

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

`galign` 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 `galign` from CRAN using:

```
install.packages("galign")
```

Alternatively, install the development version from [r-universe](https://yuuu.r-universe.dev) with:

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

or from [GitHub](https://github.com/Yunuuu/galign) with:

```
# install.packages("remotes")  
remotes::install_github("Yunuuu/galign")
```

1.2 General design

The core feature of `galign` lies in its integration of the **grammar of graphics** into advanced visualization through its object-oriented **Layout** system. The package provides two 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.

Both `Layout` classes support the alignment of observations (ordinal variable). Observations refer to data points or samples, allowing for consistent alignment of corresponding data across multiple plots when using the same axis values. Depending on whether you want to align observations across multiple plots within the layout, the following variants are available:

For `StackLayout`:

- `stack_align()`: Align the observations along the stack.
- `stack_free()`: Does not align the observations.

For `QuadLayout`:

- `quad_free/ggside`: Never align observations.
- `quad_alignh`: Align observations in the horizontal direction.
- `quad_alignv`: Align observations in the vertical direction.
- `quad_alignb`: Align observations in both horizontal and vertical directions.



Figure 1.1: General design of ggalign

1.3 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 using:
 - `stack_layout()`: Arrange Plots Horizontally or Vertically
 - `cross_align`: Arrange Plots Crosswise Horizontally or Vertically
 - `quad_layout()`: Arrange Plots in the Quad-Side of a main plot
 - `ggheatmap()`: Create a Complex Heatmap.
 - `ggoncoplot()`: Create OncoPrint Visualizations from Genetic Alteration Data
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_hclust()`: Reorder or group observations based on hierarchical clustering.
 - `align_reorder`: Reorder observations using an arbitrary statistical function.
3. Adding plots with
 - `ggfree()`: Initialize a ggplot object without aligning the observations.
 - `ggalign()`: Initialize a ggplot object and align the observations.
 - `align_dendro()`: Add a dendrogram to the plot, and reorder or group observations based on hierarchical clustering.
 - `align_line()/align_range()`: Add a plot to annotate selected observations.
 - `ggcross()`: Initialize a ggplot object to connect two different layout crosswise.
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_alignv(small_mat) + ①  
  align_dendro() + ②  
  theme(axis.text.y = element_text()) ③
```

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



This produces a simple dendrogram. By default, `stack_alignv()` removes the axis text on the axis used for aligning observations. 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_alignv(small_mat) + ①  
  align_dendro() + ②  
  ggalign(data = rowSums) + ③
```

```
geom_bar(aes(.discrete_x, value), stat = "identity") +  
theme(axis.text.y = element_text())
```

④

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 y-axis text.



The data in the underlying `ggplot` object of `ggalign()` function contains at least 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.

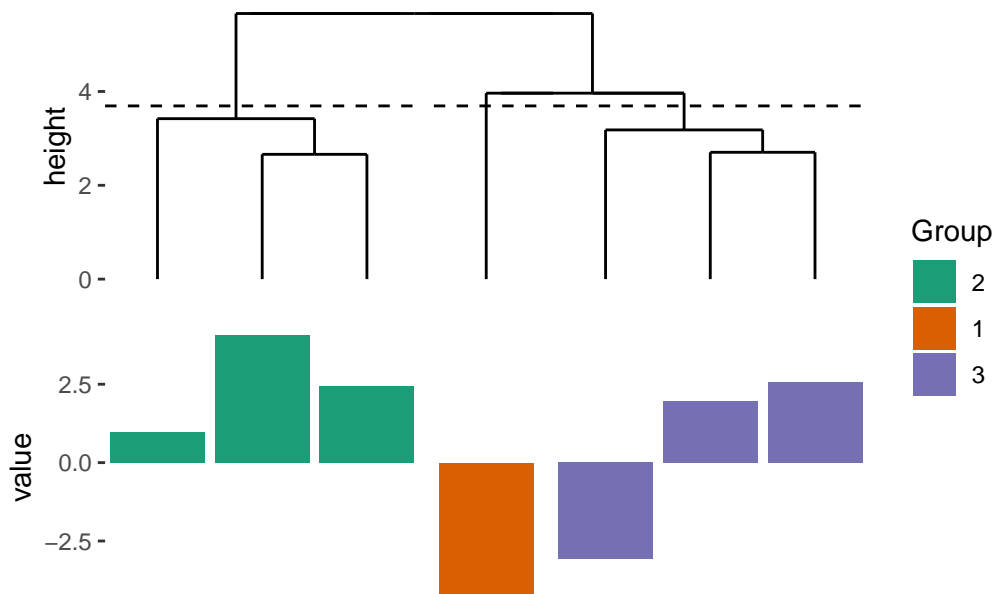
`align_dendro()` can also split the observations into groups.

```

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.y = 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 Add fill mapping scale.
- ⑥ Add y-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.

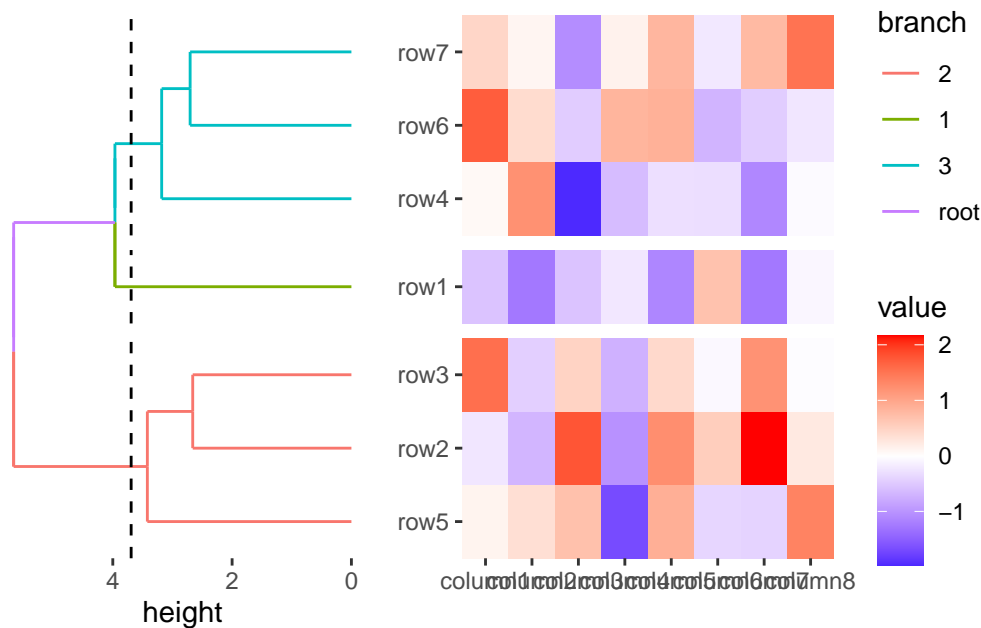
```

ggheatmap(small_mat) + ①
  anno_left() + ②
  align_dendro(aes(color = branch), k = 3) + ③

```

```
scale_fill_brewer(palette = "Dark2")
#> > heatmap built with `geom_tile()`
```

- ① We initialize a heatmap layout.
- ② 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.
- ③ Reorder and group the observations based on hierarchical clustering, and add a dendrogram tree, coloring the tree by **branch**.
- ④ Add fill mapping scale.



`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())`.

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` functionality, 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 `stack_layout()` 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 observations, there are two types of stack layouts:

- `stack_align()`: align the observations along the stack.
- `stack_free()`: don't align the observations.

Several aliases are available for convenience:

- `stack_alignv`: Aligns the stack vertically (special case of `stack_align()`).
- `stack_alignh`: Aligns the stack horizontally (special case of `stack_align()`).
- `stack_freev`: A vertical version of `stack_free()`.
- `stack_freeh`: A horizontal version of `stack_free()`.

`stack_layout(direction = 'horizontal')`



`stack_layout(direction = 'vertical')`



```
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

When aligning observations, we typically use a matrix, as it is easy to melt the matrix into a long-formatted data frame. Additionally, matrices are used to fit the observation concept,

as they can be transposed (rows to columns, columns to rows), which is necessary for use in functions like `quad_layout()` and `ggheatmap()`, where observations may be aligned in both directions simultaneously.

- For `stack_free()`, a data frame is required, and the input will be automatically converted using `fortify_data_frame()` if needed.
- For `stack_align()`, 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_align()/stack_free()` will set up the layout, but no plot will be drawn until you add a plot element:

```
stack_alignh(small_mat) +  
  layout_annotation(  
    theme = theme(plot.background = element_rect(color = "red"))  
  )  
# the same for `stack_free()`
```

- 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 be also used to control the theme of title, subtitle, caption (`layout_title()`), guides, margins, `panel.border`, `panel.spacing`.

2.2 Layout Customize

When we use `stack_align()`, it aligns the observations across multiple plots along the specified direction:

- For `stack_alignh()`: Alignment occurs along the horizontal direction (y-axis).
- For `stack_alignv()`: Alignment occurs along the vertical direction (x-axis).

The package offers a suite of `align_*` functions designed to give you precise control over the observations. These functions enable you to reorder the observations or partition the observations into multiple groups. Instead of detailing each `align_*` function individually, we will focus on the general usage and how to combine them with `stack_align()`.

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_alignh()`, the observations are aligned along the y-axis:

```
stack_alignh(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_alignv()`, the observations are aligned along the **x-axis**:

```
stack_alignv(small_mat) +  
  align_dendro()
```

①

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_alignh(small_mat) +  
  align_dendro() +  
  geom_point()
```

①

②

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_alignh(small_mat) + ①
  align_dendro(active = active(use = FALSE)) + ②
  geom_point() ③
#> Error in `stack_layout_add()` :
#> ! Cannot add `geom_point()` to `stack_align()`
#> 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()
#> `align_dendro()` object:
```

```
#> 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)
#> `align_dendro()` object:
#> 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_alignh(small_mat) +                                ①
  align_dendro(data = matrix(rnorm(56), nrow = 8)) +      ②
  theme(axis.text.y = element_text())                    ③
#> Error in `layout()`:
#> ! `align_dendro(data = matrix(rnorm(56), nrow = 8))` (nobs: 8) is not
#> compatible with the `stack_alignh()` (nobs: 7)
```

- 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_alignh(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_alignh(small_mat) +
  align_dendro(data = ~ .x[sample(nrow(.x)), ]) +
  theme(axis.text.y = element_text())
```

①
②
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:

- `align_gg()/ggalign()`: Create a ggplot object and align with the layout.
- `free_gg()/ggfree()`: Create a ggplot object without aligning.

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

For `stack_align()`, plots can be added regardless of whether they need to align observations.

```
stack_alignh(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) +
  geom_bar(aes(value, .discrete_y), stat = "identity") +
  theme(axis.text.y = element_text())
stack_alignh(small_mat) +
  align_dendro() +
  my_bar
```



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_alignh(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_alignv()`:

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



`stack_align()` can also add plot without aligning observations. `free_gg()` focuses on layout integration without enforcing strict axis alignment. `ggfree()` is an alias for `free_gg`.

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

```
stack_freev(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 `ggalen()` 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_freev(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_freev(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`

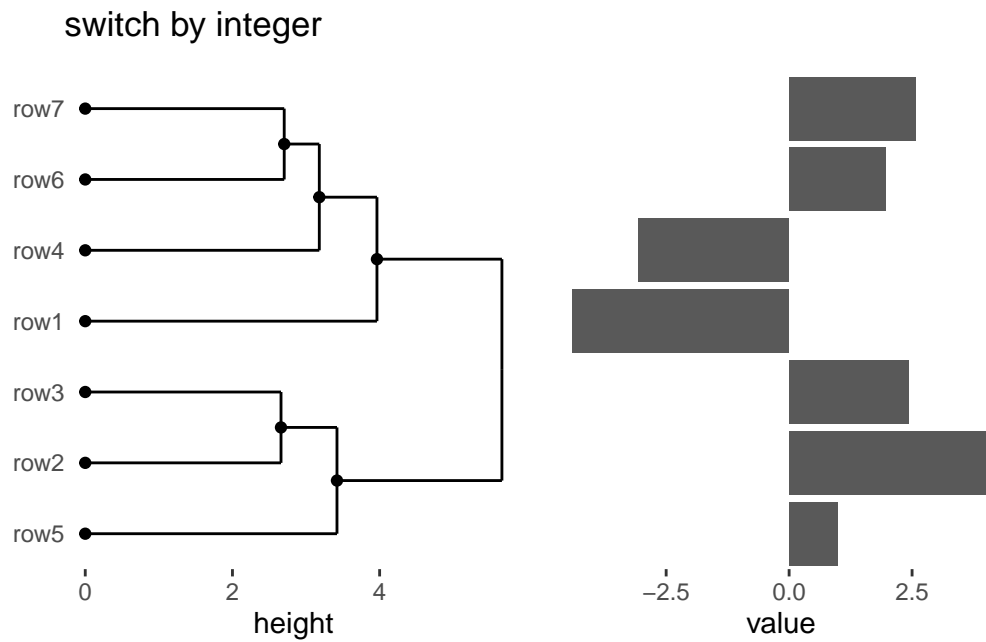
The `stack_switch()` function accepts the `what` argument, which can either be the index of the plot added (based on its adding order) or the plot name specified via the `active()` object using the `name` argument.

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() +
  ggaligned(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")) +
  ggaligned(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 directly to the `StackLayout`. We'll introduce the nested layout of `StackLayout` in Chapter 7.

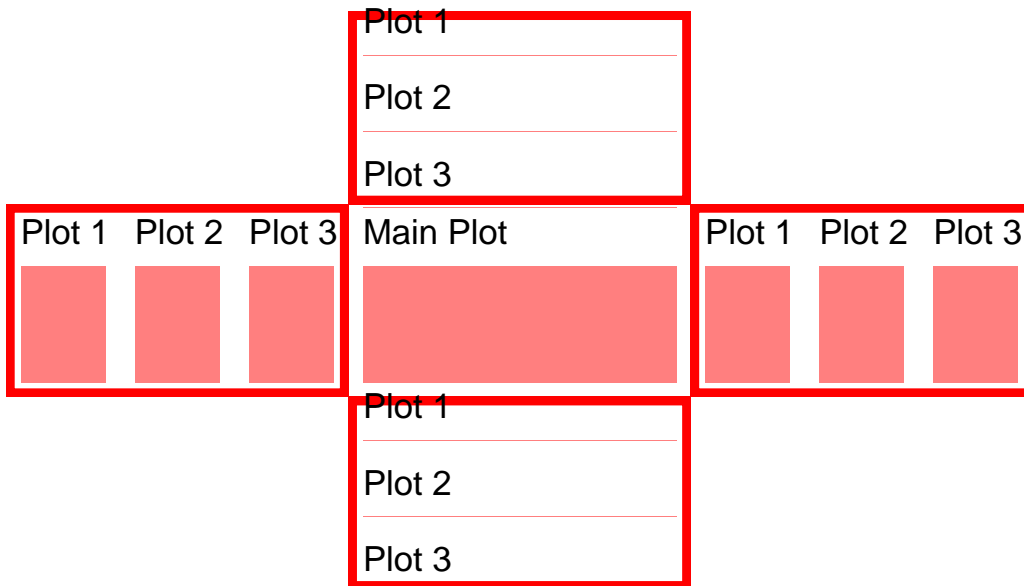
In the next chapter, we will dive into the `HeatmapLayout`, which can take the `StackLayout` as input. Heatmap layouts offer additional features for aligning observations in both directions. Let's move ahead and explore how heatmaps can be seamlessly integrated into your layout workflows.

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_alignb()`, which itself is a specific variant of `QuadLayout` (`quad_layout()`) designed to align observations 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`.

QuadLayout



`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()`.

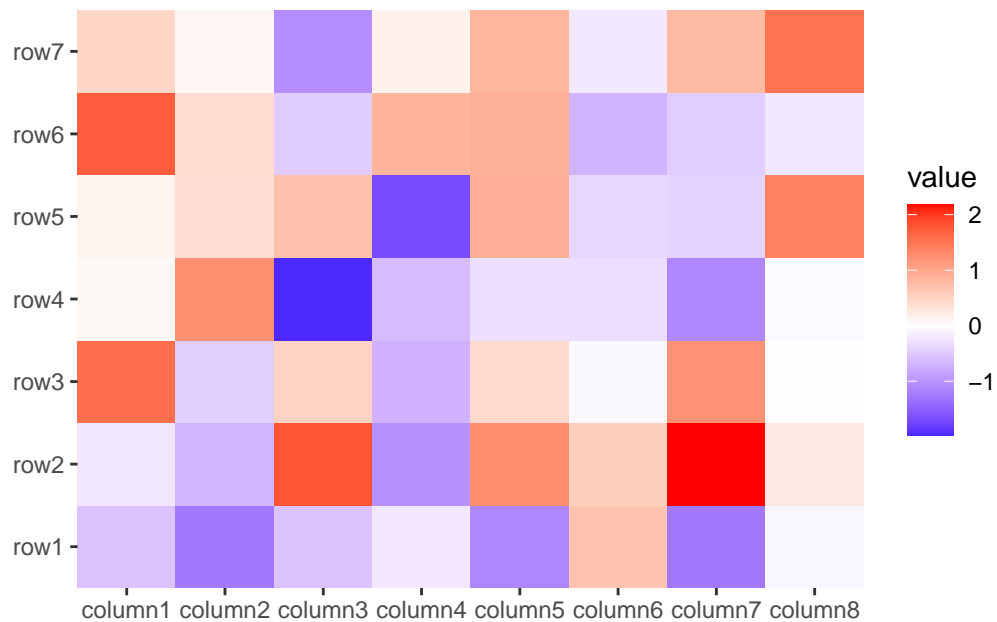
```
library(ggalign)
set.seed(123)
small_mat <- matrix(rnorm(56), nrow = 7)
```

```
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 2.1, we typically require a matrix for the **Layout** which need align observations. 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, 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).

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 automatically create a new `stack_layout()`. For top and bottom annotations, `stack_alignv()` or `stack_freev()` will be used; for left and right annotations, `stack_alignh()` or `stack_freeh()` will be applied.

`quad_anno()` will always attempt to initialize a `stack_layout()` with the same alignment as the current direction. This means that if observations need to be aligned horizontally,

`stack_alignh()` will be used for left and right annotations, otherwise, `stack_freeh()` will be initialized instead. The same logic applies for vertical alignment—`stack_alignv()` or `stack_freev()` will be applied for top and bottom annotations, depending on whether alignment is required. However, you can also manually add a `stack_free()` for directions that require alignment, which I'll cover in the following section.

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 described in Section 2.2), since the annotation is a `Layout` object.

```
ggheatmap(small_mat) +
  theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
  # we set the active context to the left annotation
  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 the observations require alignment 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 = factor(branch)))
#> > heatmap built with `geom_tile()`
```



In this example:

- `anno_right()` initialize the right annotation stack, and change the active context to the right 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 = factor(branch)))` is then added to this active plot within the annotation stack, here, it means the `align_dendro()` plot.

`ggheatmap()` aligns observations 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_alignh()` and `quad_alignv()` (which I'll discuss in more detail in a Chapter 6), which only align observations in one direction, the data in the layout may not fit the data for the annotation (when the layout requires alignment of observations, we typically use a matrix, regardless of whether alignment is needed in one or two directions)

- ``quad_alignh()``: aligning observations in horizontal direction, for column annotations, we ll need a data frame for ``stack_free()``.
- ``quad_alignv()``: aligning observations in vertical direction, for row annotations, we ll need a data frame for ``stack_free()``.

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

3.5 Adding stack layout

Similar to adding a plot in `stack_layout()` (Chapter 2), when the direction requires alignment, you can add both `stack_align()` and `stack_free()`. However, if the direction does not require alignment, you can add only `stack_free()`.

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

```
my_stack_align <- stack_alignh(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_align +
  layout_title("stack_align()")
#> > heatmap built with `geom_tile()`
```



```
my_stack_free <- stack_freeh(mpg) +
  ggfree(mapping = aes(displ, hwy, colour = class)) +
  geom_point(size = 2)
ggheatmap(small_mat) +
  theme(axis.text.x = element_text(angle = -60, hjust = 0)) +
```

```

anno_right(initialize = FALSE) +
my_stack_free +
layout_title("stack_free()")
#> > heatmap built with `geom_tile()`

```



Note when aligning the observations, 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_alignv(t(small_mat)) +
  align_dendro(aes(color = branch), k = 3L)
ggheatmap(small_mat) +
  anno_top(initialize = FALSE) +
  my_stack
#> > heatmap built with `geom_tile()`

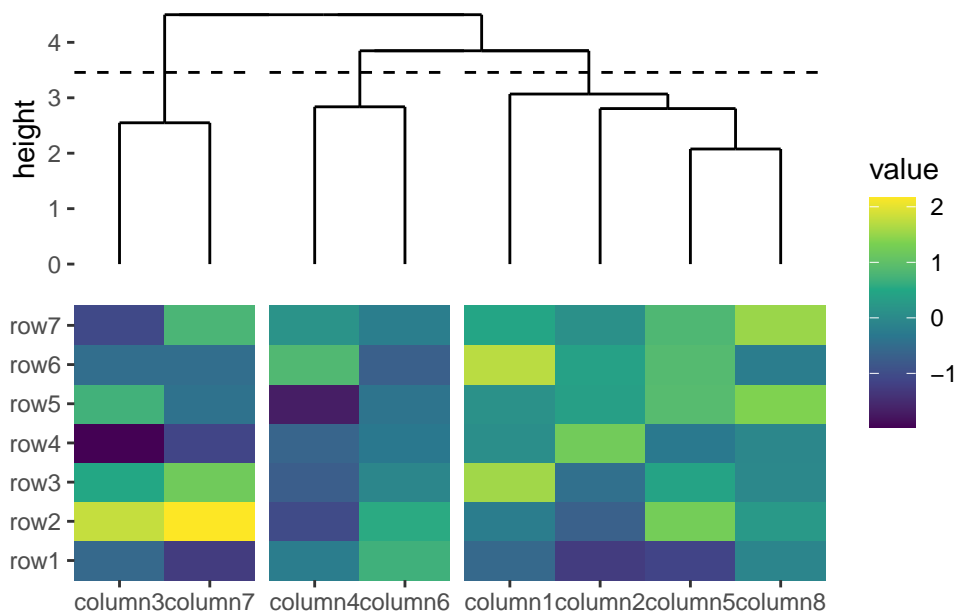
```



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()`
```



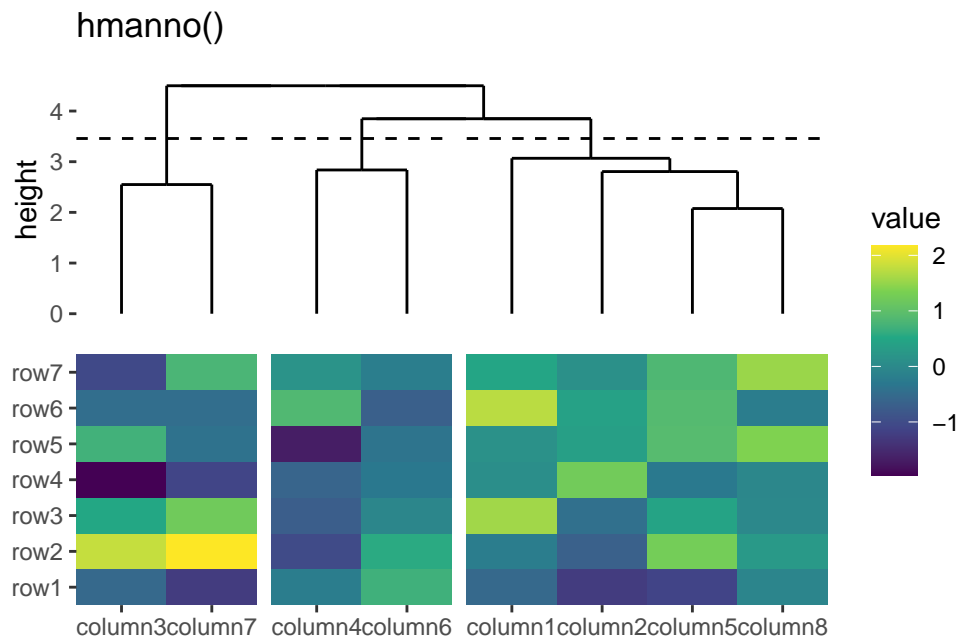
3.7 quad_switch()/hmanno()

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_order`: Reorder layout observations based on statistical weights or allows for manual reordering based on user-defined ordering index.
- `align_kmeans`: Group observations by k-means clustering results.
- `align_hclust`: Reorder or group observations based on hierarchical clustering.
- `align_reorder`: Reorder observations using an arbitrary statistical function.

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 `layout()`:
#> ! align_group(sample(letters[1:5], ncol(small_mat), replace = TRUE))
#>   disrupt the previously established panel groups of the top annotation
#>   `stack_align()`
```

4.2 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 `layout()`:
#> ! align_order(another_order) disrupt the previously established ordering
#> index of the top annotation `stack_align()`
```

4.3 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()`
```



4.4 align_hclust()

The `align_hclust()` function is designed to reorder observations and group them based on hierarchical clustering. Unlike `align_dendro()`, however, `align_hclust()` does not add a dendrogram tree to the plot. All the arguments introduced 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 building 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 correlation coefficient "pearson", "spearman" and "kendall". The correlation distance is defined as $1 - \text{cor}(x, y, \text{method} = \text{distance})$.
- a self-defined function which calculates distance from a matrix. The function should only contain one argument.

```
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()`
```

a function that calculates distance matrix



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()`
```



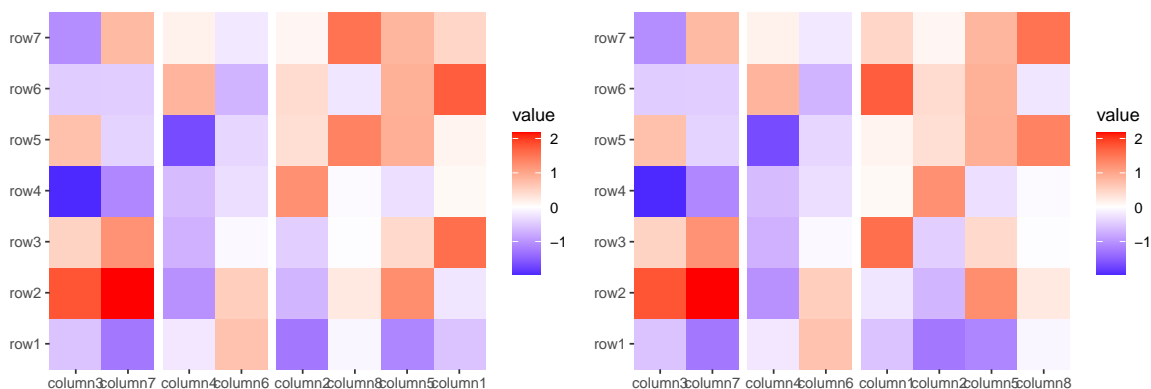

You can specify `k` or `h` to split observations into groups, which work similarly to `cutree()`:

```
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) +
  anno_top() +
  align_hclust(k = 3, reorder_dendrogram = TRUE) +
  layout_title("reorder_dendrogram = TRUE")
h2 <- ggheatmap(small_mat) +
  anno_top() +
  align_hclust(k = 3) +
  layout_title("reorder_dendrogram = FALSE")
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 `heatmap` 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 `layout()`:
#> ! align_hclust(k = 2L) disrupt the previously established panel groups
#> of the top annotation `stack_align()`
```

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.

For 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 heatmap 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 three primary functions for adding plots:

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

`ggalign()` and `ggfree()` are aliases for `align_gg()` and `free_gg()`, respectively. All three functions will set the active plot when added to the layout.

Both `ggalign()` and `align_dendro()` can only be used with a `stack_layout()` that aligns observations (`stack_align()`), whereas `ggfree()` can be added to a `stack_layout()` that does not align the observations (`stack_free()`).

```
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 align_gg()/ggalign()

`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 matrix.

`ggalign()` always applies a default mapping for the axis of the data index in the layout. This mapping is `aes(y = .data$.y)` for horizontal stacking (including left and right quad layout annotation) and `aes(x = .data$.x)` for vertical stacking (including top and bottom quad layout annotation).

The data in the underlying `ggplot` object will contain following columns:

- `.panel`: the panel for the aligned axis. It means `x-axis` for vertical stack layout (including top and bottom annotation), `y-axis` for horizontal stack layout (including left and right annotation).
- `.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 ([vec_names()][vctrs::vec_names])` and `.index ([vec_size()][vctrs::vec_size()]/[NROW()])`: a character names (only applicable when `names` exists) and an integer of index of the original data.
- `.row_names` and `.row_index`: the row names and an integer of row index of the original matrix (only applicable if `data` is a `matrix`).
- `.column_names` and `.column_index`: the column names and column index of the original matrix (only applicable if `data` is a `matrix`).
- `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.

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



In the case where the input data is already a data frame, following columns (`.panel`, `.index`, `.names`, `.x/.y`, `.discrete_x/.discrete_y`) are added to the data frame. Note, `NROW(data)` must match 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()`
```



You may wonder if the strict data requirements will prevent us from preparing the data for plotting. Don't worry! In the later chapters, I'll introduce powerful way to prepare data for your plots.

If `data = NULL`, the data in the underlying `ggplot` object contains following columns:

- `.panel`: the panel for the axis used for alignment.
- `.index`: the index of the original layout data.
- `.x` or `.y`: the x or y coordinates

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



5.1.1 Cross panel summary

When used in a `quad_layout()`, and the data is inherited from the `quad_layout()`, a special column `.extra_panel` will be added if applicable, which is the panel information for column (for left or right annotation) or row (for top or bottom annotation). This is useful if you want to create summary plot using another axis panel groups. In such cases, it's often necessary to disable the automatic setting of limits (`limits = FALSE` in `ggalign()`).

```
set.seed(1234)
ggheatmap(small_mat) +
  anno_right() +
  align_kmeans(2) +
  anno_top(size = 0.5) +
  ggalign(limits = FALSE) +
  geom_boxplot(aes(.extra_panel, value, fill = .extra_panel)) +
  scale_fill_brewer(palette = "Dark2", name = "row groups")
#> > heatmap built with `geom_tile()`
```



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.

5.2 `free_gg()/ggfree()`

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

Internally, the function uses `fortify_data_frame()` to transform the input into a data frame. For matrices, it converts them into a long-formatted data frame. Note that `ggfree()` does not provide a default aesthetic mapping, which contrasts with `ggalign()`. You will need to manually provide the default mappings.

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



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()`
```



5.3 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.

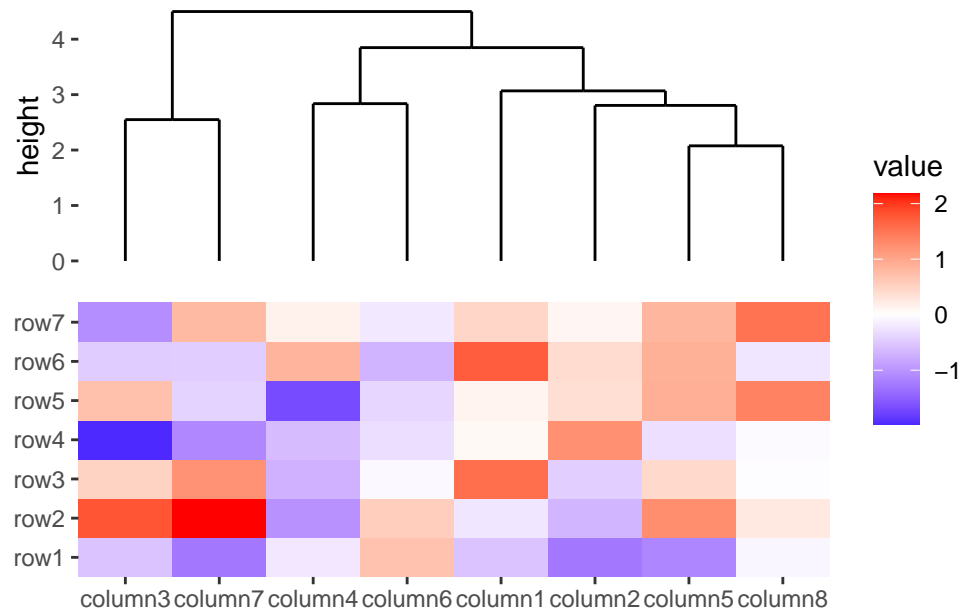
`align_dendro()` will initialize a ggplot object, the data underlying the ggplot object contains the dendrogram `node` data with dendrogram `edge` data attached in a special attribute.

dendrogram `node` and `edge` contains following columns: - `index`: the original index in the tree for the current node - `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 `galign_attr()`. The `edge` data is stored in the `edge` field of `galign_attr()`:

```
ggheatmap(small_mat) +
  anno_top() +
  align_dendro() +
  geom_segment(
    aes(x = .data$x, y = .data$y, xend = .data$xend, yend = .data$yend),
    data = function(x) galign_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 setting `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()`
```

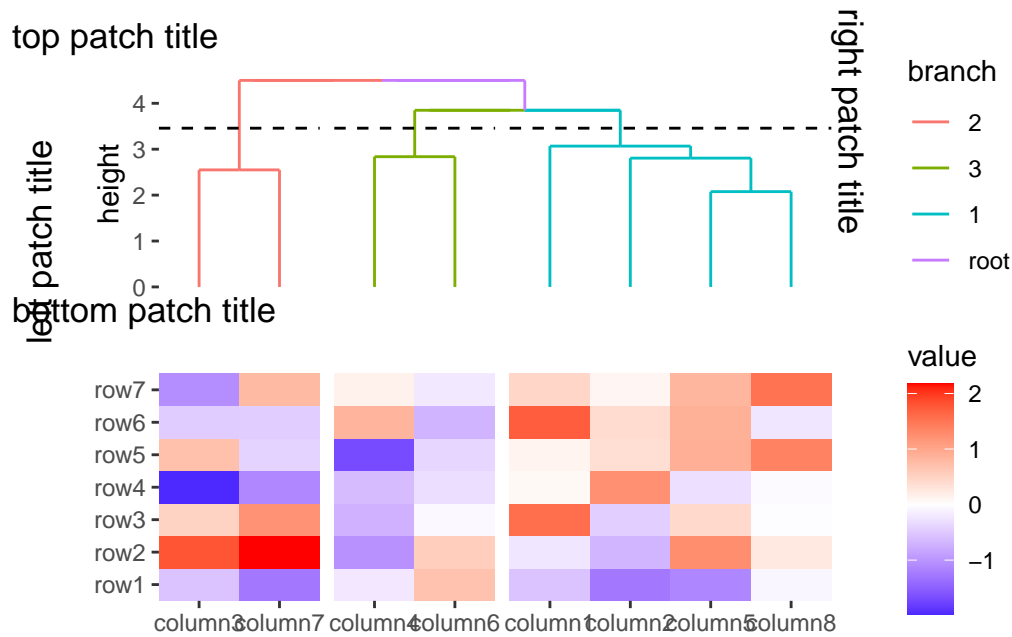



The appearance and alignment of these patch titles can be customized using `ggplot2::theme()`:

- `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, 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.

6 quad-layout

`quad_layout()` arranges plots in the Quad-Side of a main plot.

QuadLayout



```
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)))
```

6.1 introduction

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

Alignment of Observations	horizontal	vertical	Data Format
<code>quad_free()/ggside()</code>			data frame
<code>quad_alignh()</code>			matrix
<code>quad_alignv()</code>			matrix
<code>quad_alignb()/ggheatmap()</code>			matrix

When the layout requires alignment of observations, we typically use a matrix, regardless of whether alignment is needed in one or two directions.

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

6.2 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
<code>quad_free()/ggside()</code>	<code>stack_freeh()</code>	<code>stack_freev()</code>
<code>quad_alignh()</code>	<code>stack_freeh()/stack_alignh()</code>	<code>stack_freev()</code>
<code>quad_alignv()</code>	<code>stack_freeh()</code>	<code>stack_freev()/stack_alignv()</code>
<code>quad_alignb()/ggheatmap()</code>	<code>stack_freeh()/stack_alignh()</code>	<code>stack_freev()/stack_alignv()</code>

6.3 quad_alignb()

`quad_alignb()` aligns observations 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()`, 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_alignb(small_mat, aes(.x, .y)) +
  geom_tile(aes(fill = value)) +
  scale_fill_viridis_c()
```



6.4 quad_alignh()/quad_alignv()

`quad_alignh()` aligns observations horizontally, while `quad_alignv()` aligns observations vertically.

The underlying `ggplot` data is the same with `ggheatmap()/heatmap_layout()`, it is recommended to use `.y`, or `.discrete_y` as the `y` mapping in the main plot for `quad_alignh()` but use `.x` or `.discrete_x` as the `x` mapping in the main plot for `quad_alignv()`.

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



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



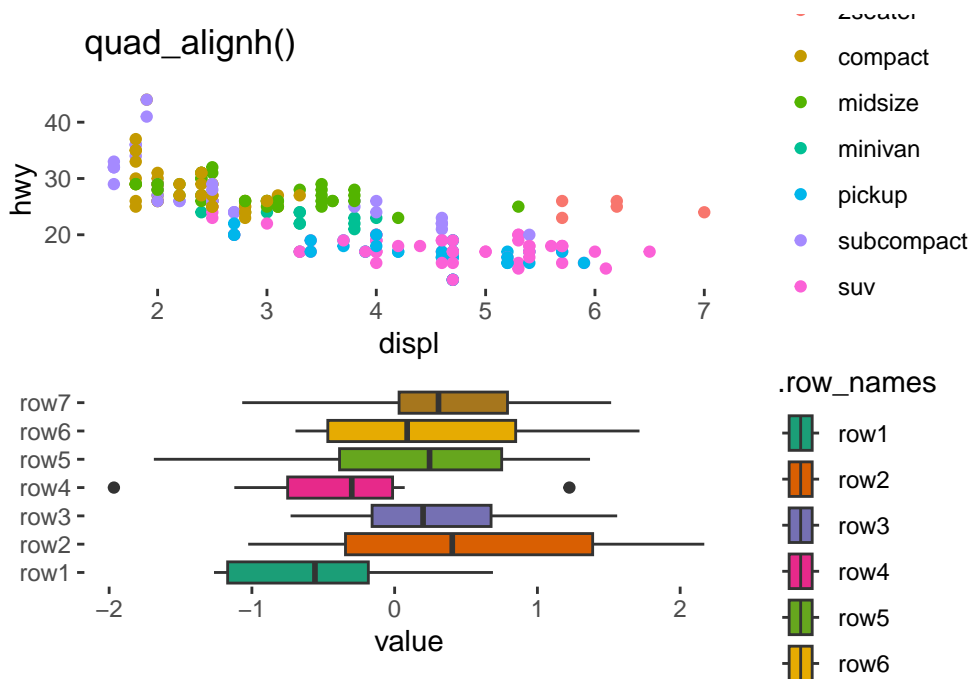
As discussed in Section 3.4, `quad_anno()` will always attempt to initialize a `stack_layout()` with the same alignment as the current direction. For top and bottom annotations in `quad_alignh()`, and left and right annotations in `quad_alignv()`, `quad_anno()` will not initialize the annotation due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

```
quadh <- quad_alignh(small_mat) +
  anno_top()
#> Warning: `data` in `quad_alignh()` is a double matrix, but the top annotation stack need
#> a <data.frame>, won't initialize the top annotation stack
quadv <- quad_alignv(small_mat) +
  anno_left()
#> Warning: `data` in `quad_alignv()` 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_alignh(small_mat) +
  anno_top(initialize = FALSE)
quadv <- quad_alignv(small_mat) +
  anno_left(initialize = FALSE)
```

```
quadh +
  stack_freev(mpg) +
  # add a plot in the top annotation
  ggfree(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()")
```

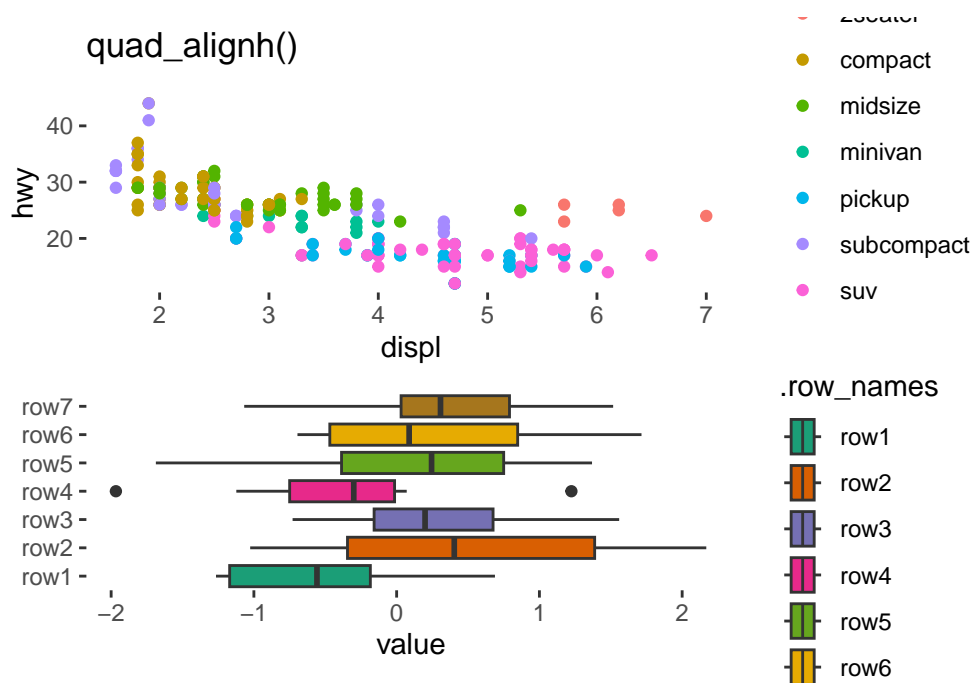


```
quadv +
  stack_freeh(data = mpg) +
  # add a plot in the top annotation
  ggfree(mapping = aes(displ, hwy, colour = class)) +
  geom_point(aes(displ, hwy, colour = class)) +
  quad_active() +
  geom_boxplot(aes(.discrete_x, value, fill = .column_names)) +
  scale_fill_brewer(palette = "Dark2") +
  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_alignh(small_mat) +
  geom_boxplot(aes(value, .discrete_y, fill = .row_names)) +
  scale_fill_brewer(palette = "Dark2") +
  anno_top(initialize = TRUE) +
  ggfree(data = mpg, aes(displ, hwy, colour = class)) +
  geom_point(aes(displ, hwy, colour = class)) +
  layout_title("quad_alignh()")
```



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



6.5 quad_free()

`quad_free()` does not align observations and is functionally equivalent to the [ggside](#) package. For convenience, `ggside()` is provided as an alias for `quad_free()`. 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
  ggfree() +
  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
  ggfree() +
  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) +
  ggfree() +
  geom_density(aes(Sepal.Width, y = after_stat(density), colour = Species),
    position = "stack"
  ) +
  facet_grid(cols = vars(Species2)) +
  anno_right(size = 0.3) +
  ggfree() +
  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 a later chapter, I will introduce another operator that seamlessly combines with the `+` operator, allowing you to add elements to multiple plots at once.

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.

7 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()`.

7.1 `stack_align()`

As discussed in Section 2.3, `stack_align()` can accept plots regardless of whether alignment of observations is required.

```
stack_alignh(small_mat) +
  ggheatmap() +
  theme(axis.text.x = element_text(hjust = -60, angle = -90)) +
  ggheatmap() +
  theme(axis.text.x = element_text(hjust = -60, angle = -90))
#> > heatmap built with `geom_tile()`
#> > 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_alignv(small_mat) +
  ggheatmap() +
  ggheatmap() +
  scale_fill_viridis_c()
#> > heatmap built with `geom_tile()`
#> > heatmap built with `geom_tile()`
```

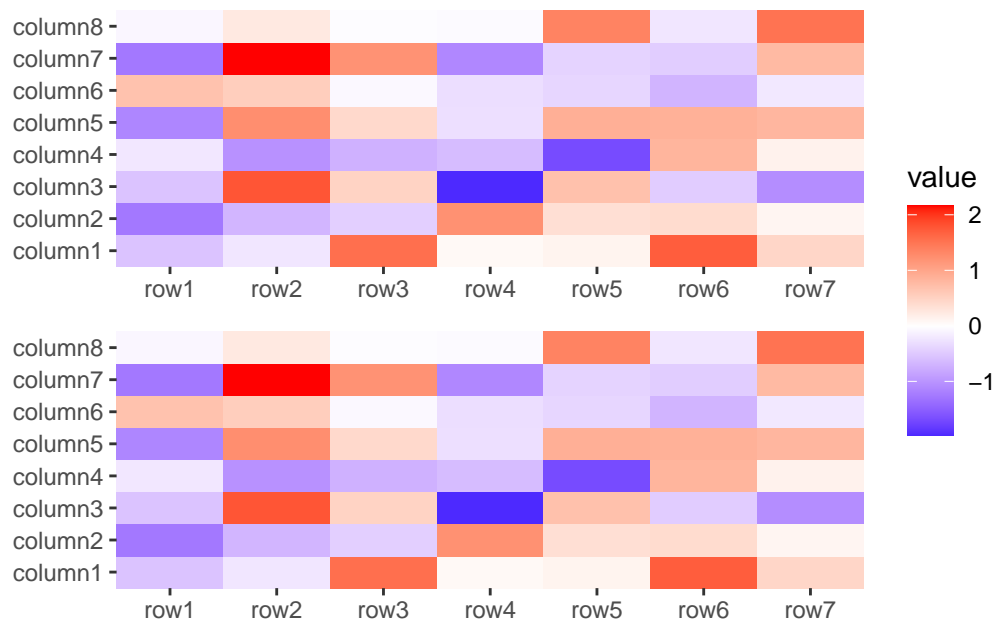


The data of `ggheatmap()/quad_layout()` can inherit from the `stack_layout()`, but the data format must match. Otherwise, you will need to manually provide the data. For `stack_align()`, the data is always expected to be a matrix, if you try to add a `ggside()` (which uses a data frame), it will result in an error.

```
stack_alignh(small_mat) +
  ggside()
#> Error in `stack_layout_add()`:
#> ! Cannot add `quad_free()` to `stack_align()`
#> i `data` in `stack_align()` is a double matrix, but `quad_free()` need a
#>   <data.frame>.
#> i Try provide `data` in `quad_free()`
```

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

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

`stack_align()` ensures that all plots aligned along the stack have the same ordering index or groups for the observations. Here's a table summarizing which `quad_layout()` will be aligned in `stack_align()`.

	<code>stack_alignh()</code>	<code>stack_alignv()</code>
<code>quad_free()/ggside()</code>		
<code>quad_alignh()</code>		
<code>quad_alignv()</code>		
<code>quad_alignb()/ggheatmap()</code>		

We can customize the layout in the `stack_align()` 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_alignv(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()`
```

dendrogram in ggheatmap()



```
stack_alignv(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.

7.2 stack_free()

However, `stack_free()` is designed to only accept plots that are not aligned along the axis (Section 2.3). Below is a table summarizing which `quad_layout()` are compatible with `stack_free()`:

	<code>stack_freeh()</code>	<code>stack_freev()</code>
<code>quad_free()/ggside()</code>		
<code>quad_alignh()</code>		
<code>quad_alignv()</code>		
<code>quad_alignb()/ggheatmap()</code>		

```
alignh_quad_plot <- quad_alignh(small_mat) +
  geom_boxplot(aes(value, .discrete_y, fill = .row_names)) +
  scale_fill_brewer(palette = "Dark2")
stack_freev() +
  alignh_quad_plot +
  alignh_quad_plot
```



7.3 Control sizes

A numeric or a unit object of length 3 should be provided in `stack_align()/stack_free()` 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_alignv(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_alignv(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_alignv(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()`
```



Next, we will build on these concepts and explore even more advanced strategies for integrating elements across multiple plots or annotations in a layout.

8 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, modifying, or removing elements across multiple plots or annotations 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)))
```

8.1 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 7). 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.

```
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()`

```

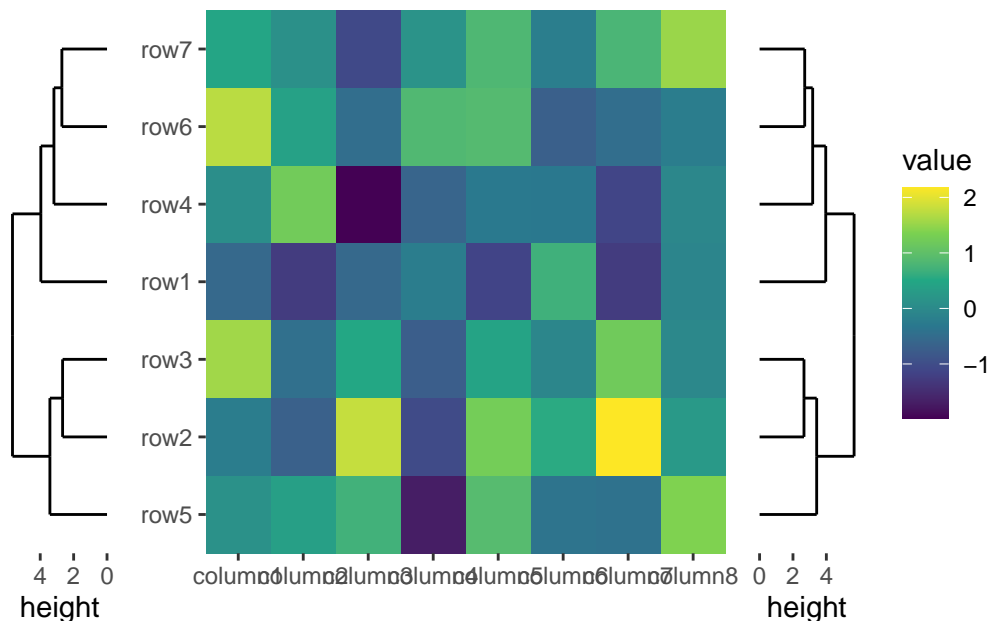


In `quad_layout()`, four nested layouts are available for annotations: `top`, `left`, `bottom`, and `right`. If no active annotation is set, `quad_layout()` treat itself as the active layout. Since there is only one main plot in the `quad_layout()`, the main plot is always treated as the active plot 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()`

```



8.2 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()`
```



8.3 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 `+`.

8.3.1 `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_layout`
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()`
```



8.3.2 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 8.3.1.

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

8.4 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 modifications are applied to specific annotation stacks or the main plot, without changing the currently active layout or plot.

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.

8.4.1 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`
```



8.4.2 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 layout)
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()`.

9 schemes

Schemes control the actions of plots within the layout. These schemes 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)))
```

9.1 `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"))
```



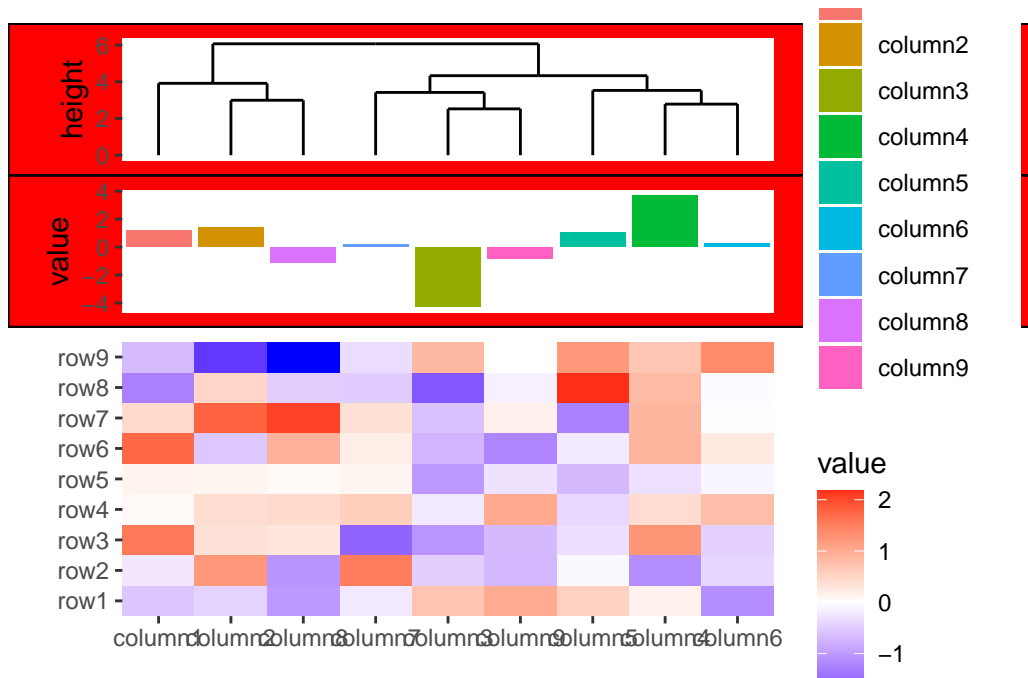
Note that `scheme_theme()` serves as the default theme and will always be overridden by any `theme()` settings applied directly to the plot. The default theme (`scheme_theme()`) is applied first, followed by any specific `theme()` settings, even if `theme()` is added before `scheme_theme()`.

```
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()`
```



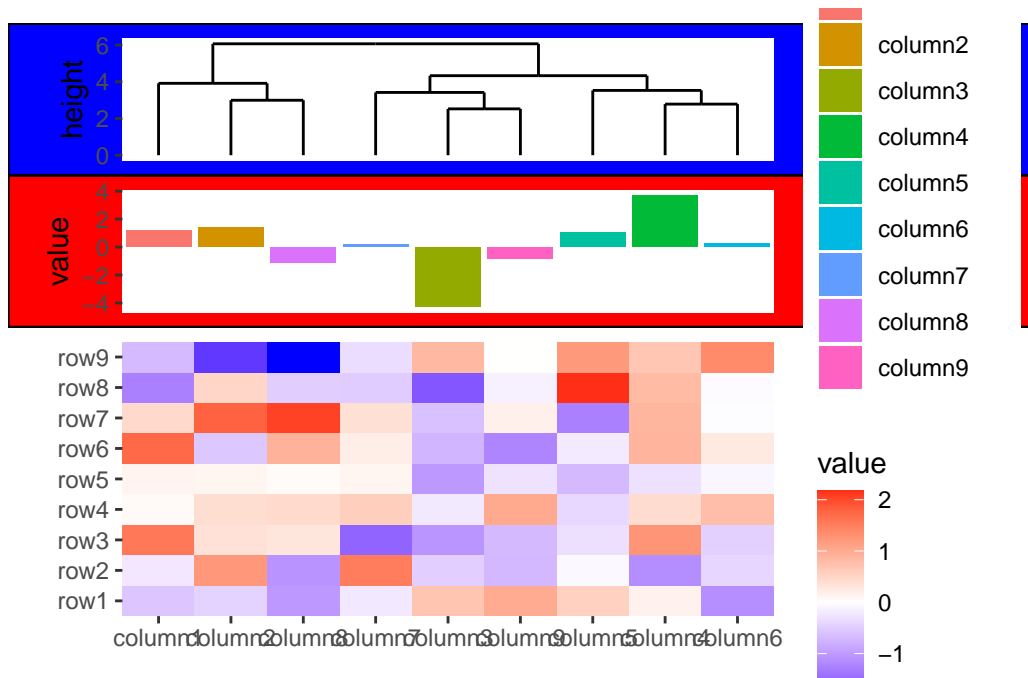
By using the `-` operator with schemes, we apply the scheme directly to the active layout.

```
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()`
```



9.2 scheme_data()

`align_gg()/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 subset the plot data
  scheme_data(~ subset(.x, .panel == 1L)) +
```

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



9.3 scheme_align()

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

9.3.1 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 9.3.2](#).

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.

9.3.2 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 = "1"`.

```

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 = "1") +
  # 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.

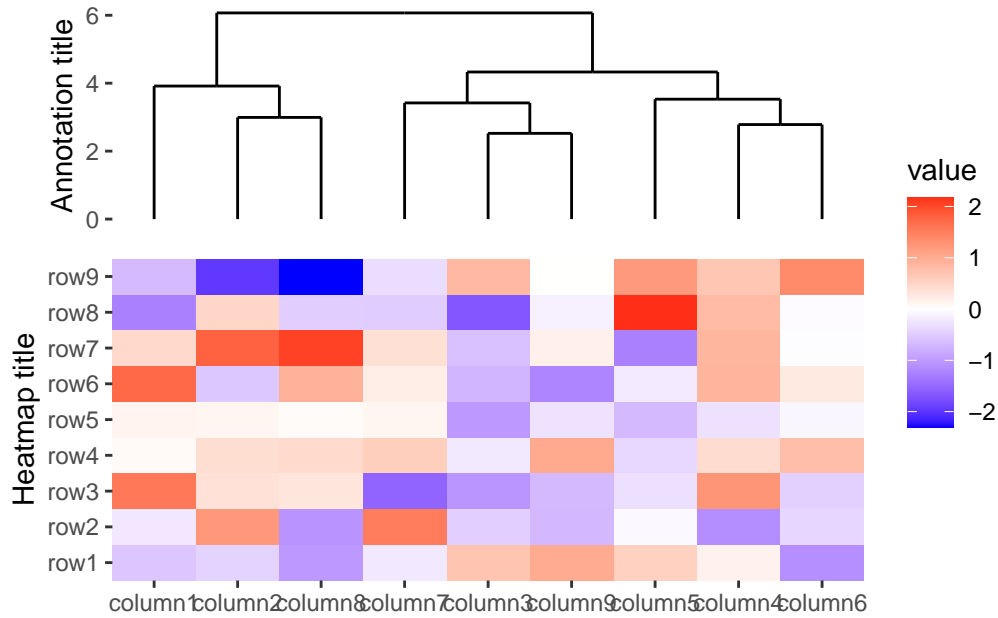
In `ggheatmap()/quad_layout()`, the behavior of the `free_spaces` and `free_labs` arguments differs from `guides` arguments in `scheme_align()` when inheriting from the parent layout:

- 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.

9.3.3 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()`
```



10 Difference with ggplot2

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

The following syntax applies to all **align_*** functions that add a plot area, and to the main plot in **quad_layout()** when alignment is needed.

10.1 Axes used for alignment

Axes used for alignment in **ggalign** refer to: - x-axis in vertical stack layouts

- x-axis in horizontal stack layouts
- x- and y- axes in the **quad_layout()** main plot

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.

10.2 Position Scales

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

10.2.1 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()`
```

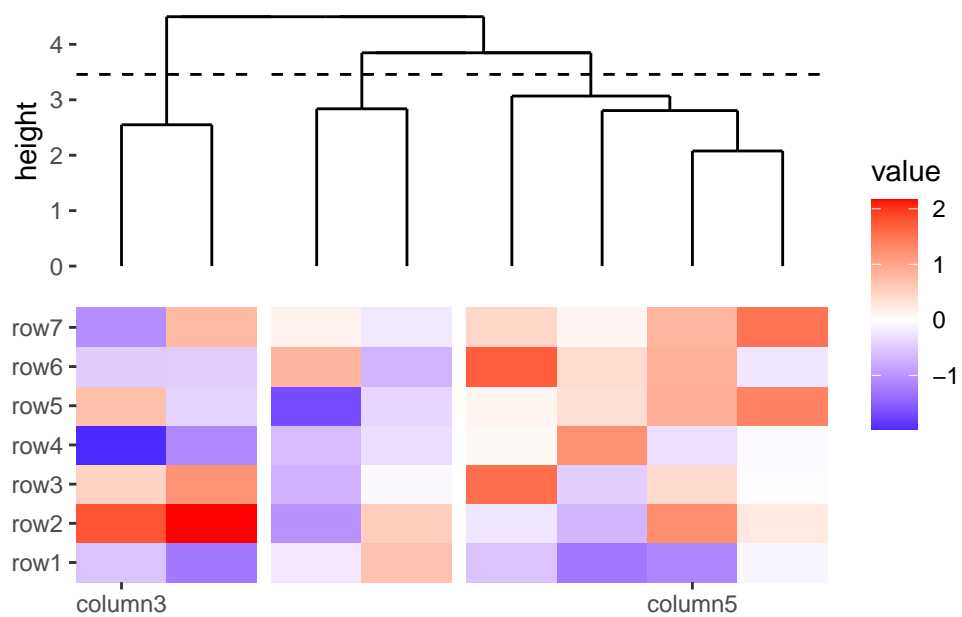


```
ggheatmap(small_mat, filling = FALSE) +
  geom_tile(aes(.discrete_x, .discrete_y, fill = value)) +
  scale_x_discrete(breaks = NULL)
```

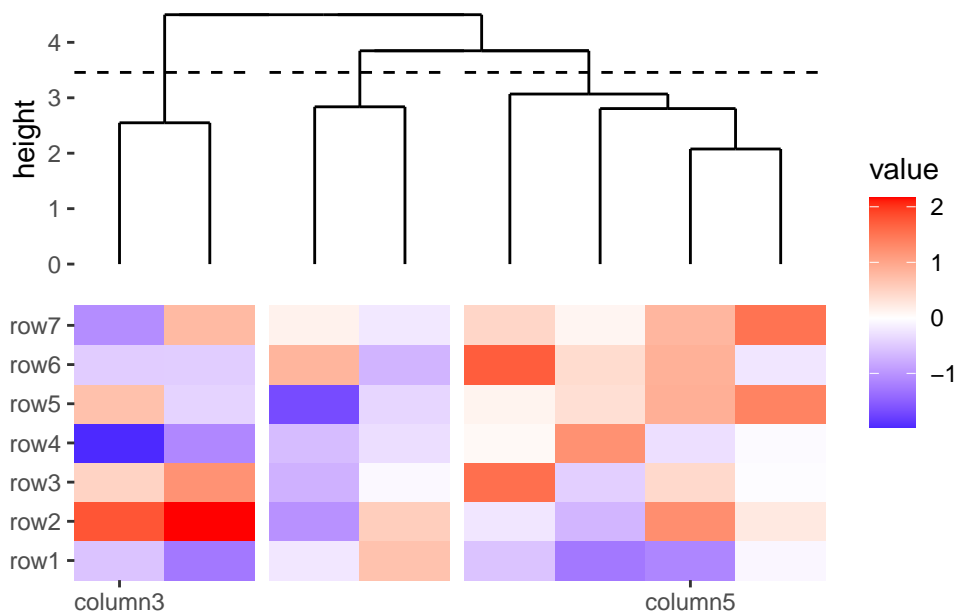


Character-based **breaks** use data names (or **indices** if names are absent)

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

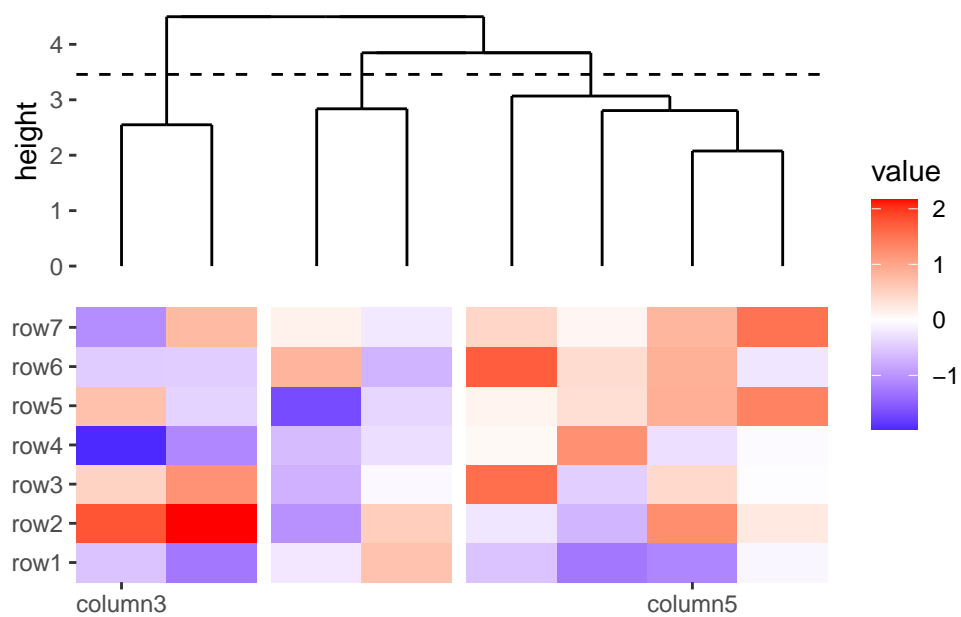


```
ggheatmap(small_mat, filling = FALSE) +
  geom_tile(aes(.discrete_x, .discrete_y, fill = value)) +
  scale_x_discrete(breaks = c("column3", "column5")) +
  anno_top() +
  align_dendro(k = 3L)
```



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()`
```




10.2.2 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.

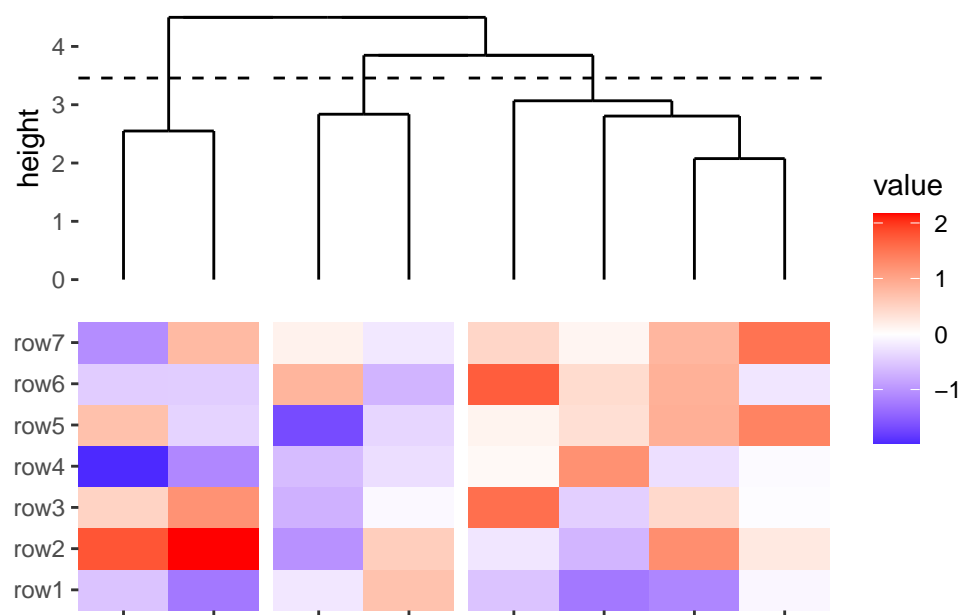
The default labels are the data names (or indices if names are absent):

```
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()`
```



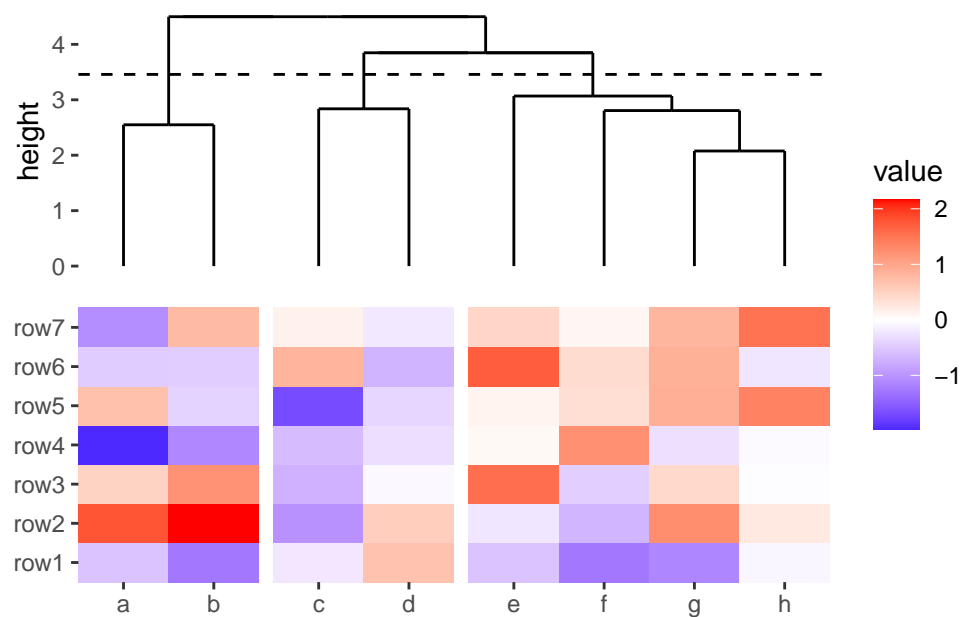
Character labels will be reordered based on the data's ordering:

```
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()`
```



10.2.3 expand

By default, we utilize zero expansion for the aligned axis. This is typically the desired setting. If you wish to introduce expansion, you must manually adjust it and apply it to each plot to ensure proper axis alignment.

```
ggheatmap(small_mat) +
  scale_x_continuous(expand = expansion(mult = 0.1)) +
  anno_top() +
  align_dendro(aes(color = branch), k = 3L) +
  scale_x_continuous(expand = expansion(mult = 0.1))
#> > heatmap built with `geom_tile()`
```



You can utilize `gg4x::facetted_pos_scales()` to set scales for each panel.

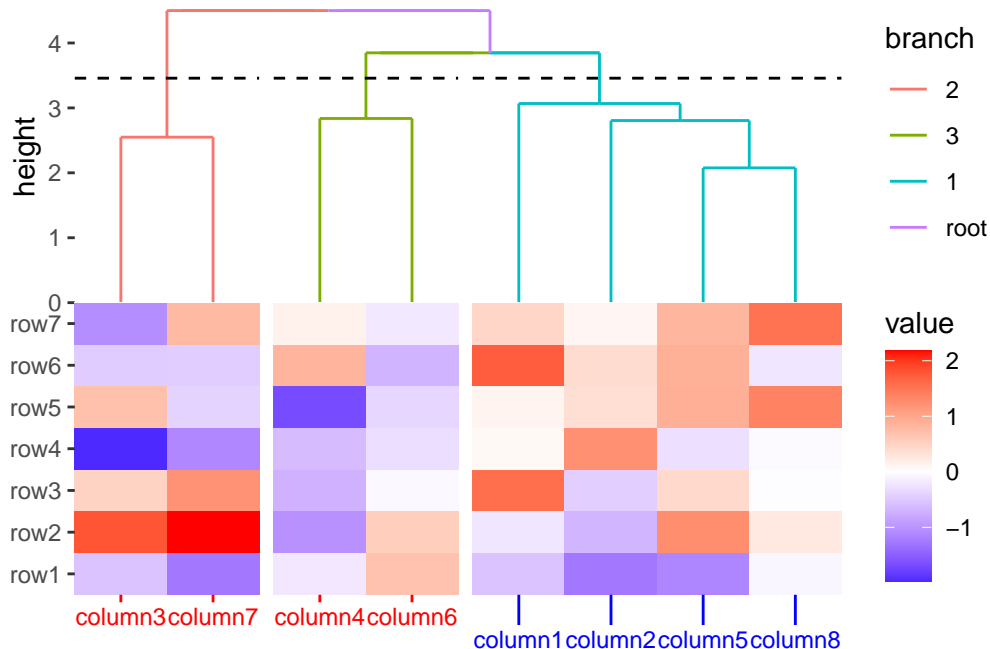
10.3 theme

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()`
```



10.4 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()`
```



10.5 Coords

Currently, only cartesian coordinate can be used to align axis well. Internally, the limits will always be set to the number of observations, with an additional range expansion of 0.5 added on both ends.

11 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
```

11.1 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)
```



11.2 Empty area

You can use NULL to indicate the empty area.

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



11.3 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))
```



11.4 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.

11.5 free_guide

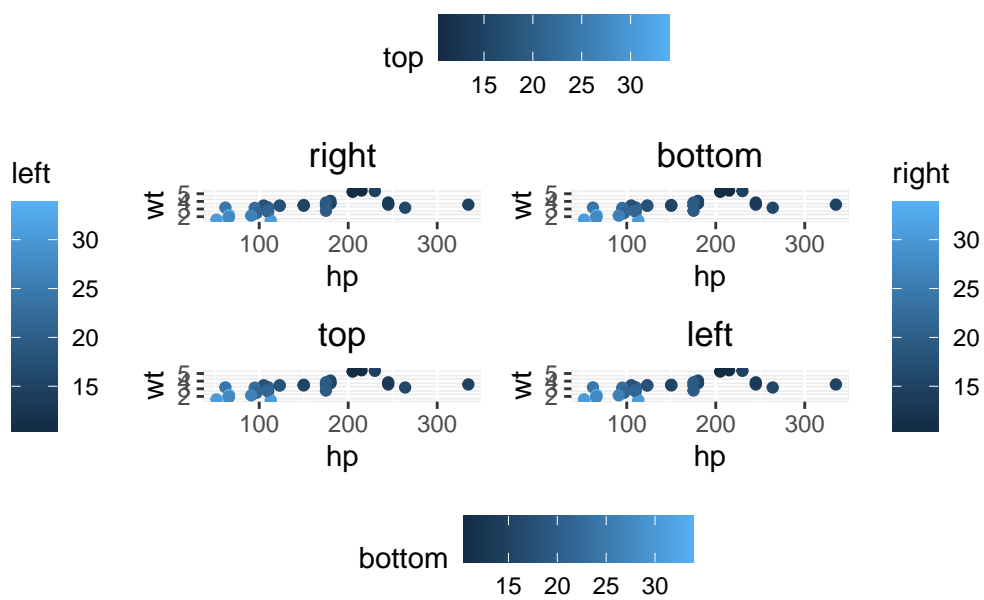
The `free_guide()` function allows you to override the `guides` argument for a single plot.

```
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")
)
```



Part II

Advanced

12 ggoncplot

The `ggoncplot()` 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
```

12.1 Input data

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

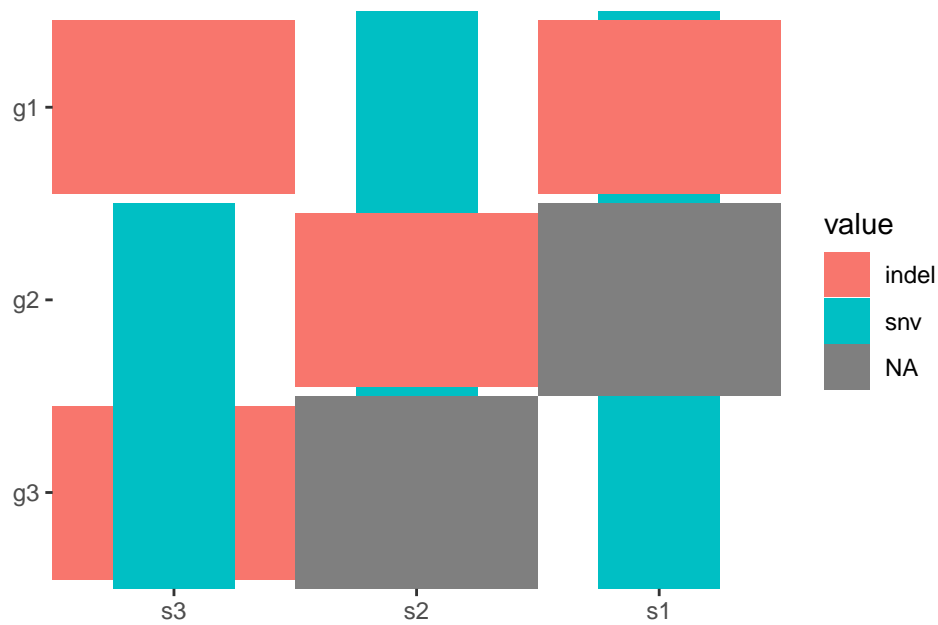
```
ggoncoplot(mat)
```



12.2 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):

```
ggoncoplex(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`:

```
ggoncoplex(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")`.

```
ggoncplot(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)
```




12.3 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 `ggoncplot()`.

```
ggoncplot(mat, map_width = c(snv = 0.5), map_height = c(indel = 0.9)) +
  anno_top(size = 0.2) +
  ggalign() +
  # by setting `inherit = TRUE`, we apply the parent layout `scheme_data()`
  # (from the `ggoncplot()` 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: `ggoncplot()` 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)
```



12.4 Integration with maftools

The `ggoncplot()` function supports MAF objects from the `maftools` package using the `fortify_matrix.MAF()` method. It includes options to control data generation for `ggoncplot()`, 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
ggoncplot(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(
  ggoncplot(laml, n_top = 20L, remove_empty_samples = FALSE) +
    scale_fill_brewer(palette = "Dark2", na.translate = FALSE) +
    theme_no_axes("x") +
    ggtitle("Keep empty samples"),
  ggoncplot(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"
)
```



12.5 Specialized Geoms

12.5.1 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.

```
ggoncplot(laml, n_top = 20, collapse_vars = FALSE, filling = FALSE) +
  geom_subtile(aes(fill = value), direction = "vertical") +
  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()`:

```
ggoncoplex(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 unnest the columns.
  }, inherit = TRUE) +
  geom_subtile(aes(fill = value), direction = "vertical") +
  scale_fill_brewer(palette = "Dark2", na.translate = FALSE) +
  theme_no_axes("x")
#> `geom_subtile()` subdivide tile into a maximal of 3 rectangles
```



12.5.2 geom_draw()

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

Key Features of `geom_draw()`:

- 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_draw()` 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)
    )
  }
)
```



```

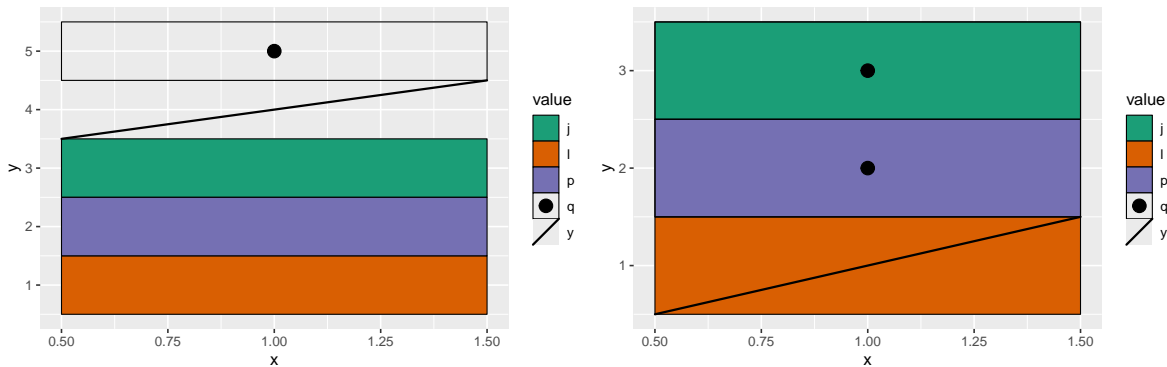
    )
  }
)

```

```

value <- sample(letters, 5L)
ggplot(data.frame(value = value, y = seq_len(5))) +
  geom_draw(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_draw(aes(x = 1, y = y, draw = value, fill = value)) +
  scale_draw_manual(values = draw_mapping) +
  scale_fill_brewer(palette = "Dark2")

```



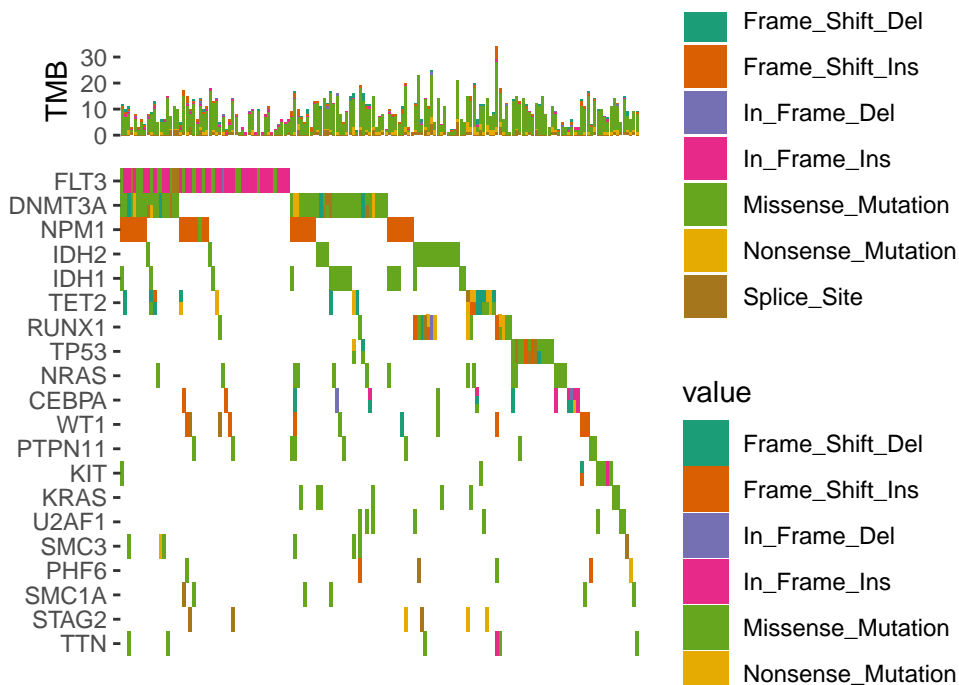
12.6 ggalgn attributes

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 = "vertical") +
  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](#).

```

ggoncplot(laml, n_top = 20, collapse_vars = FALSE, filling = FALSE) +
  geom_subtile(aes(fill = value), direction = "vertical") +
  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) +
  ggalignment(data = function(data) {
    data <- ggalignment_attr(data, "sample_summary")
    # matrix input will be automatically melted into a long formatted data
    # frame in `ggalignment()` 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 altered samples in the right annotation
  ggalignment(data = function(data) {
    # Atomic vector will be put in the `value` column of the data frame.
    ggalignment_attr(data, "gene_summary")$AlteredSamples /
    ggalignment_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
  ggalignment(data = function(data) {
    data <- ggalignment_attr(data, "gene_summary")
    # matrix input will be automatically melted into a long formatted data
    # frame in `ggalignment()` 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()`).

```



12.7 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
ggoncplot(laml.gistic) +
  scale_fill_brewer("CNV", palette = "Dark2", na.translate = FALSE) +
  theme_no_axes("x")

```



Part III

Cases

13 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)))
```

13.1 Simple heatmap

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



13.2 heatmap layout customize

13.2.1 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()`
```



13.2.2 Based on kmeans

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



13.2.3 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()`
```



13.2.4 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()`
```



13.3 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()`
```



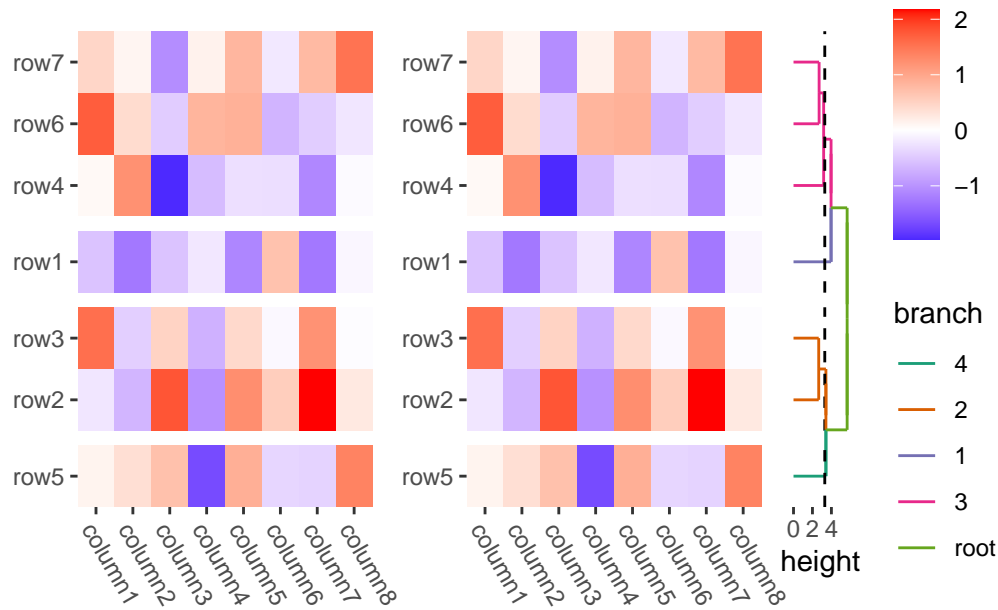
```
ggheatmap(small_mat) +
  anno_top(size = 0.5) +
  align_dendro(aes(color = branch), k = 3L) +
  ggalign(rowSums, aes(y = value)) +
  geom_bar(stat = "identity", aes(fill = factor(.panel))) +
  scale_fill_brewer(name = NULL, palette = "Dark2") +
  anno_left(size = 0.5) +
  align_dendro(aes(color = 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()`
```



13.4 Multiple heatmaps

13.4.1 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()`
```



13.4.2 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()`
```



13.5 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
ggfree() +
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
ggfree() +
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 `galign` 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.

14 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))
```

14.1 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 palette 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](#) package.

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())
```



14.2 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()`
```




14.3 Clustering

14.3.1 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()`
```

pre-defined distance method (1 – pearson)



```
# 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()`
```

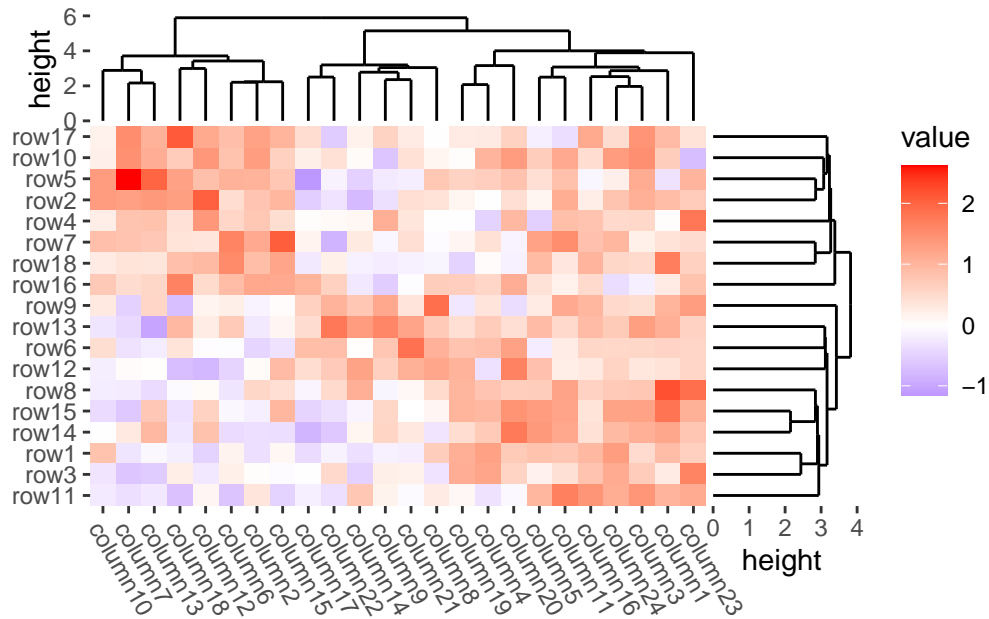
a function that calculates distance matrix



14.3.2 Clustering methods

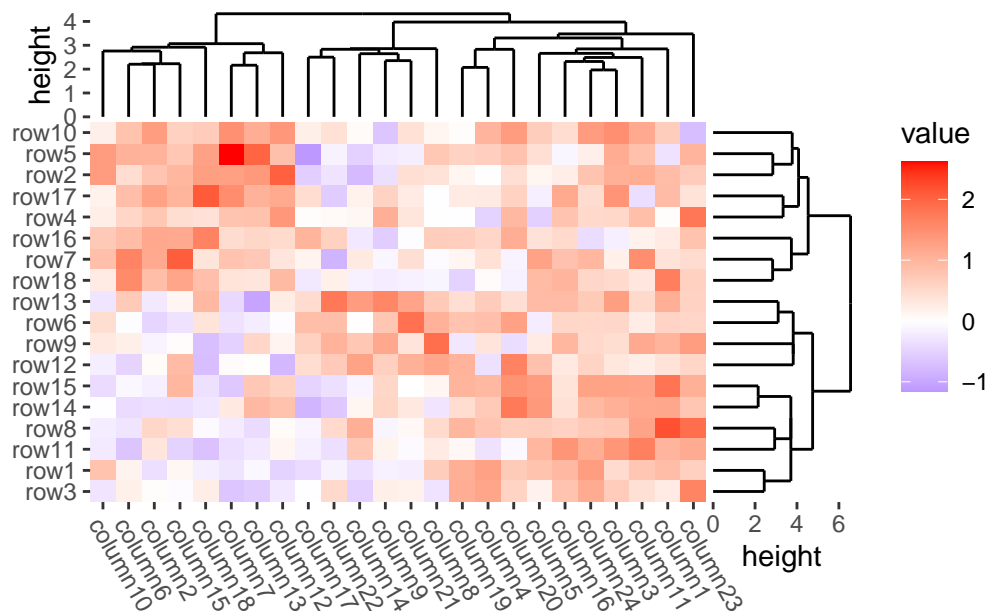
Method to perform hierarchical clustering can be specified by `method` argument, Possible methods are those supported in `hclust()` function.

```
# 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()`
```



14.3.3 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()`
```



14.4 Set row and column orders

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

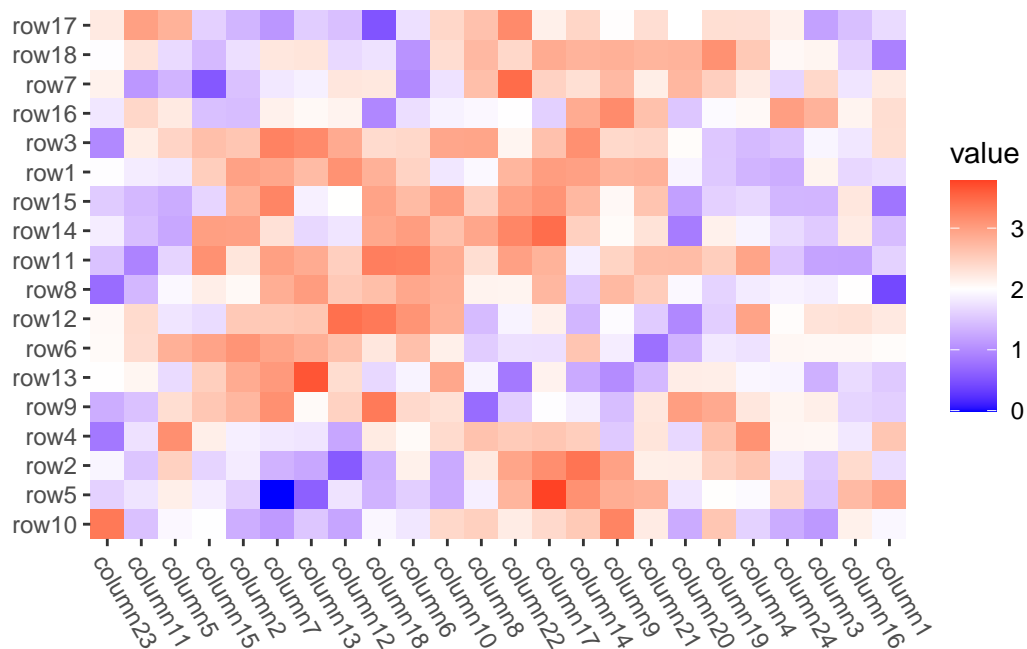
```
# ComplexHeatmap::Heatmap(mat,
#   name = "mat",
#   row_order = order(as.numeric(gsub("row", "", rownames(mat)))),
#   column_order = order(as.numeric(gsub("column", "", colnames(mat)))),
#   column_title = "reorder matrix"
# )
ggheatmap(mat) +
  theme(axis.text.x = element_text(angle = -60, hjust = 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()`
```



14.5 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.

14.6 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()`
```



14.7 Heatmap split

14.7.1 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.

14.7.2 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()`
```




14.7.3 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()`
```



14.7.4 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()`
```



14.7.5 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 ...

14.7.6 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>

```

15 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>.

15.1 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 = "1") +
  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(limits = FALSE) +
  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 +

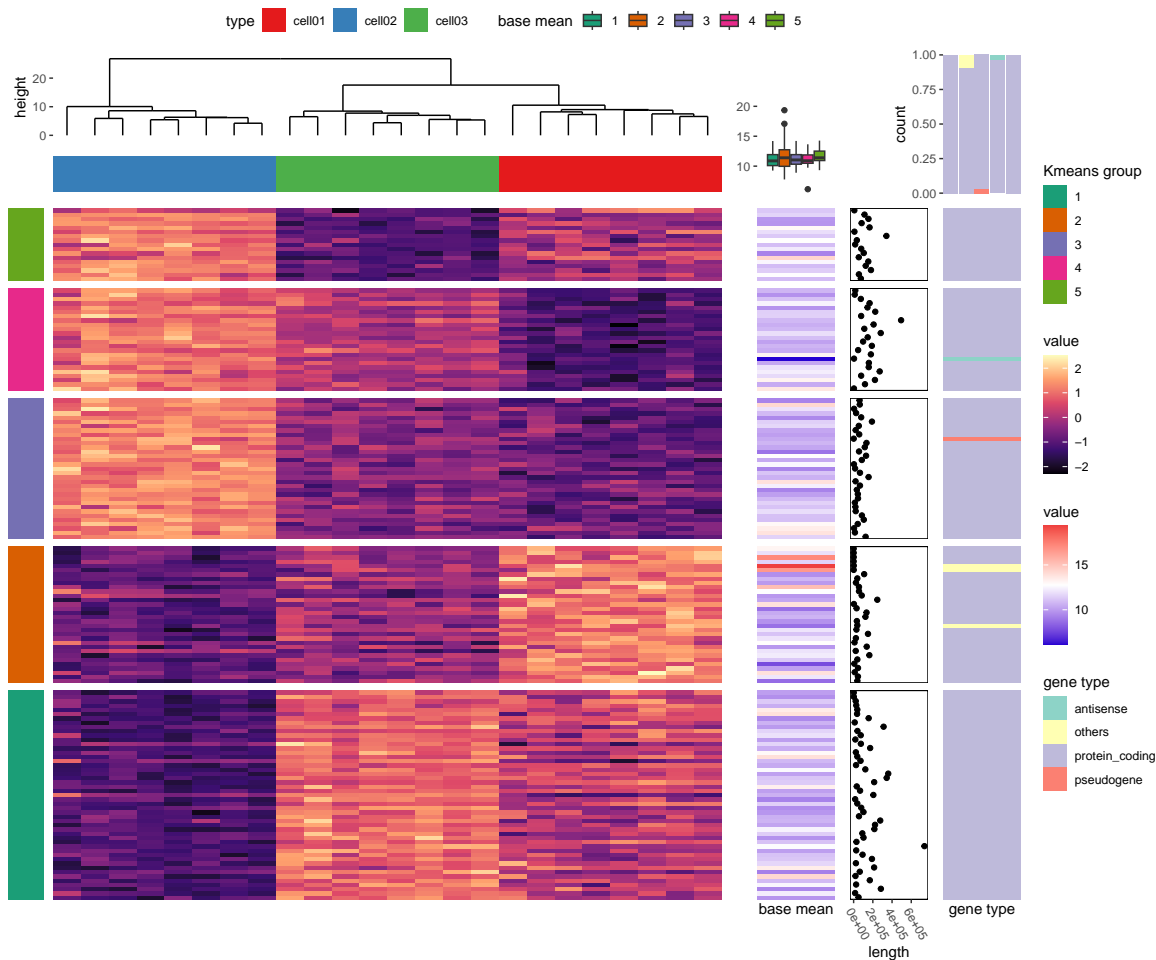
```



```

# 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()`

```



15.2 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))

```

