How I use ggplot2

true

6/4/23

A brief introduction to ggplot2. Be warned: This chapter provides detailed insight into certain aspects, while other components are not discussed at all.

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1 Before we start

1.1 Who this is for

This tutorial serves as an introductory guide to ggplot2, tailored specifically for beginners with no prior exposure to ggplot2. However, it's worth mentioning that as we delve deeper into the subject, we'll employ both BaseR and tidyverse code for some data preparations.

In addition, this ggplot2 guide reflects my personal approach and application of visualization techniques, focusing on the disciplines that align with the theme of this website - from agricultural sciences to experimental data from biology or life sciences at large. This tutorial, therefore, may not encompass all facets of ggplot2, but rather those elements that I frequently utilize in these specific domains.

1.2 Other resources

Here are some other ggplot2 tutorials and resources that I like:

- Chapter 3: Data Visualisation in (Wickham and Grolemund 2017)
- Cédric Scherer's (2022a) A ggplot2 tutorial for beautiful plotting in R
- Cédric Scherer's (2022b) Graphic Design with ggplot2
- Andrew Heiss' (2023) Data visualization with R
- Claus Wilke's (2019) Fundamentals of Data Visualization

1.3 Packages to install & load

We are using the `p_load()` function of the {pacman} package to install and load all necessary packages for this tutorial.

```
pacman::p_load(
  ggplot2,
  ggrepel,
  ggtext
  )
```

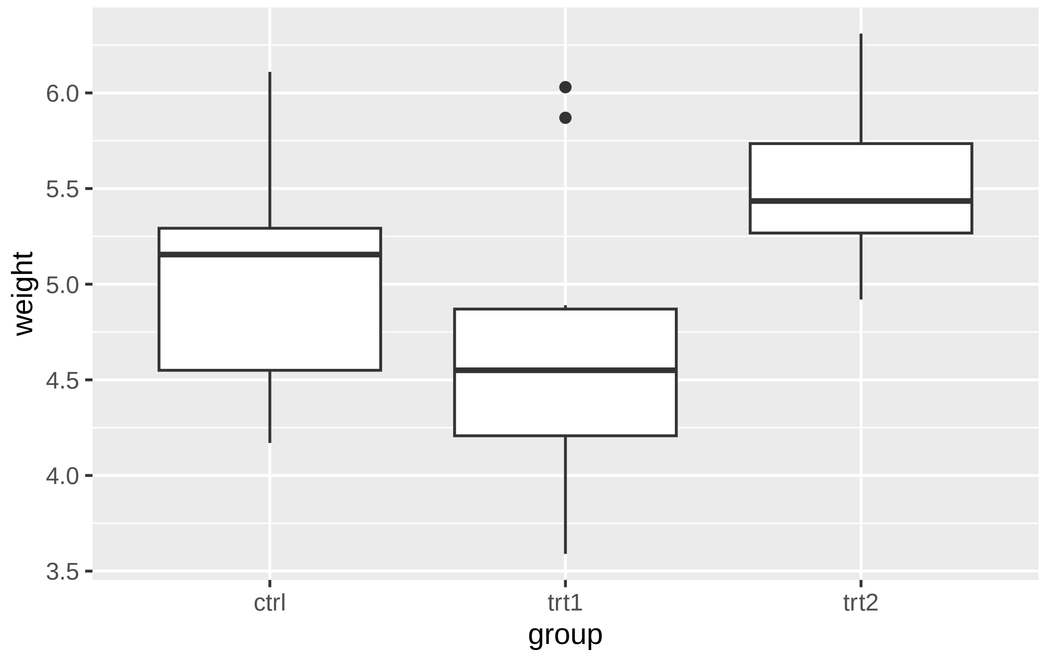
1.4 Showcase

Here are some beautiful ggplots

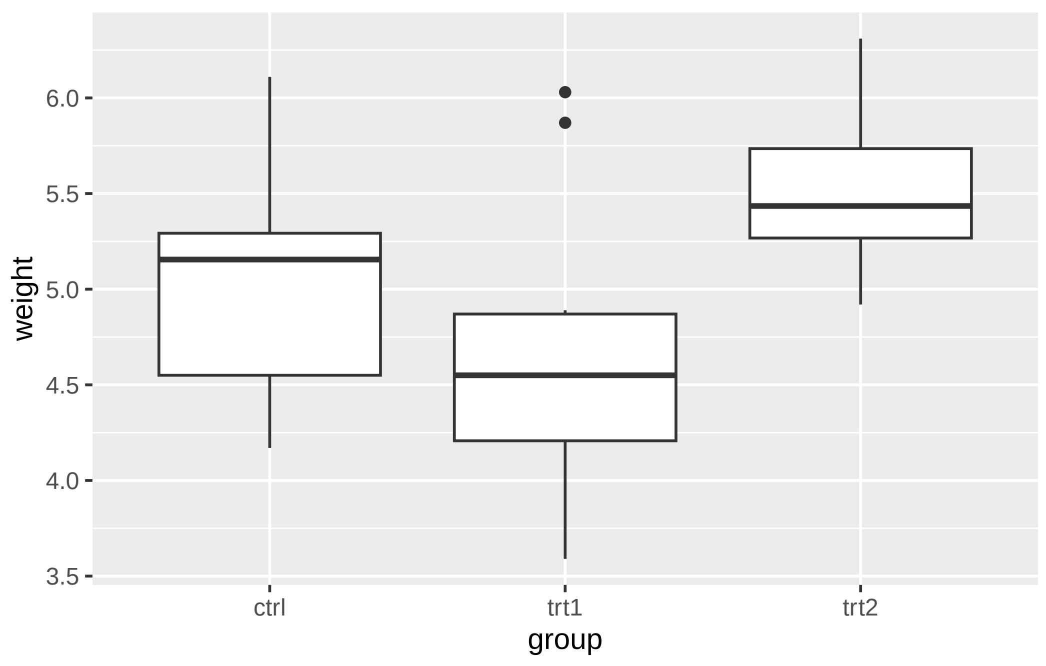
2 Let's start

Let us start by creating a plot that requires a minimum amount of code, but is still informative. We make use the `PlantGrowth` data, which is directly accessible in R.

```r
ggplot(data = PlantGrowth,
       mapping = aes(y = weight, x = group)) +
  geom_boxplot()
```



```r
ggplot(data = PlantGrowth) +
  aes(y = weight, x = group) +
  geom_boxplot()
```



Actually, you can see we created the same plot twice using slightly different code. Apologies for immediately confusing you with this, but it would be even more confusing if we postpone this topic.

Let's try to understand the general approach by looking at the first version of the code. The code for any ggplot always starts with the `ggplot()` function and then **layers** are added to it via the `+` operator.

The `data =` argument in `ggplot()` is where you specify the dataset you want to visualize. Think of it as telling ggplot "Here is the data I want you to work with."

The `mapping = aes()` argument is where you define the aesthetic mappings, like which columns of the data should be represented on the x and y axes. It's like giving ggplot specific instructions on "How should you represent this data?" For instance, `mapping = aes(x = column1, y = column2)` would tell ggplot to use `column1` for the x-axis and `column2` for the y-axis.

So, together, these two arguments form the fundamental instructions for any ggplot: "Here is my data, and this is how I want you to represent it."

Looking at our two versions of code that result in the same plot, you can see that they only differ in how the `aes()` is included. The far more common approach is to include it inside the `ggplot()` function as in the first version. However, I am not the only one who argues that the second version is simply easier to read, which is why I am using it. Other than that, there is no difference between the two versions.

Finally, there is `geom_boxplot()`. This function, known as a geometric object or "geom", represents the type of plot you want to create. In ggplot2, every type of plot is associated with a specific geom function. For our example,`geom_boxplot()` is used to create a boxplot, which is a great way to visualize the distribution of numerical data and compare it across different groups. The `geom_boxplot()` function is added to the base `ggplot()` call using the `+` operator, just like the other layers. In this way, it's as if we're telling ggplot: "And here is the type of plot I want you to create.". Again - it know already *how* to draw the boxes because we told it about the data and aesthetic mapping.

Other geoms you might use include `geom_point()` for scatter plots, `geom_line()` for line graphs, and many more. Each geom function has its own set of aesthetics and other arguments that you can specify to customize your plot. By using these different geoms, you can create a wide variety of plots to meet your specific data visualization needs.

Now you understand the absolute minimum of how to create a ggplot.

- List of all `geom_*()` functons

3 Axes

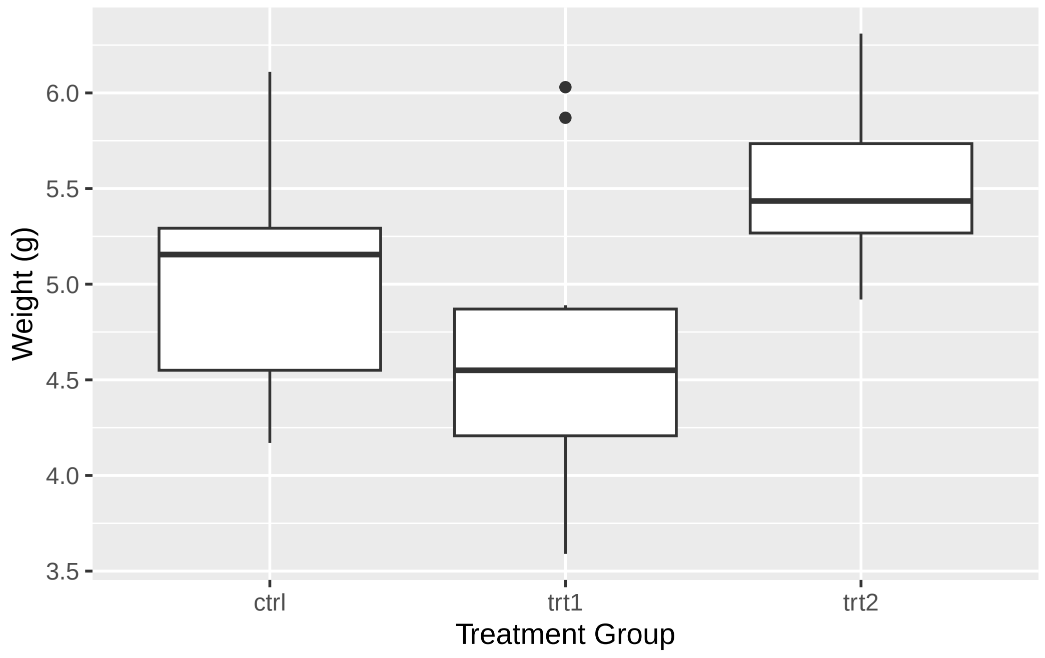
In ggplot2, the `scale_x_*` and `scale_y_*` functions are used to control the appearance of the x and y axes, respectively. These functions allow you to set the scale type (continuous, discrete, etc.), the axis labels, the tick mark labels, and the range of values displayed on the axis.

Regarding the scale type, we need to use `scale_y_continuous()` (since `weight` is a continous, metric variable) and `scale_x_discrete()` (since `group` is a discrete, categorical variable) for our boxplot.

3.1 Name

The `name =` allows you to change the axis titles.

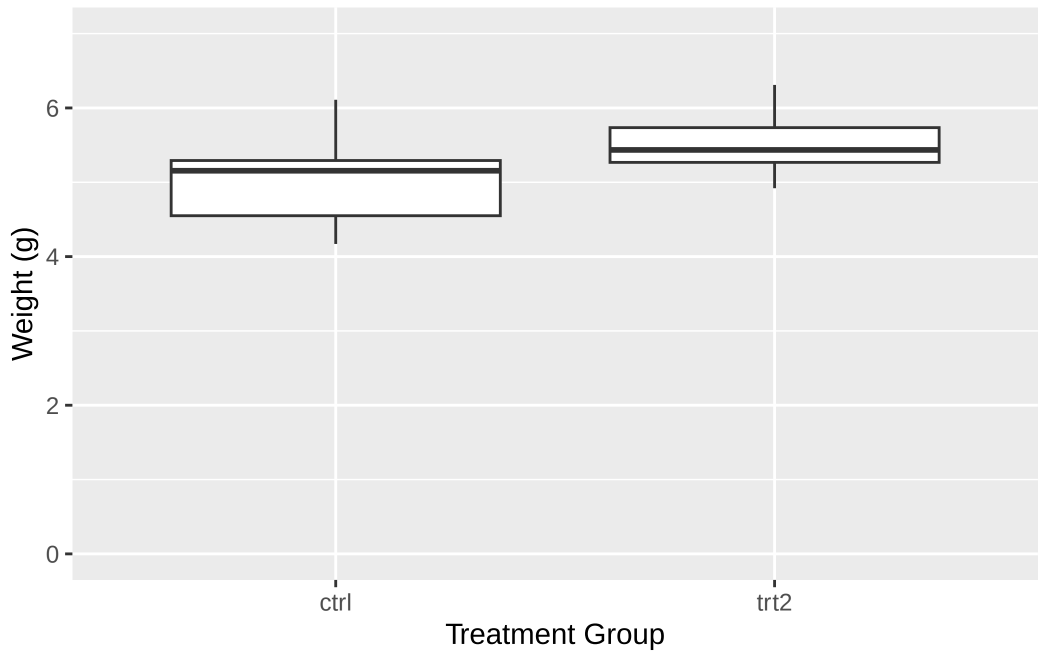
```r
ggplot(data = PlantGrowth) +
  aes(y = weight, x = group) +
  geom_boxplot() +
  scale_y_continuous(name = "Weight (g)") +
  scale_x_discrete(name = "Treatment Group")
```



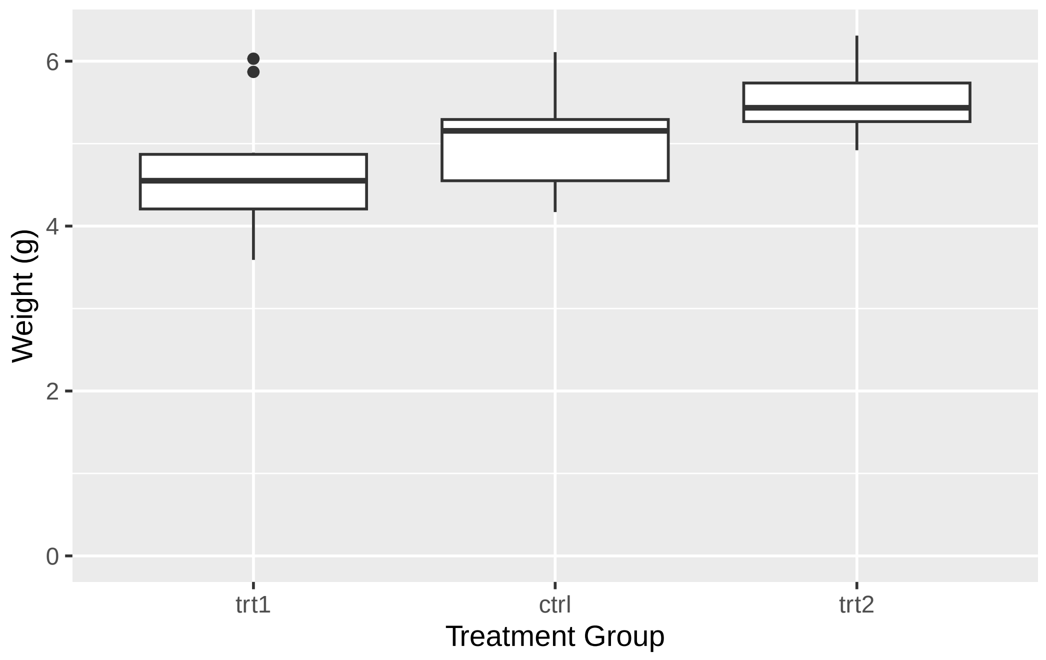
3.2 Limits

The `limits =` argument in the scale_*_* functions allows you to specify the range of values displayed on the axis. This can be particularly useful when you want to focus on a specific part of your data. Let's see how this works in practice with our boxplot example.

```
ggplot(data = PlantGrowth) +
  aes(y = weight, x = group) +
  geom_boxplot() +
  scale_y_continuous(
    name = "Weight (g)",
    limits = c(0, 7)
  ) +
  scale_x_discrete(
    name = "Treatment Group",
    limits = c("ctrl", "trt2")
  )
```



```r
ggplot(data = PlantGrowth) +
  aes(y = weight, x = group) +
  geom_boxplot() +
  scale_y_continuous(
    name = "Weight (g)",
    limits = c(0, NA)
  ) +
  scale_x_discrete(
    name = "Treatment Group",
    limits = c("trt1", "ctrl", "trt2")
  )
```



In the left plot, we use the `limits =` argument in `scale_y_continuous()` to set the y-axis to range from 0 to 7. This works as expected, showing all weights from 0 to 7. However, including only "ctrl" and "trt2" (i.e. the first and last level) in the `limits =` argument of in `scale_x_discrete()`, results in only these two groups being displayed on the x-axis. The key point here is that for a discrete scale, the `limits =` argument needs to include all the levels you want to display.

In the right plot, we again use the `limits =` argument in `scale_y_continuous()`, but this time we only specify the lower limit (0) and use `NA` for the upper limit. This tells ggplot2 to start the y-axis at 0 and end it at the maximum value in the data, which is the default behavior. For the x-axis, we provide all three levels ("trt1", "ctrl", "trt2") in the `limits =` argument of `scale_x_discrete()`. This not only ensures that all groups are displayed, but also allows us to control the order in which they appear.

This demonstrates how the `limits =` argument can be used differently in `scale_*_continuous()` and `scale_*_discrete()`. In a continuous scale, it defines the range of values, while in a discrete scale, it specifies which levels to include and their order.

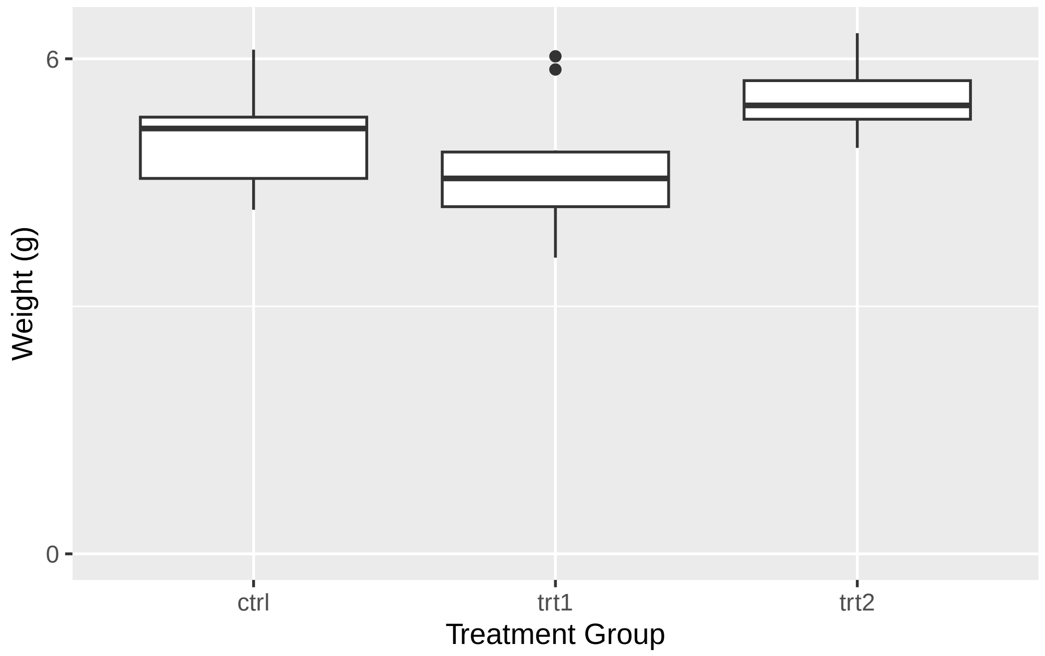
In the end, it's important to note that setting the limits can exclude data outside the specified range from the plot. This means that the excluded data will not be considered when calculating statistics or generating geoms. In other words, while setting limits can help focus your plot on specific aspects of your data, it can also exclude important information. Always consider the implications of setting limits on your data visualization.

- List of all scales functions

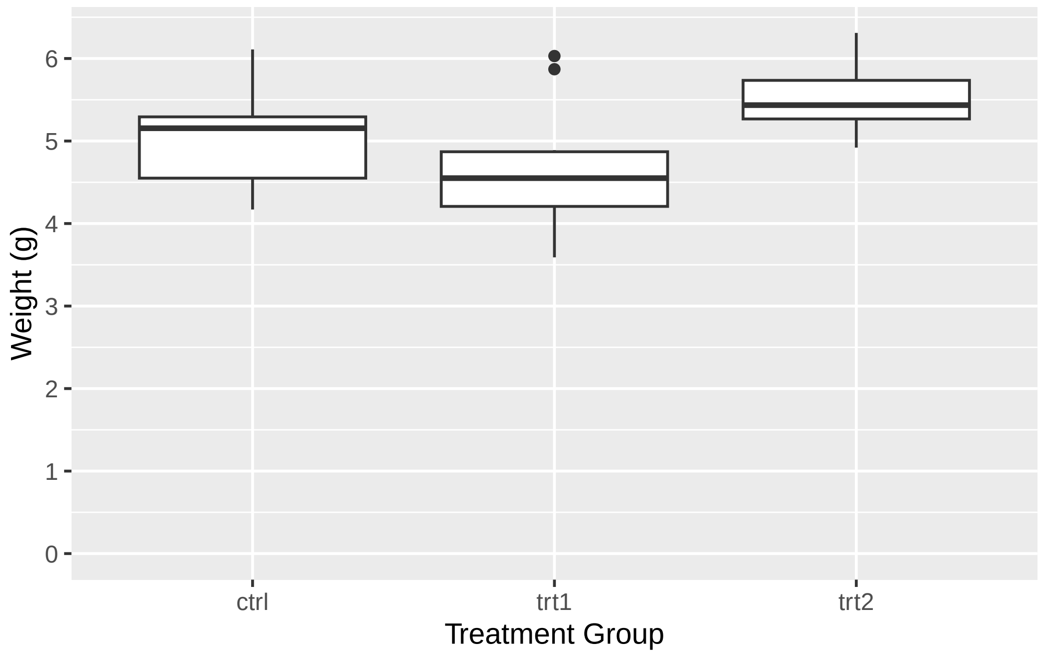
3.3 Breaks

The breaks = argument in these functions allows you to specify the locations of the tick marks on the axis.

```r
ggplot(data = PlantGrowth) +
  aes(y = weight, x = group) +
  geom_boxplot() +
  scale_y_continuous(
    name = "Weight (g)",
    limits = c(0, NA),
    breaks = c(0, 6)
  ) +
  scale_x_discrete(
    name = "Treatment Group"
  )
```



```r
ggplot(data = PlantGrowth) +
  aes(y = weight, x = group) +
  geom_boxplot() +
  scale_y_continuous(
    name = "Weight (g)",
    limits = c(0, NA),
    breaks = seq(0, 6)
  ) +
  scale_x_discrete(
    name = "Treatment Group"
  )
```



In the left plot, we use the `breaks =` argument in `scale_y_continuous()` to set the y-axis tick marks at 0 and 6. This really results in only two tick marks being displayed on the y-axis. While this is not typically useful for data representation, it serves to illustrate that the `breaks =` argument can be used to place tick marks at any specified values.

In the right plot, we use the `seq()` function in the `breaks =` argument to set the y-axis tick marks at every integer value from 0 to 6. This provides a more informative view of the data, as it allows us to see the weight values at regular intervals.

Tip

Instead of having to manually write “6” in `breaks = seq(0, 6)` you can instead do this:

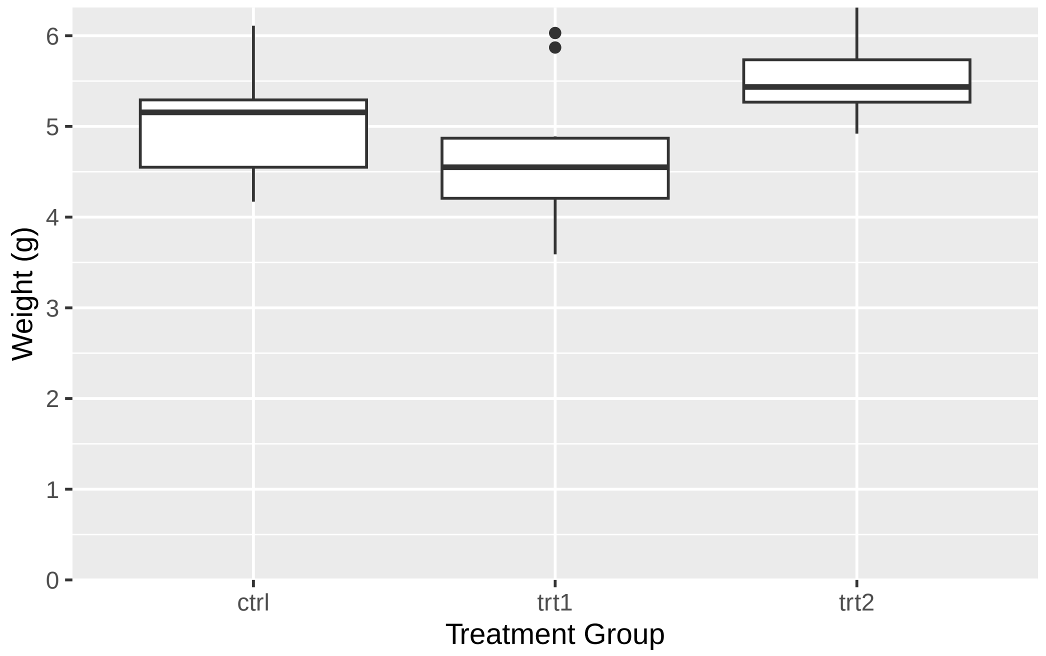
- `breaks = seq(0, max(PlantGrowth$weight))` automatically finds the maximum value in the data
- `breaks = scales::breaks_width(1)` makes use of the `breaks_width()` function in the {scales} package to simply define the width of the breaks

3.4 Expand

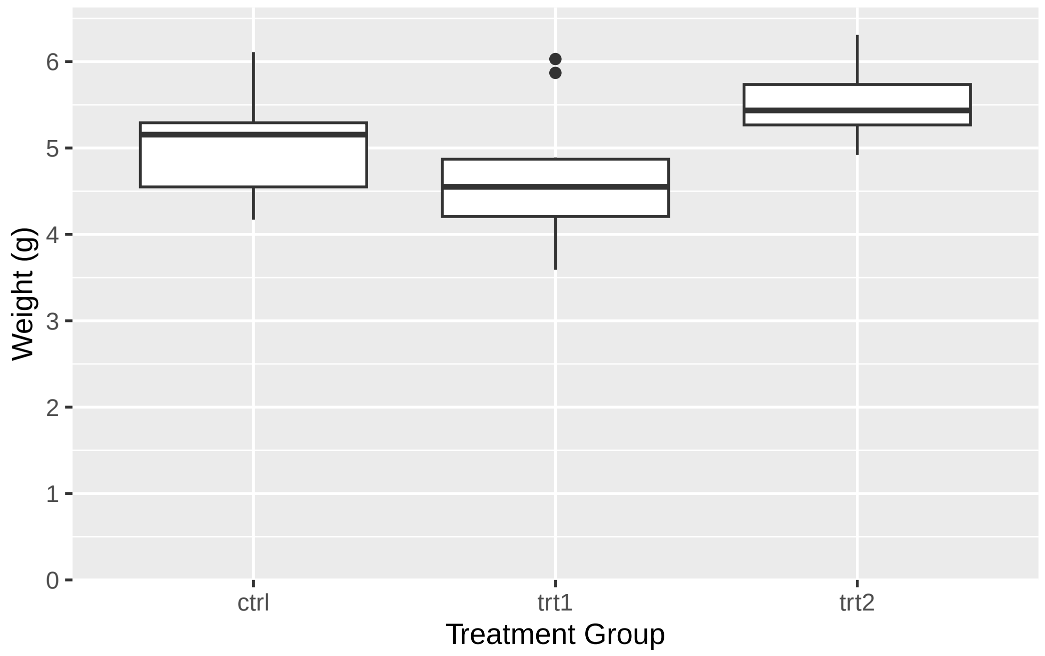
The `expand =` argument in the scale_*_* functions allows you to control the expansion of the scale. This is particularly useful when you want to adjust the space between the plotted data and the axes.

By default, ggplot2 adds a small amount of space around the data to ensure that the data doesn’t overlap with the axes. However, there might be situations where you want to adjust this space. For instance, you might want to remove the space below the 0 on the y-axis.

```r
ggplot(data = PlantGrowth) +
  aes(y = weight, x = group) +
  geom_boxplot() +
  scale_y_continuous(
    name = "Weight (g)",
    limits = c(0, NA),
    breaks = seq(0, 6),
    expand = c(0, 0)
  ) +
  scale_x_discrete(
    name = "Treatment Group"
  )
```



```r
ggplot(data = PlantGrowth) +
  aes(y = weight, x = group) +
  geom_boxplot() +
  scale_y_continuous(
    name = "Weight (g)",
    limits = c(0, NA),
    breaks = seq(0, 6),
    expand = expansion(mult = c(0, 0.05))
  ) +
  scale_x_discrete(
    name = "Treatment Group"
  )
```



In the left plot, we use the `expand = c(0, 0)` argument in `scale_y_continuous()` to simply set the expansion to 0 on both sides of the scale. This removes all extra space around the data. However, this also results in the plot being cut off right at the maximum observation, which might not be desirable.

In the right plot, we use the `expansion()` function in the `expand =` argument. This function allows us to set different expansion multipliers for the lower and upper limits of the scale. Here, we set the lower multiplier to 0 to remove the space below 0, and the upper multiplier to 0.05 to add a small amount (= 5%) of space above the maximum observation.

Tip

For a better understanding of how this expansion-thing works, I found this cheat sheet to be really insightful.

End

Heiss, Andrew. 2023. "Data Visualization with R - Data Visualization." https://datavizs23.classes.andrewheiss.com/.

Scherer, Cédric. 2022a. "A Ggplot2 Tutorial for Beautiful Plotting in r." *Cédric Scherer Blog*. https://www.cedricscherer.com/2019/08/05/a-ggplot2-tutorial-for-beautiful-plotting-in-r/.

———. 2022b. “Graphic Design with Ggplot2 - Graphic Design with Ggplot2.” *Rstudio::conf(2022) Workshop*. https://rstudio-conf-2022.github.io/ggplot2-graphic-design/.

Wickham, Hadley, and Garrett Grolemund. 2017. *R for Data Science: Import, Tidy, Transform, Visualize, and Model Data*. 1st ed. O’Reilly Media, Inc. https://r4ds.had.co.nz/.

Wilke, Claus O. 2019. *Fundamentals of data visualization*. O’Reilly Media. https://clauswilke.com/dataviz/.