems to have changed, right? This is because guide legends within annotation stacks are first collected by the annotation `stack_layout()` and only then passed to the top-level layout for further integration.

By default, the annotation stack inherits the `guides` arguments from the heatmap layout, followed by the inherited of individual plot in the annotation. So `guides` argument set at top-level (heatmap layout) will affect all guide collection behaviour.

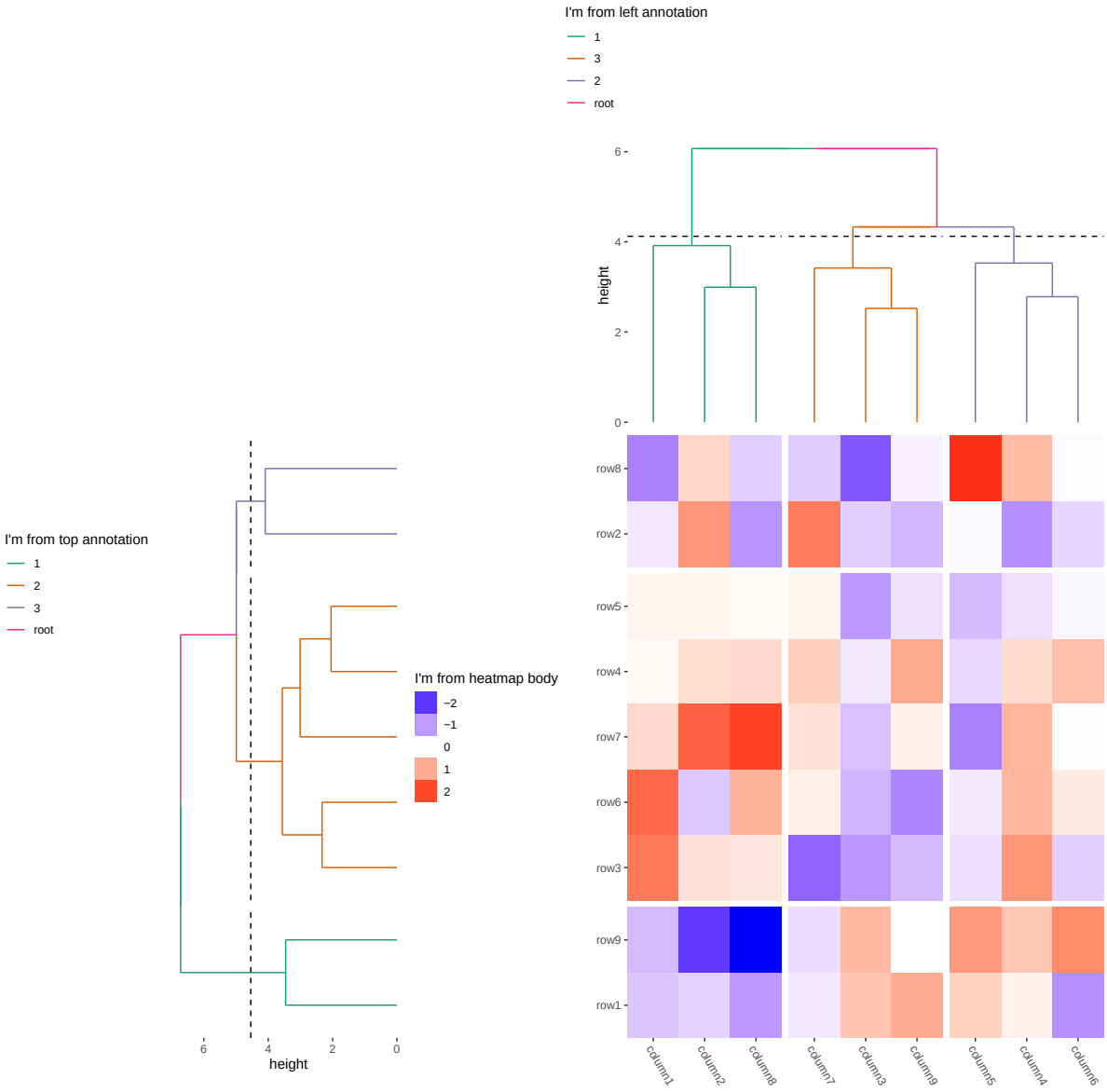
In this example:

- The legend on the left side of the dendrogram in the top annotation is collected first at the annotation level.

- Since the heatmap layout is not set to collect legends from the left side, it remains at the left side within the annotation stack.
- For this specific case, the top annotation contains only one plot, so its annotation-level placement is identical to plot-level placement.

To override this, you can use the `free_guides` argument of the `quad_anno()`/`anno_*()` function. This differs from the `guides` argument in `scheme_align()`, which schemes the behavior for the plots in the layout. The `free_guides` argument specifies which guide legends from at the annotation stack layout level should be collected by the heatmap layout.

```
heatmap_collect_all_guides -
    # we set global `guides` argument for `the heatmap layout`
    # we only collect guides in the top side in the heatmap layout
    with_quad(scheme_align(guides = "t"), NULL) +
    # we also collect guides in the left side for the top annotation stack
    # in the heatmap layout
    anno_top(free_guides = "l") +
    # `+` apply it to the active plot
    # for the dendrogram in the top annotation, we collect guide in the left side
    scheme_align(guides = "l")
#> > heatmap built with `geom_tile()`
```

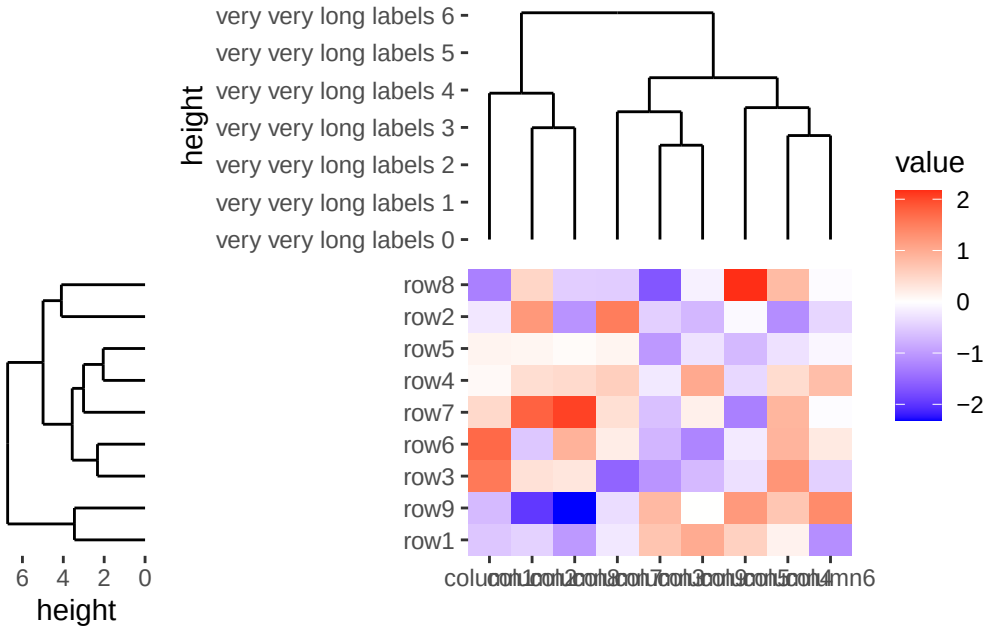


Note: The heatmap layout will only collect guide legends from the annotation stack if the stack layout collects its own guides first.

11.3.2 free_spaces

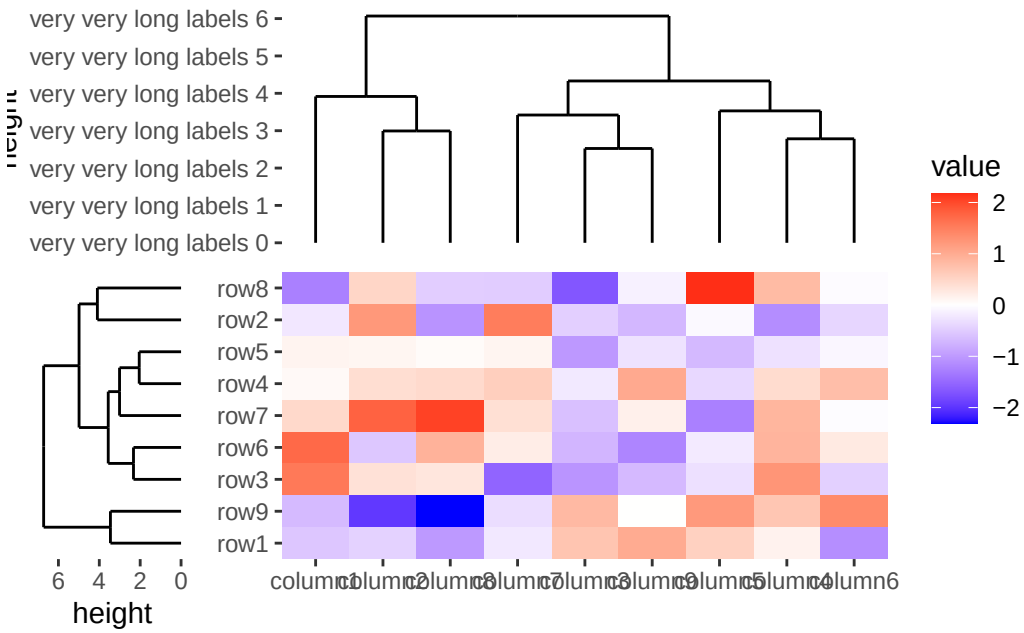
By default, `ggheatmap()` will align all elements of the plot, which can sometimes lead to unwanted spacing. Consider the following example:

```
ggheatmap(small_mat) +
    # add top annotation
    anno_top(size = unit(30, "mm")) +
    # add a dendrogram to the top annotation
    align_dendro() +
    # here, we use long labels for visual example
    scale_y_continuous(
        expand = expansion(),
        labels = ~ paste("very very long labels", .x)
    ) +
    # add left annotation
    anno_left(unit(20, "mm")) +
    # add a dendrogram to the left annotation
    align_dendro()
#> > heatmap built with `geom_tile()`
```



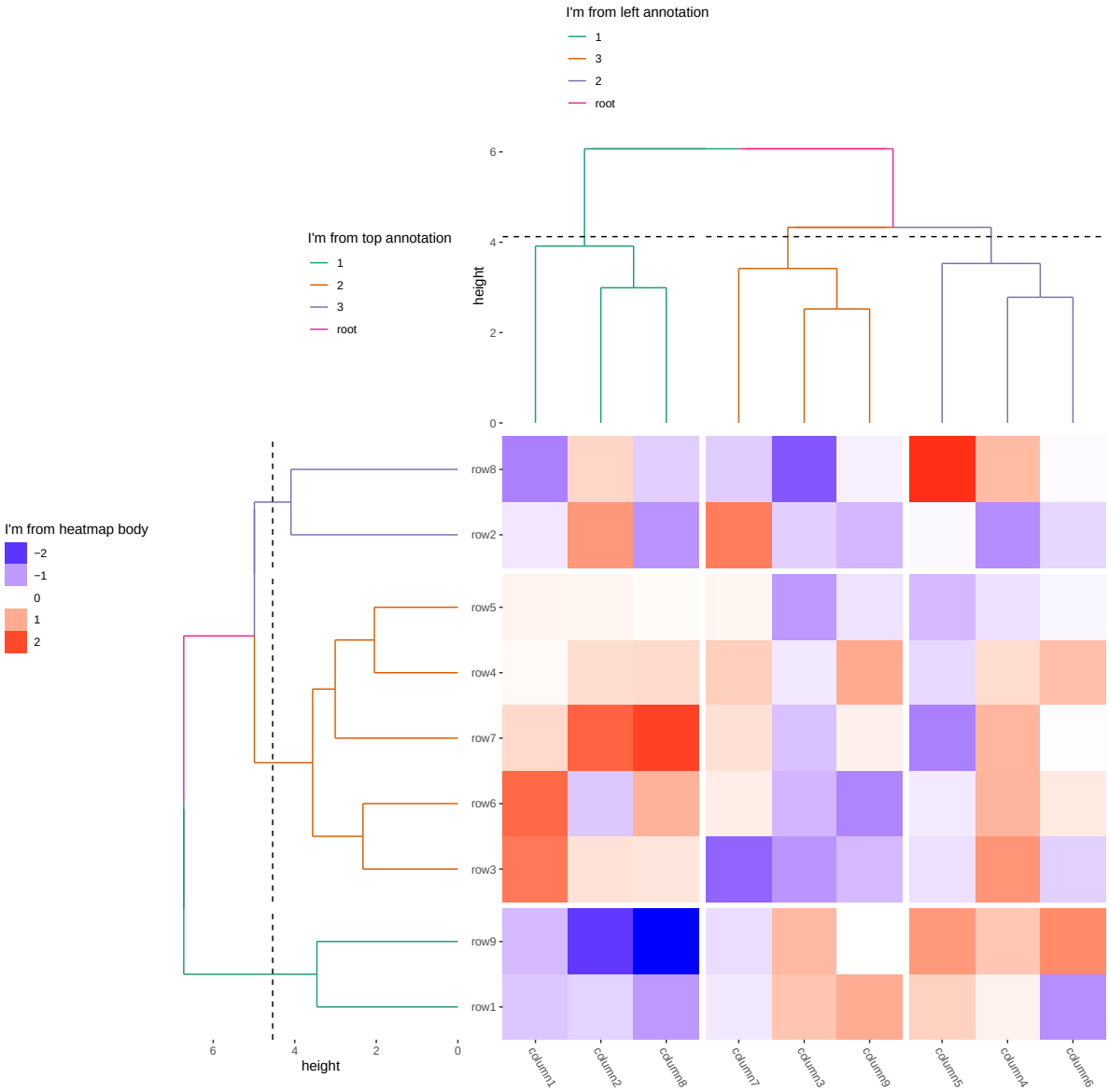
In this case, the left annotation stack is positioned far from the heatmap body due to the wide axis labels in the top annotation stack. This occurs because the top annotation stack is aligned with the heatmap body. To fix this, you can remove the left borders around the panel of the top annotation stack by setting `free_spaces = "l"`.

```
ggheatmap(small_mat) +
    # add top annotation
    anno_top(size = unit(30, "mm")) -
    # we remove the spaces of the left borders in the top annotation
    scheme_align(free_spaces = "l") +
    # add a dendrogram to the top annotation
    align_dendro() +
    # here, we use long labels for visual example
    scale_y_continuous(
        expand = expansion(),
        labels = ~ paste("very very long labels", .x)
    ) +
    # add left annotation
    anno_left(unit(20, "mm")) +
    # add a dendrogram to the left annotation
    align_dendro()
#> > heatmap built with `geom_tile()`
```



One useful way to utilize `free_spaces` is to position the guide legends next to the annotations. (Note the guide legend from the bottom annotation):

```
heatmap_collect_all_guides +
    # reset the active context to the heatmap layout
    quad_active() -
    # we set global `guides` argument for the heatmap layout
    # we only collect guides in the top side
    scheme_align(guides = "t") +
    # `+` apply it to the current active plot
    # for the heatmap body, we collect guide in the left side
    scheme_align(guides = "l") -
    with_quad(scheme_align(free_spaces = "l"), "t")
#> > heatmap built with `geom_tile()`
```



Usually you want to apply `free_spaces` with the whole layout, instead of individual plots.

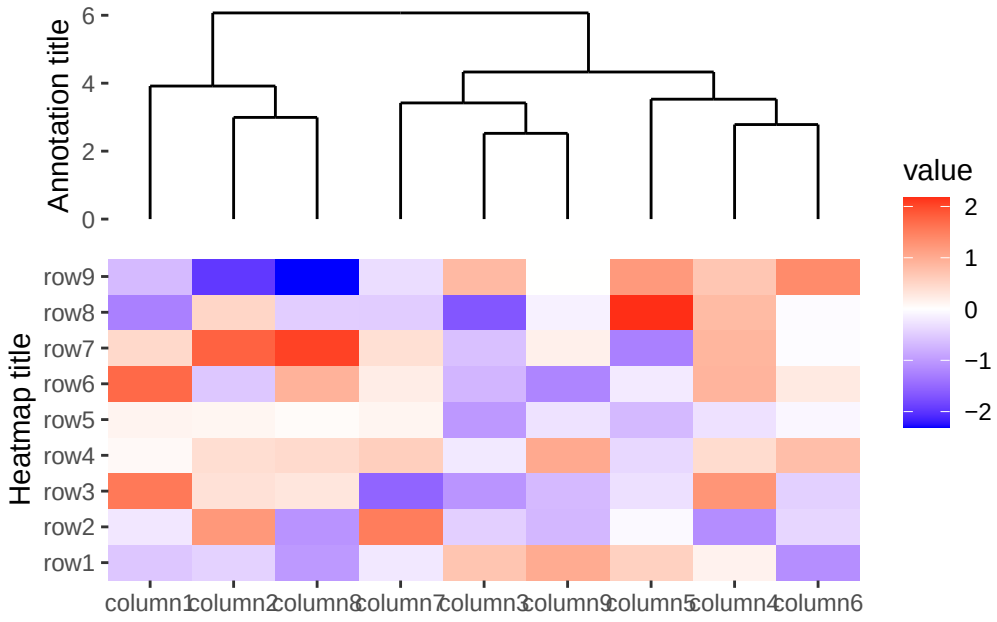
In `ggheatmap()`/`quad_layout()`, the behavior of the `free_spaces` and `free_labs` arguments differs from `guides` arguments in `scheme_align()` when inheriting from the parent layout:

- For `top` and `bottom` annotations, it inherits from the left ("l") and right ("r") axes.
- For `left` and `right` annotations, it inherits from the top ("t") and bottom ("b") axes.

11.3.3 free_labs

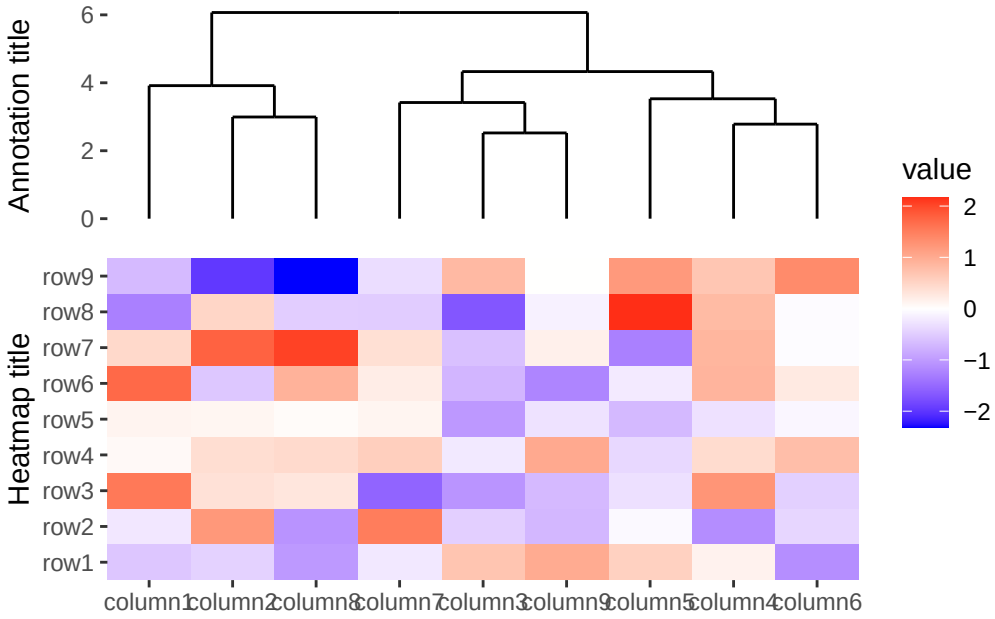
By default, we won't align the axis titles.

```
ggheatmap(small_mat) +
    ylab("Heatmap title") +
    anno_top(size = unit(30, "mm")) +
    align_dendro() +
    ylab("Annotation title")
#> > heatmap built with `geom_tile()`
```



To align axis titles, you can set `free_labs = NULL`. Alternatively, A single string containing one or more of axis positions ("t", "l", "b", "r") to indicate which axis titles should be free from alignment.

```
ggheatmap(small_mat) -
    scheme_align(free_labs = NULL) +
    ylab("Heatmap title") +
    anno_top(size = unit(30, "mm")) +
    align_dendro() +
    ylab("Annotation title")
#> > heatmap built with `geom_tile()`
```


Annotation title
6
4
2
0
Heatmap title
row9
row8
row7
row6
row5
row4
row3
row2
row1
column1
column2
column8
column7
column3
column9
column5
column4
column6
value
2
1
0
−1
−2

12 Difference with ggplot2

`ggalign` focuses on aligning axes across multiple plots. While it builds on the `ggplot2` framework, there are key differences in how scales, facets, and coordinates are handled. This vignette highlights these syntax differences.

12.1 Position Scales

To better fit the alignment-based layout, `ggalign` introduces adjustments to `breaks`, `labels`, and `expand` arguments.

For `discrete` values, `ggalign` introduces special syntax and handling for these axes, differing from the default behavior in `ggplot2`. These adjustments ensure that observations are properly aligned and operations are user-friendly.

The following syntax applies to the axes used to align observations (discrete values).

12.1.1 breaks

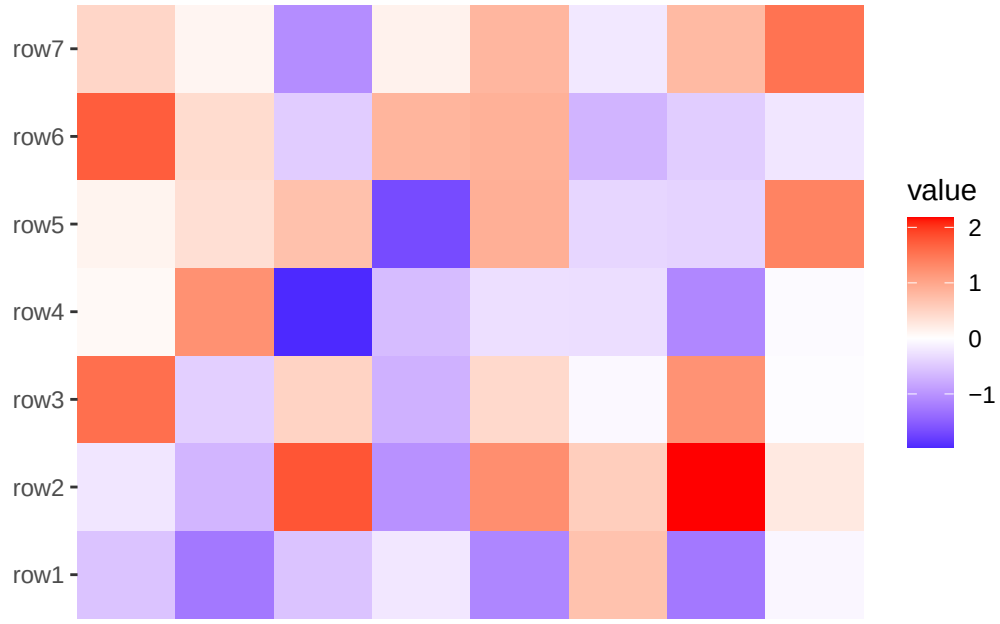
`breaks` and `labels` are typically handled similarly to discrete scales, as we focus on aligning observations (which should be regarded as discrete variables); no matter what you use is continuous scale or discrete scale.

`breaks` should be one of:

```
- `NULL` for no breaks

- `waiver()` for the default breaks (the full data index or `NULL` if no
data names and `labels` is `waiver()`)

- A character vector of breaks (rownames / colunames of the matrix).

- A numeric vector of data index (must be an integer).

- A function that takes the data names or the data index as input and
returns breaks as output. Also accepts rlang lambda function notation.
```

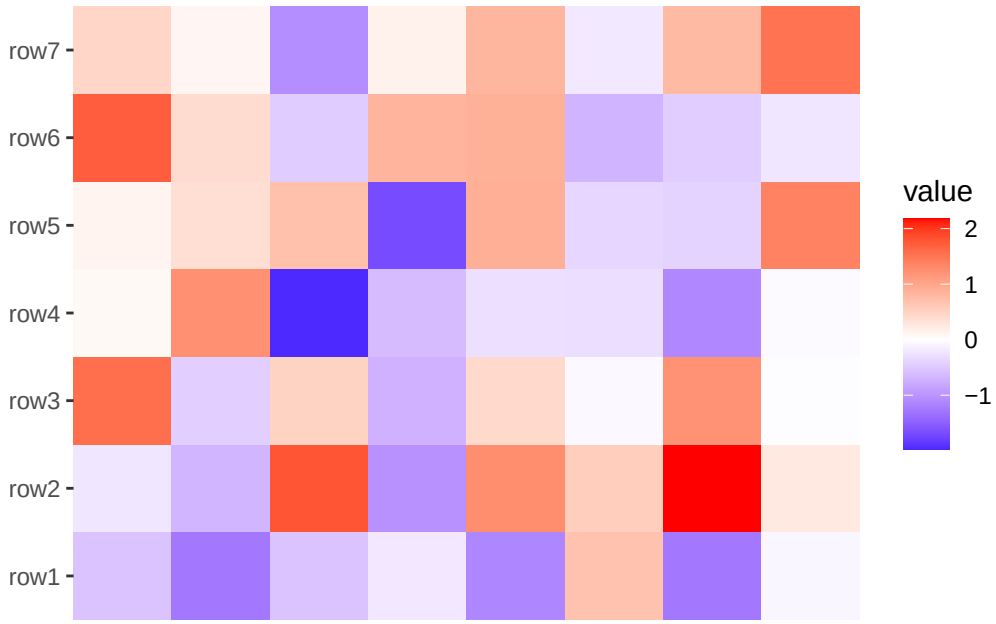
Default `breaks` without names:

```
no_names <- small_mat
colnames(no_names) <- NULL
ggheatmap(no_names) + scale_x_continuous()
#> > heatmap built with `geom_tile()`
```

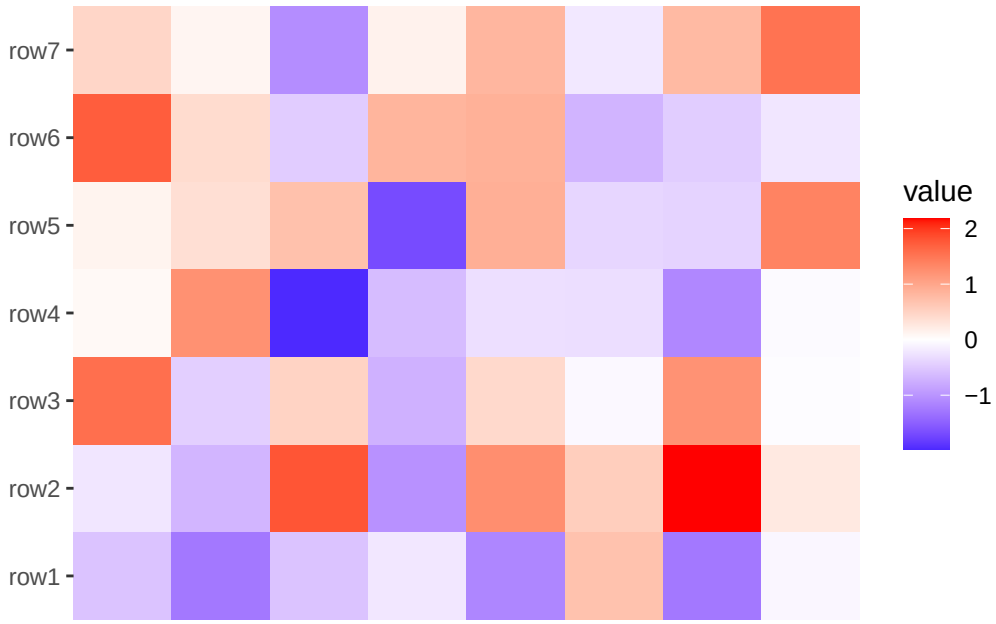


No breaks:

```
ggheatmap(small_mat) + scale_x_continuous(breaks = NULL)
#> > heatmap built with `geom_tile()`
```

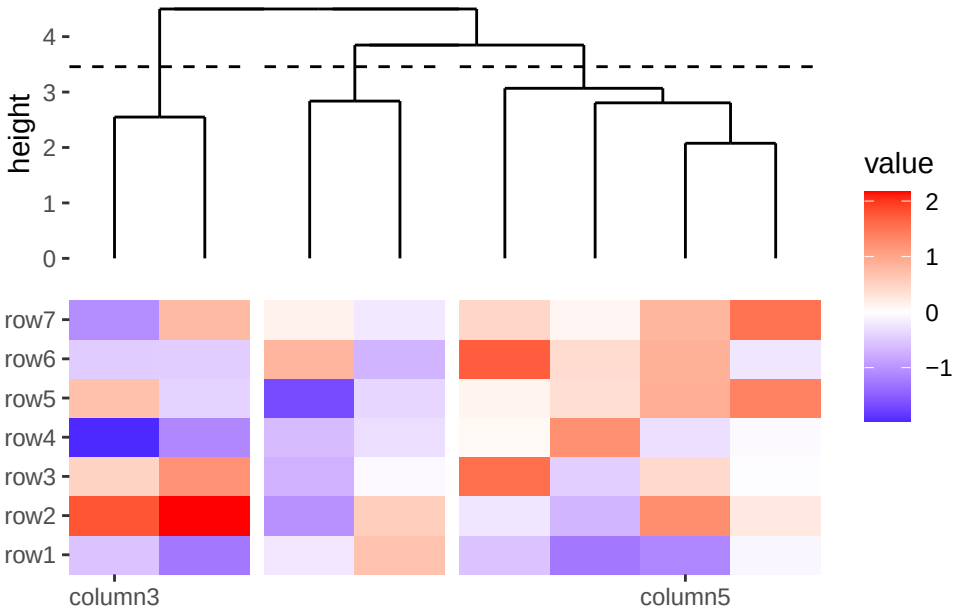



```
ggheatmap(small_mat, filling = FALSE) +
    geom_tile(aes(.discrete_x, .discrete_y, fill = value)) +
    scale_x_discrete(breaks = NULL)
```

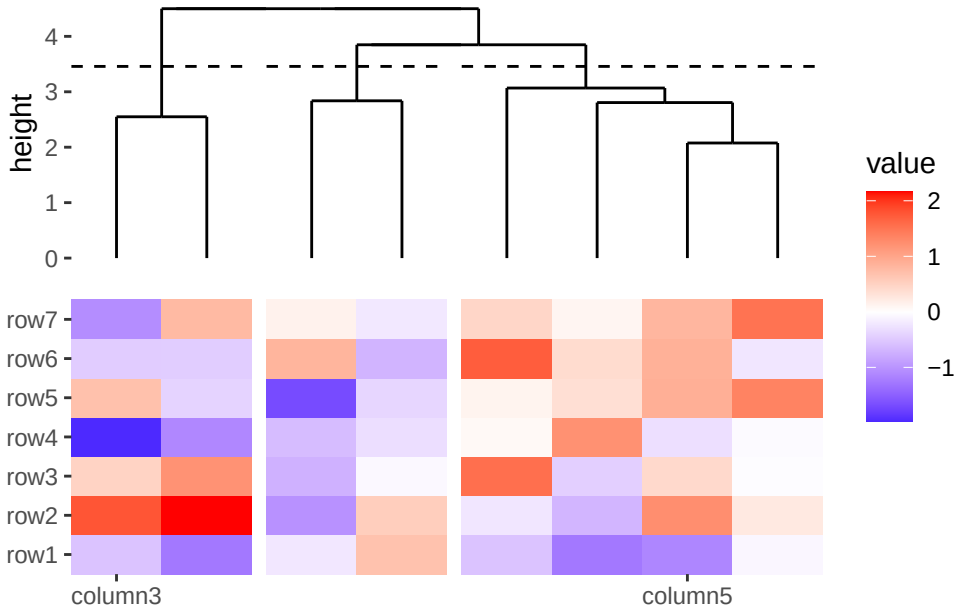


Character-based `breaks` use data names (or `indices` if names are absent)

```
ggheatmap(small_mat) +
    scale_x_continuous(breaks = c("column3", "column5")) +
    anno_top() +
    align_dendro(k = 3L)
#> > heatmap built with `geom_tile()`
```

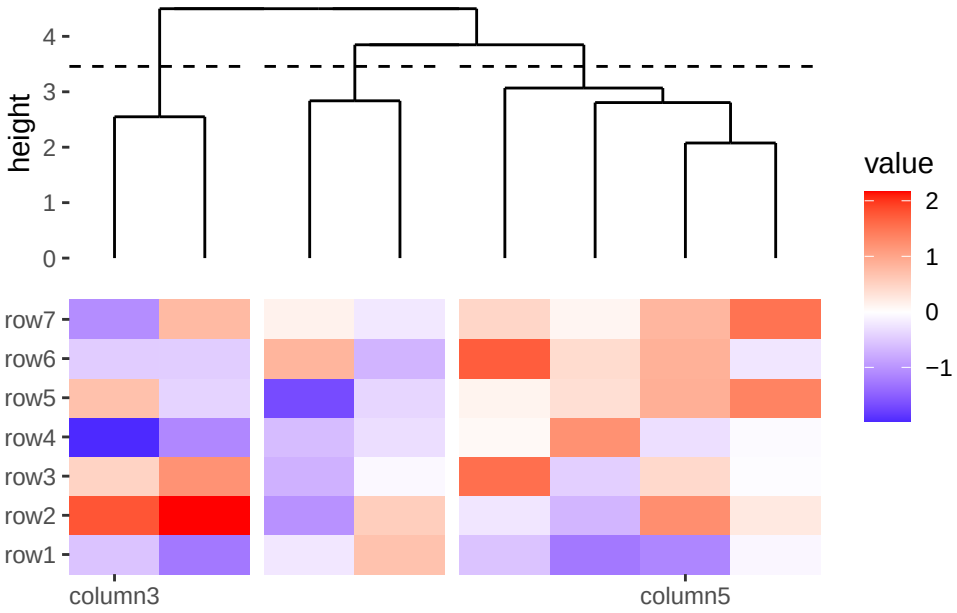



```
ggheatmap(small_mat, filling = FALSE) +
    geom_tile(aes(.discrete_x, .discrete_y, fill = value)) +
    scale_x_discrete(breaks = c("column3", "column5")) +
    anno_top() +
    align_dendro(k = 3L)
```

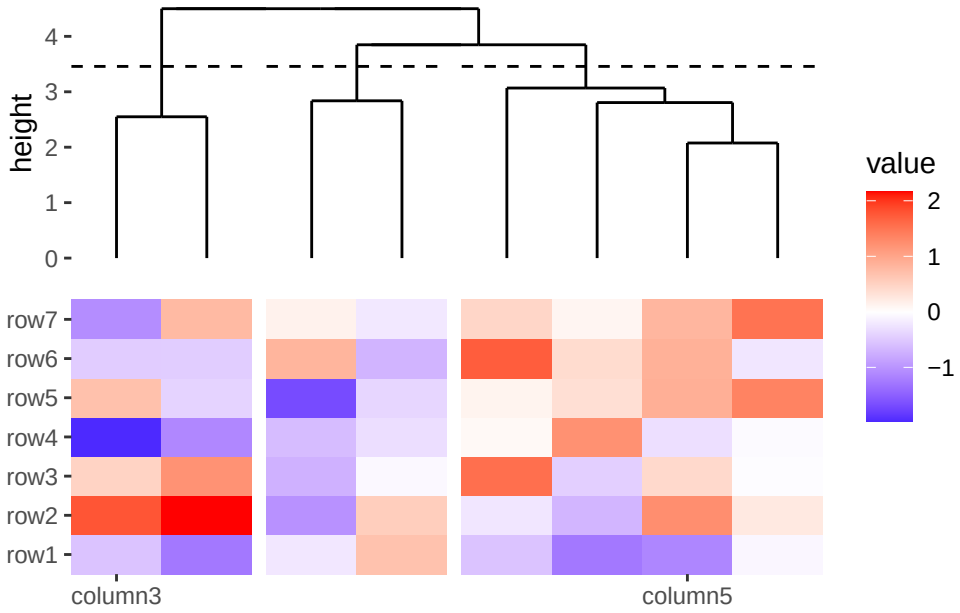


Integer-based `breaks` are interpreted as data indices:

```
ggheatmap(small_mat) +
    scale_x_continuous(breaks = c(3, 5)) +
    anno_top() +
    align_dendro(k = 3L)
#> > heatmap built with `geom_tile()`
```




```
ggheatmap(small_mat, filling = FALSE) +
    geom_tile(aes(.discrete_x, .discrete_y, fill = value)) +
    scale_x_discrete(breaks = c(3, 5)) +
    anno_top() +
    align_dendro(k = 3L)
```

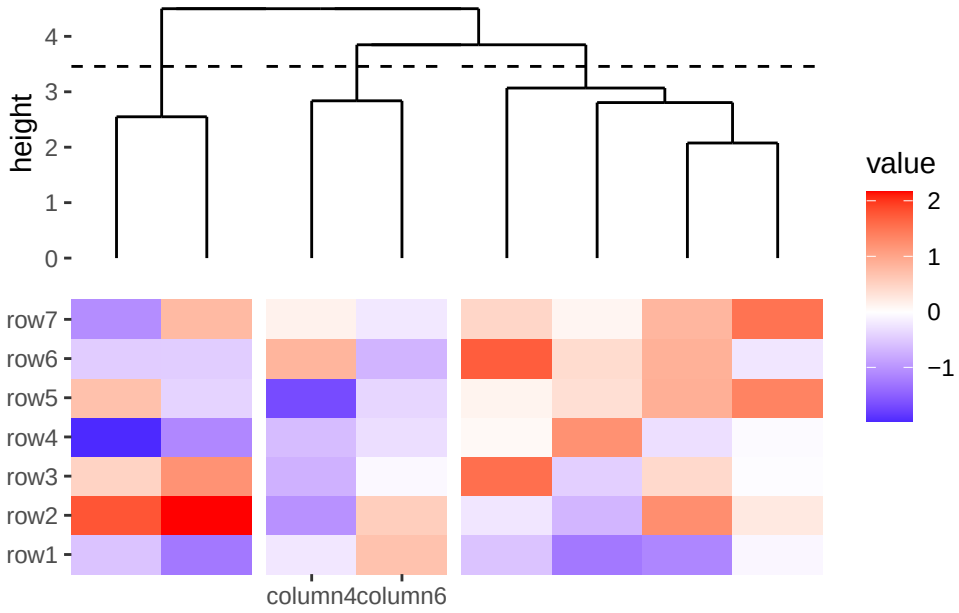


Floating numbers are invalid for `breaks`:

```
ggheatmap(small_mat) + scale_x_continuous(breaks = c(3.5, 5))
#> > heatmap built with `geom_tile()`
#> Error in `scale_x_continuous()`:
#> ! Can't convert from `breaks` <double> to <integer> due to loss of precision.
#> * Locations: 1
```

To interpret integers as plot-specific coordinate indices, wrap them with `I()`:

```
ggheatmap(small_mat) +
    scale_x_continuous(breaks = I(3:4)) +
    anno_top() +
    align_dendro(k = 3L)
#> > heatmap built with `geom_tile()`
```



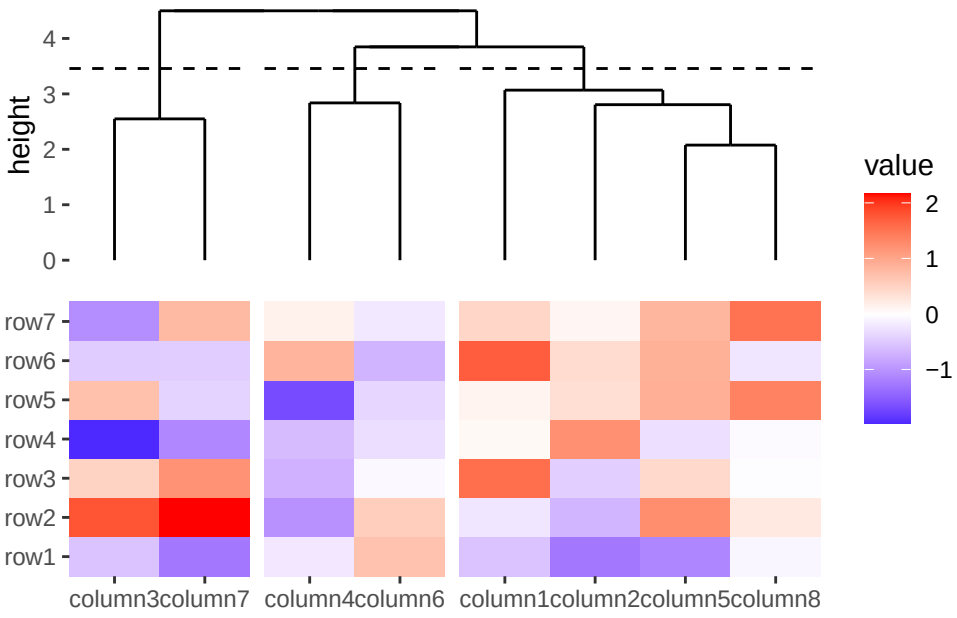
12.1.2 labels

`labels` should be one of:

```
- `NULL` for no labels

- `waiver()` for the default labels (data names)

- A character vector giving labels (must be same length as breaks)

- An expression vector (must be the same length as breaks). See `?plotmath`
for details.

- A function that takes the data names (or data index if data has no names)
as input and returns labels as output. This can be also a rlang lambda
function.
```

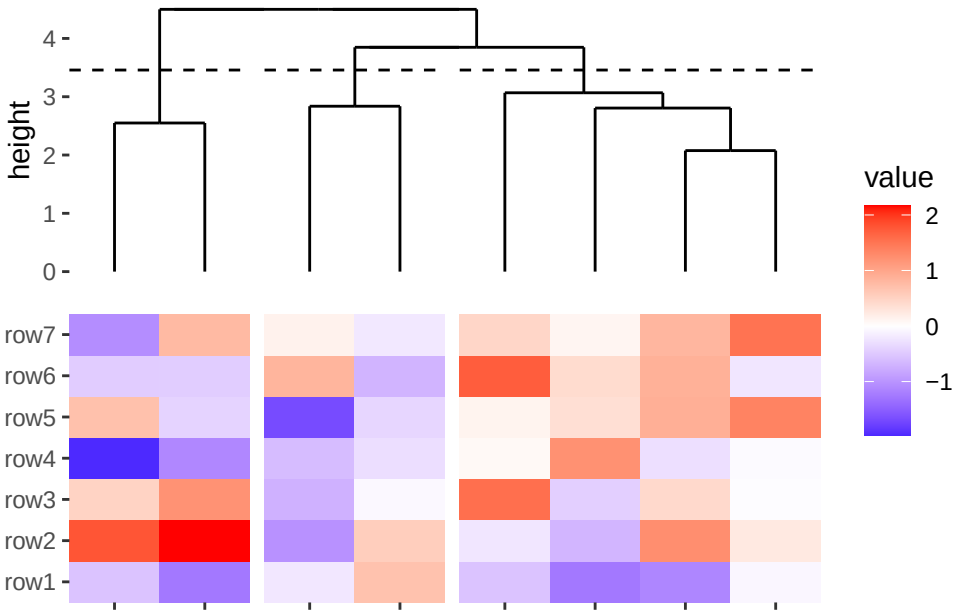
The default labels are the data names (or indices if names are absent):

```
ggheatmap(small_mat) + scale_x_continuous() +
    anno_top() +
    align_dendro(k = 3L)
#> > heatmap built with `geom_tile()`
```



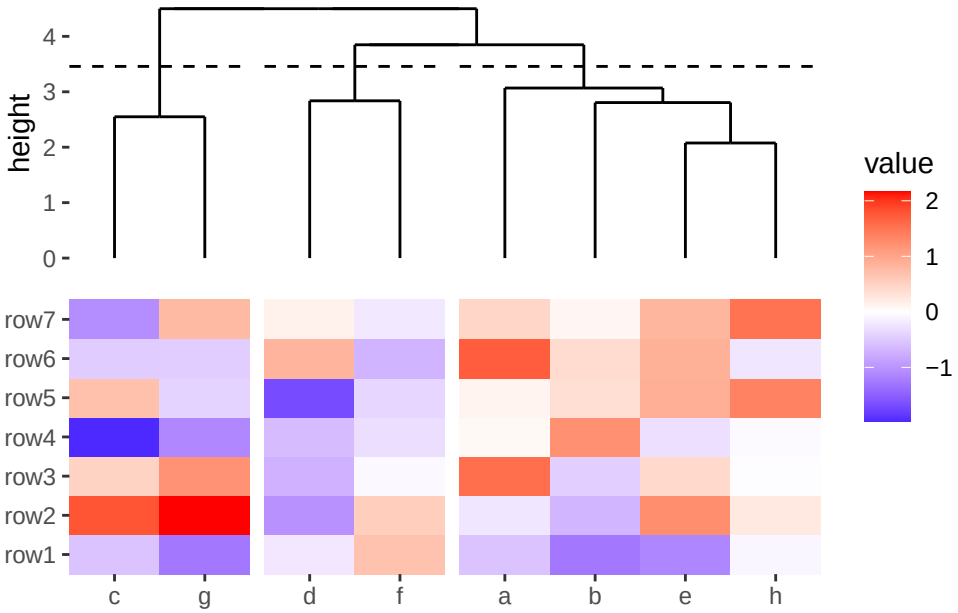
No labels:

```
ggheatmap(small_mat) +
    scale_x_continuous(labels = NULL) +
    anno_top() +
    align_dendro(k = 3L)
#> > heatmap built with `geom_tile()`
```



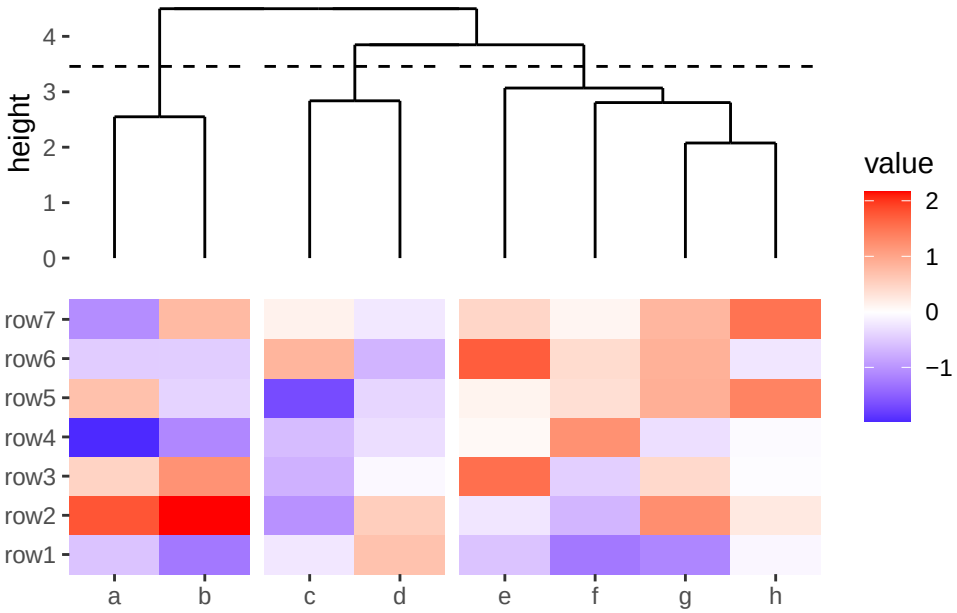
Character labels will be reordered based on the data's ordering:

```
ggheatmap(small_mat) +
    scale_x_continuous(labels = letters[seq_len(ncol(small_mat))]) +
    anno_top() +
    align_dendro(k = 3L)
#> > heatmap built with `geom_tile()`
```



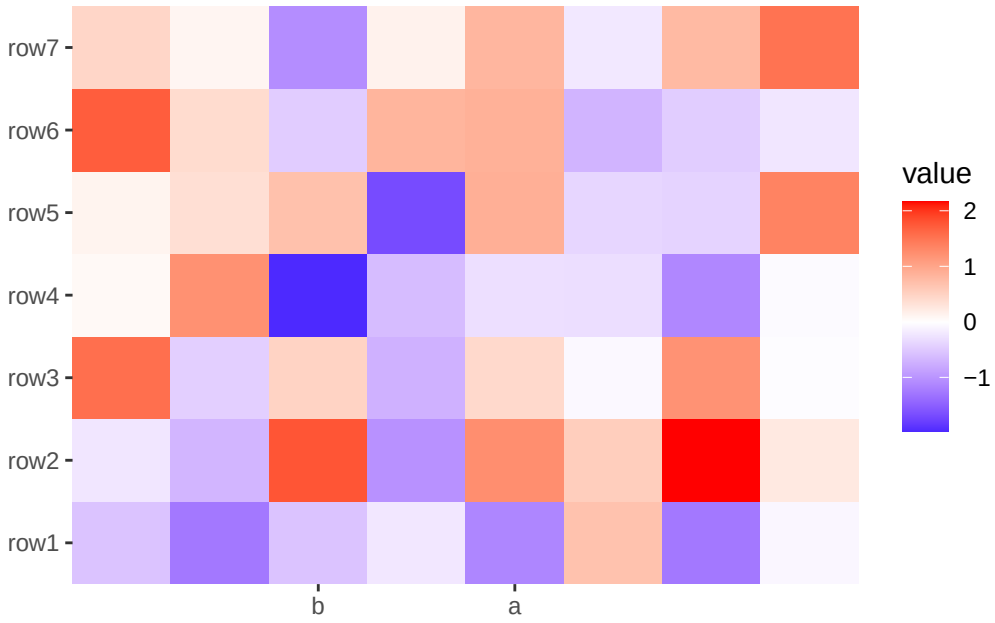
To retain the original order of character labels, wrap them with `I()`:

```
ggheatmap(small_mat) +
    scale_x_continuous(labels = I(letters[seq_len(ncol(small_mat))])) +
    anno_top() +
    align_dendro(k = 3L)
#> > heatmap built with `geom_tile()`
```



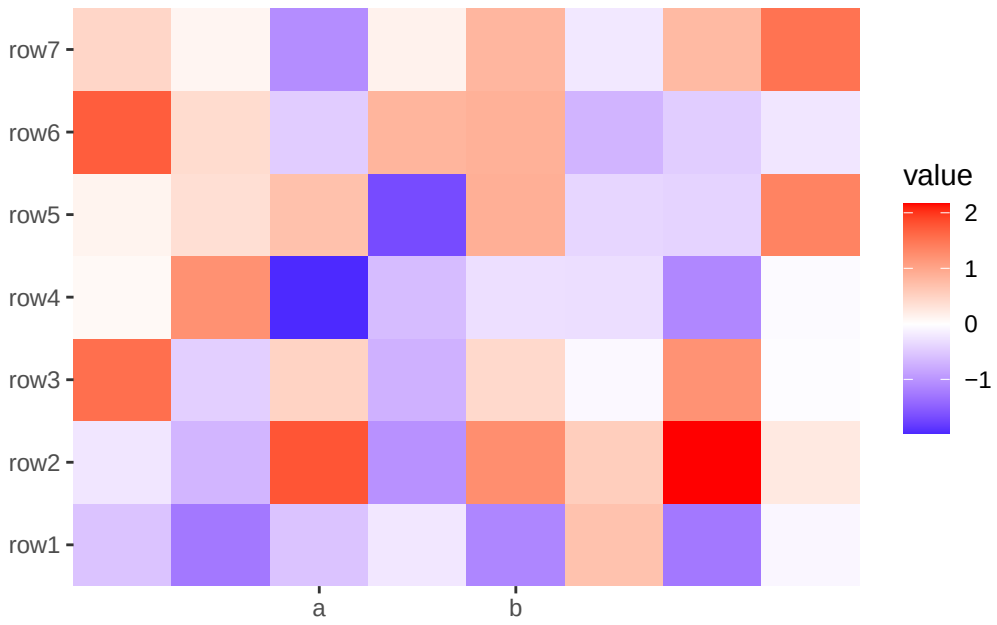
By default, labels correspond to `breaks`:

```
ggheatmap(small_mat) +
    scale_x_continuous(breaks = c(5, 3), labels = c("a", "b"))
#> > heatmap built with `geom_tile()`
```



To override the default matching, wrap the labels vector with `I()`:

```
ggheatmap(small_mat) +
    scale_x_continuous(breaks = c(5, 3), labels = I(c("a", "b")))
#> > heatmap built with `geom_tile()`
```

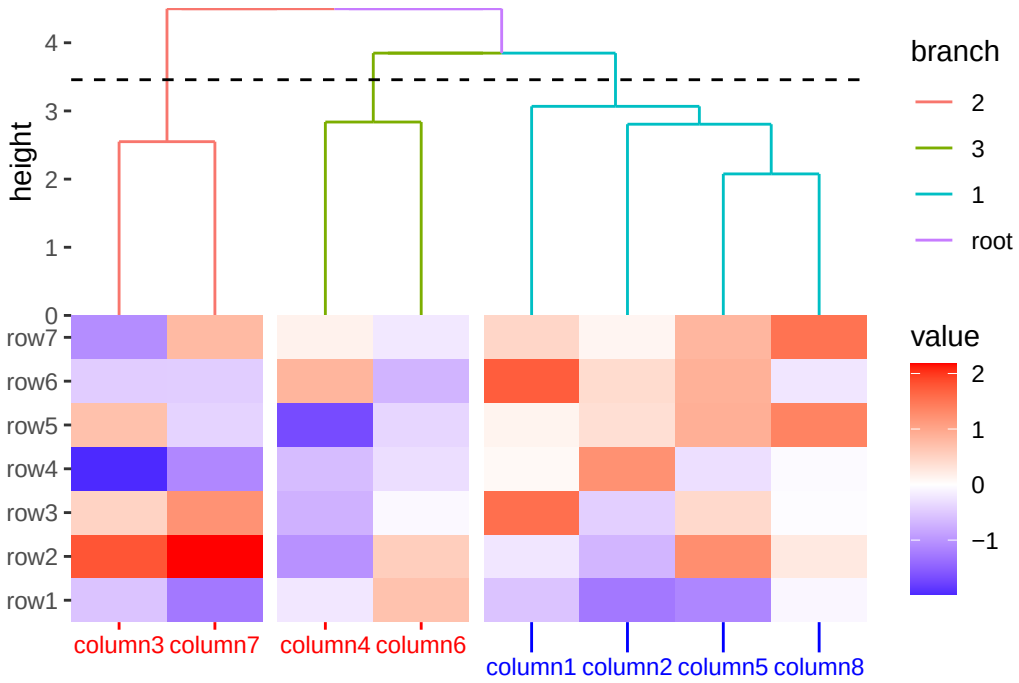


12.2 theme

Although ggplot2 does not officially support vectorized input for theme elements, we can still utilize it. `ggalign` extends this feature, allowing theme elements to be vectorized and applied across panels.

```
ggheatmap(small_mat) +
    theme(
        axis.text.x = element_text(
            colour = c(rep("red", 4), rep("blue", 5))
        ),
        axis.ticks.x = element_line(
            colour = c(rep("red", 4), rep("blue", 5))
        ),
        axis.ticks.length.x = unit(rep(c(1, 4), times = c(4, 5)), "mm")
    ) +
    anno_top() +
    align_dendro(aes(color = branch), k = 3L) +
    scale_y_continuous(expand = expansion()) &
    theme(plot.margin = margin())
#> Warning: Vectorized input to `element_text()` is not officially supported.
```

```
#> i Results may be unexpected or may change in future versions of ggplot2.
#> > heatmap built with `geom_tile()`
```

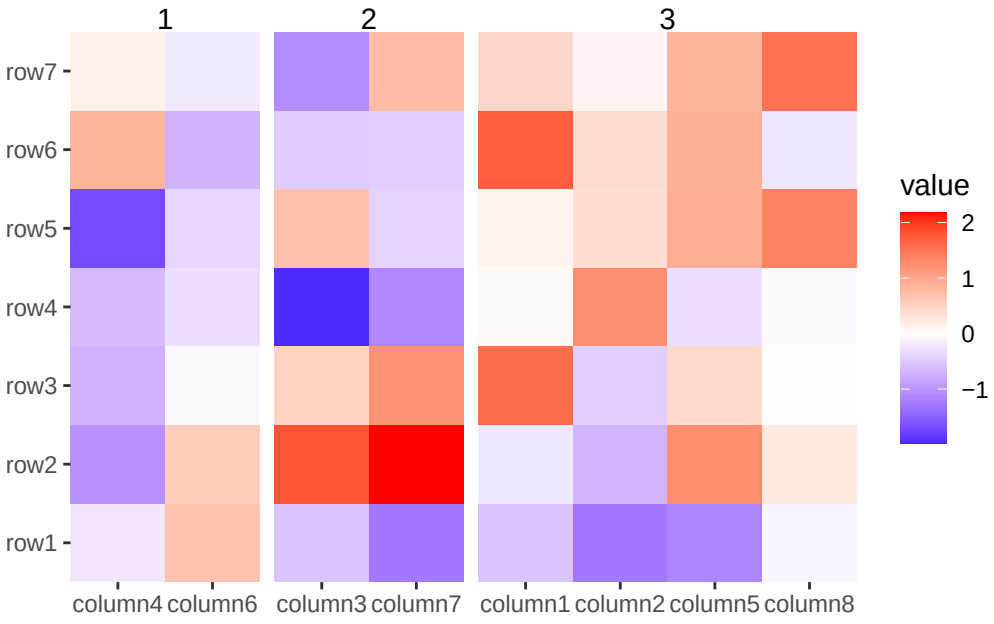


12.3 Facets

When working with facets, manual configuration of the panel using the `facet_*()` functions is not possible since the internal structure will use `facet_grid()` to set the row/column groups defined by `align_*()` functions. However, you can still use `facet_grid()` or `facet_null()` (if no panel) to control other arguments except aligned panels (`rows` in horizontal stack layout or `cols` in vertical stack layout, or both `rows` and `cols` in heatmap body).

A common use case is to modify the panel strip text. The default theme (`theme_ggalign()`) will always remove the panel strip text, you can override this behaviour with `theme(strip.text = element_text())` to add the panel title in the plot area.

```
ggheatmap(small_mat) +
    facet_grid(labeller = labeller(.column_panel = function(x) letters[as.integer(x)])) +
    theme(strip.text = element_text()) +
    anno_top() +
    align_kmeans(centers = 3L)
#> > heatmap built with `geom_tile()`
```


1
2
3
row7
row6
row5
row4
row3
row2
row1
column4
column6
column3
column7
column1
column2
column5
column8
value
2
1
0
−1

13 Plot Composer

Special thanks to the `patchwork` project—many core codes of the plot composer process were adapted from `patchwork`. We have added new features to better implement `ggalign`'s layout functions (`stack_layout()` and `quad_layout()`), including:

- `free_align()`
- `free_border()`
- `free_guide()`
- `free_lab()`
- `free_space()`
- `free_vp()`

These features have not been pushed to `patchwork` because they required significant modification of core code. We attempted to merge them, but the author of `patchwork` decided to implement some of these features independently. The latest version of patchwork now includes `free_align()`, `free_lab()`, and `free_space()` functionality under a single function: `patchwork::free()`. For more details, see: https://www.tidyverse.org/blog/2024/09/patchwork-1-3-0/.

The plot composer function in `ggalign` is `align_plots()`, which behaves similarly to `cowplot::align_plots()` and `patchwork::wrap_plots()`. However, you can directly use `align_plots()` with `quad_layout()`/`ggheatmap()` and `stack_layout()`, ensuring that they align correctly by plot panel. Additionally, `align_plots()` can align `pheatmap` and `ComplexHeatmap` objects, although they won't align by panel area with ggplot2.

```
library(ggalign)
#> Loading required package: ggplot2
```

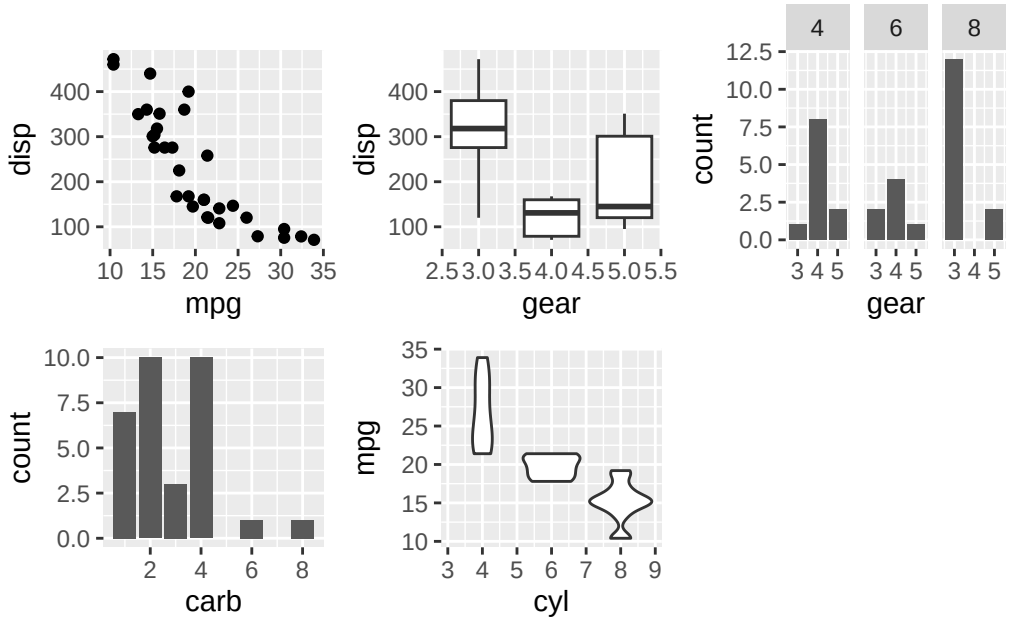
13.1 Plot Assembly

We'll start with a few well-known example plots:

```
p1 <- ggplot(mtcars) +
    geom_point(aes(mpg, disp))
p2 <- ggplot(mtcars) +
    geom_boxplot(aes(gear, disp, group = gear))
p3 <- ggplot(mtcars) +
    geom_bar(aes(gear)) +
    facet_wrap(~cyl)
p4 <- ggplot(mtcars) +
    geom_bar(aes(carb))
p5 <- ggplot(mtcars) +
    geom_violin(aes(cyl, mpg, group = cyl))
```

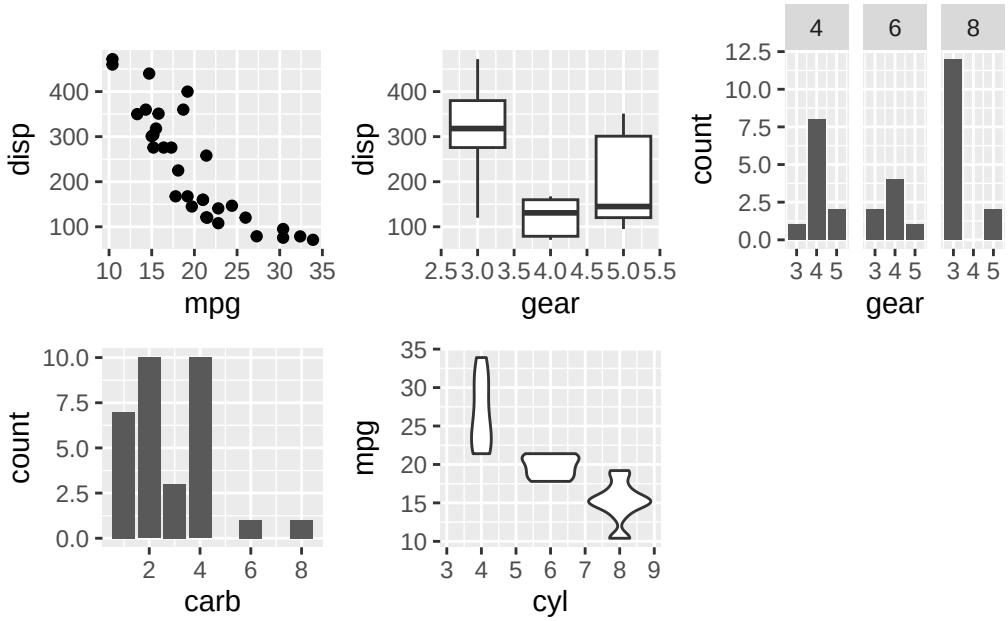
Either add the plots as single arguments

```
align_plots(p1, p2, p3, p4, p5)
```



Or use bang-bang-bang to add a list of plots

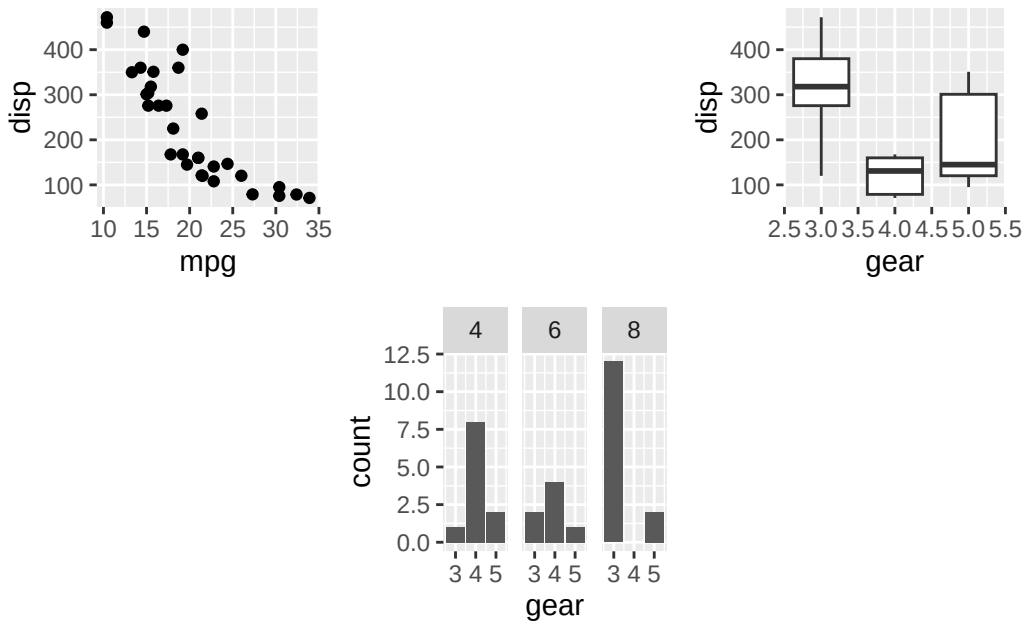
```
align_plots(!!!list(p1, p2, p3), p4, p5)
```



13.2 Empty area

You can use `NULL` to indicate the empty area.

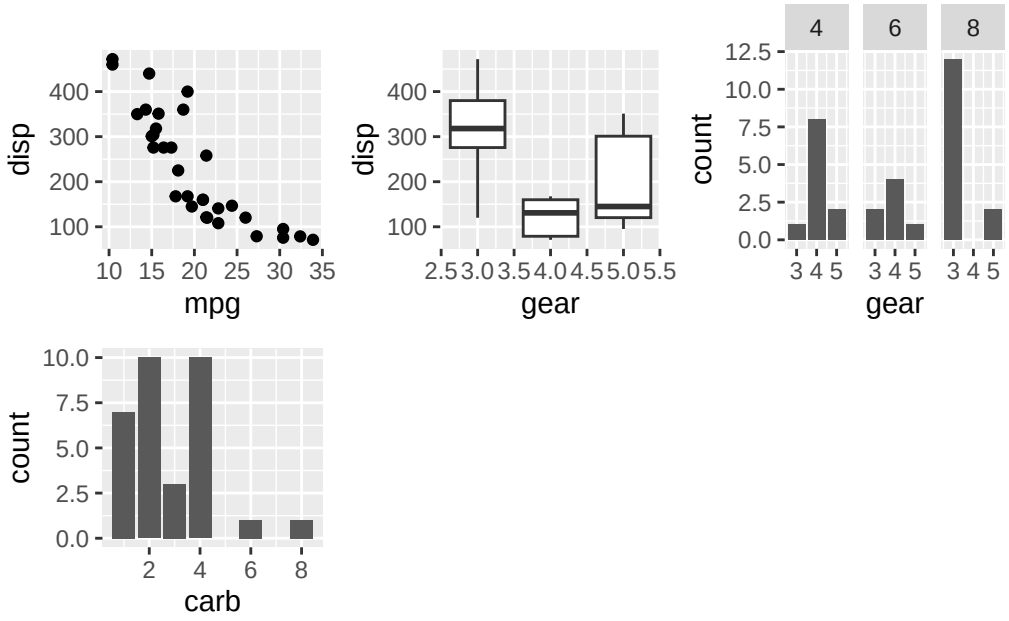
```
align_plots(p1, NULL, p2, NULL, p3, NULL)
```



13.3 Controlling the grid

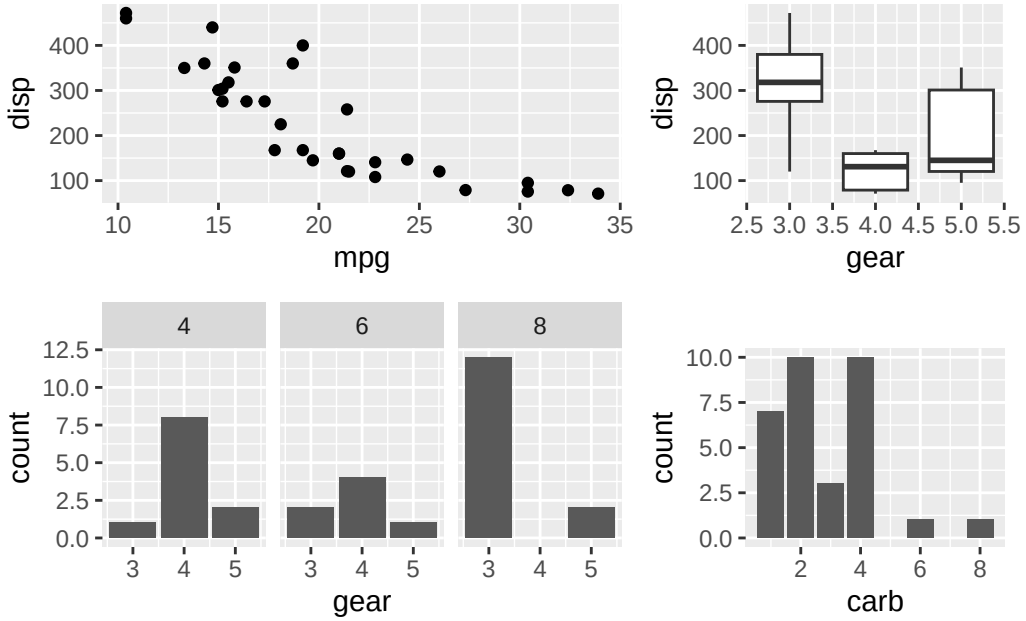
Like `patchwork`, if no specific layout is provided, `align_plots()` will attempt to create a grid that is as square as possible, with each column and row taking up equal space:

```
align_plots(p1, p2, p3, p4, ncol = 3)
```



To adjust the widths of columns, use:

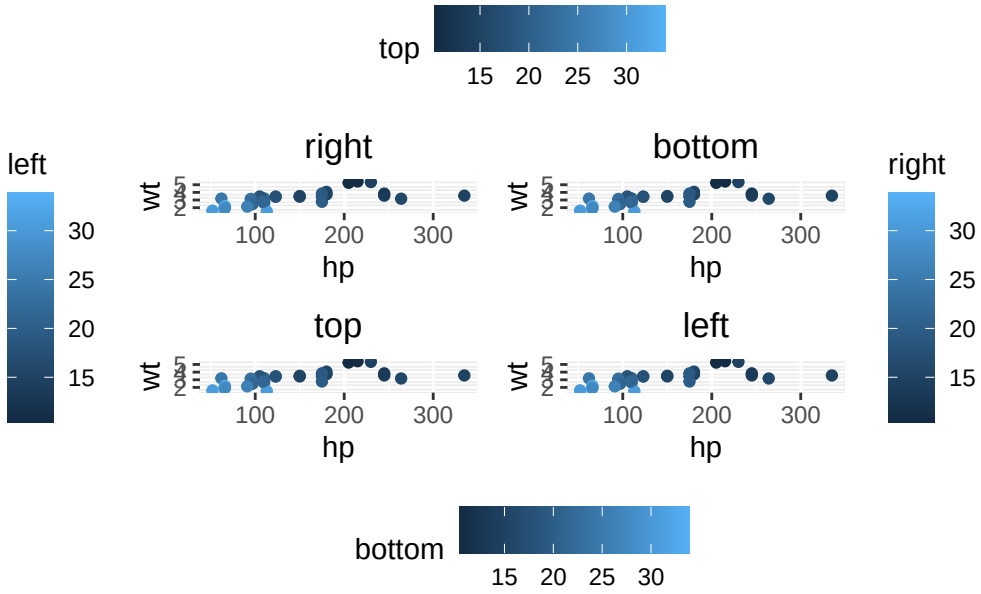
```
align_plots(p1, p2, p3, p4, widths = c(2, 1))
```



13.4 Guide legends

By default, `align_plots()` won't collect any guide legends. You can use the `guides` argument to control which side of the guide legends should be collected. They will be collected to their original side. Here, we use `patch_titles()` to indicate the guide legend position (instead of using `ggtitle()`). `patch_titles()` can add titles on four sides, and the title will be placed between the plot panel and the guide legend.

```
p_right <- ggplot(mtcars) +
    geom_point(aes(hp, wt, colour = mpg)) +
    patch_titles("right") +
    labs(color = "right")
p_top <- p_right +
    patch_titles("top") +
    scale_color_continuous(
        name = "top",
        guide = guide_colorbar(position = "top")
    )
p_left <- p_right +
    patch_titles("left") +
    scale_color_continuous(
        name = "left",
        guide = guide_colorbar(position = "left")
    )
p_bottom <- p_right +
    patch_titles("bottom") +
    scale_color_continuous(
        name = "bottom",
        guide = guide_colorbar(position = "bottom")
    )
align_plots(p_right, p_bottom, p_top, p_left, guides = "tlbr")
```

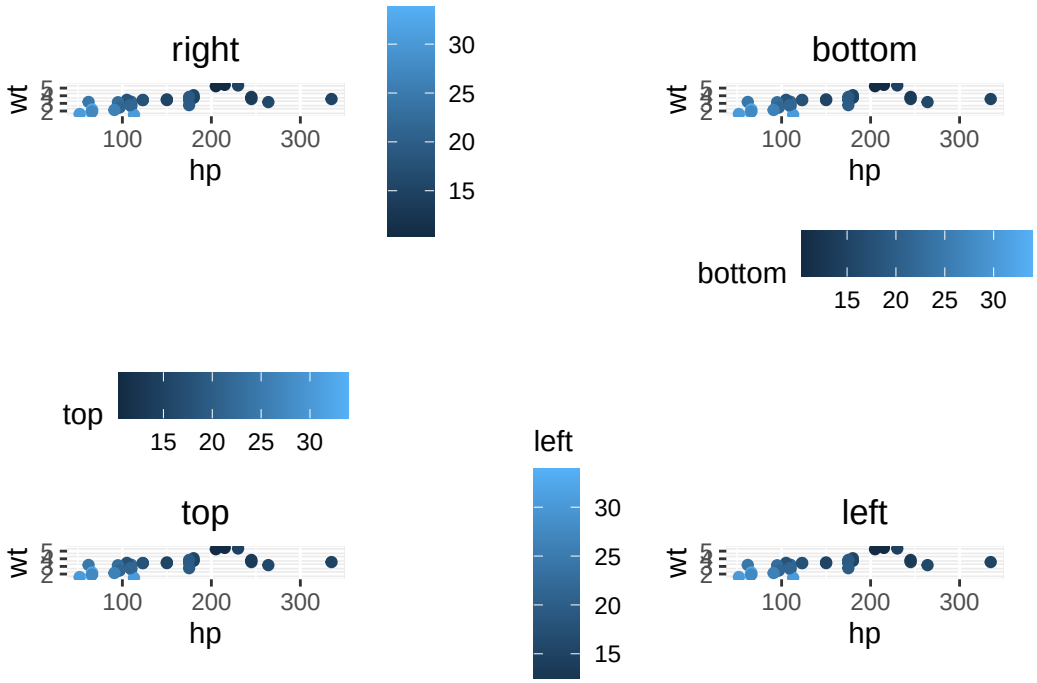


If `align_plots()` is nested in another `align_plots()`, the nested `align_plots()` will inherit the `guides` argument from the upper-level `align_plots()`. And the top-level `align_plots()` won't collect guide legends from plots within the nested `align_plots()` unless the nested `align_plots()` collects them first.

13.5 free_guide

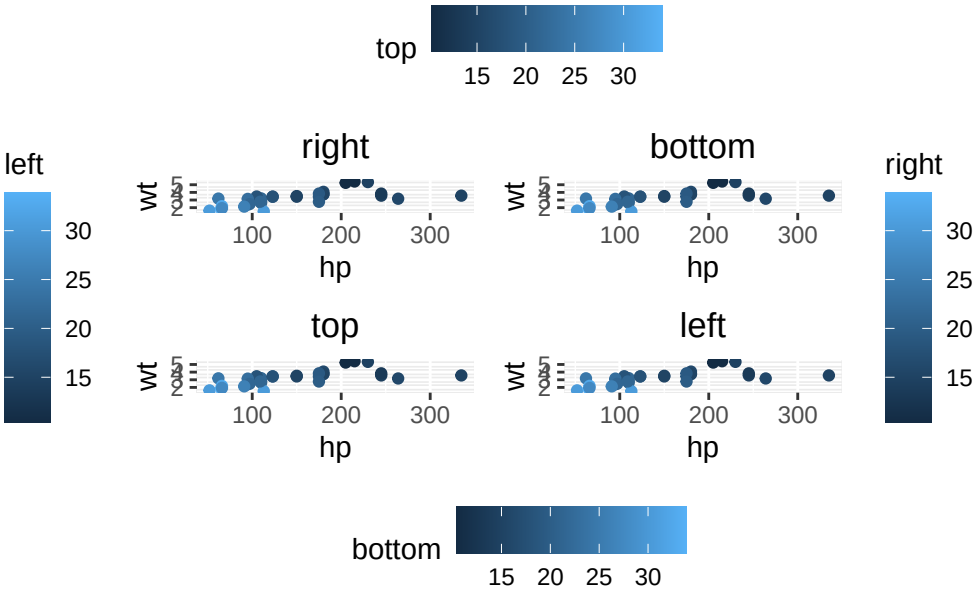
The `free_guide()` function allows you to override the `guides` argument for a single plot.

```
align_plots(
    free_guide(p_right, NULL),
    free_guide(p_bottom, NULL),
    free_guide(p_top, NULL),
    free_guide(p_left, NULL),
    guides = "tlbr"
)
```



You can also specify which guide positions to be collected for individual plots.

```
align_plots(
    free_guide(p_right, "r"),
    free_guide(p_bottom, "b"),
    free_guide(p_top, "t"),
    free_guide(p_left, "l")
)
```


top
15 20 25 30
left
30
25
20
15
right
wt
hp
100 200 300
bottom
top
left
right
30
25
20
15
bottom
15 20 25 30

Part II

Advanced

14 ggoncoplot

The `ggoncoplot()` function generates `oncoPrint` visualizations that display genetic alterations in a matrix format. This function is especially useful for visualizing complex genomic data, such as mutations, copy number variations, and other genomic alterations in cancer research.

```
library(ggalign)
#> Loading required package: ggplot2
```

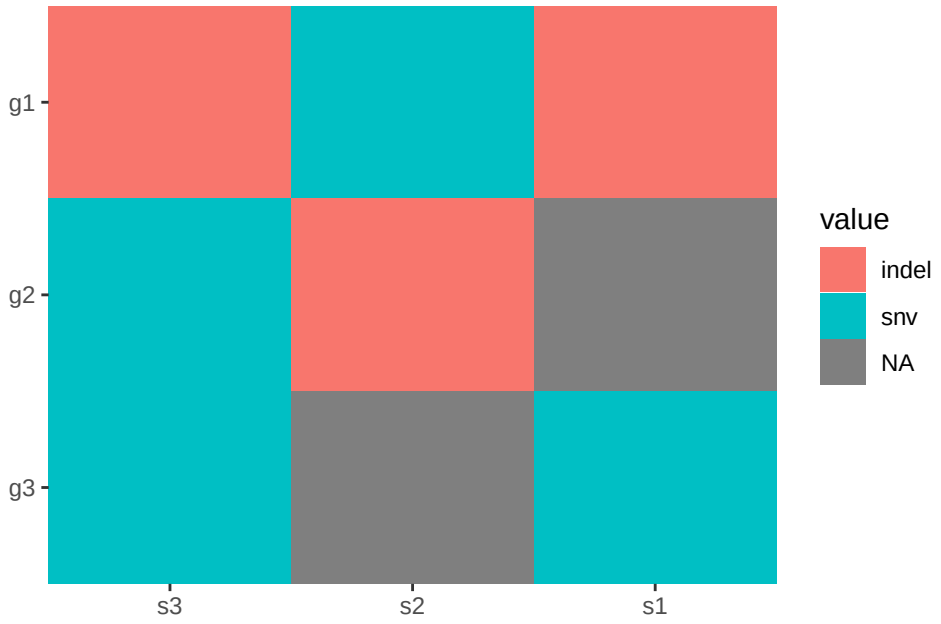
14.1 Input data

The input should be a character matrix which encodes the alterations, you can use string of `";"`, `":"`, `","`, and `"|"` to separate multiple alterations. Internally, `ggoncoplot()` will use `fortify_matrix()` to get such matrix.

```
mat <- read.table(
    textConnection(
        "s1,s2,s3
         g1,snv;indel,snv,indel
         g2,,snv;indel,snv
         g3,snv,,indel;snv"
    ),
    row.names = 1, header = TRUE, sep = ",", stringsAsFactors = FALSE
)
mat
#>                    s1        s2        s3
#>          g1 snv;indel       snv     indel
#>          g2           snv;indel       snv
#>          g3       snv           indel;snv
```

A basic oncoprint can be generated as follows:

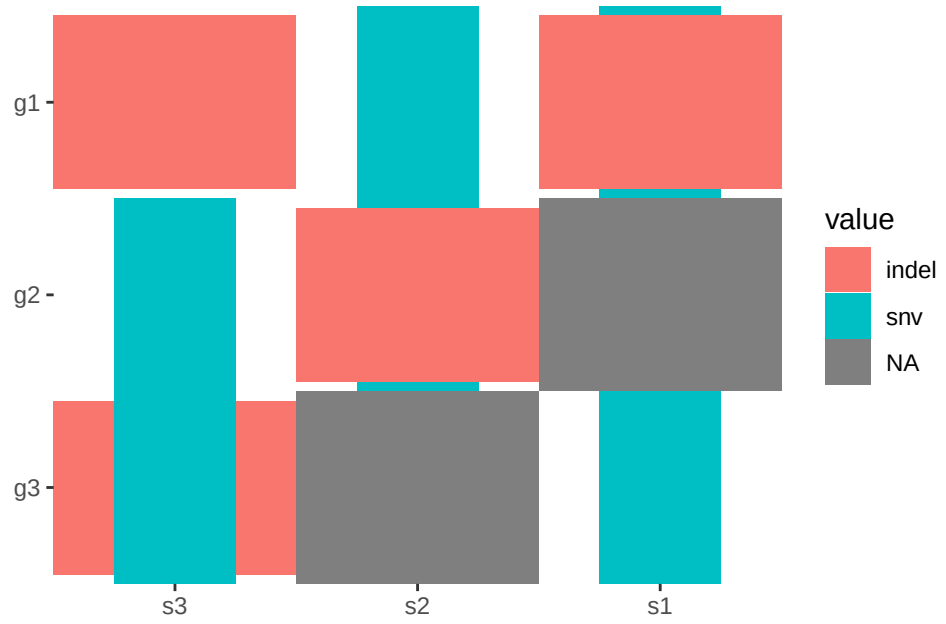
```
ggoncoplot(mat)
```



14.2 oncoPrint Customization

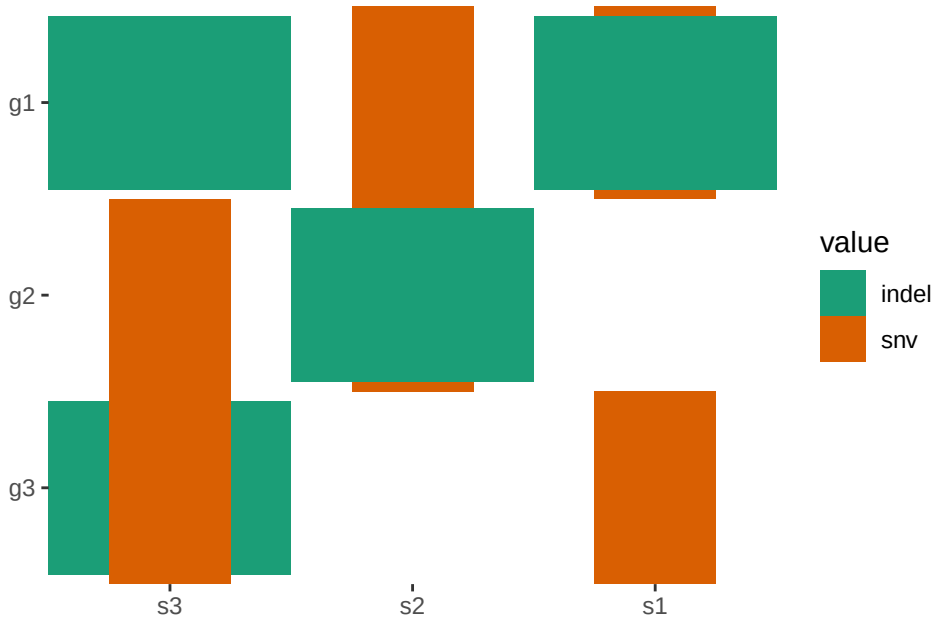
By default, all alterations are represented with tiles of equal width and height, which may lead to overlapping. You can control the `width` and `height` of the tiles using the `map_width` and `map_height` arguments (we will introduce another more effective ways to handle this in the `Specialized Geoms` section):

```
ggoncoplot(mat, map_width = c(snv = 0.5), map_height = c(indel = 0.9))
```



By default, all empty string will be converted to `NA` value and `ggplot2` will translate the `NA` values and render it in the legend. To prevent this, you can turn off the translation using `na.translate = FALSE`:

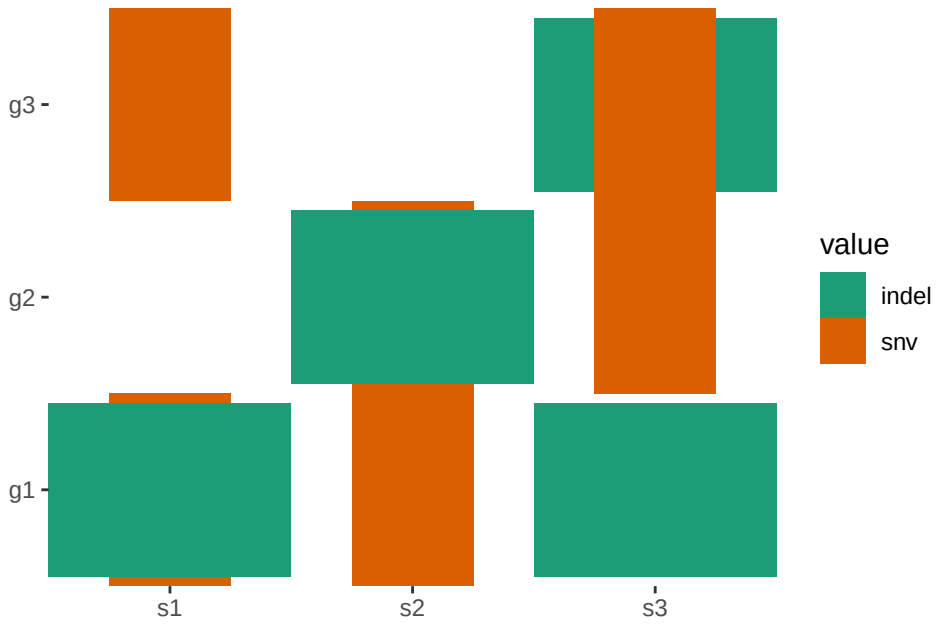
```
ggoncoplot(mat, map_width = c(snv = 0.5), map_height = c(indel = 0.9)) +
    scale_fill_brewer(palette = "Dark2", na.translate = FALSE)
```



The function automatically reorders rows and columns based on alteration frequency. Disable this with `reorder_row = FALSE` and `reorder_column = FALSE`.

You can further customize layouts using methods from `vignette("layout-customize")`.

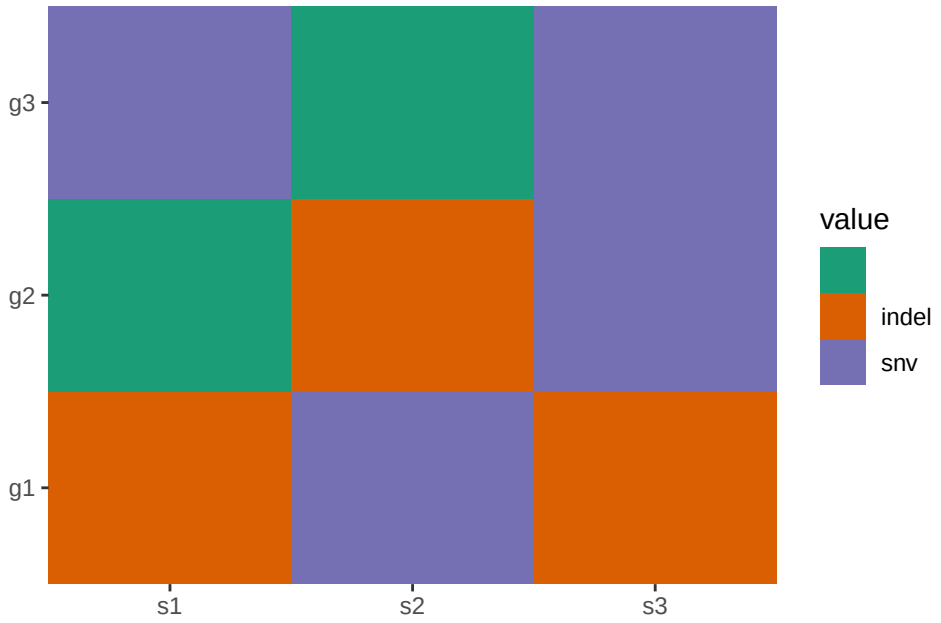
```
ggoncoplot(mat,
    map_width = c(snv = 0.5), map_height = c(indel = 0.9),
    reorder_row = FALSE, reorder_column = FALSE
) +
    scale_fill_brewer(palette = "Dark2", na.translate = FALSE)
```



14.3 Advanced Data Handling

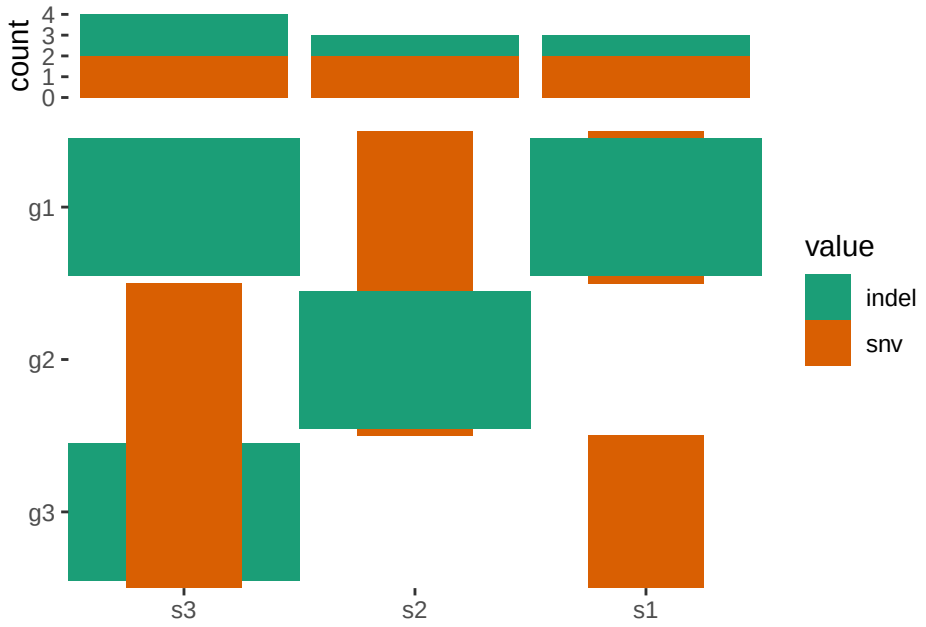
`ggoncoplot()` is built on `ggheatmap()` with a default `scheme_data()` (see `vignette("plot-options")` for details), which splits alterations into separate entries for visualization. (See `ggplot2 specification` section in `ggheatmap()` for the input data of `scheme_data()`):

```
pdata <- function(data) {
    tidyr::separate_longer_delim(data,
        cols = value,
        delim = stringr::regex("\\s*[;:,|]\\s*")
    )
}
# Note: this figure will contain an empty string value.
#
# `ggoncoplot()` will automatically convert any empty strings to `NA`
# before pass it to `ggheatmap`.
ggheatmap(mat) -
    scheme_data(pdata) +
    scale_fill_brewer(palette = "Dark2", na.translate = FALSE)
#> > heatmap built with `geom_tile()`
```



By default, the `scheme_data()` is inherited from the parent layout if the data of the plot is inherited from the layout. You can apply the parent `scheme_data()` first and then apply another transformation by setting `inherit = TRUE`. This functionality is especially useful when working with `ggoncoplot()`.

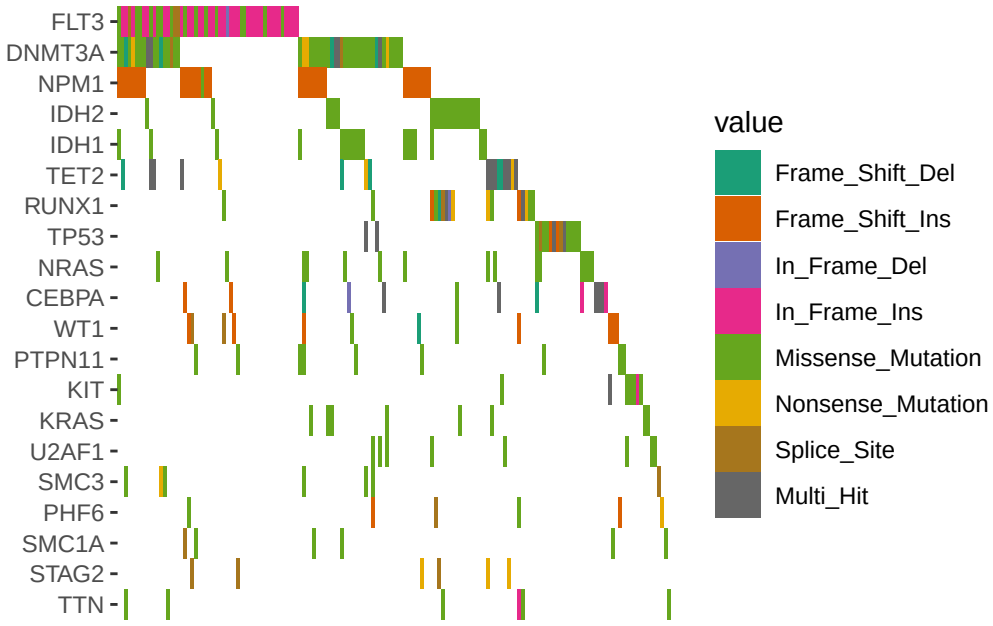
```
ggoncoplot(mat, map_width = c(snv = 0.5), map_height = c(indel = 0.9)) +
    anno_top(size = 0.2) +
    ggalign() +
    # by setting `inherti = TRUE`, we apply the parent layout `scheme_data()`
    # (from the `ggoncoplot()` layout) firstly, which will split the alteration
    # string and unnested the columns.
    # Here: We then remove `NA` value
    scheme_data(~ subset(.x, !is.na(value)), inherit = TRUE) +
    geom_bar(aes(.x, after_stat(count), fill = value)) +
    # note: `ggoncoplot()` use `geom_tile()` to draw the oncoPrint,
    # the guide is different from `geom_bar()`, though both looks
    # like the same, we remove the guide of `geom_bar()` plot
    guides(fill = "none") &
    scale_fill_brewer(palette = "Dark2", na.translate = FALSE)
```



14.4 Integration with maftools

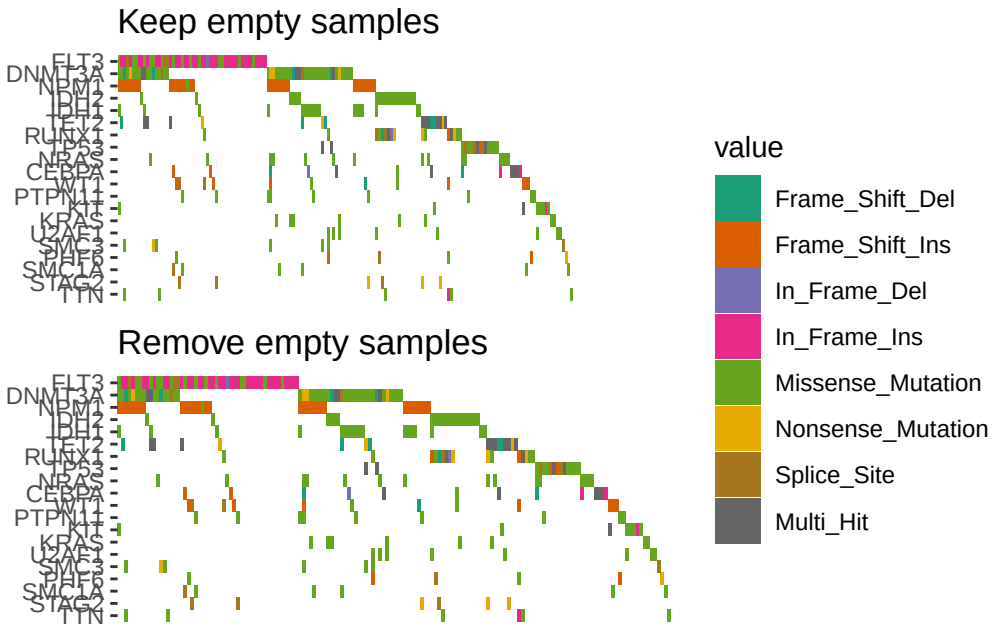
The `ggoncoplot()` function supports `MAF` objects from the `maftools` package using the `fortify_matrix.MAF()` method. It includes options to control data generation for `ggoncoplot()`, such as drawing the top `n_top` genes.

```
# load data from `maftools`
laml.maf <- system.file("extdata", "tcga_laml.maf.gz", package = "maftools")
# clinical information containing survival information and histology. This is optional
laml.clin <- system.file("extdata", "tcga_laml_annot.tsv", package = "maftools")
laml <- maftools::read.maf(
    maf = laml.maf,
    clinicalData = laml.clin,
    verbose = FALSE
)
# Visualizing the Top 20 Genes
ggoncoplot(laml, n_top = 20) +
    scale_fill_brewer(palette = "Dark2", na.translate = FALSE) +
    theme_no_axes("x")
```



By default, samples without alterations in the selected genes are removed. To include all samples, set `remove_empty_samples = FALSE`:

```
align_plots(
    ggoncoplot(laml, n_top = 20L, remove_empty_samples = FALSE) +
        scale_fill_brewer(palette = "Dark2", na.translate = FALSE) +
        theme_no_axes("x") +
        ggtitle("Keep empty samples"),
    ggoncoplot(laml, n_top = 20L, remove_empty_samples = TRUE) +
        scale_fill_brewer(palette = "Dark2", na.translate = FALSE) +
        theme_no_axes("x") +
        ggtitle("Remove empty samples"),
    ncol = 1L,
    guides = "tlbr"
)
```



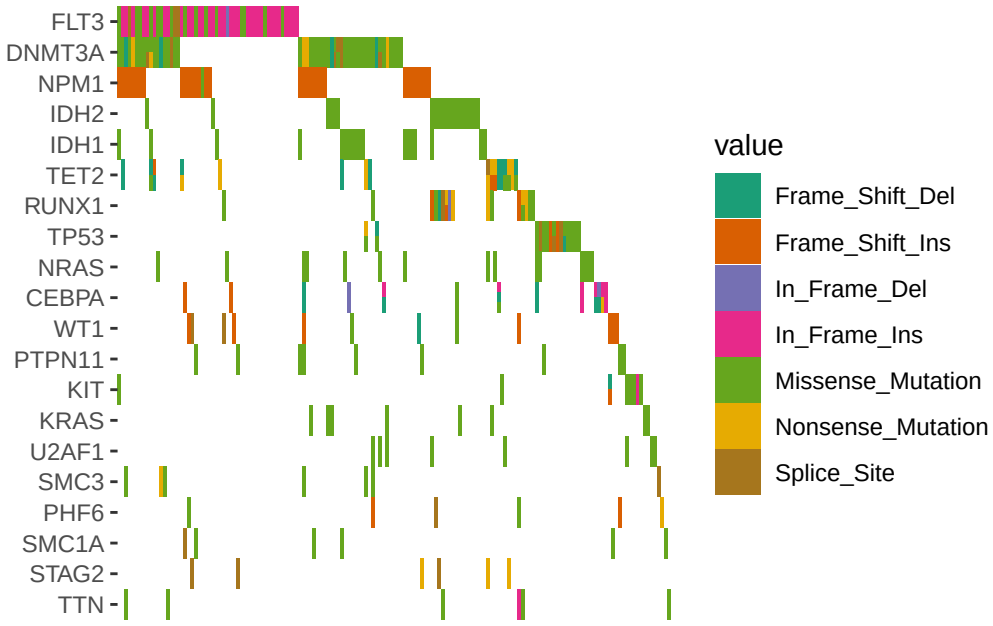
14.5 Specialized Geoms

14.5.1 geom_subtile()

When multiple alterations occur in the same sample and gene, they are combined into a single value, `"Multi_Hit"`, by default. To visualize these alterations separately, you can set `collapse_vars = FALSE`. However, doing so can lead to overlapping alterations within the same cell, making the visualization cluttered and hard to interpret.

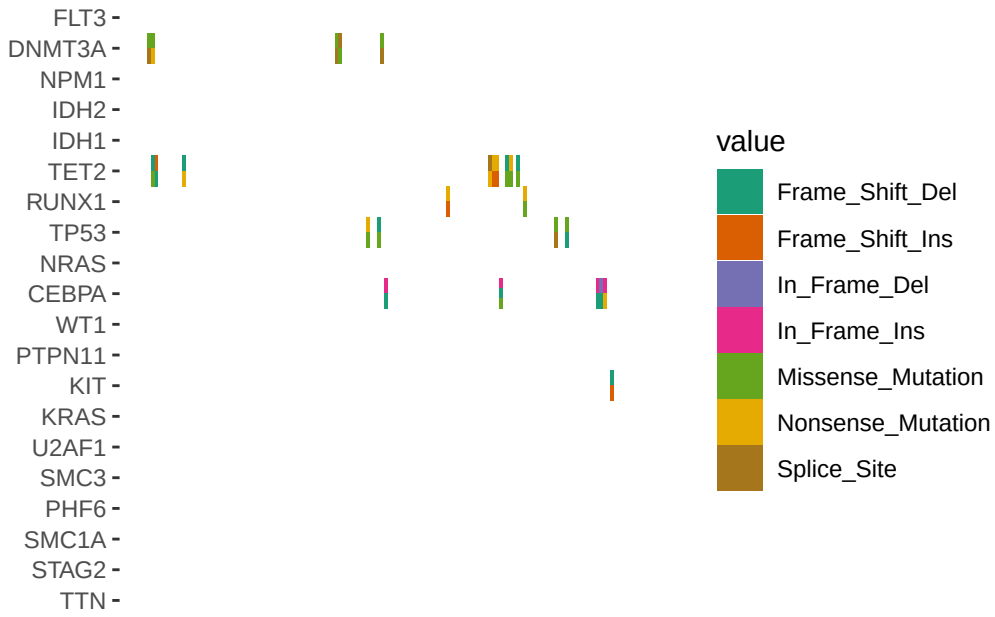
In such cases, disabling the default filling and defining a custom heatmap layer with `geom_subtile()` is more effective. This function subdivides each cell into smaller rectangles, allowing the distinct alterations to be clearly displayed.

```
ggoncoplot(laml, n_top = 20, collapse_vars = FALSE, filling = FALSE) +
    geom_subtile(aes(fill = value), direction = "v") +
    scale_fill_brewer(palette = "Dark2", na.translate = FALSE) +
    theme_no_axes("x")
#> `geom_subtile()` subdivide tile into a maximal of 3 rectangles
```



We focus exclusively on cells with multiple alterations to highlight the differences, by filtering the data before applying `geom_subtile()`:

```
ggoncoplot(laml, n_top = 20, collapse_vars = FALSE, filling = FALSE) +
    scheme_data(function(data) {
        dplyr::filter(data, dplyr::n() > 1L, .by = c(".x", ".y"))
        # we apply the parent layout `scheme_data()` first (`inherit = TRUE`),
        # which will split the alteration string and unnested the columns.
    }, inherit = TRUE) +
    geom_subtile(aes(fill = value), direction = "v") +
    scale_fill_brewer(palette = "Dark2", na.translate = FALSE) +
    theme_no_axes("x")
#> `geom_subtile()` subdivide tile into a maximal of 3 rectangles
```



14.5.2 geom_draw2()

`geom_subtile()` often suffices for most scenarios. However, if you require a strategy similar to that of `ComplexHeatmap`, consider using `geom_draw2()`, which offers greater flexibility for complex customizations.

Key Features of `geom_draw2()`:

- Custom Drawing Logic: Accepts a `draw` aesthetic, allowing each cell to be rendered as a specific graphical object (`grob`).
- Manual Scaling: Requires `scale_draw_manual()` to map `draw` values to corresponding drawing functions.
- Flexible Aesthetic Mapping: Functions mapped through `scale_draw_manual()` can utilize any number of ggplot2 aesthetics and output custom graphical objects (`grob`). Beyond the `x`, `y`, `xmin`, `xmax`, `width`, and `height` aesthetics, you may want to rely solely on mapped aesthetics (`aes()`). Unmapped aesthetics will default to ggplot2's behavior, which might not produce the desired outcome. And always use `native` unit.

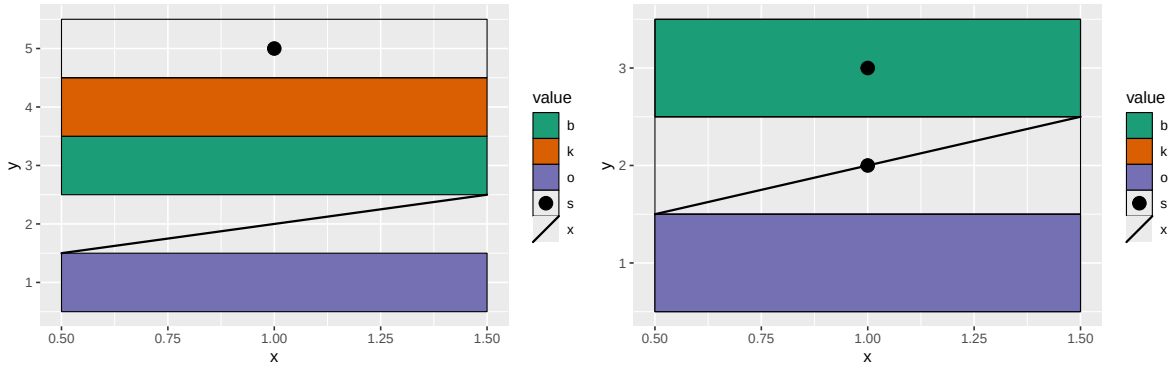
:) Sorry, I cannot deal with a pretty example for this, but the function provided in `values` argument of `scale_draw_manual` operates similarly to `alter_fun` in ComplexHeatmap. Currently, `geom_subtile()` performs well enough for most cases, making `geom_draw2()` somewhat cumbersome to use. Managing alteration types, especially in the case of overlapping

alterations, requires meticulous design to ensure that the visual elements do not interfere with each other.

```
library(grid)
draw_mapping <- list(
    function(x, y, width, height, fill) {
        rectGrob(x, y,
            width = width, height = height,
            gp = gpar(fill = fill),
            default.units = "native"
        )
    },
    function(x, y, width, height, fill) {
        rectGrob(x, y,
            width = width, height = height,
            gp = gpar(fill = fill),
            default.units = "native"
        )
    },
    function(x, y, width, height, fill) {
        rectGrob(x, y,
            width = width, height = height,
            gp = gpar(fill = fill),
            default.units = "native"
        )
    },
    function(x, y, width, height, shape) {
        gList(
            pointsGrob(x, y, pch = shape),
            # To ensure the rectangle color is shown in the legends, you
            # must explicitly provide a color argument and include it in
            # the `gpar()` of the graphical object
            rectGrob(x, y, width, height,
                gp = gpar(col = "black", fill = NA)
            )
        )
    },
    function(xmin, xmax, ymin, ymax) {
        segmentsGrob(
            xmin, ymin,
            xmax, ymax,
            gp = gpar(lwd = 2)
        )
```

```
    }
)
```

```
value <- sample(letters, 5L)
ggplot(data.frame(value = value, y = seq_len(5))) +
    geom_draw2(aes(x = 1, y = y, draw = value, fill = value)) +
    scale_draw_manual(values = draw_mapping) +
    scale_fill_brewer(palette = "Dark2")
ggplot(data.frame(value = c(value, value[5L]), y = c(1, 2, 3, 1, 2, 3))) +
    geom_draw2(aes(x = 1, y = y, draw = value, fill = value)) +
    scale_draw_manual(values = draw_mapping) +
    scale_fill_brewer(palette = "Dark2")
```



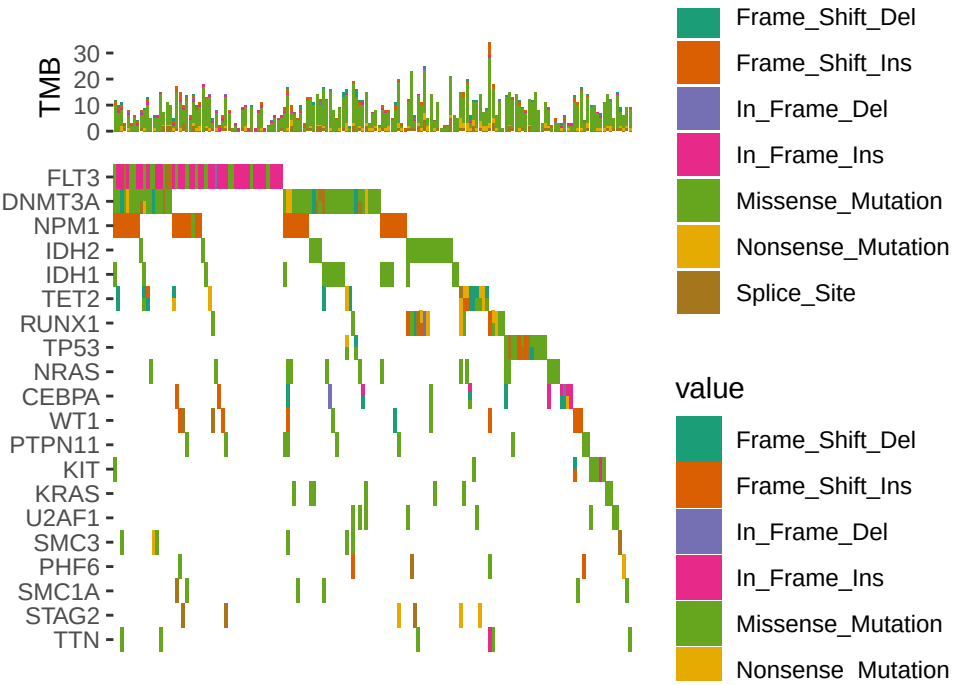
14.6 ggalign attributes

Except for the data used for the main plot, `fortify_matrix.MAF()` also attaches several useful attributes.

- `gene_summary`: gene summary informations. See `maftools::getGeneSummary()` for details.
- `sample_summary`: sample summary informations. See `maftools::getSampleSummary()` for details.
- `sample_anno`: sample clinical informations. See `maftools::getClinicalData()` for details.
- `n_genes`: Total of genes.
- `n_samples`: Total of samples.
- `titv`: A list of `data.frames` with Transitions and Transversions summary. See `maftools::titv()` for details.

You can extract these attributes using the `ggalign_attr()` function. Below is an example of how to extract the sample summary data (e.g., TMB) using `ggalign_attr()` and add it to the top annotation of an oncoplot:

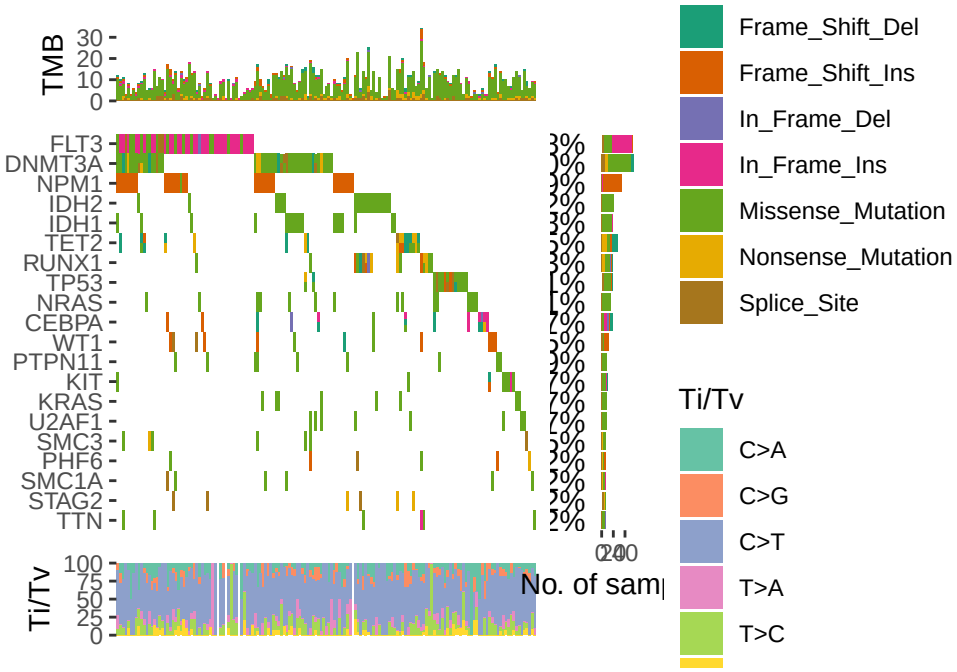
```
ggoncoplot(laml, n_top = 20, collapse_vars = FALSE, filling = FALSE) +
    geom_subtile(aes(fill = value), direction = "v") +
    theme_no_axes("x") +
    anno_top(size = 0.2) +
    ggalign(data = function(data) {
        data <- ggalign_attr(data, "sample_summary")
        # matrix input will be automatically melted into a long foramted data
        # frame in `ggalign()` function.
        as.matrix(data[2:(ncol(data) - 1L)])
    }) +
    geom_bar(aes(.x, value, fill = .column_names),
        stat = "identity"
    ) +
    ylab("TMB") &
    scale_fill_brewer(palette = "Dark2", na.translate = FALSE)
#> `geom_subtile()` subdivide tile into a maximal of 3 rectangles
```



We can draw the example from maftools vignette.

```r
ggoncoplot(laml, n_top = 20, collapse_vars = FALSE, filling = FALSE) +
    geom_subtile(aes(fill = value), direction = "v") +
    theme_no_axes("x") +
    # since legends from geom_tile (oncoPrint body) and `geom_bar`
    # is different, though both looks like the same, the internal
    # won't merge the legends. we remove the legends of oncoPrint body
    guides(fill = "none") +
    # add top annotation
    anno_top(size = 0.2) +
    ggalign(data = function(data) {
        data <- ggalign_attr(data, "sample_summary")
        # matrix input will be automatically melted into a long foramted data
        # frame in `ggalign()` function.
        as.matrix(data[2:(ncol(data) - 1L)])
    }) +
    geom_bar(aes(.x, value, fill = .column_names),
        stat = "identity"
    ) +
    ylab("TMB") +
    # add right annotation
    anno_right(size = 0.2) -
    # remove bottom spaces of the right annotation when aligning
    scheme_align(free_spaces = "b") +
    # add the text percent for the alterated samples in the right annotation
    ggalign(data = function(data) {
        # Atomic vector will be put in the `value` column of the data frame.
        ggalign_attr(data, "gene_summary")$AlteredSamples /
            ggalign_attr(data, "n_samples")
    }) +
    geom_text(aes(1, label = scales::label_percent()(value)), hjust = 1) +
    scale_x_continuous(
        expand = expansion(),
        name = NULL, breaks = NULL,
        limits = c(0, 1)
    ) +
    theme(plot.margin = margin()) +
    # add the bar plot in the right annotation
    ggalign(data = function(data) {
        data <- ggalign_attr(data, "gene_summary")
        # matrix input will be automatically melted into a long foramted data
        # frame in `ggalign()` function.
        as.matrix(data[2:8])
```

```
    }) +
    geom_bar(aes(value, fill = .column_names),
        stat = "identity",
        orientation = "y"
    ) +
    xlab("No. of samples") -
    # we apply the scale mapping to the top and right annotation: `position = "tr"`
    # and the main plot: `main = TRUE`
    with_quad(
        scale_fill_brewer("Mutations",
            palette = "Dark2", na.translate = FALSE
        ),
        position = "tr",
        main = TRUE
    ) +
    # add bottom annotation
    anno_bottom(size = 0.2) +
    # add bar plot in the bottom annotation
    ggalign(data = function(data) {
        data <- ggalign_attr(data, "titv")$fraction.contribution
        # matrix input will be automatically melted into a long foramted data
        # frame in `ggalign()` function.
        as.matrix(data[2:7])
    }) +
    geom_bar(aes(y = value, fill = .column_names), stat = "identity") +
    ylab("Ti/Tv") +
    scale_fill_brewer("Ti/Tv", palette = "Set2")
#> `geom_subtile()` subdivide tile into a maximal of 3 rectangles
#> Warning: Removed 24 rows containing missing values or values outside the scale range
#> (`geom_bar()`).
```



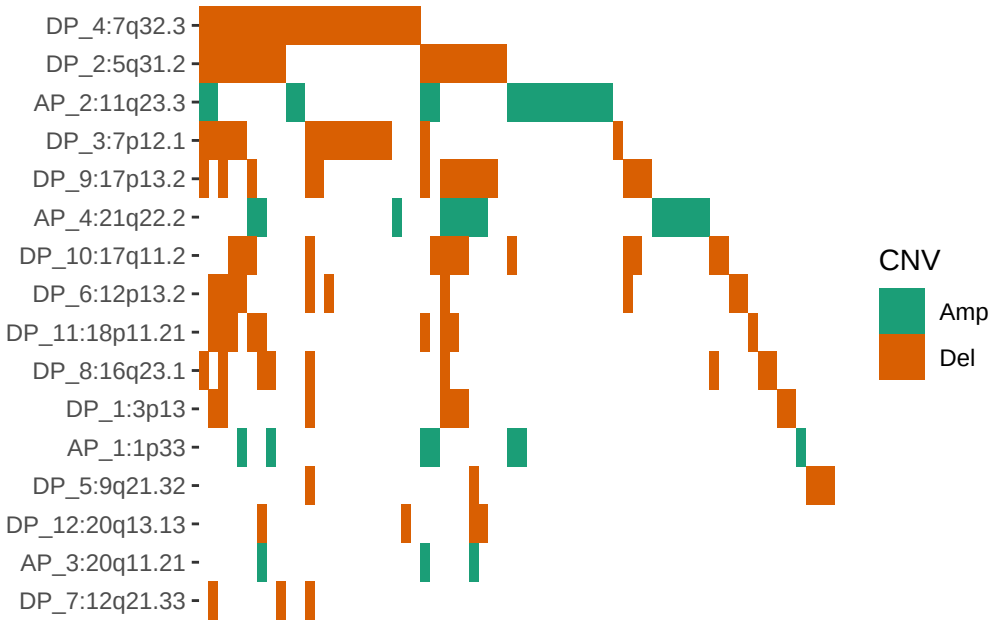
14.7 Integration with GISTIC results from maftools

The package also includes a `fortify_matrix.GISTIC()` method designed to handle `GISTIC` objects from the `maftools` package. This allows you to seamlessly apply the same operations to visualize `GISTIC` results. The following ggalign attributes are generated as part of the analysis:

- `sample_anno`: sample clinical informations provided in `sample_anno` argument.
- `sample_summary`: sample copy number summary informations. See `data@cnv.summary` for details.
- `cytoband_summary`: cytoband summary informations. See `data@cytoband.summary` for details.
- `gene_summary`: gene summary informations. See `data@gene.summary` for details.
- `summary`: A data frame of summary information. See `data@summary` for details.

```
# Ensure the maftools package is installed and load the example GISTIC data
all.lesions <- system.file("extdata", "all_lesions.conf_99.txt", package = "maftools")
amp.genes <- system.file("extdata", "amp_genes.conf_99.txt", package = "maftools")
del.genes <- system.file("extdata", "del_genes.conf_99.txt", package = "maftools")
scores.gistic <- system.file("extdata", "scores.gistic", package = "maftools")
laml.gistic <- maftools::readGistic(
    gisticAllLesionsFile = all.lesions, gisticAmpGenesFile = amp.genes,
```

```
    gisticDelGenesFile = del.genes, gisticScoresFile = scores.gistic
)
#> -Processing Gistic files..
#> --Processing amp_genes.conf_99.txt
#> --Processing del_genes.conf_99.txt
#> --Processing scores.gistic
#> --Summarizing by samples
ggoncoplot(laml.gistic) +
    scale_fill_brewer("CNV", palette = "Dark2", na.translate = FALSE) +
    theme_no_axes("x")
```



Part III

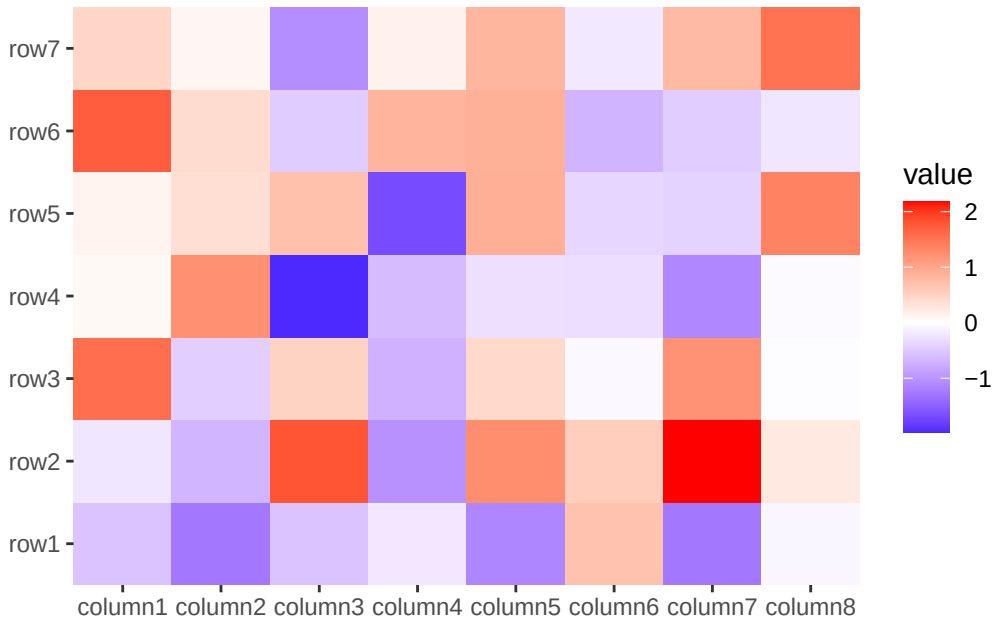
Cases

15 Complete examples

```
library(ggalign)
#> Loading required package: ggplot2
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
rownames(small_mat) <- paste0("row", seq_len(nrow(small_mat)))
colnames(small_mat) <- paste0("column", seq_len(ncol(small_mat)))
```

15.1 Simple heatmap

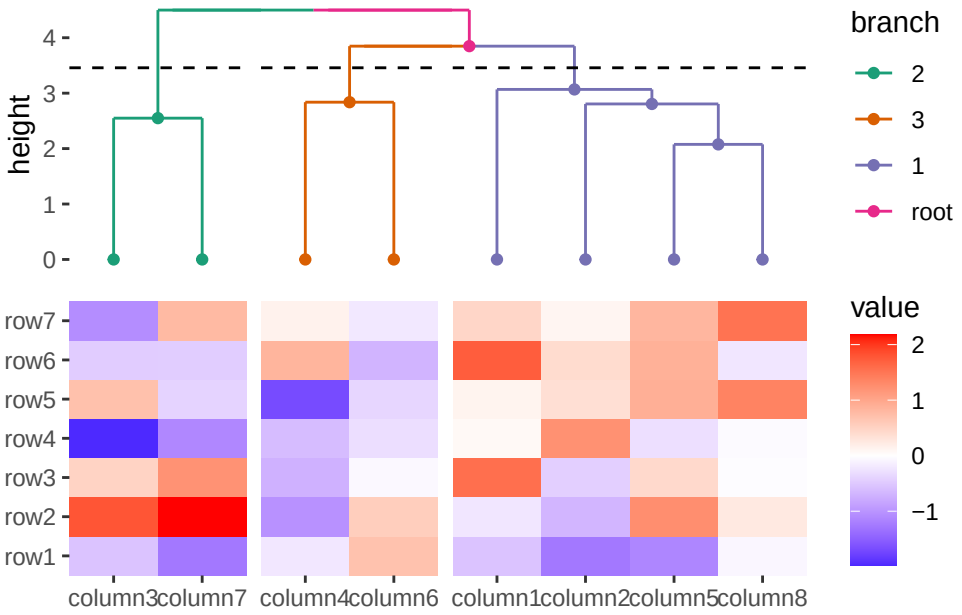
```
ggheatmap(small_mat)
#> > heatmap built with `geom_tile()`
```



15.2 heatmap layout customize

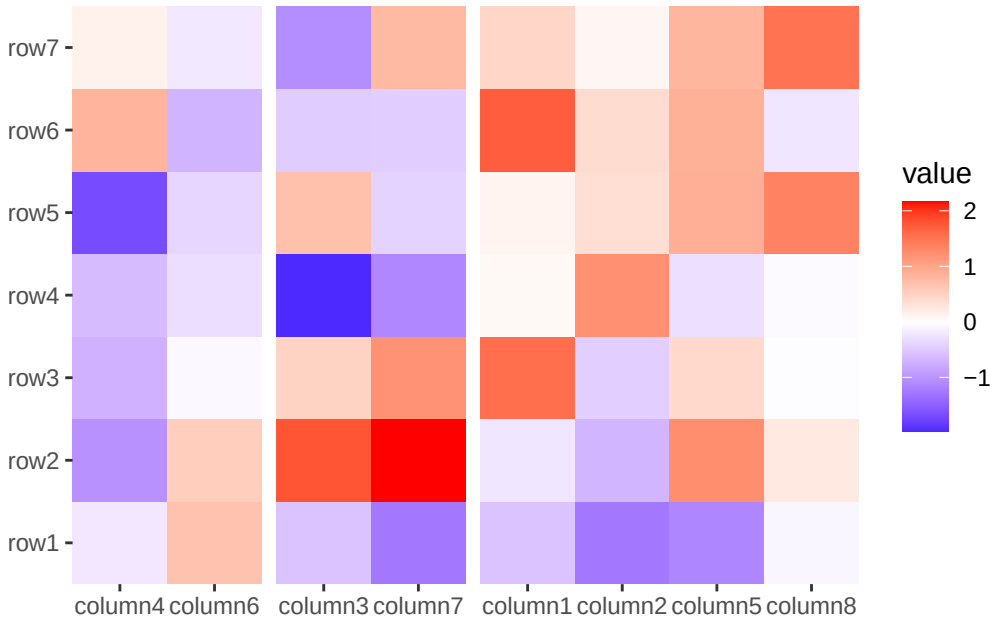
15.2.1 Based on dendrogram

```
ggheatmap(small_mat) +
    anno_top() +
    align_dendro(aes(color = branch), k = 3) +
    geom_point(aes(color = branch, y = y)) +
    scale_color_brewer(palette = "Dark2")
#> > heatmap built with `geom_tile()`
```



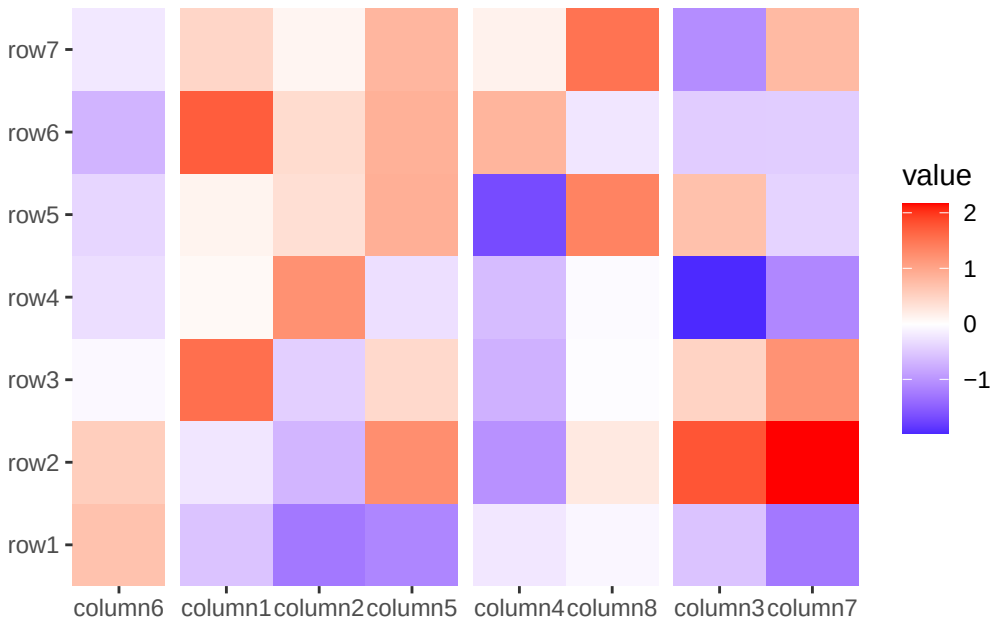
15.2.2 Based on kmeans

```
ggheatmap(small_mat) +
    anno_top() +
    align_kmeans(3L)
#> > heatmap built with `geom_tile()`
```



15.2.3 Based on a group variable

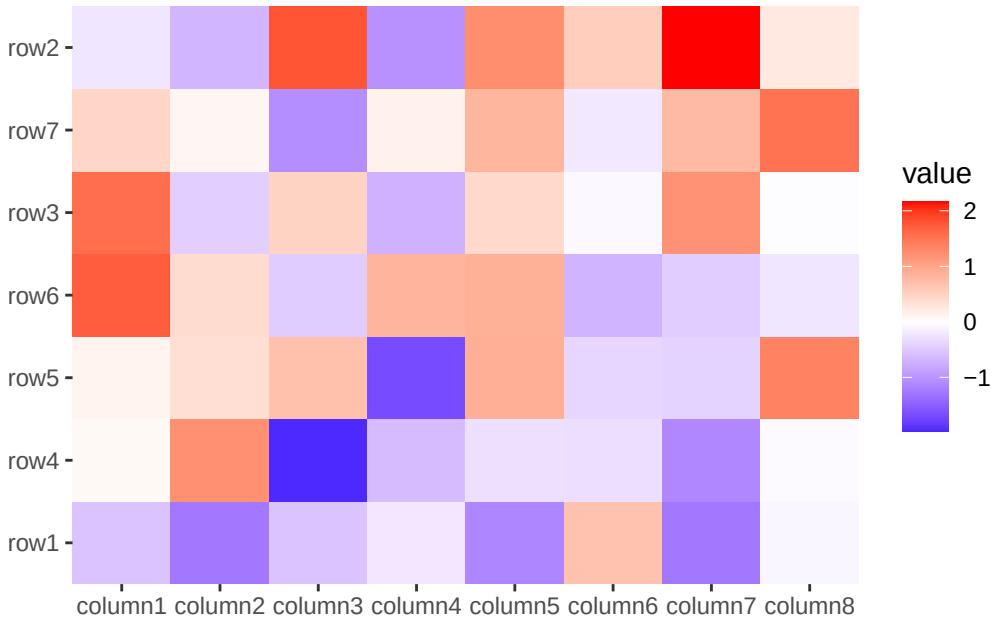
```
ggheatmap(small_mat) +
    anno_top() +
    align_group(sample(letters[1:4], ncol(small_mat), replace = TRUE))
#> > heatmap built with `geom_tile()`
```



15.2.4 Based on an ordering weights

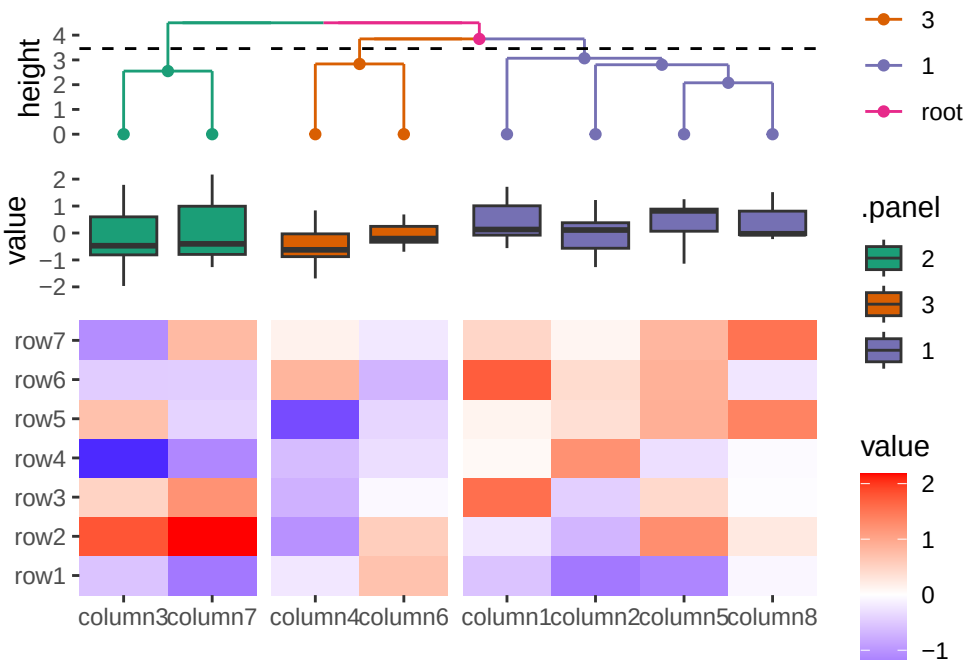
Here, we ordered the heatmap rows based on the row means.

```
ggheatmap(small_mat) +
    anno_left() +
    align_order(rowMeans)
#> > heatmap built with `geom_tile()`
```

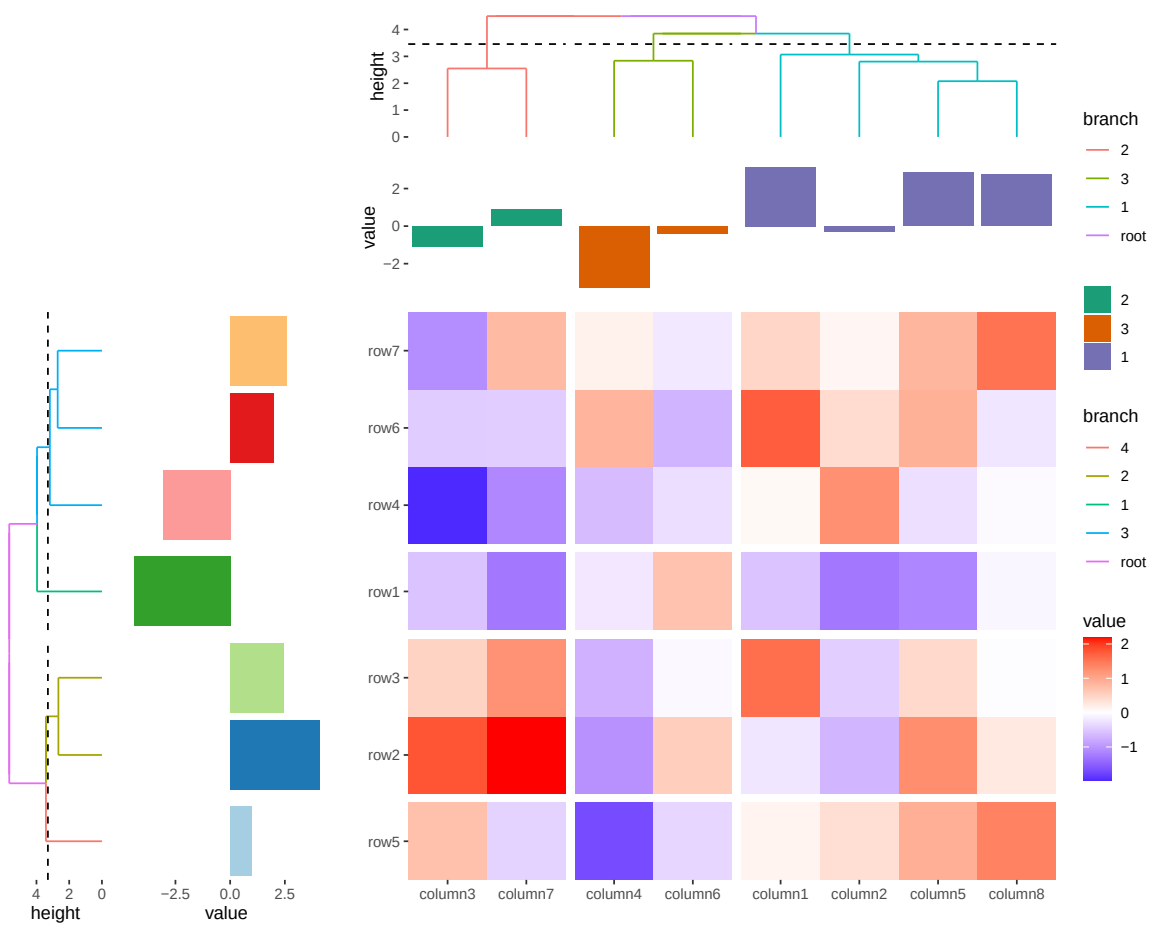


15.3 Heatmap annotation plot

```
ggheatmap(small_mat) +
    anno_top() +
    align_dendro(aes(color = branch), k = 3) +
    geom_point(aes(color = branch, y = y)) +
    scale_color_brewer(palette = "Dark2") +
    ggalign(mapping = aes(y = value)) +
    geom_boxplot(aes(factor(.x), fill = .panel)) +
    scale_fill_brewer(palette = "Dark2")
#> > heatmap built with `geom_tile()`
```



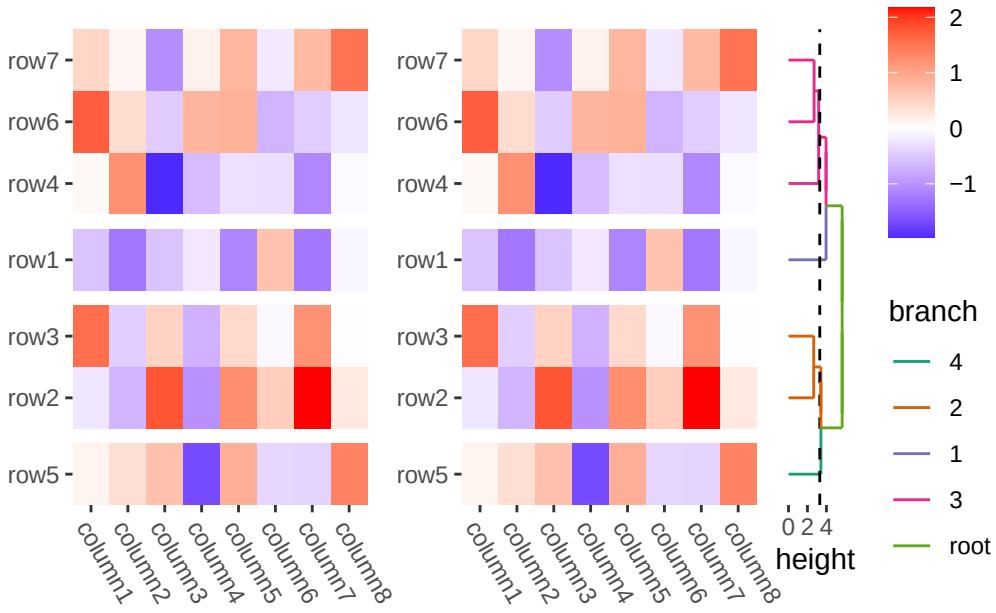

```
ggheatmap(small_mat) +
    anno_top(size = 0.5) +
    align_dendro(aes(color = branch), k = 3L) +
    ggalign(rowSums, aes(y = value)) +
    geom_bar(stat = "identity", aes(fill = factor(.panel))) +
    scale_fill_brewer(name = NULL, palette = "Dark2") +
    anno_left(size = 0.5) +
    align_dendro(aes(color = branch), size = 0.5, k = 4L) +
    ggalign(rowSums, aes(x = value)) +
    geom_bar(
        aes(y = .y, fill = factor(.y)),
        stat = "identity",
        orientation = "y"
    ) +
    scale_fill_brewer(name = NULL, palette = "Paired", guide = "none")
#> > heatmap built with `geom_tile()`
```



15.4 Multiple heatmaps

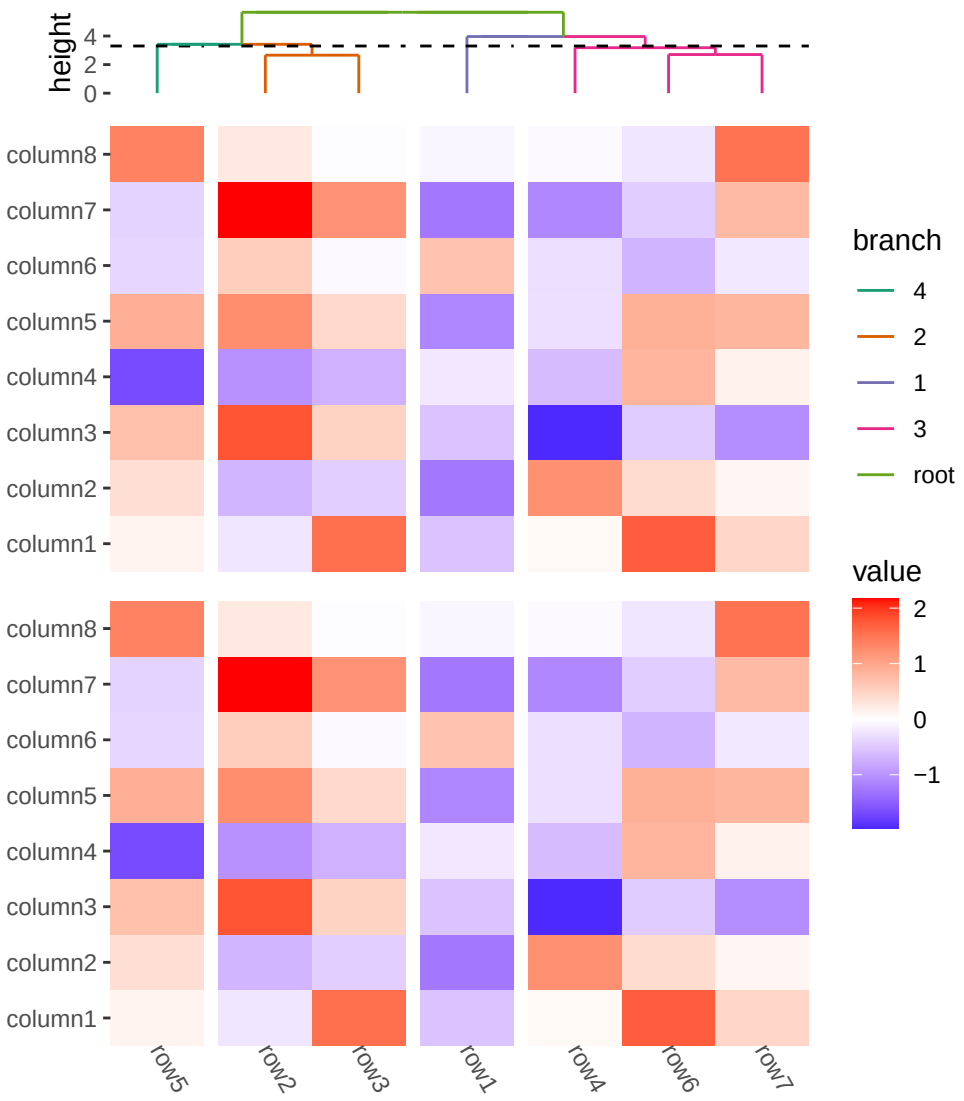
15.4.1 Horizontal layout

```
(stack_alignh(small_mat) +
    ggheatmap() +
    ggheatmap() &
    theme(axis.text.x = element_text(angle = -60, hjust = 0))) +
    stack_active() +
    align_dendro(aes(color = branch), k = 4L, size = 0.2) +
    scale_color_brewer(palette = "Dark2")
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```



15.4.2 Vertical layout

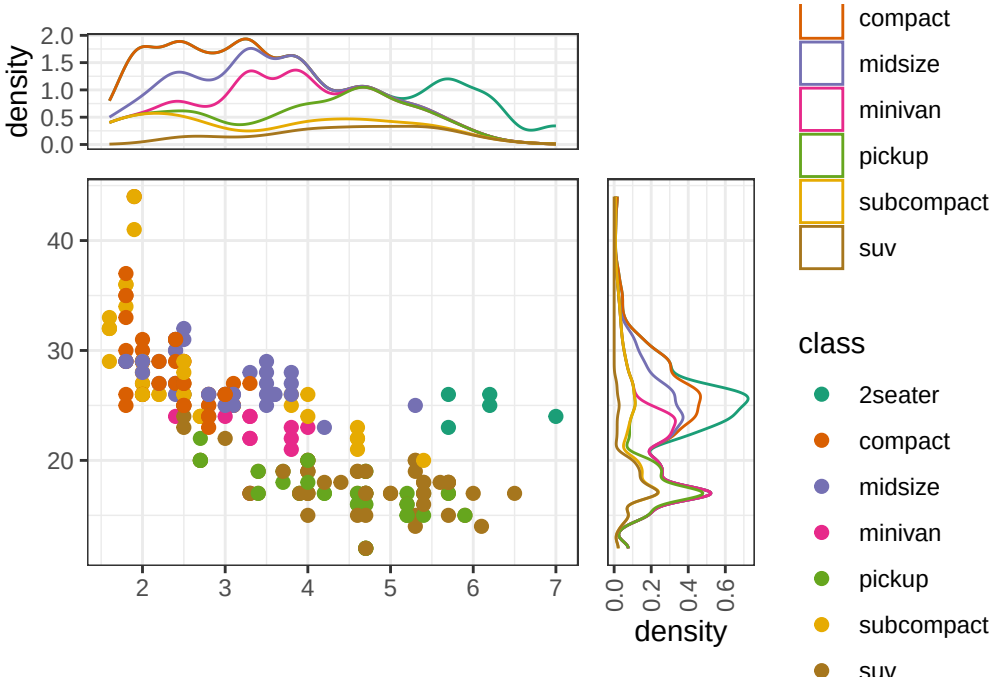
```
stack_alignv(small_mat) -
    scheme_theme(
        axis.text.x = element_blank(),
        axis.ticks.x = element_blank()
    ) +
    align_dendro(aes(color = branch), k = 4L, size = 0.2) +
    scale_color_brewer(palette = "Dark2") +
    ggheatmap() +
    ggheatmap() +
    theme(axis.text.x = element_text(angle = -60, hjust = 0))
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```



15.5 marginal plots

```
ggside(mpg, aes(displ, hwy, colour = class)) -
    # set default theme for all plots in the layout
    scheme_theme(theme_bw()) +
    geom_point(size = 2) +
    # add top annotation
```

```
    anno_top(size = 0.3) -
    # set default theme for the top annotation
    scheme_theme(theme_no_axes("tb")) +
    # add a plot in the top annotation
    ggalign() +
    geom_density(aes(displ, y = after_stat(density), colour = class), position = "stack") +
    anno_right(size = 0.3) -
    # set default theme for the right annotation
    scheme_theme(theme_no_axes("lr")) +
    # add a plot in the right annotation
    ggalign() +
    geom_density(aes(x = after_stat(density), hwy, colour = class),
        position = "stack"
    ) +
    theme(axis.text.x = element_text(angle = 90, vjust = .5)) &
    scale_color_brewer(palette = "Dark2")
```



Part IV

ComplexHeatmap

In this chapter, we'll use `ggalign` to draw all the heatmap in https://jokergoo.github.io/ComplexHeatmap-reference/book/index.html.

The chapter is divided into several sections, following the structure of the original book.

16 A Single Heatmap

In this thread, we'll use `ggalign` to draw all the heatmap in https://jokergoo.github.io/ComplexHeatmap-reference/book/a-single-heatmap.html

```
library(ggalign)
#> Loading required package: ggplot2
```

```
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), nrow = nr1),
        matrix(rnorm(nr2 * nc1, mean = 0, sd = 0.5), nrow = nr2),
        matrix(rnorm(nr3 * nc1, mean = 0, sd = 0.5), nrow = nr3)
    ),
    rbind(
        matrix(rnorm(nr1 * nc2, mean = 0, sd = 0.5), nrow = nr1),
        matrix(rnorm(nr2 * nc2, mean = 1, sd = 0.5), nrow = nr2),
        matrix(rnorm(nr3 * nc2, mean = 0, sd = 0.5), nrow = nr3)
    ),
    rbind(
        matrix(rnorm(nr1 * nc3, mean = 0.5, sd = 0.5), nrow = nr1),
        matrix(rnorm(nr2 * nc3, mean = 0.5, sd = 0.5), nrow = nr2),
        matrix(rnorm(nr3 * nc3, mean = 1, sd = 0.5), nrow = nr3)
    )
)
mat <- mat[sample(nr, nr), sample(nc, nc)]
rownames(mat) <- paste0("row", seq_len(nr))
colnames(mat) <- paste0("column", seq_len(nc))
```

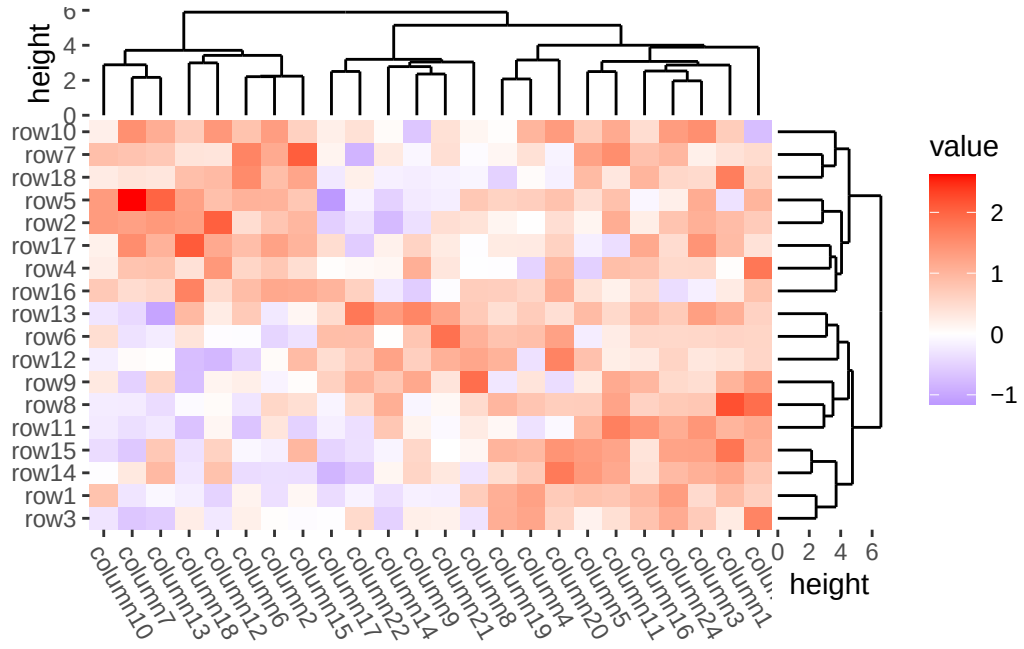
16.1 Colors

It is important to note that the `ComplexHeatmap` package reorders the dendrogram by default, while `align_dendro()` in `ggalign` does not modify the tree layout.

Another key difference is in how the two packages treat the starting point. `ggalign` considers the left-bottom as the starting point, whereas `ComplexHeatmap` starts from the left-top. When reordering the dendrogram, `ComplexHeatmap` does so in decreasing order, while `ggalign` uses an ascending order.

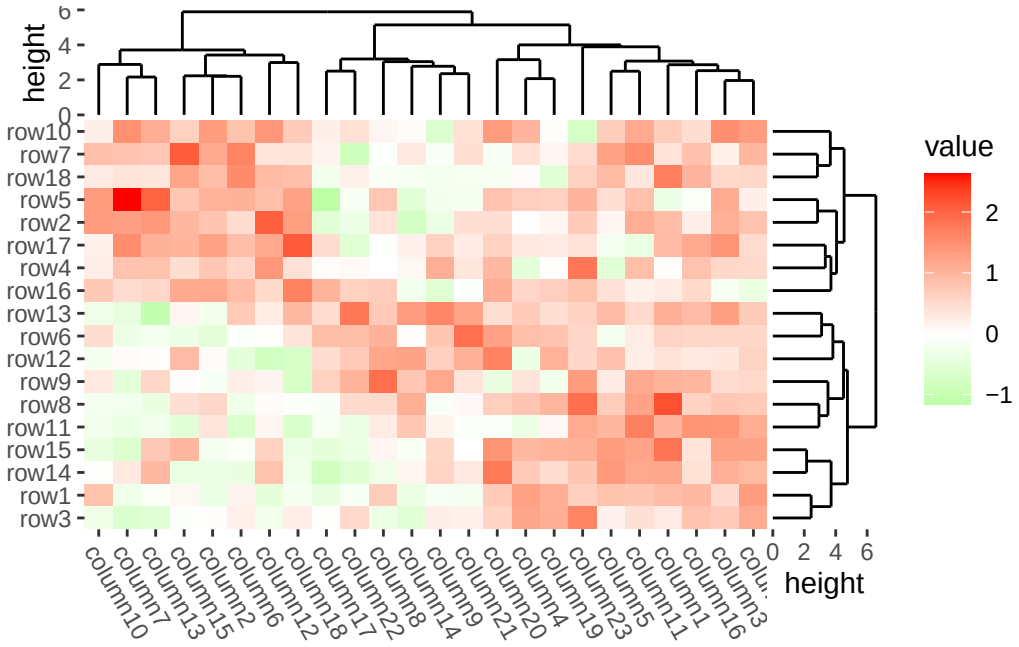
To modify colors in the heatmap, you can use the `scale_fill_*()` function from `ggplot2`, which provides a flexible way and enriched pallete to adjust color schemes.

```
dim(mat)
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



```
# ComplexHeatmap::Heatmap(mat)
#> [1] 18 24
```

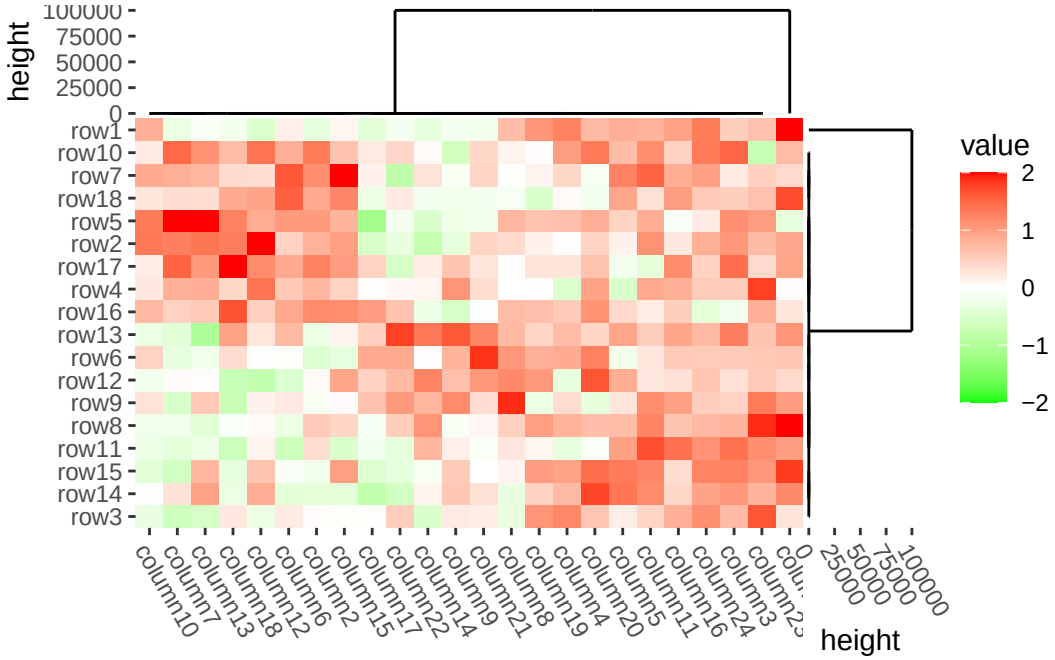
```
ggheatmap(mat) +
    scale_fill_gradient2(low = "green", high = "red") +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro() +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



`oob` argument in the `scale_fill_*` function can be used to deal with the outliers.

```
mat2 <- mat
mat2[1, 1] <- 100000
ggheatmap(mat2) +
    scale_fill_gradient2(
        low = "green", high = "red",
        limits = c(-2, 2),
```

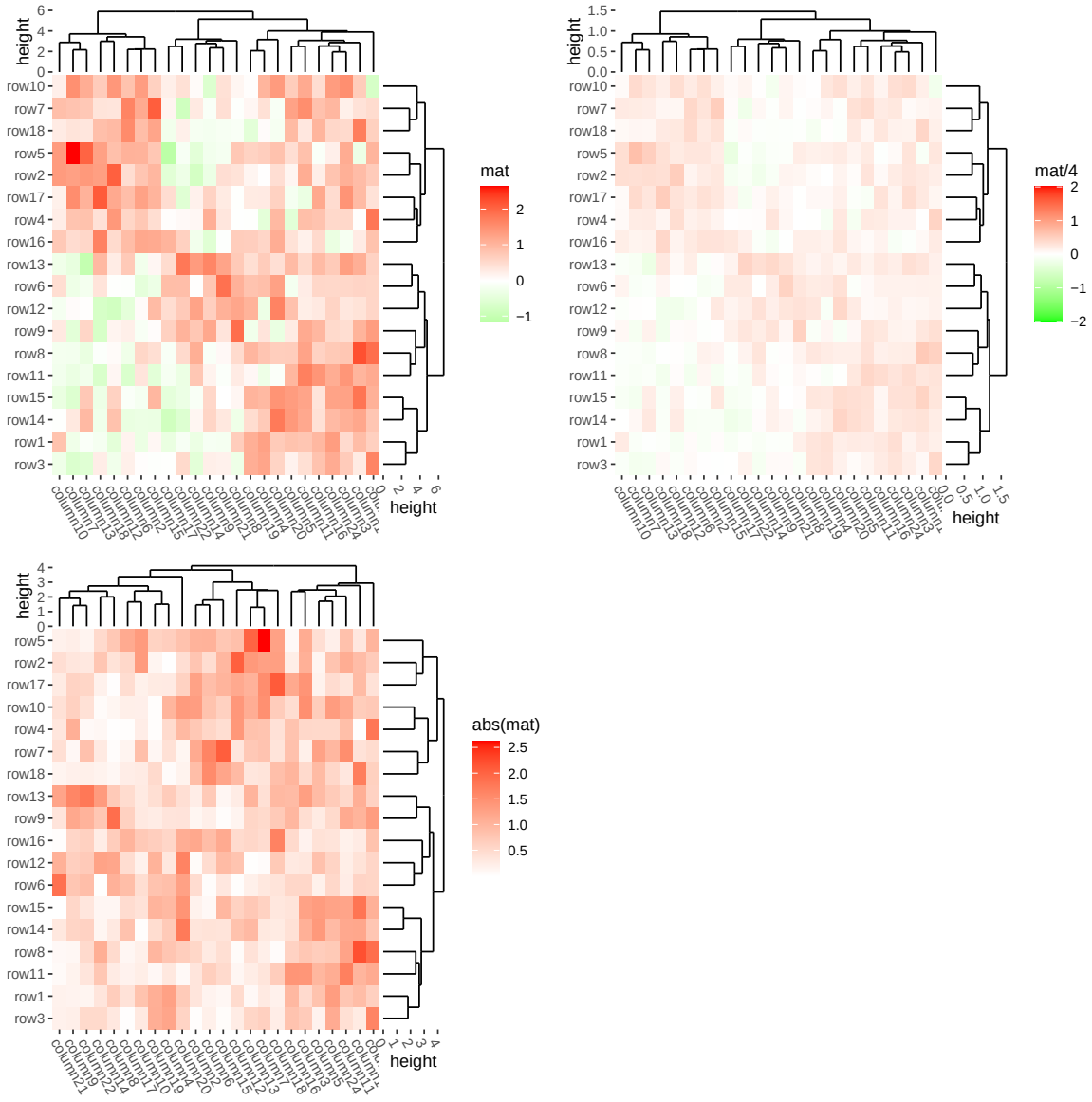
```
        oob = scales::squish
    ) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



We can use `align_plots()` to arrange them.

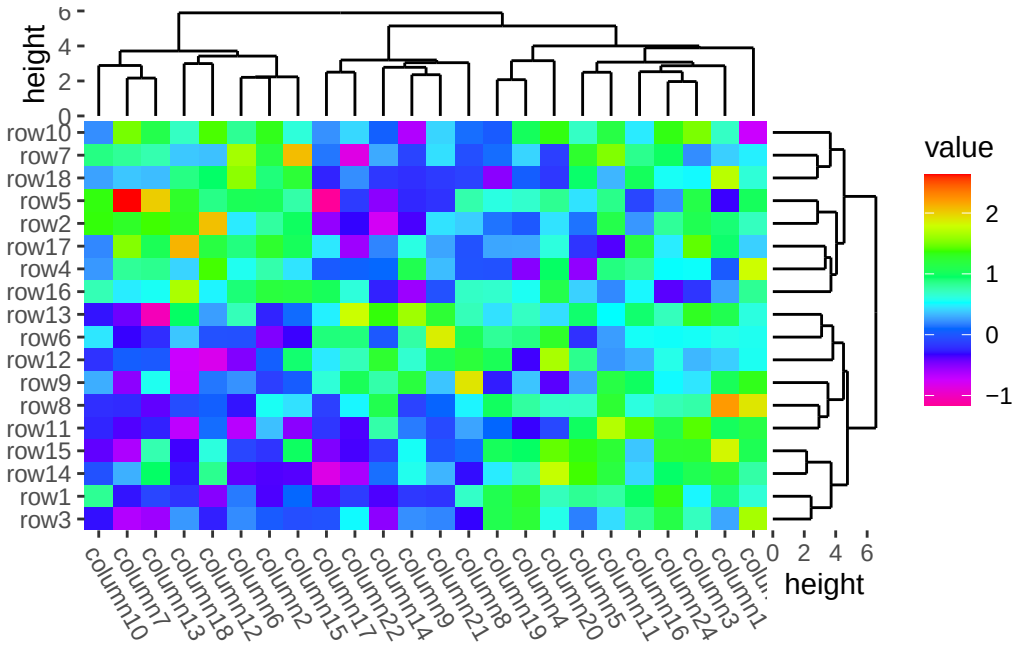
```
h1 <- ggheatmap(mat) +
    scale_fill_gradient2(name = "mat", low = "green", high = "red") +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
```

```
    theme(plot.margin = margin())

h2 <- ggheatmap(mat / 4) +
    scale_fill_gradient2(
        name = "mat/4", limits = c(-2, 2L),
        oob = scales::squish,
        low = "green", high = "red"
    ) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())

h3 <- ggheatmap(abs(mat)) +
    scale_fill_gradient2(name = "abs(mat)", low = "green", high = "red") +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
align_plots(h1, h2, h3, ncol = 2L)
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```



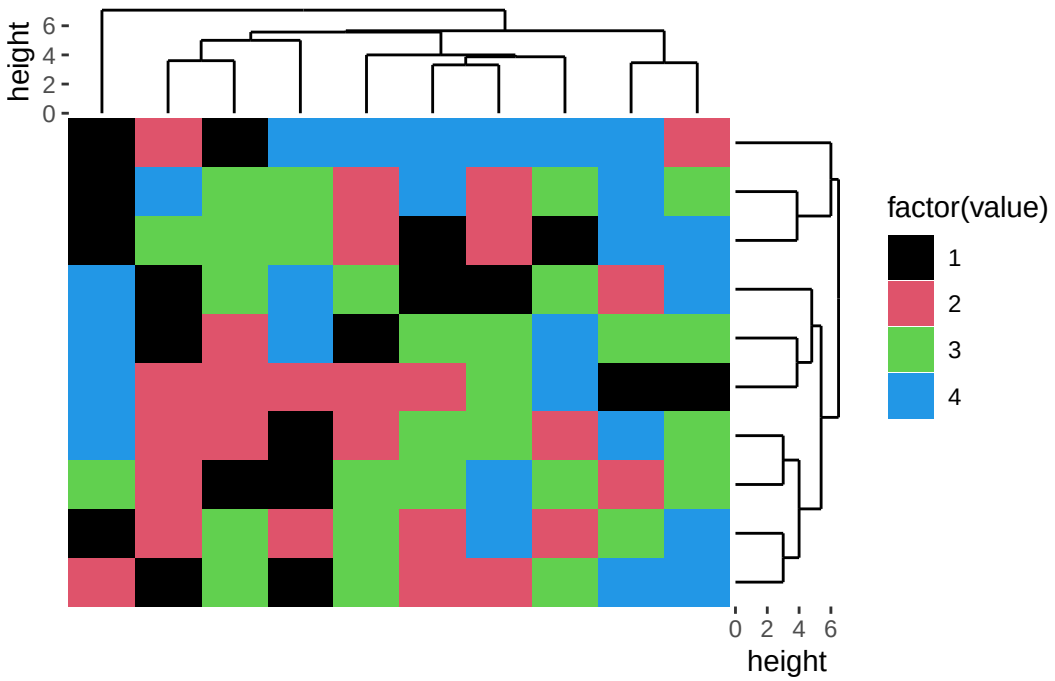

```
ggheatmap(mat) +
    scale_fill_gradientn(colors = rev(rainbow(10))) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
```

```
#> > heatmap built with `geom_tile()`
```

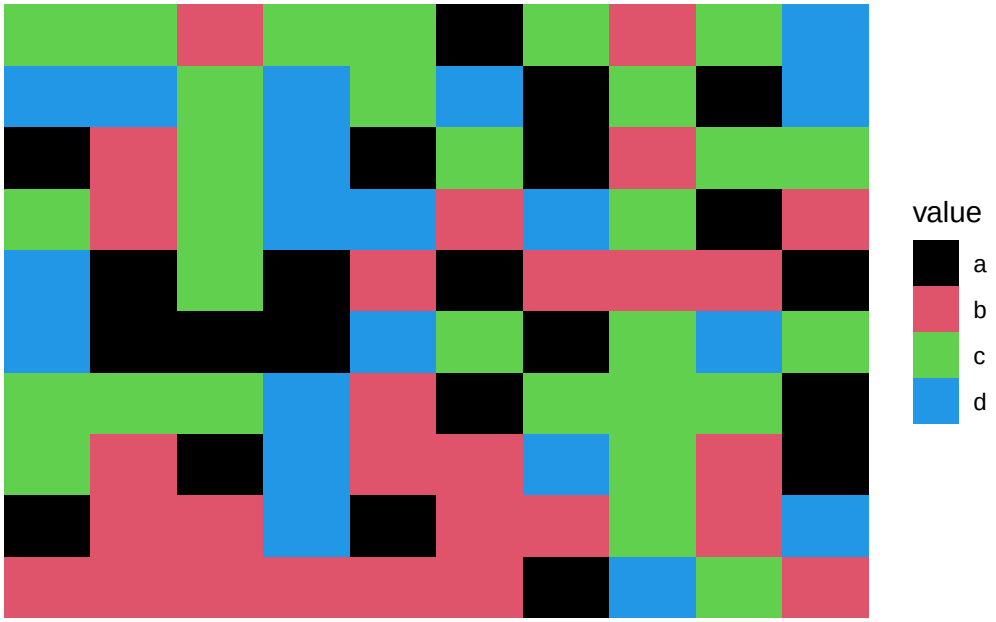


For character matrix, you can use ggplot2 discrete filling scales.

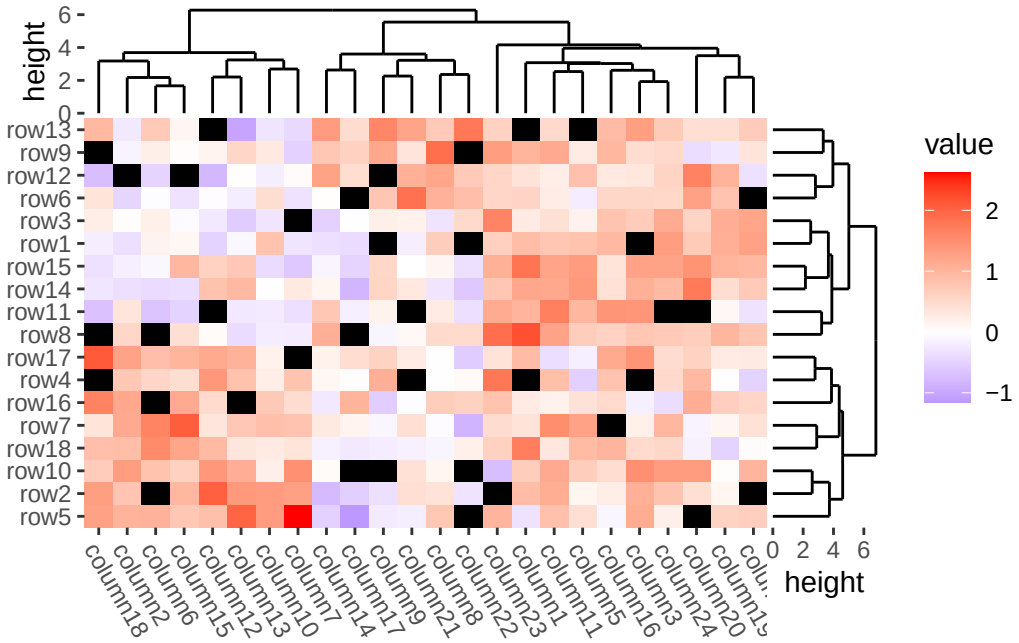
```
discrete_mat <- matrix(sample(1:4, 100, replace = TRUE), 10, 10)
colors <- structure(1:4, names = c("1", "2", "3", "4")) # black, red, green, blue
ggheatmap(discrete_mat, aes(fill = factor(value))) +
    scale_fill_manual(values = colors) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```




```
discrete_mat <- matrix(sample(letters[1:4], 100, replace = TRUE), 10, 10)
colors <- structure(1:4, names = letters[1:4])
ggheatmap(discrete_mat) +
    scale_fill_manual(values = colors)
#> > heatmap built with `geom_tile()`
```



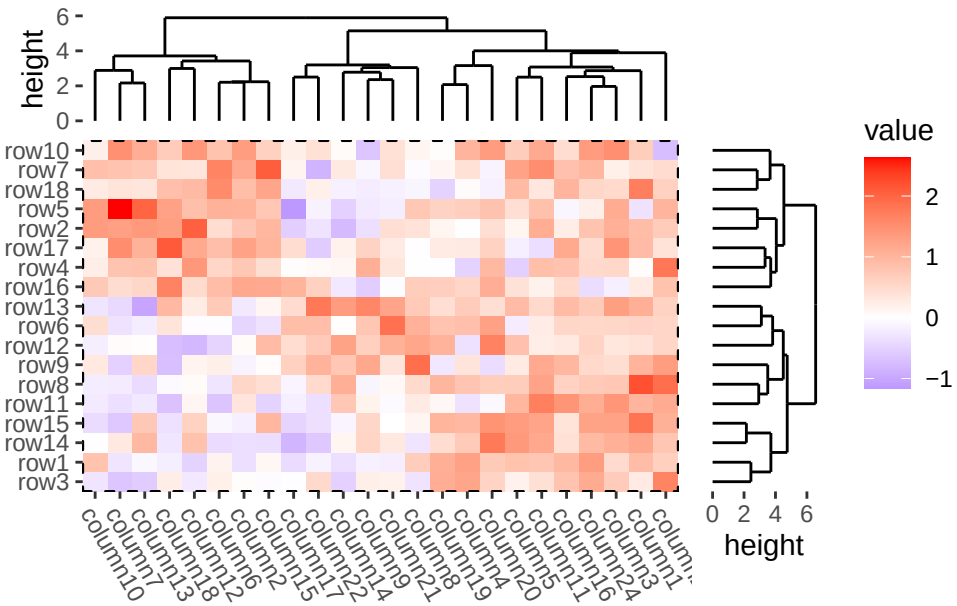

```
mat_with_na <- mat
na_index <- sample(c(TRUE, FALSE),
    nrow(mat) * ncol(mat),
    replace = TRUE, prob = c(1, 9)
)
mat_with_na[na_index] <- NA
ggheatmap(mat_with_na) +
    scale_fill_gradient2(low = "blue", high = "red", na.value = "black") +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



We won't compare the LAB and RGB space. If you want to convert color between different color space, try to use farver pacakge.

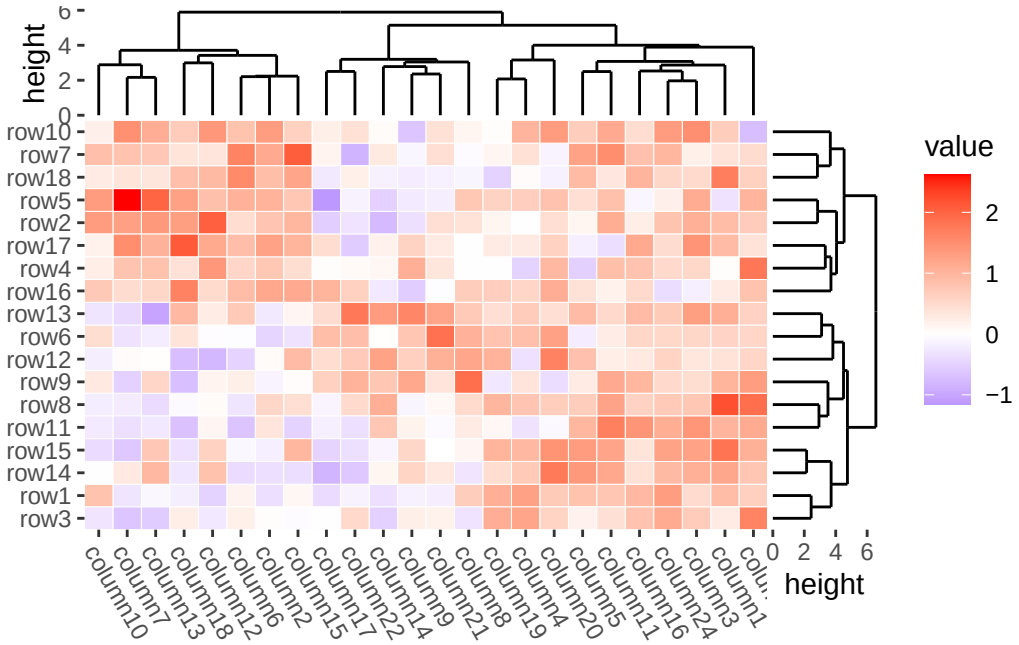
In ggplot2, you can use `panel.border` argument in `theme()` function to control the Heatmap body border.

```
ggheatmap(mat) +
    theme(
        axis.text.x = element_text(angle = -60, hjust = 0),
        panel.border = element_rect(linetype = "dashed", fill = NA)
    ) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



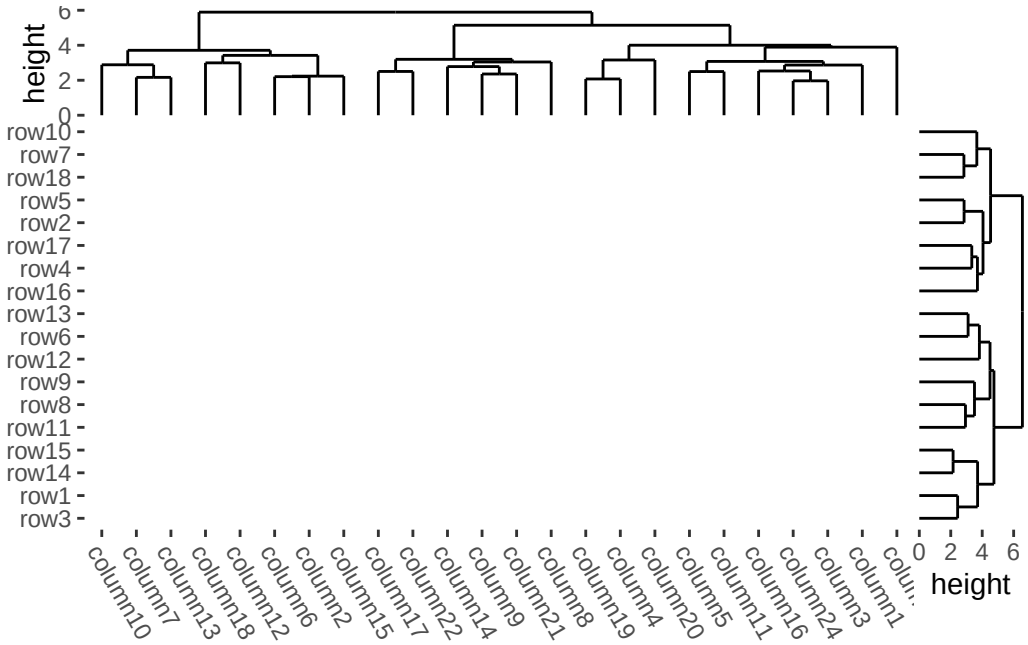
You can use the `filling` argument to turn off the heatmap cell filling, allowing you to customize the heatmap body geoms. Use the `color` aesthetic to specify the cell border color and the `linewidth` aesthetic to set the border width.

```
ggheatmap(mat, filling = NULL) +
    geom_tile(aes(fill = value), color = "white") +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) &
    theme(plot.margin = margin())
```



To draw a blank heatmap body:

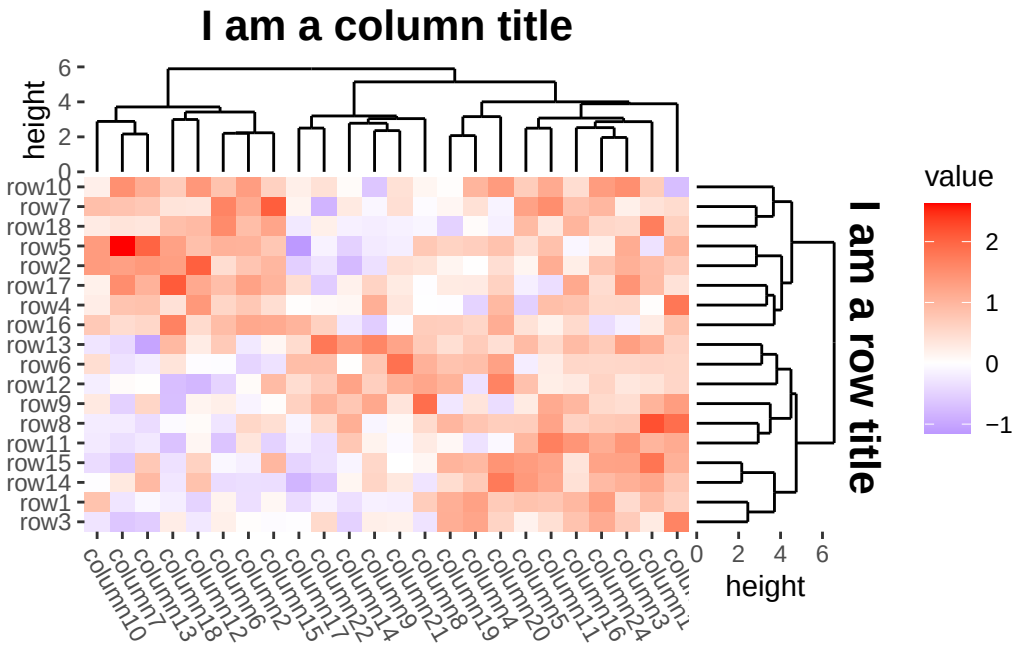
```
ggheatmap(mat, filling = NULL) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) &
    theme(plot.margin = margin())
```



16.2 Titles

We can use `patch_titles()` to add titles around each border of the plot. You can use `theme()` to control the text appearance.

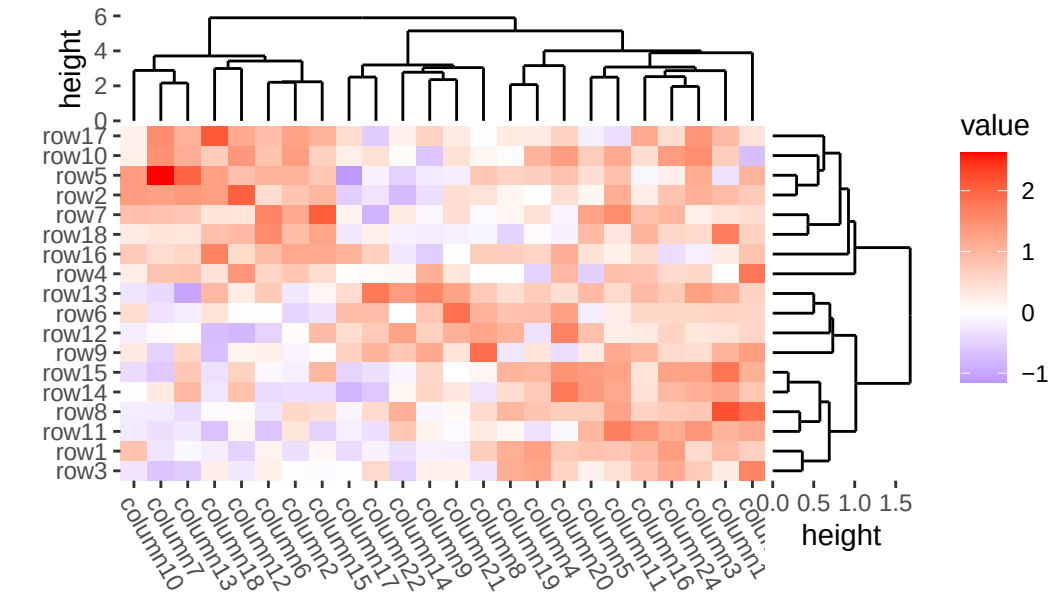
```
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(20, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    patch_titles(right = "I am a row title") +
    theme(plot.patch_title.right = element_text(face = "bold", size = 16)) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    patch_titles(top = "I am a column title") +
    theme(plot.patch_title.top = element_text(face = "bold", size = 16)) &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



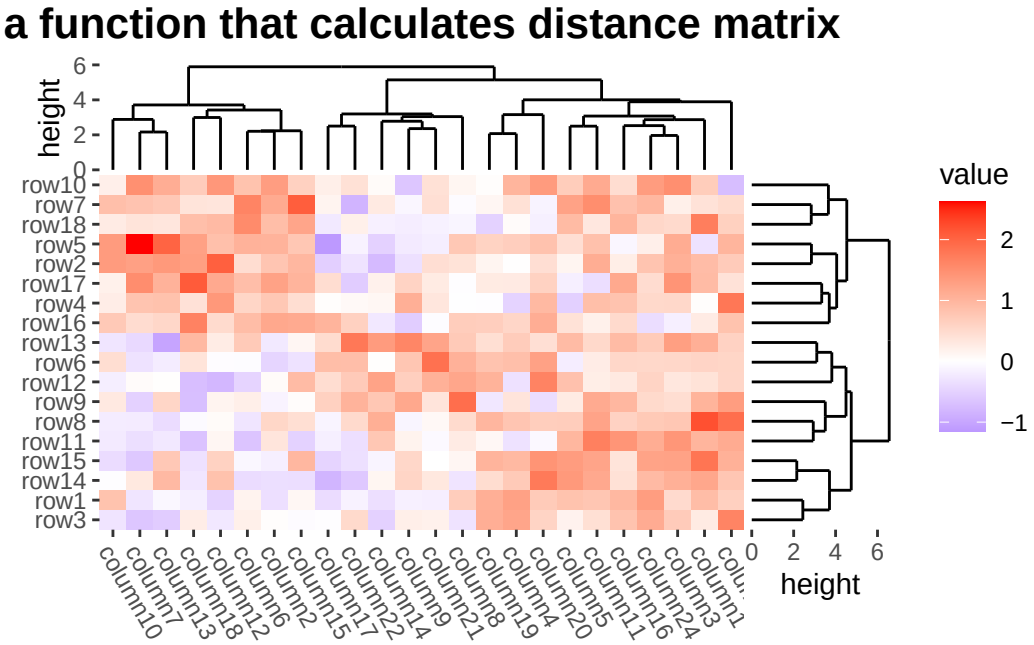
16.3 Clustering

16.3.1 Distance methods

```
# ComplexHeatmap::Heatmap(mat,
#   name = "mat", clustering_distance_rows = "pearson",
#   column_title = "pre-defined distance method (1 - pearson)"
# )
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(20, "mm")) +
    align_dendro(distance = "pearson", reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    patch_titles(top = "pre-defined distance method (1 - pearson)") +
    theme(plot.patch_title.top = element_text(face = "bold", size = 16)) &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



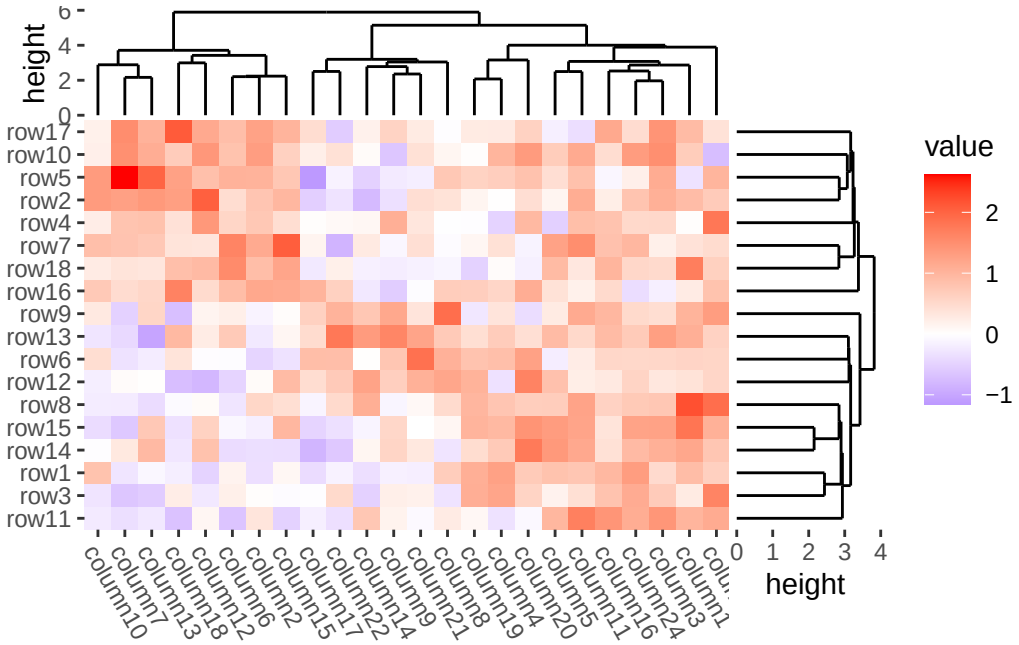

```
# ComplexHeatmap::Heatmap(mat,
#     name = "mat", clustering_distance_rows = function(m) dist(m),
#     column_title = "a function that calculates distance matrix"
# )
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(20, "mm")) +
    align_dendro(distance = dist, reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    patch_titles(top = "a function that calculates distance matrix") +
    theme(plot.patch_title.top = element_text(face = "bold", size = 16)) &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



16.3.2 Clustering methods

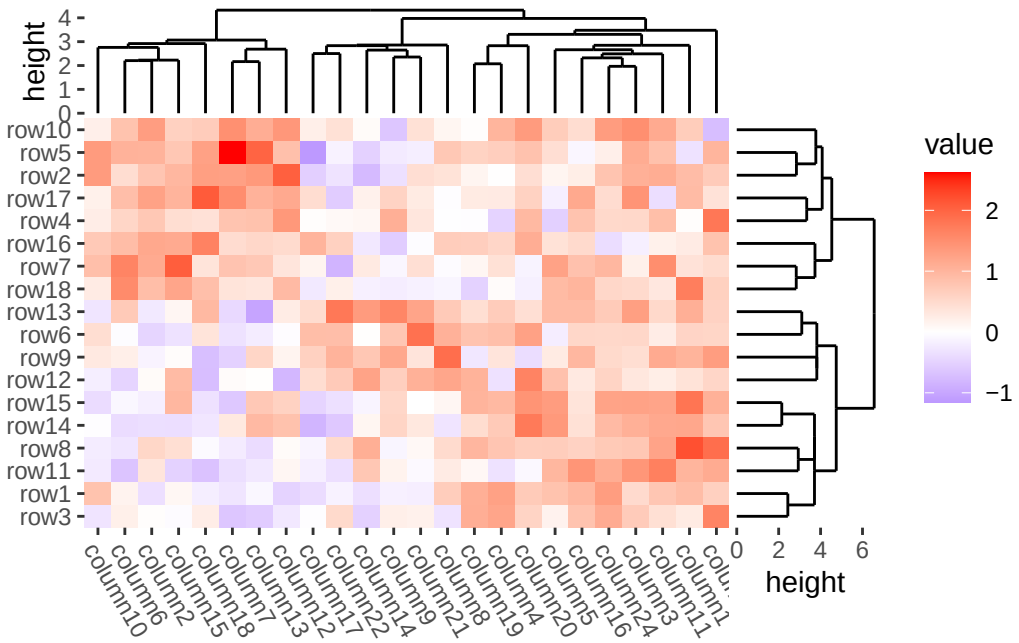
Method to perform hierarchical clustering can be specified by `method` argument, Possible methods are those supported in `hclust()` function.

```
# ComplexHeatmap::Heatmap(mat,
#     name = "mat",
#     clustering_method_rows = "single"
# )
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(20, "mm")) +
    align_dendro(method = "single", reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



Use `distance = NULL` if you don't want to calculate the distance.

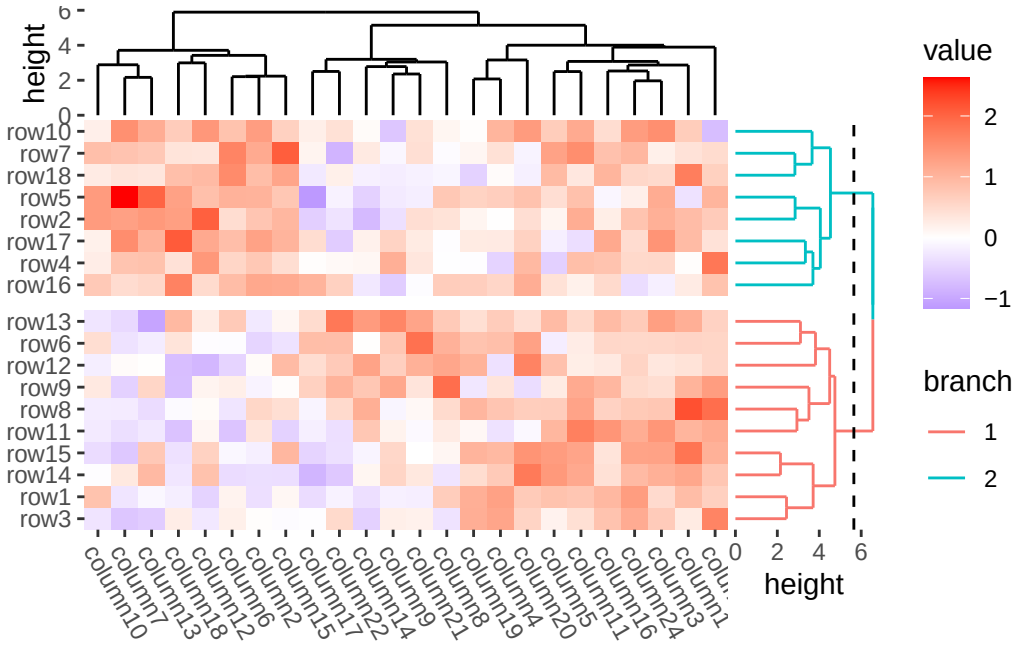
```
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(20, "mm")) +
    align_dendro(
        distance = NULL, method = cluster::diana,
        reorder_dendrogram = TRUE
    ) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(
        distance = NULL, method = cluster::agnes,
        reorder_dendrogram = TRUE
    ) &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



16.3.3 Render dendrograms

It's easy for `ggalign` to color the branches by setting the color mapping, since `ggalign` will add the `cutree()` results into the underlying data.

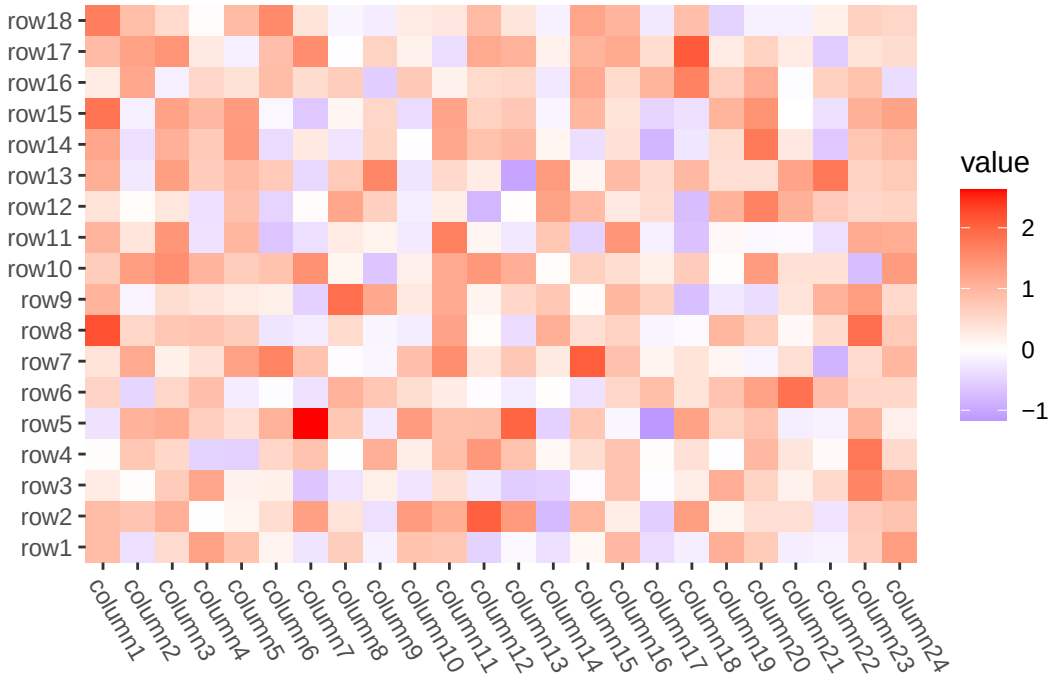
```
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(20, "mm")) +
    align_dendro(aes(color = branch), k = 2L, reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



16.4 Set row and column orders

We can use `align_order()` to set the order.

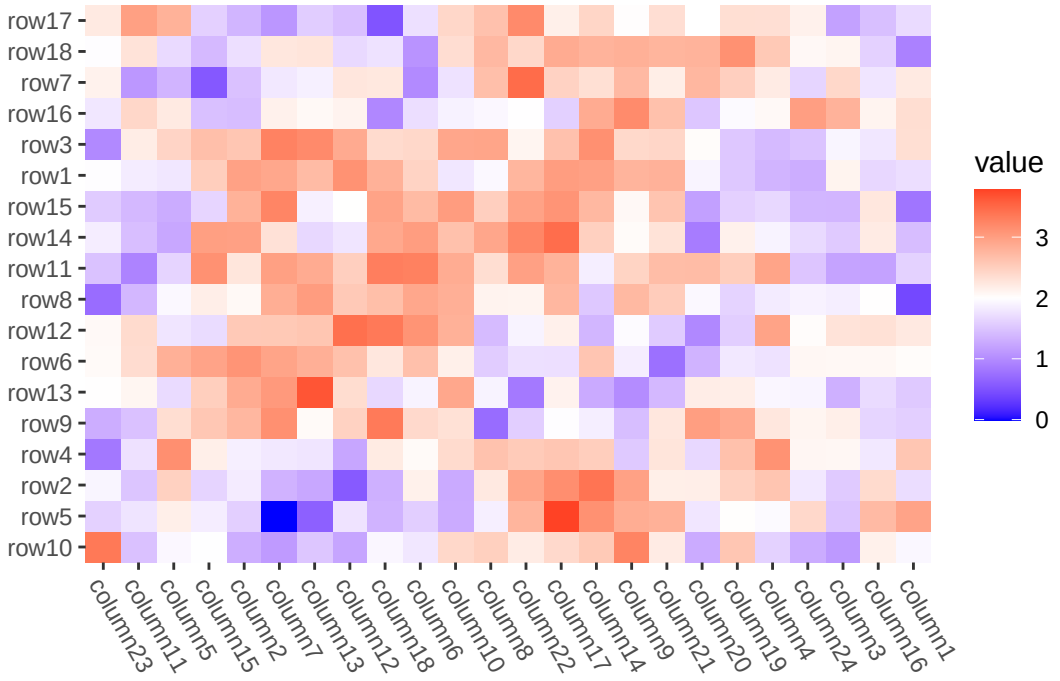
```
# ComplexHeatmap::Heatmap(mat,
#     name = "mat",
#     row_order = order(as.numeric(gsub("row", "", rownames(mat)))),
#     column_order = order(as.numeric(gsub("column", "", colnames(mat)))),
#     column_title = "reorder matrix"
# )
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(20, "mm")) +
    align_order(as.numeric(gsub("row", "", rownames(mat)))) +
    anno_top(size = unit(15, "mm")) +
    align_order(as.numeric(gsub("column", "", colnames(mat)))) &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



16.5 Seriation

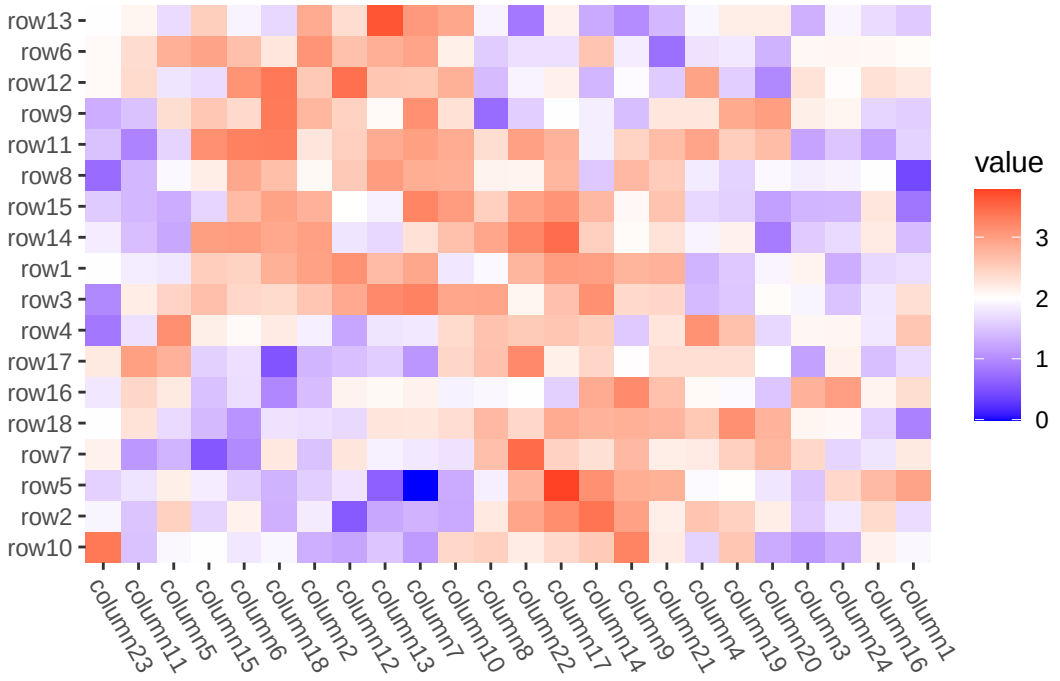
`align_reorder()` can directly take the `seriate()` function as the input and extract the ordering information.

```
mat2 <- max(mat) - mat
ggheatmap(mat2) +
    scale_fill_gradient2(low = "blue", high = "red", midpoint = 2L) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(20, "mm")) +
    align_reorder(seriation::seriate, method = "BEA_TSP") +
    anno_top(size = unit(15, "mm")) +
    align_reorder(seriation::seriate, method = "BEA_TSP") &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



The above code will execute `seriate()` twice—once for each dimension. However, since a single run of `seriate()` can provide the ordering for both dimensions, we can manually extract the ordering indices to avoid redundancy.

```
o <- seriation::seriate(mat2, method = "BEA_TSP")
ggheatmap(mat2) +
    scale_fill_gradient2(low = "blue", high = "red", midpoint = 2L) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(20, "mm")) +
    align_order(seriation::get_order(o, 1L)) +
    anno_top(size = unit(15, "mm")) +
    align_order(seriation::get_order(o, 2L)) &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



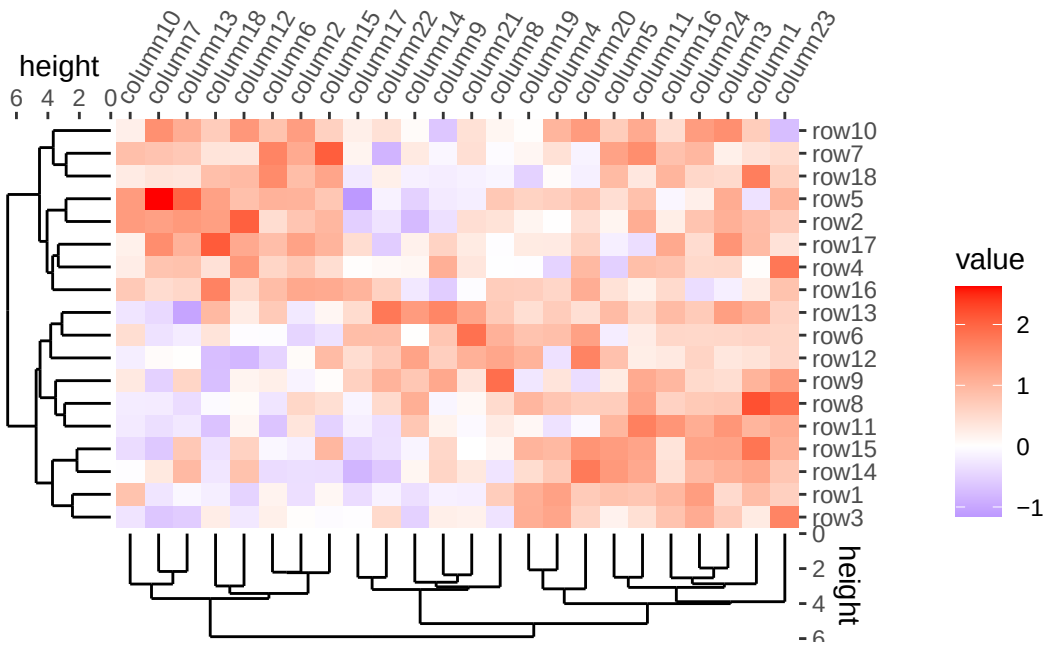
For more use of the `seriate()` function, please refer to the seriation package.

16.6 Dimension labels

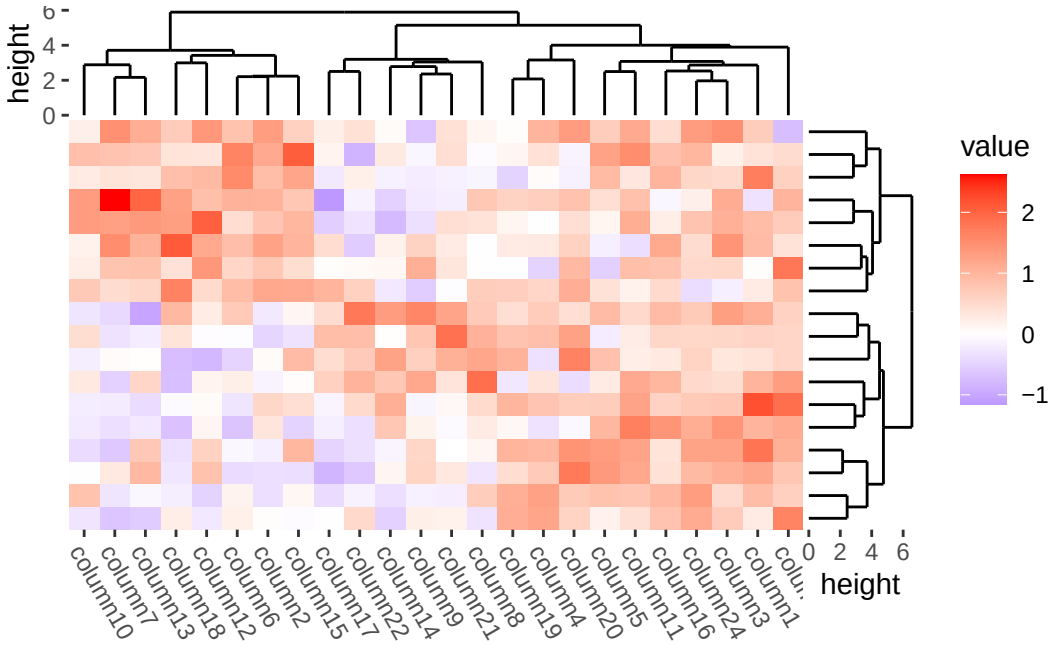
`ggplot2` use scales and theme to control the axis labels, Please see chapter for more details.

```
# ComplexHeatmap::Heatmap(mat,
#     name = "mat", row_names_side = "left", row_dend_side = "right",
#     column_names_side = "top", column_dend_side = "bottom"
# )
ggheatmap(mat) +
    scale_x_continuous(position = "top") +
    scale_y_continuous(position = "right") +
    theme(axis.text.x = element_text(angle = 60, hjust = 0)) +
    anno_left(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    scale_x_continuous(position = "top") +
    anno_bottom(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    scale_y_continuous(position = "right") +
    quad_active() &
```

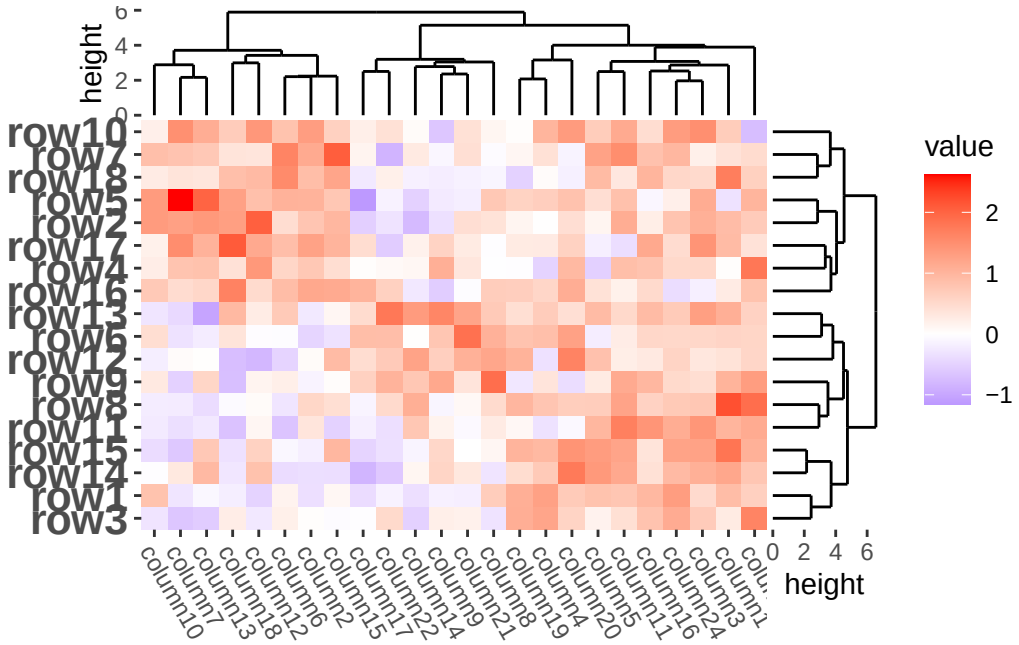
```
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



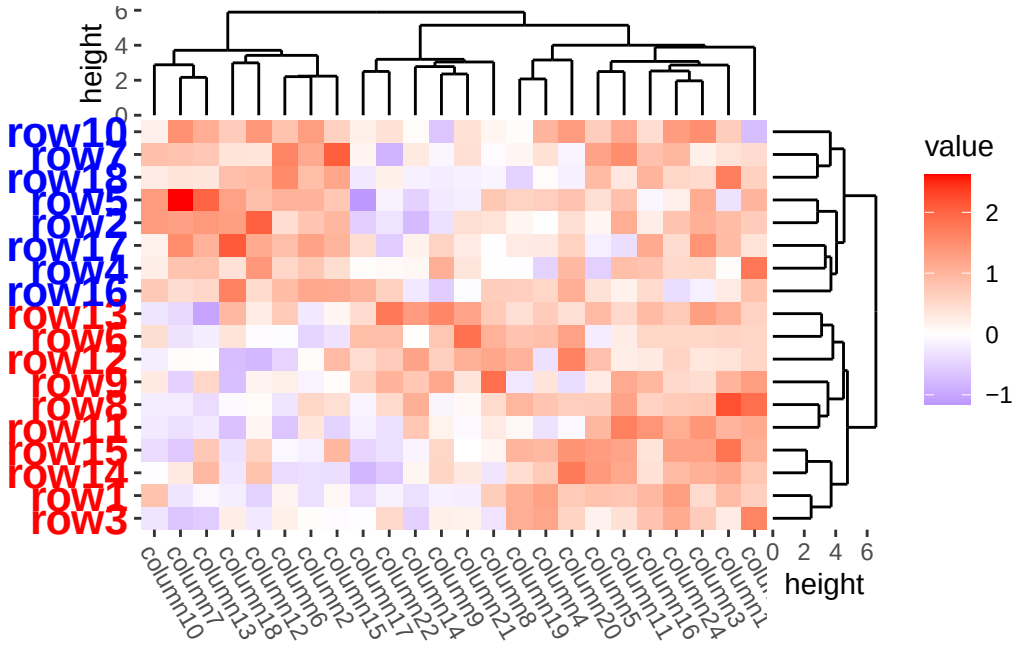

```
ggheatmap(mat) +
    scale_y_continuous(breaks = NULL) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```




```
ggheatmap(mat) +
    theme(
        axis.text.x = element_text(angle = -60, hjust = 0),
        axis.text.y = element_text(face = "bold", size = 16)
    ) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



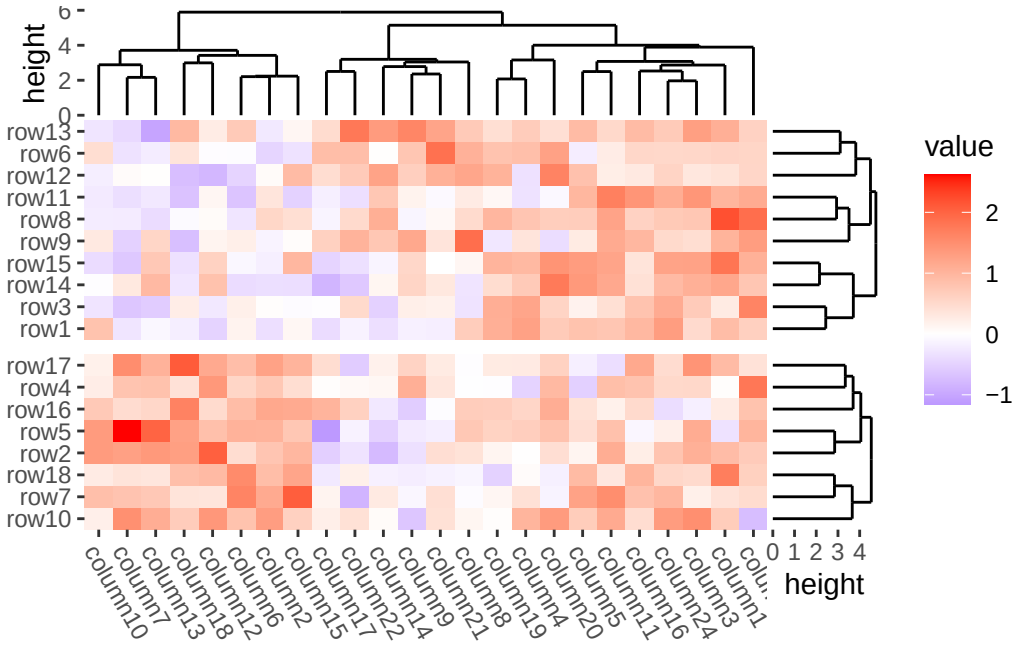

```
ggheatmap(mat) +
    theme(
        axis.text.x = element_text(angle = -60, hjust = 0),
        axis.text.y = element_text(
            face = "bold", size = 16,
            colour = c(rep("red", 10), rep("blue", 8))
        )
    ) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> Warning: Vectorized input to `element_text()` is not officially supported.
#> i Results may be unexpected or may change in future versions of ggplot2.
#> > heatmap built with `geom_tile()`
```



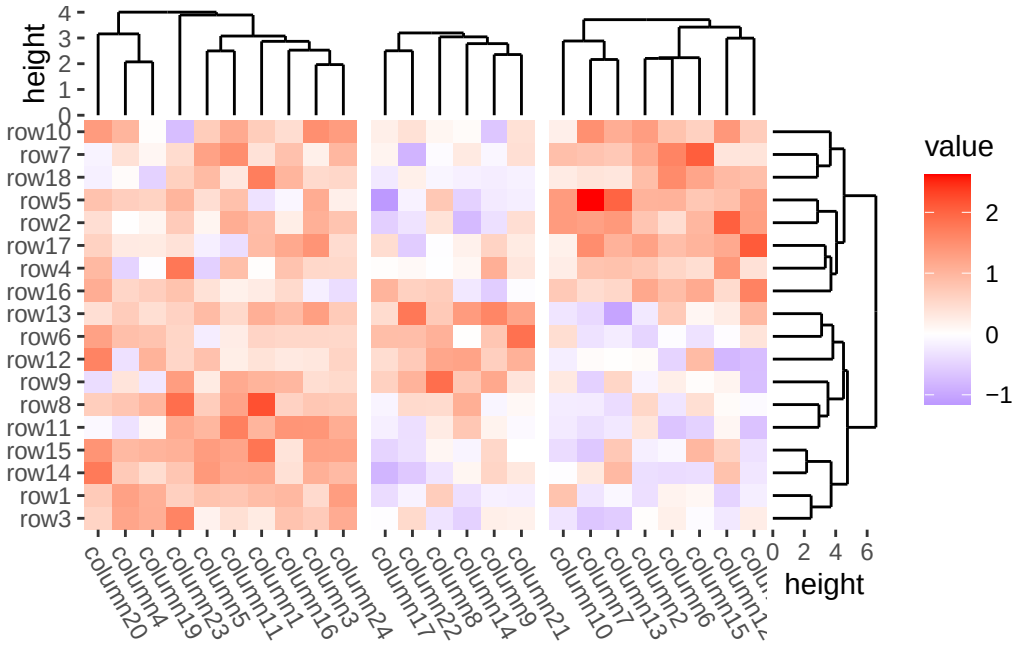
16.7 Heatmap split

16.7.1 Split by k-means clustering

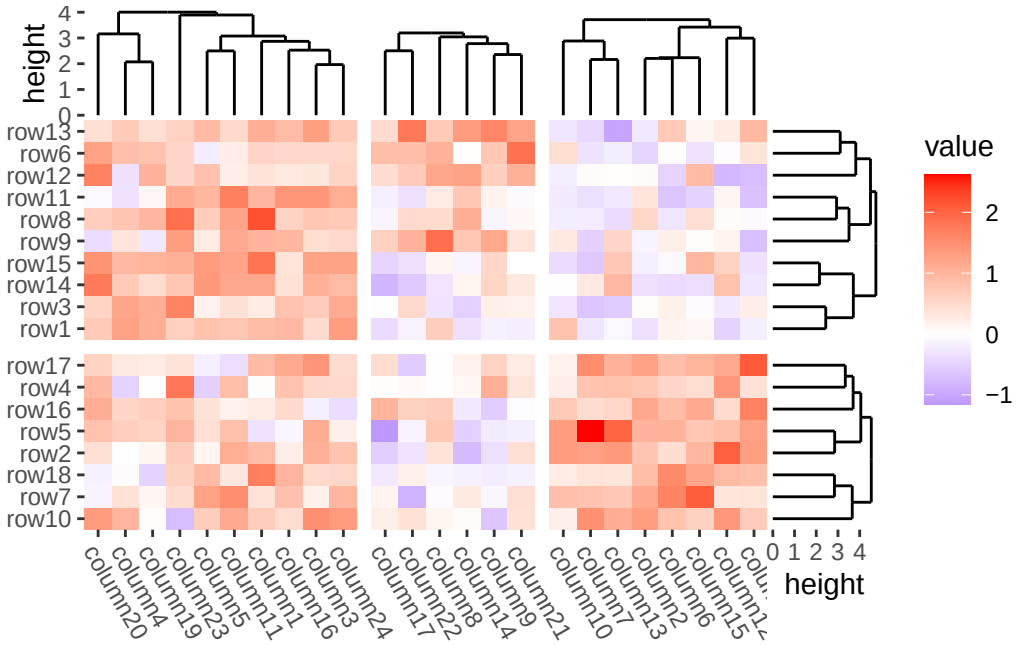
```
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_kmeans(2L) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```




```
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_kmeans(3L) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



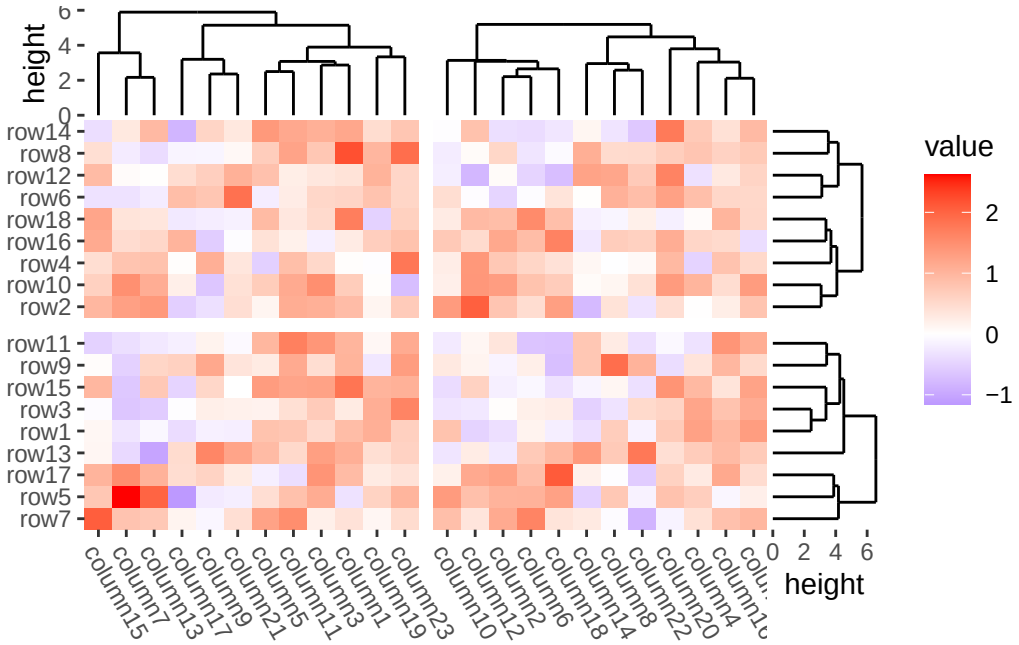

```
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_kmeans(2L) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_kmeans(3L) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



The dendrogram was calculated in each group defined by kmeans.

16.7.2 Split by categorical variables

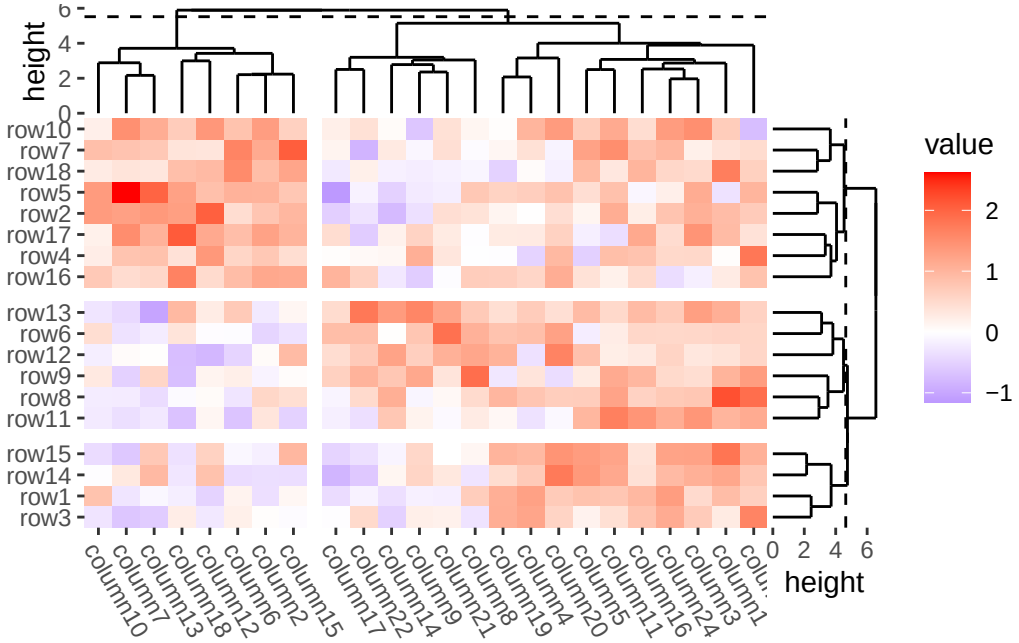
```
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_group(rep(c("A", "B"), 9)) +
    align_dendro(reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_group(rep(c("C", "D"), 12)) +
    align_dendro(reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



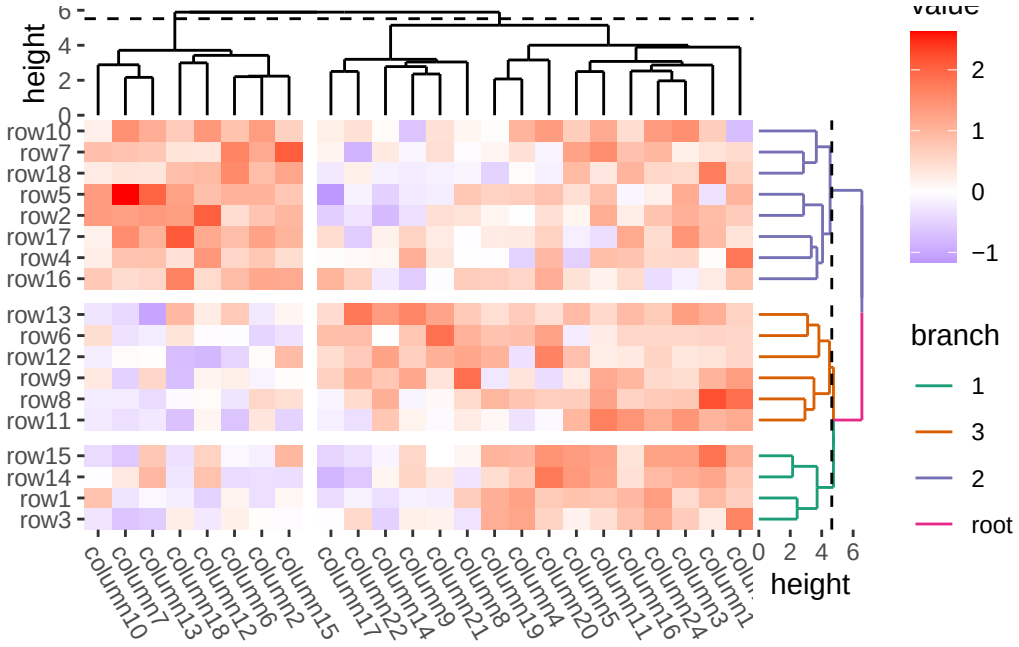
16.7.3 Split by dendrogram

When you splitted by a dendrogram, the cutted height will be indicated with a dashed line.

```
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(k = 3L, reorder_dendrogram = TRUE) +
    anno_top(size = unit(15, "mm")) +
    align_dendro(k = 2L, reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```




```
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_dendro(aes(color = branch), k = 3L, reorder_dendrogram = TRUE) +
    scale_color_brewer(palette = "Dark2") +
    anno_top(size = unit(15, "mm")) +
    align_dendro(k = 2L, reorder_dendrogram = TRUE) +
    quad_active() &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```

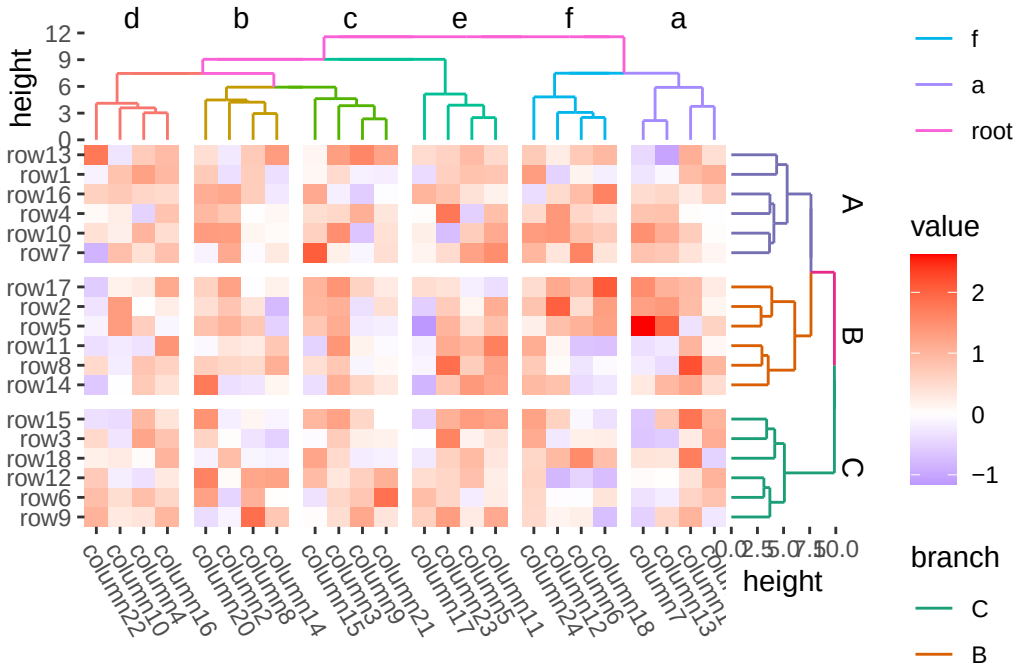


16.7.4 Order of slices (panels)

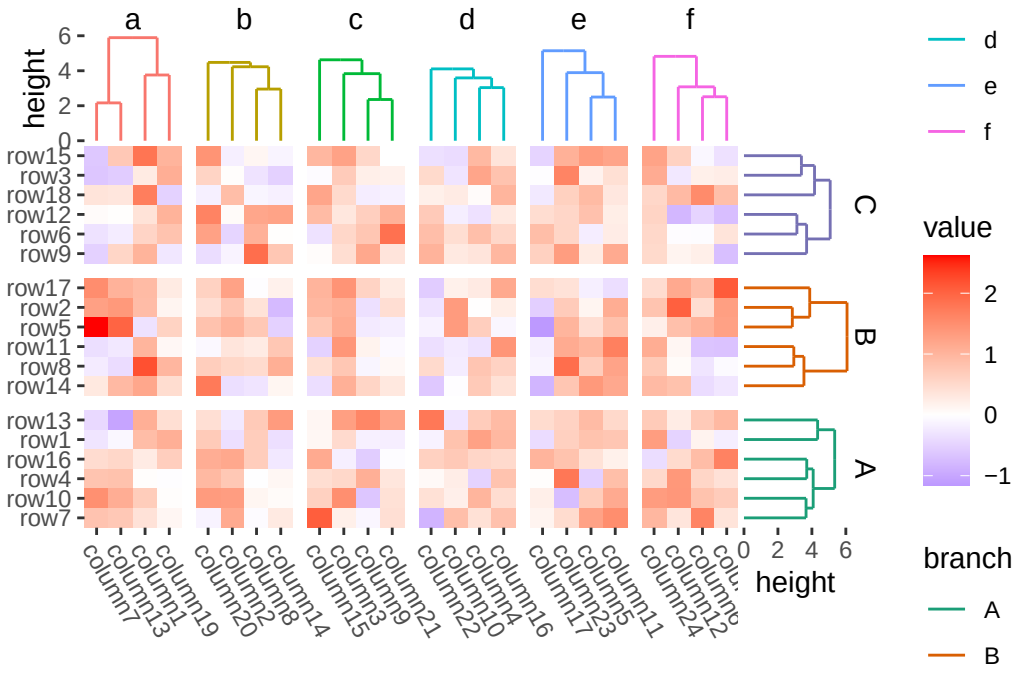
The order of the panels always follow the factor level. Note: the merging of dendrogram between `ComplexHeatmap` and `ggalign` is a little different.

```
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_group(rep(LETTERS[1:3], 6)) +
    align_dendro(aes(color = branch),
        reorder_dendrogram = TRUE,
        reorder_group = TRUE,
        merge_dendrogram = TRUE
    ) +
    scale_color_brewer(palette = "Dark2") +
    anno_top(size = unit(15, "mm")) +
    align_group(rep(letters[1:6], 4)) +
    align_dendro(aes(color = branch),
        reorder_dendrogram = TRUE,
        reorder_group = TRUE,
        merge_dendrogram = TRUE
    ) +
```

```
    quad_active() -
    with_quad(theme(strip.text = element_text()), "tr") &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```




```
ggheatmap(mat) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right(size = unit(15, "mm")) +
    align_group(rep(LETTERS[1:3], 6)) +
    align_dendro(aes(color = branch), reorder_dendrogram = TRUE) +
    scale_color_brewer(palette = "Dark2") +
    anno_top(size = unit(15, "mm")) +
    align_group(rep(letters[1:6], 4)) +
    align_dendro(aes(color = branch), reorder_dendrogram = TRUE) +
    quad_active() -
    with_quad(theme(strip.text = element_text()), "tr") &
    theme(plot.margin = margin())
#> > heatmap built with `geom_tile()`
```



16.7.5 Titles for splitting (facet strip text)

By default, the facet strip text is removed. You can override this behavior with `theme(strip.text = element_text())`. Since `align_group()` does not create a new plot, the panel title can only be added to the heatmap plot.

waiting for complete ...

16.7.6 Graphic parameters for splitting

```
ggh4x::facet_grid2(strip = ggh4x::strip_themed(
    background_x = list(
        element_rect(fill = "red"),
        element_rect(fill = "blue"),
        element_rect(fill = "green")
    )
))
#> <ggproto object: Class FacetGrid2, FacetGrid, Facet, gg>
#>     attach_axes: function
#>     compute_layout: function
#>     draw_back: function
```

```
#>     draw_front: function
#>     draw_labels: function
#>     draw_panels: function
#>     finish_data: function
#>     finish_panels: function
#>     init_scales: function
#>     map_data: function
#>     params: list
#>     setup_aspect_ratio: function
#>     setup_axes: function
#>     setup_data: function
#>     setup_panel_table: function
#>     setup_params: function
#>     shrink: TRUE
#>     strip: <ggproto object: Class StripElemental, Strip, gg>
#>         assemble_strip: function
#>         build_strip: function
#>         clip: inherit
#>         draw_labels: function
#>         elements: list
#>         finish_strip: function
#>         get_strips: function
#>         given_elements: list
#>         incorporate_grid: function
#>         incorporate_wrap: function
#>         init_strip: function
#>         params: list
#>         setup: function
#>         setup_elements: function
#>         strips: list
#>         super:  <ggproto object: Class StripElemental, Strip, gg>
#>     train_scales: function
#>     vars: function
#>     vars_combine: function
#>     super:  <ggproto object: Class FacetGrid2, FacetGrid, Facet, gg>
```

17 More examples

```
library(ggalign)
#> Loading required package: ggplot2
```

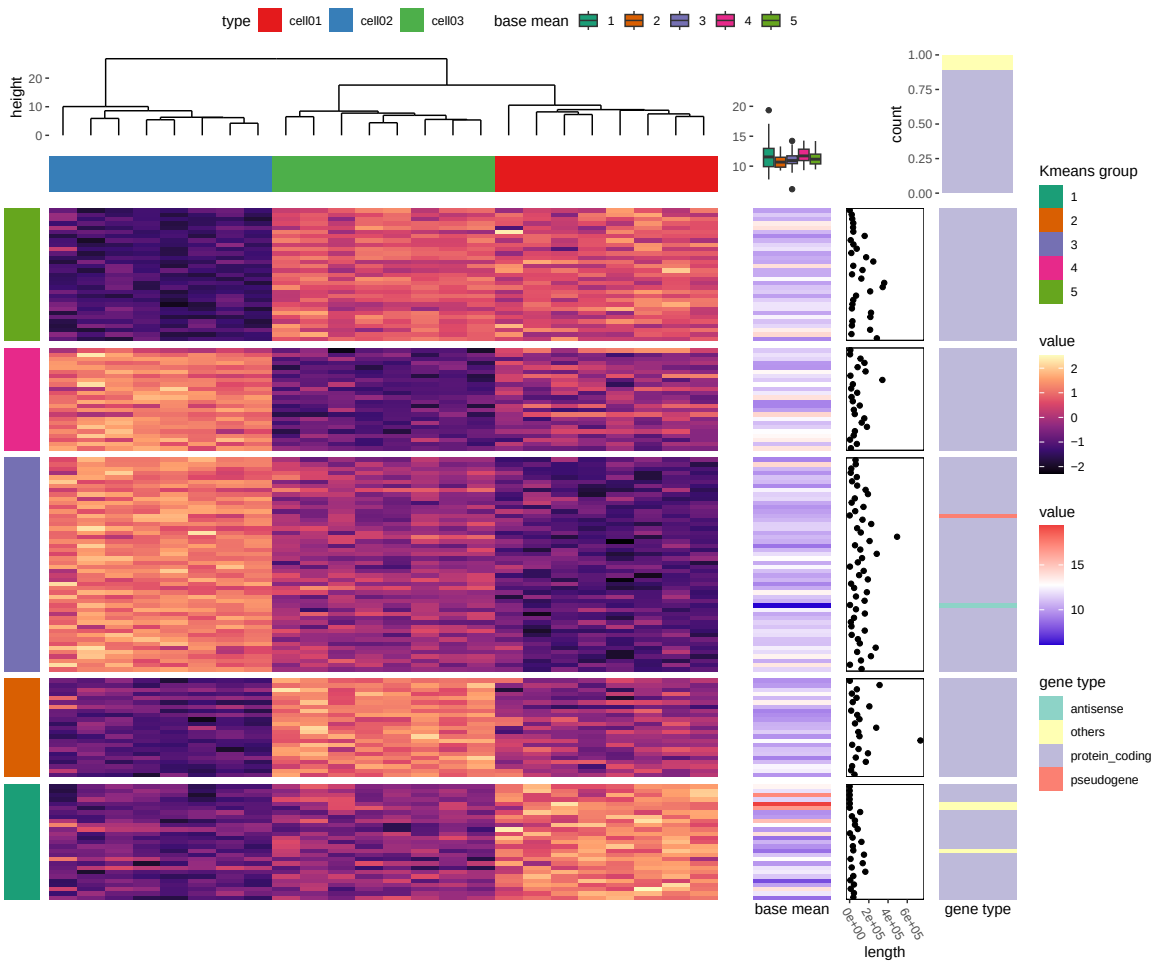
In this section, we'll use `ggalign` to draw all the heatmap in https://jokergoo.github.io/ComplexHeatmap-reference/book/more-examples.html.

17.1 Add more information for gene expression matrix

```
expr <- read_example("gene_expression.rds")
mat <- as.matrix(expr[, grep("cell", colnames(expr))])
base_mean <- rowMeans(mat)
mat_scaled <- t(apply(mat, 1, scale))
type <- gsub("s\\d+_", "", colnames(mat))

heat1 <- ggheatmap(mat_scaled) +
    scheme_align(free_spaces = "l") +
    scale_y_continuous(breaks = NULL) +
    scale_fill_viridis_c(option = "magma") +
    # add dendrogram for this heatmap
    anno_top() +
    align_dendro() +
    # add a block for the heatmap column
    ggalign(data = type, size = unit(1, "cm")) +
    geom_tile(aes(y = 1, fill = factor(value))) +
    scale_y_continuous(breaks = NULL, name = NULL) +
    scale_fill_brewer(
        palette = "Set1", name = "type",
        guide = guide_legend(position = "top")
    )

heat2 <- ggheatmap(base_mean, width = unit(2, "cm")) +
```

```
    scale_y_continuous(breaks = NULL) +
    scale_x_continuous(name = "base mean", breaks = FALSE) +
    scale_fill_gradientn(colours = c("#2600D1FF", "white", "#EE3F3FFF")) +
    # set the active context of the heatmap to the top
    # and set the size of the top stack
    anno_top(size = unit(4, "cm")) +
    # add box plot in the heatmap top
    ggalign() +
    geom_boxplot(aes(y = value, fill = factor(.extra_panel))) +
    scale_x_continuous(expand = expansion(), breaks = NULL) +
    scale_fill_brewer(
        palette = "Dark2", name = "base mean",
        guide = guide_legend(position = "top")
    ) +
    theme(axis.title.y = element_blank())

heat3 <- ggheatmap(expr$type, width = unit(2, "cm")) +
    scale_fill_brewer(palette = "Set3", name = "gene type") +
    scale_x_continuous(breaks = NULL, name = "gene type") +
    # add barplot in the top annotation, and remove the spaces in the y-axis
    anno_top() -
    scheme_align(free_spaces = "lr") +
    ggalign() +
    geom_bar(
        aes(.extra_panel, fill = factor(value)),
        position = position_fill()
    ) +
    scale_y_continuous(expand = expansion()) +
    scale_fill_brewer(palette = "Set3", name = "gene type", guide = "none") -
    scheme_theme(plot.margin = margin())

stack_alignh(mat_scaled) +
    stack_active(sizes = c(0.2, 1, 1)) +
    # group stack rows into 5 groups
    align_kmeans(centers = 5L) +
    # add a block plot for each group in the stack
    ggalign(size = unit(1, "cm"), data = NULL) +
    geom_tile(aes(x = 1, fill = factor(.panel))) +
    scale_fill_brewer(palette = "Dark2", name = "Kmeans group") +
    scale_x_continuous(breaks = NULL, name = NULL) +
    # add a heatmap plot in the stack
    heat1 +
```

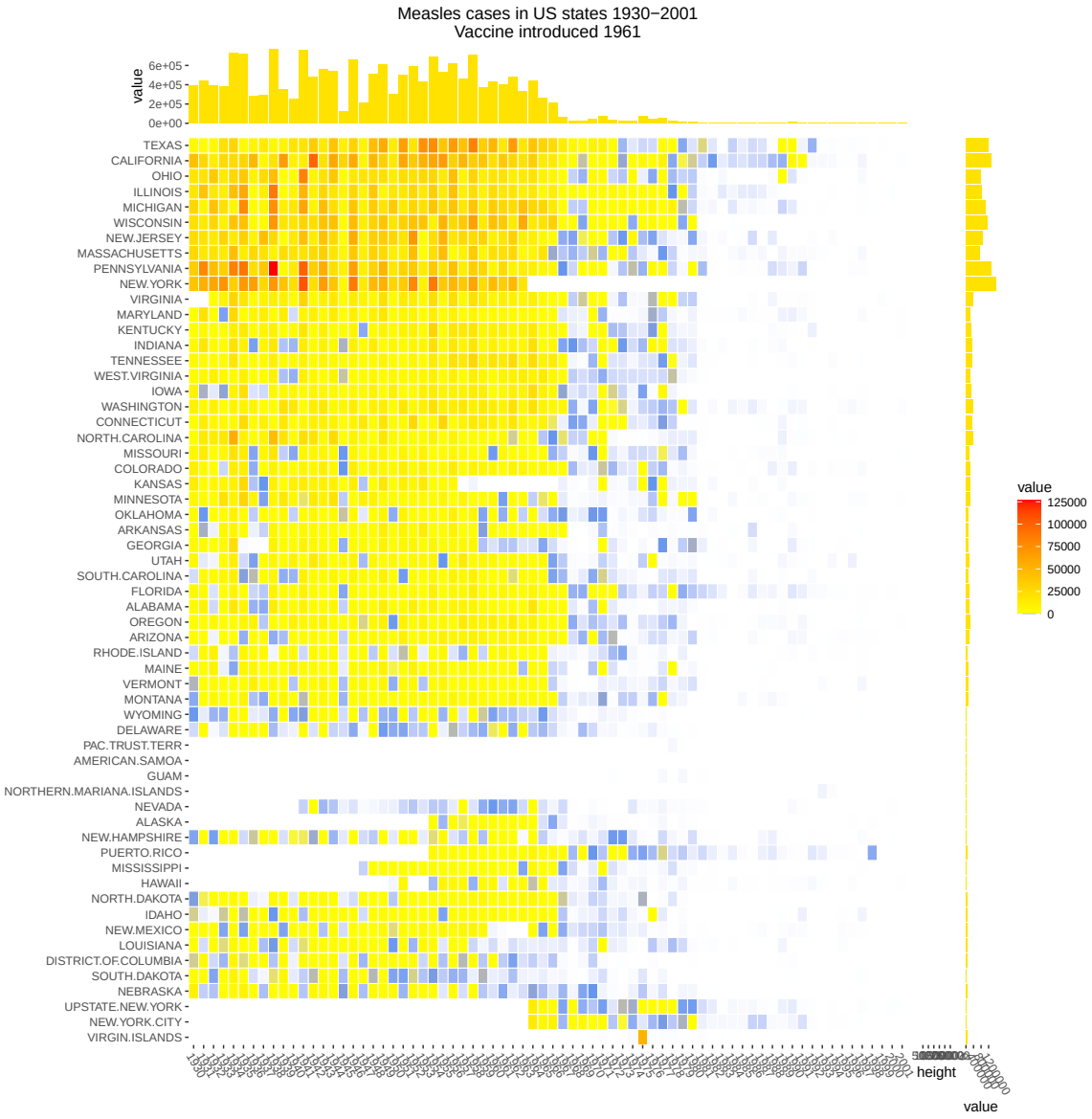
```
    # add another heatmap in the stack
    heat2 +
    # we move into the stack layout
    stack_active() +
    # add a point plot
    ggalign(data = expr$length, size = unit(2, "cm")) +
    geom_point(aes(x = value)) +
    labs(x = "length") +
    theme(
        panel.border = element_rect(fill = NA),
        axis.text.x = element_text(angle = -60, hjust = 0)
    ) +
    # add another heatmap
    heat3 &
    theme(
        plot.background = element_blank(),
        panel.background = element_blank(),
        legend.background = element_blank()
    )
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```



17.2 The measles vaccine heatmap

```
mat <- read_example("measles.rds")
ggheatmap(mat, filling = FALSE) +
    geom_tile(aes(fill = value), color = "white") +
    scale_fill_gradientn(
        colours = c("white", "cornflowerblue", "yellow", "red"),
        values = scales::rescale(c(0, 800, 1000, 127000), c(0, 1))
    ) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
    anno_right() +
    align_dendro(plot_dendrogram = FALSE) +
```

```
    anno_top(size = unit(2, "cm")) +
    ggalign(data = rowSums) +
    geom_bar(aes(y = value), fill = "#FFE200", stat = "identity") +
    scale_y_continuous(expand = expansion()) +
    ggtitle("Measles cases in US states 1930-2001\nVaccine introduced 1961") +
    theme(plot.title = element_text(hjust = 0.5)) +
    anno_right(size = unit(2, "cm")) +
    ggalign(data = rowSums) +
    geom_bar(aes(x = value),
        fill = "#FFE200", stat = "identity",
        orientation = "y"
    ) +
    scale_x_continuous(expand = expansion()) +
    theme(axis.text.x = element_text(angle = -60, hjust = 0))
```


Measles cases in US states 1930−2001
Vaccine introduced 1961
value
6e+05
4e+05
2e+05
0e+00
TEXAS
CALIFORNIA
OHIO
ILLINOIS
MICHIGAN
WISCONSIN
NEW.JERSEY
MASSACHUSETTS
PENNSYLVANIA
NEW.YORK
VIRGINIA
MARYLAND
KENTUCKY
INDIANA
TENNESSEE
WEST.VIRGINIA
IOWA
WASHINGTON
CONNECTICUT
NORTH.CAROLINA
MISSOURI
COLORADO
KANSAS
MINNESOTA
OKLAHOMA
ARKANSAS
GEORGIA
UTAH
SOUTH.CAROLINA
FLORIDA
ALABAMA
OREGON
ARIZONA
RHODE.ISLAND
MAINE
VERMONT
MONTANA
WYOMING
DELAWARE
PAC.TRUST.TERR
AMERICAN.SAMOA
GUAM
NORTHERN.MARIANA.ISLANDS
NEVADA
ALASKA
NEW.HAMPSHIRE
PUERTO.RICO
MISSISSIPPI
HAWAII
NORTH.DAKOTA
IDAHO
NEW.MEXICO
LOUISIANA
DISTRICT.OF.COLUMBIA
SOUTH.DAKOTA
NEBRASKA
UPSTATE.NEW.YORK
NEW.YORK.CITY
VIRGIN.ISLANDS
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
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1996
1997
1998
1999
2000
2001
height
value
value
125000
100000
75000
50000
25000
0