GGplot

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Contents

Chapter 5 Graphics with ggplot (*Introduction to R book*)

First steps:

1. The first step in producing a plot with ggplot() is the easiest! We just need to install and then make the package avaialble.

```
library(ggplot2)
```

2. Always take care of the order of the categorical variables right from the start For example, `flowergg$nitrogen <- factor(flowergg$nitrogen, levels = c("high", "medium", "low"))`

With that taken care of, let's make our first ggplot!

First GGplot

```
flowergg <- read.table(file = "/Users/apoorv/Desktop/RMarkdown/data/Apoorv/flowerr.txt",
                       header = TRUE, sep = "\t",
                       stringsAsFactors = TRUE)
str(flowergg)
```

```
## 'data.frame':    96 obs. of  8 variables:
##  $ treat    : Factor w/ 2 levels "notip","tip": 2 2 2 2 2 2 2 2 2 2 ...
##  $ nitrogen : Factor w/ 3 levels "high","low","medium": 3 3 3 3 3 3 3 3 3 3 ...
##  $ block    : int  1 1 1 1 1 1 1 1 2 2 ...
##  $ height   : num  7.5 10.7 11.2 10.4 10.4 9.8 6.9 9.4 10.4 12.3 ...
##  $ weight   : num  7.62 12.14 12.76 8.78 13.58 ...
##  $ leafarea : num  11.7 14.1 7.1 11.9 14.5 12.2 13.2 14 10.5 16.1 ...
##  $ shootarea: num  31.9 46 66.7 20.3 26.9 72.7 43.1 28.5 57.8 36.9 ...
##  $ flowers  : int  1 10 10 1 4 9 7 6 5 8 ...
```

We know from the "final figure" that we want the variable shootarea on the y axis (response/dependent variable) and weight on the x axis (explanatory/independent variable).

aes

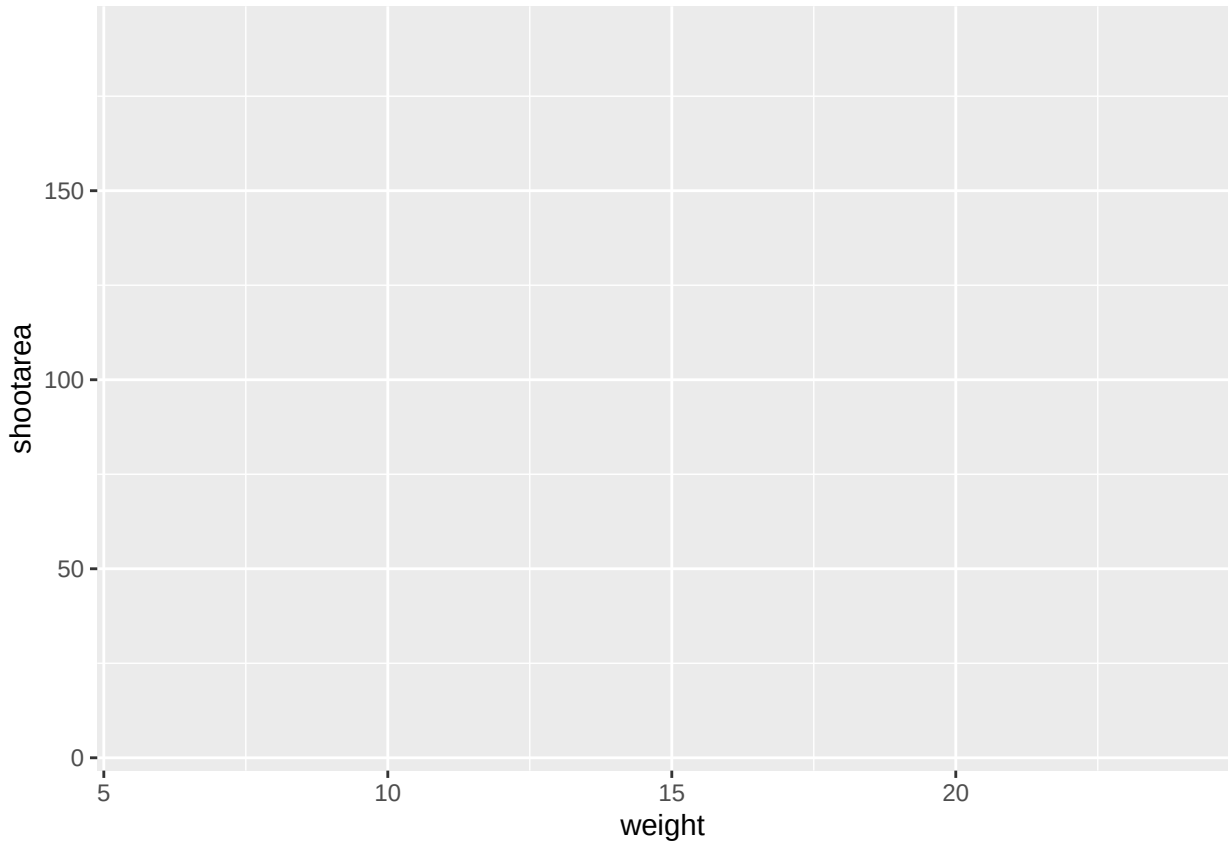
To do this in ggplot2 we need to make use of the aes() function and also add a data = argument.

aes is short for aesthetics, and it's the function we use to specify what we want displayed in the figure.

If we did not include the aes() function, then the x = and y = arguments would produce an error saying that the object was not found. A good rule to keep in mind when using ggplot2 is that the variables which we want displayed on the figure must be included in aes() function via the mapping = argument

All features in the figure which alter the displayed information, not based on a variable in our dataset (e.g. increasing the size of points to an arbitrary value), is included outside of the aes() function.

```
# Including aesthetics for x and y axes as well as specifying the dataset
ggplot(mapping = aes(x = weight, y = shootarea), data = flowergg)
```



geoms

That's already much better. At least it's no longer a blank grey canvas. We've now told ggplot2 what we want as our x and y axes as well as where to find that data. But, what's missing here is where we tell ggplot2 how to display that data. This is now the time to introduce you to 'geoms' or geometry layers.Geometries are the way that ggplot2 displays information.

For instance,

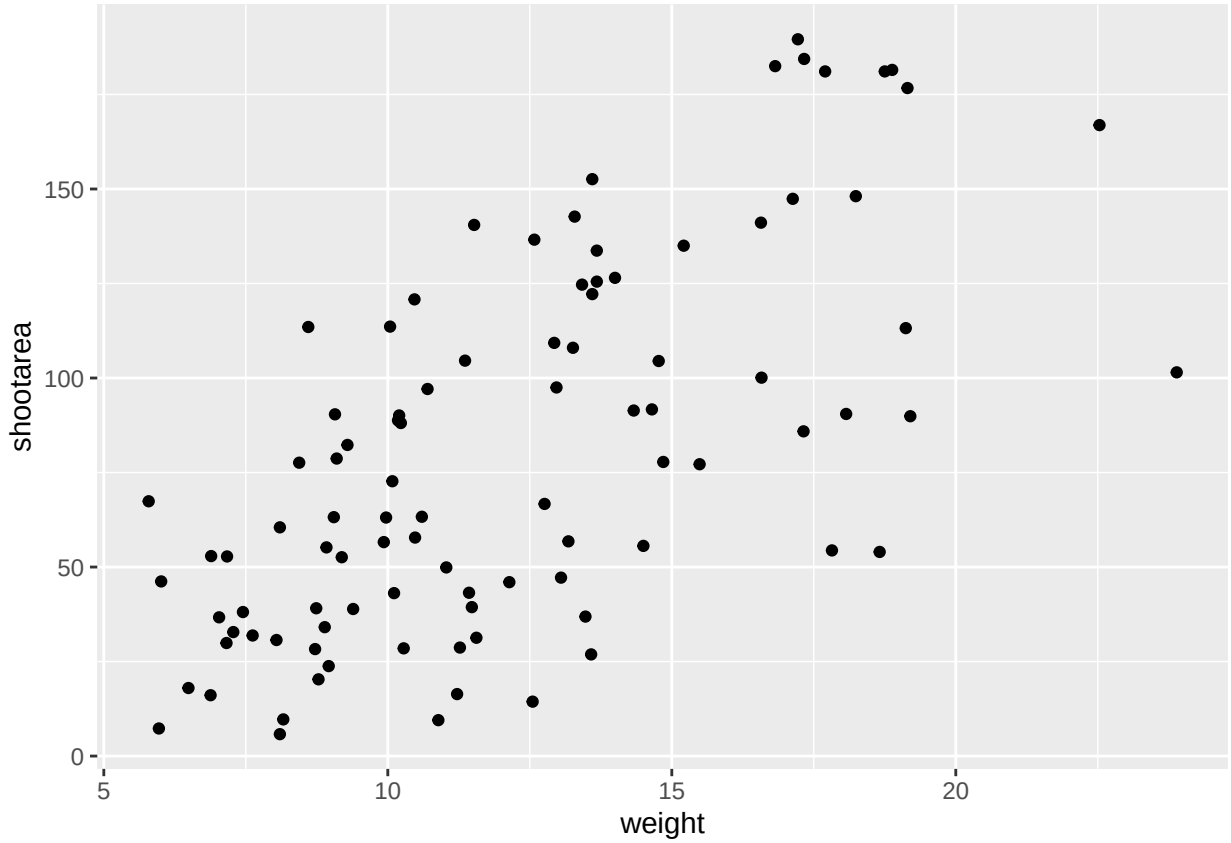
```
geom_point()
```

```
## geom_point: na.rm = FALSE
## stat_identity: na.rm = FALSE
## position_identity
```

```
# tells ggplot2 that you want the information to be displayed as points
# (making scatterplots possible for example). Given that the "final figure" uses points,
# this is clearly the appropriate geom to use here.
```

Before we can do that, we need to talk about the coding structure used by ggplot2. The analogy that we and many others use is to say that making a figure in ggplot2 is much like painting. What we've did in the above code was to make our "canvas". Now we are going to add sequential layers to that painting, increasing the complexity and detail over time. Each time we want to include a new layer we need to end a preceding layer with a + at the end to tell ggplot2 that there are additional layers coming. Let's add (+) a new geometry layer now:

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point() # Adding a geom to display data as point data
```



When you first start using ggplot2 there are three crucial layers that require your input. You can safely ignore the other layers initially as they all receive sensible (if sometimes ugly) defaults.

The three crucial layers are:

1. Data - the information we want to plot
2. Mapping - which variables we want displayed and where
3. Geometry - how we want that data displayed

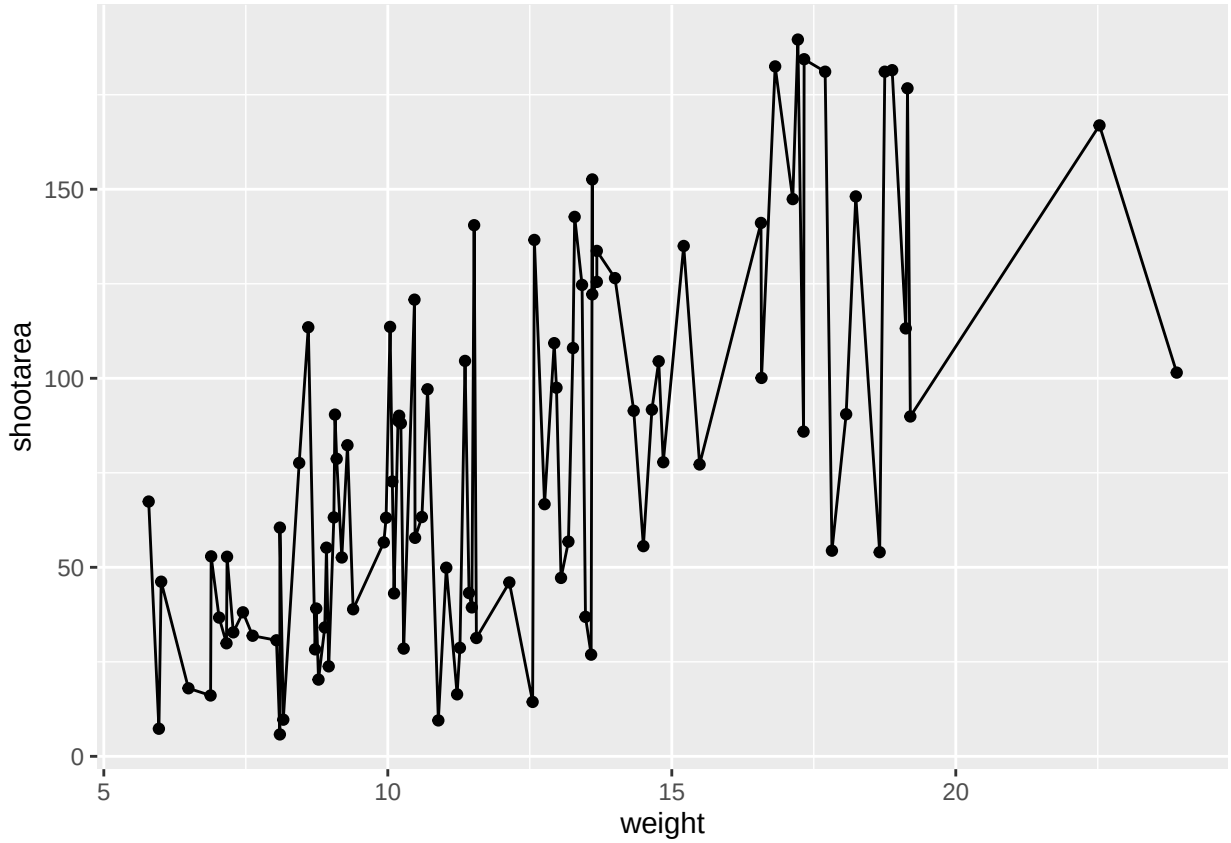
Given that 'data' only requires us to specify the dataset we want to use, it is trivially easy to complete. 'Mapping' only requires you to specify what variables in the data to use, often just the x- and y-axes (specified using aes()). Lastly, 'geometry' is where we choose how we want the data to be visualised. With just these three fundamentals, you will be able to produce a large variety of plots (see later in this Chapter for a bestiary of plots). If what we wanted was a quick and dirty figure to get a grasp of the trend in the data we can stop here. From the scatterplot that we've produced, we can see that shootarea looks like it's increasing with weight in a linear fashion. So long as this answers the question we were asking from these data, we have a figure that is fit for purpose.

geom_line and geom_smooth

However, for showing to other people we might want something a bit more developed. If we glance back to our "final figure" we can see that we have lines representing the different nitrogen concentrations. We can

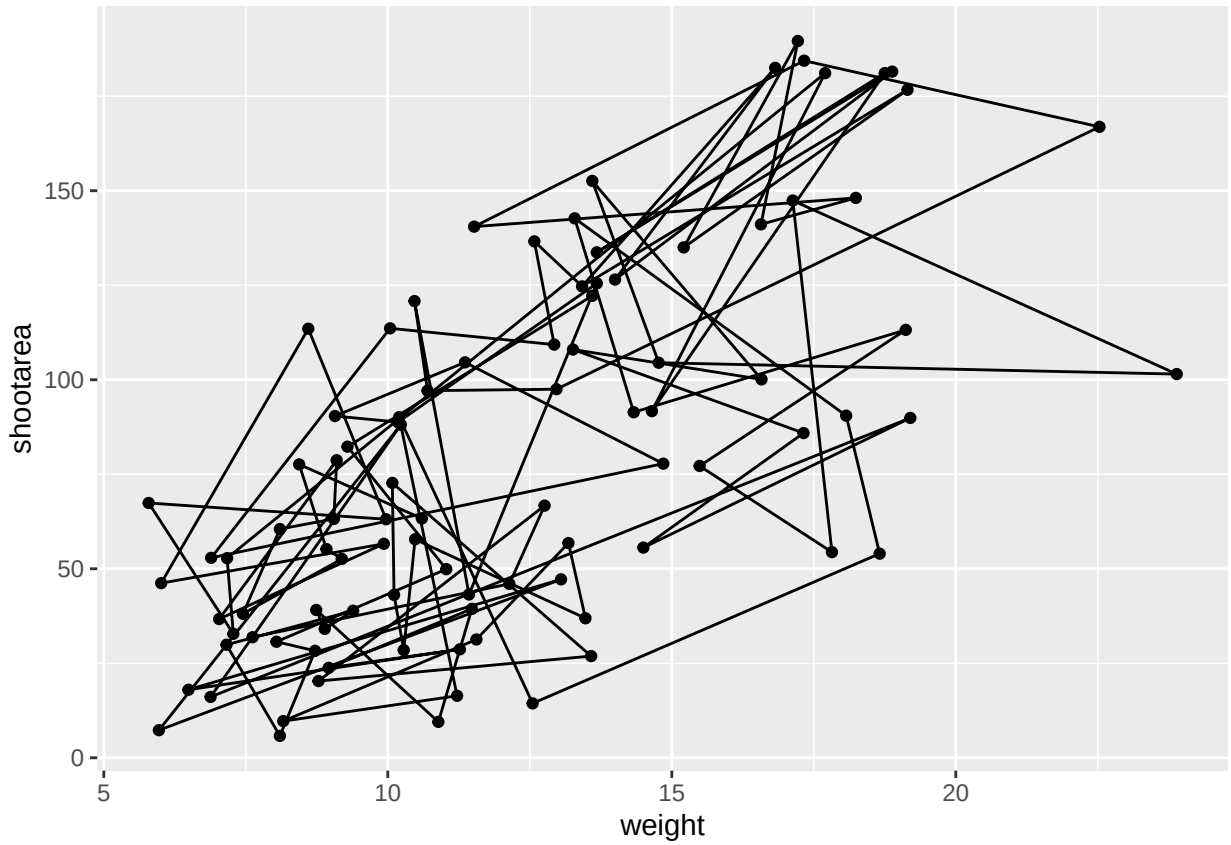
include lines using a geom. If you have a quick look through the available geoms here, you might think that geom_line() would be appropriate. Let's try it

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point() +
  geom_line() # Adding geom_line
```



ALTERNATIVE,

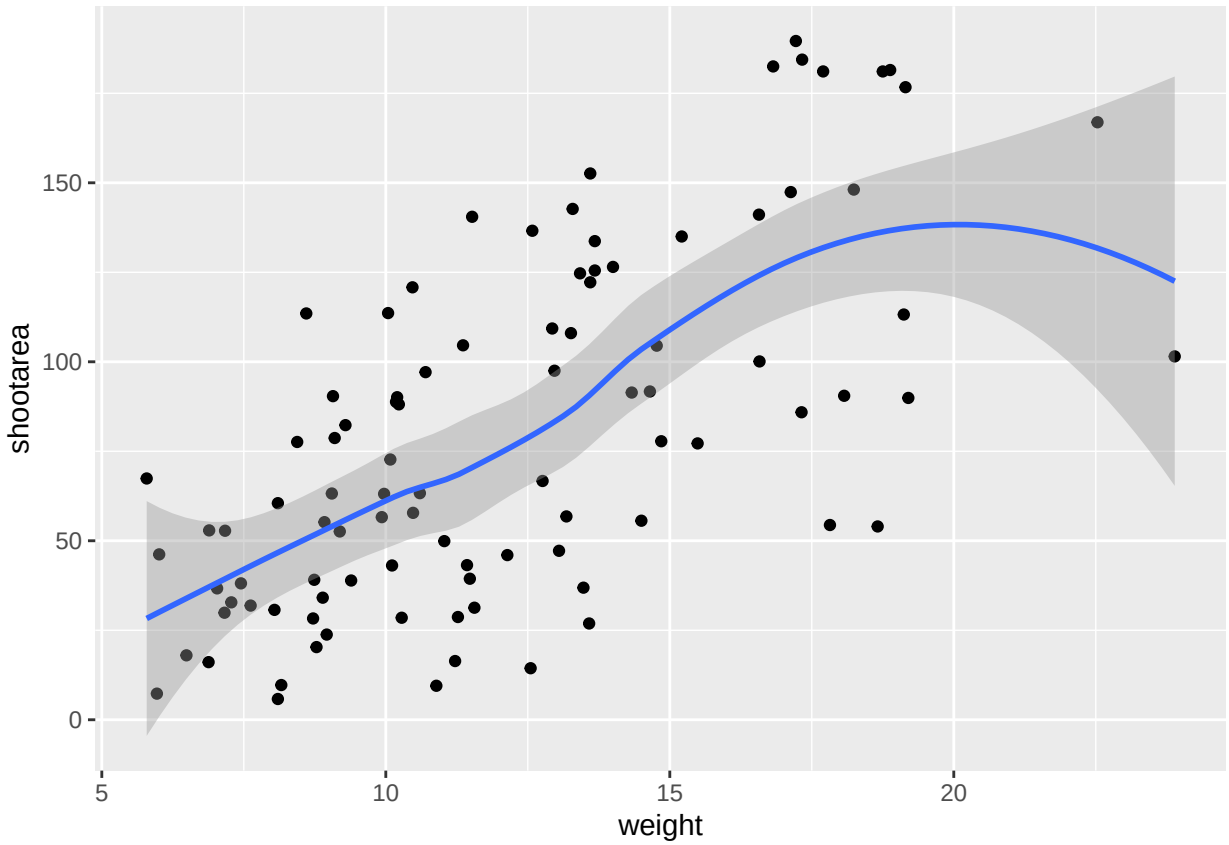
```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point() +
  geom_path()
```



Not quite what we were going for. The problem that we have is that geom_line() is actually just playing join-the-dots in the order they appear in the data (an alternative to geom_path()). The geom we actually want to use is

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point() +
  geom_smooth() # Changing to geom_smooth
```

```
## `geom_smooth()` using method = 'loess' and formula = 'y ~ x'
```

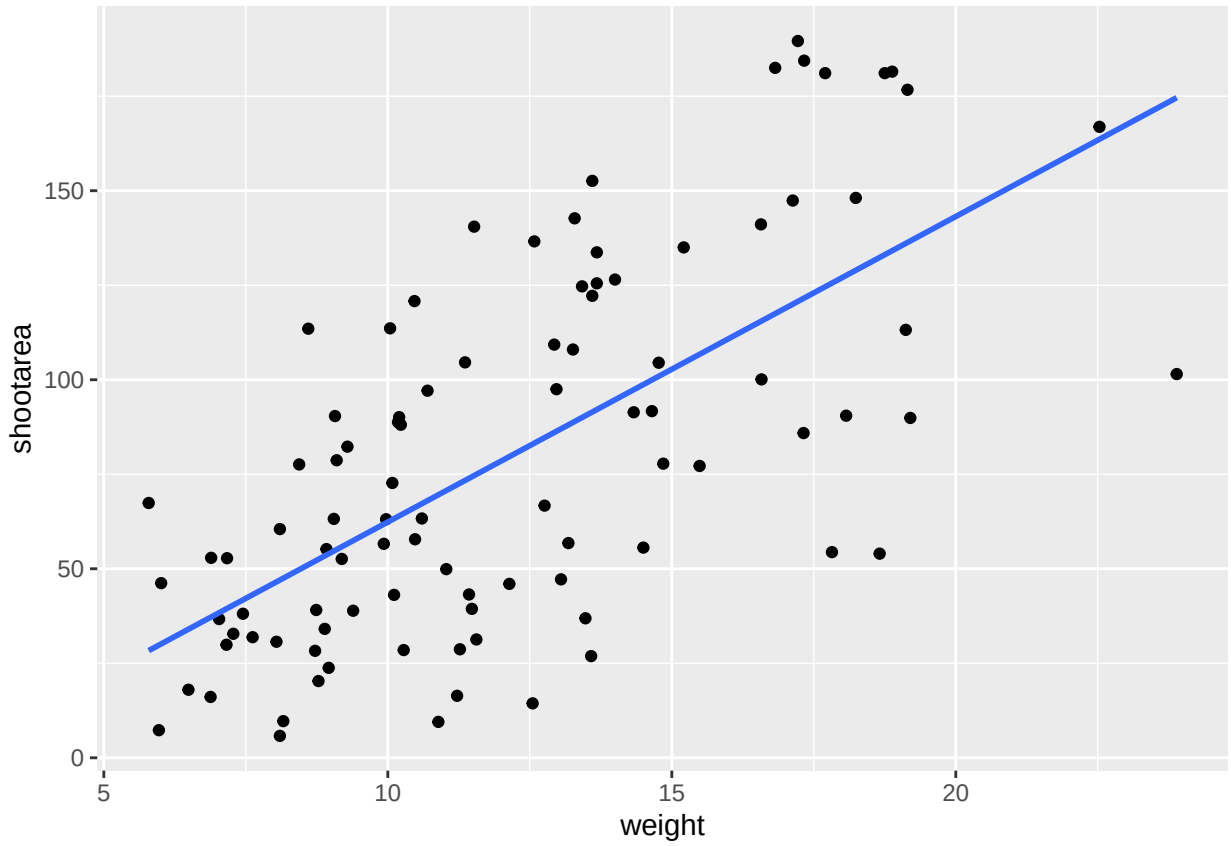


Better, but still not what we wanted. The challenge here is that drawing a line is actually somewhat complicated. The way our line above was drawn was by using a method called "LOESS" (locally estimated scatterplot smoothing) which gives something very close to a moving average; useful in some cases, less so in others. ggplot2 will use LOESS as default when you have < 1000 observations, so we'll need to manually specify the method. Instead of a wiggly line, we want a nice simple 'line of best fit' to be drawn using a method called "lm" (short for linear model - see Chapter 6 for more details). Try looking at the help file, using ?geom_smooth, to see what other options are available for the method = argument.

While we're at it, let's get rid of the confidence interval ribbon around the line. We prefer to do this as we think it's clearer to the audience that this isn't a properly analysed line and to treat it as a visual aid only. We can do this at the same time as changing the method by setting the se = argument (short for standard error) to FALSE. Let's update the code to use a linear model without confidence intervals.

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) # method and se
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



For diiferent factors or a Categorical variable

We get the straight line that we wanted, though it's still not matching the "final figure".

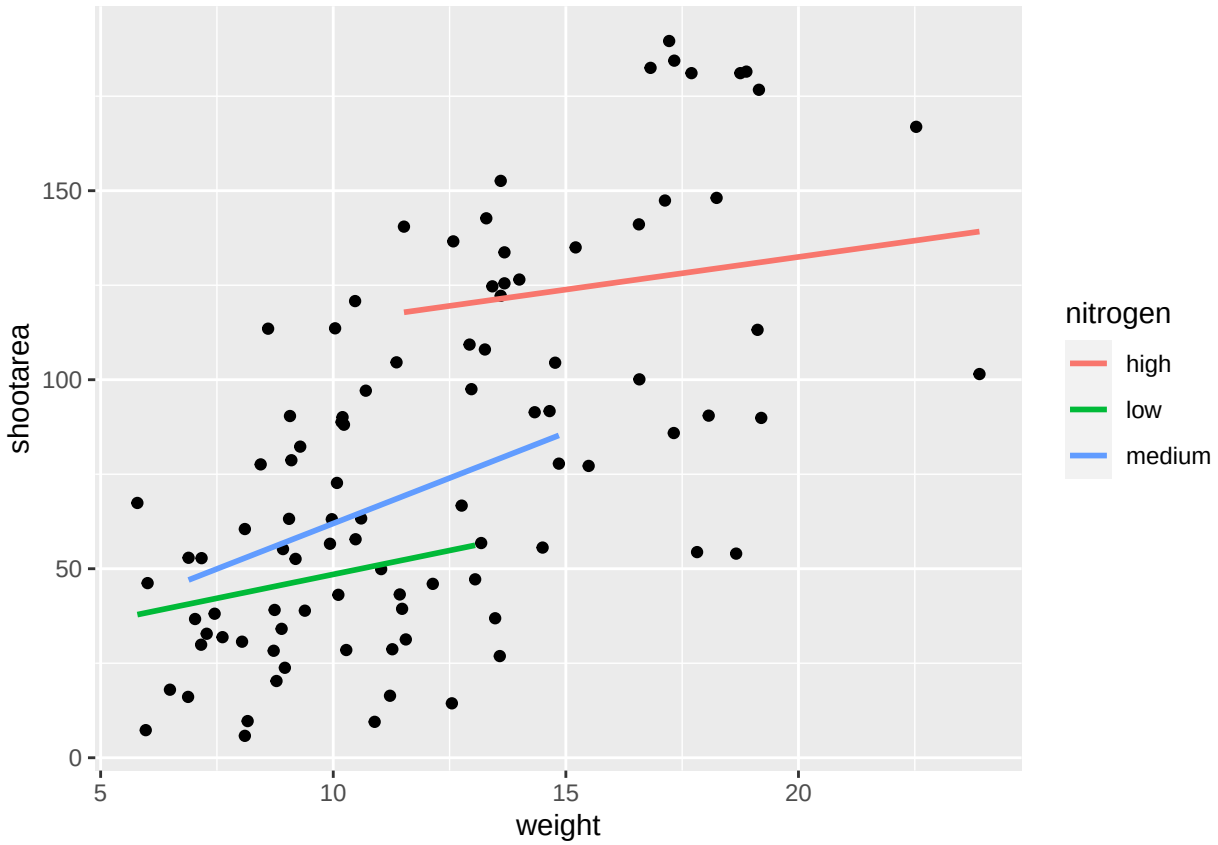
We need to alter geom_smooth() so that it draws lines for each level of nitrogen concentration. Getting ggplot2 to do that is pretty straightforward

We can use the colour = argument within `aes()`

(remember whatever we include in `aes()` will be something displayed in the figure) to tell ggplot2 to draw a different coloured lines depending on the nitrogen variable. Keep in mind that we have no variable in our dataset called "nitrogen_colour", so ggplot2 is taking care of that for us here and assigning a colour to each unique nitrogen level. An aside: ggplot2 was written with both UK English and American English in mind, so both colour and color spellings work in ggplot2

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point() +
  # Including colour argument in aes()
  geom_smooth(aes(colour = nitrogen), method = "lm", se = FALSE)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



We're getting closer, especially since ggplot2 has automatically created a legend for us.

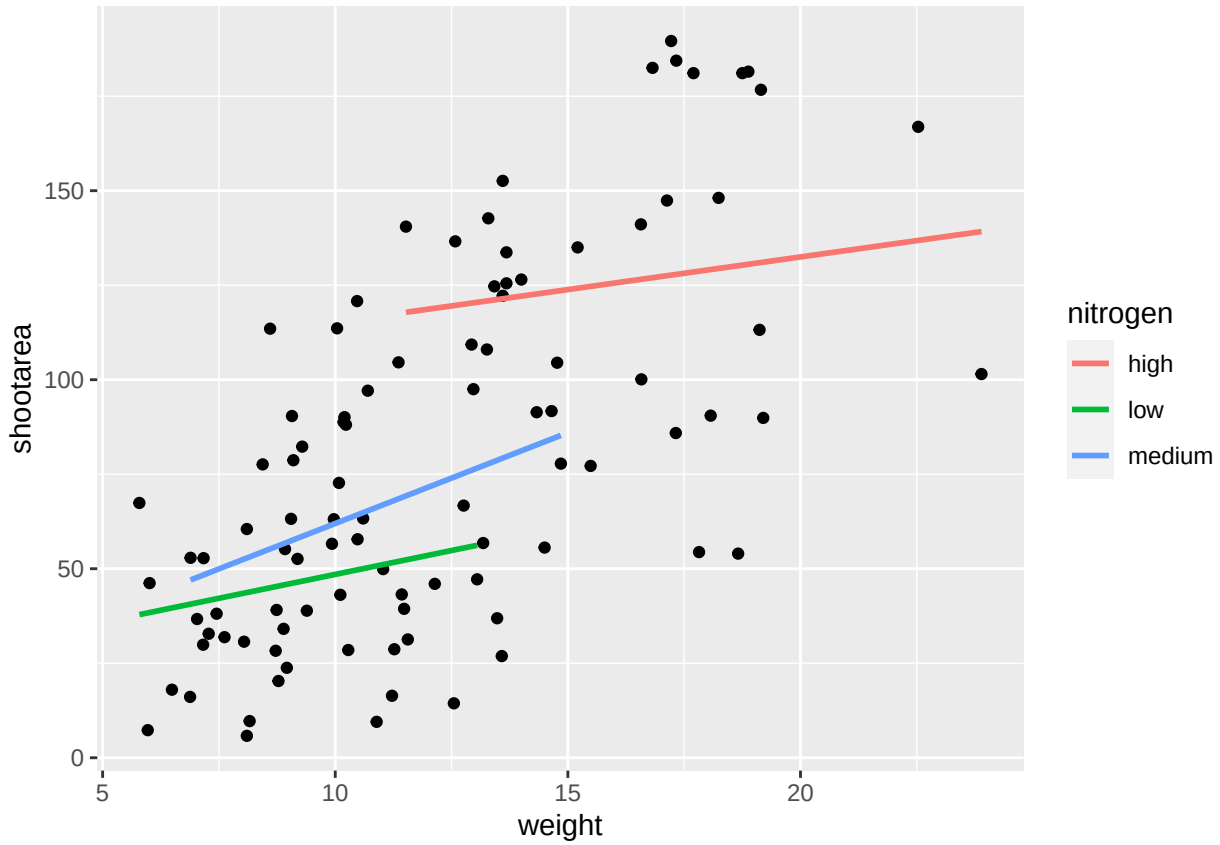
Where to include information

At this point it's a good time to talk about where to include information - whether to include it within a geom or in the main call to ggplot().

When we include information such as data = and aes() in ggplot() we are setting those as the default, universal values which all subsequent geoms use. Whereas if we were to include that information within a geom, only that geom would use that specific information. In this case, we can easily move the information around and get exactly the same figure.

```
ggplot() +
  # Moved aes() and data into geoms
  geom_point(aes(x = weight, y = shootarea), data = flowergg) +
  geom_smooth(aes(x = weight, y = shootarea, colour = nitrogen),
              data = flowergg, method = "lm", se = FALSE)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Doing so we get exactly the same figure. This ability to move information between the main ggplot() call or in specific geoms is surprisingly powerful (although sometime confusing!).

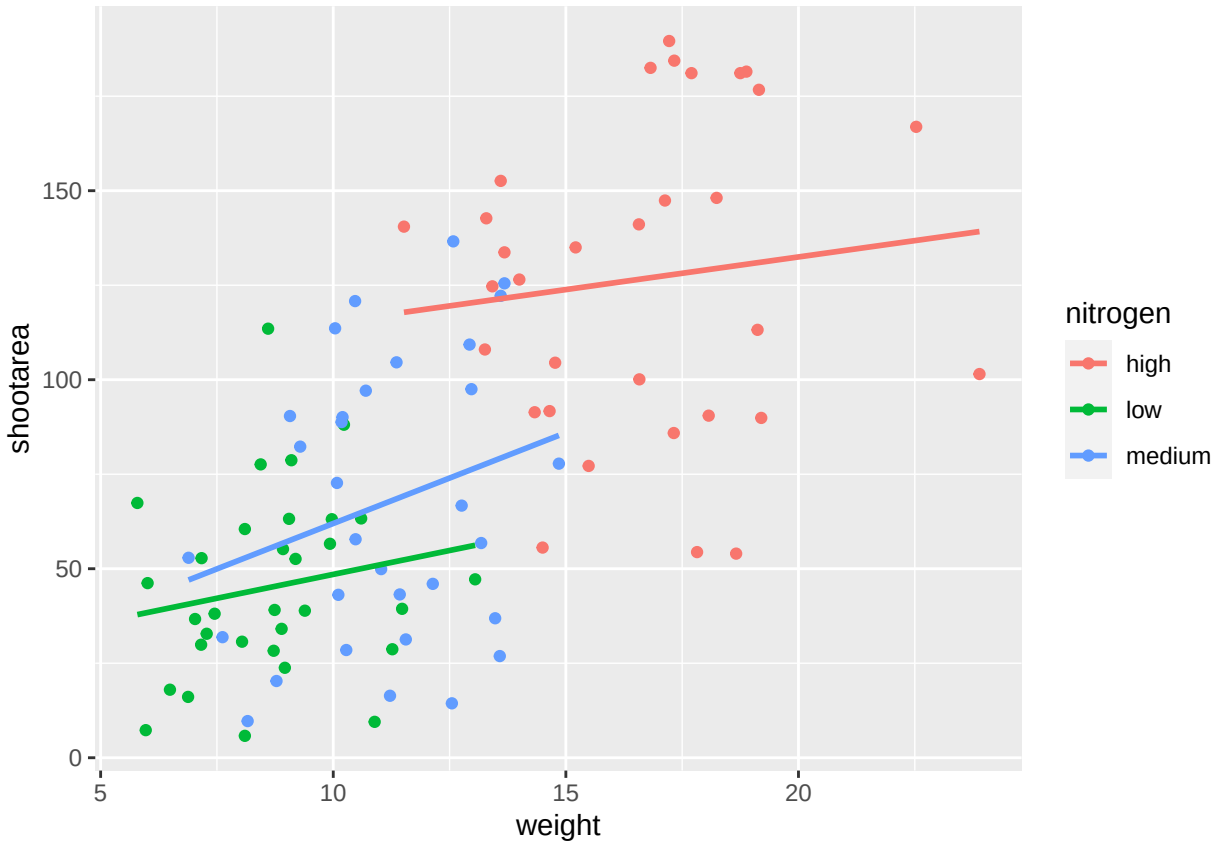
It can allow different geoms to display different (albeit similar) information (see more on this later). For this worked example, we'll move the same information back to the universal ggplot(),#

Points according to different concentrations

NOW TO GET POINTS COLOURED ACC TO DIFFERENT CONCENTRATIONS, but we'll also move colour = nitrogen into ggplot() so that we can have the points coloured according to nitrogen concentration as well Moved colour = nitrogen into the universal ggplot()

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



This figure is now what we would consider to be the typical ggplot2 figure (once you know to look for it, you'll see it everywhere). We have specified some information, with only a few lines of code, yet we have something that looks quite attractive. While it'snot yet the "final figure" it's perfectly suited for displaying the information we need from these data. You have now created your first "pure" ggplot using only the 'data','mapping' and 'geom' layers (as well as others indirectly).

Let's keep going as we're aiming for something a bit more "sophisticated

Wrapping grids (2 Conditional variables)

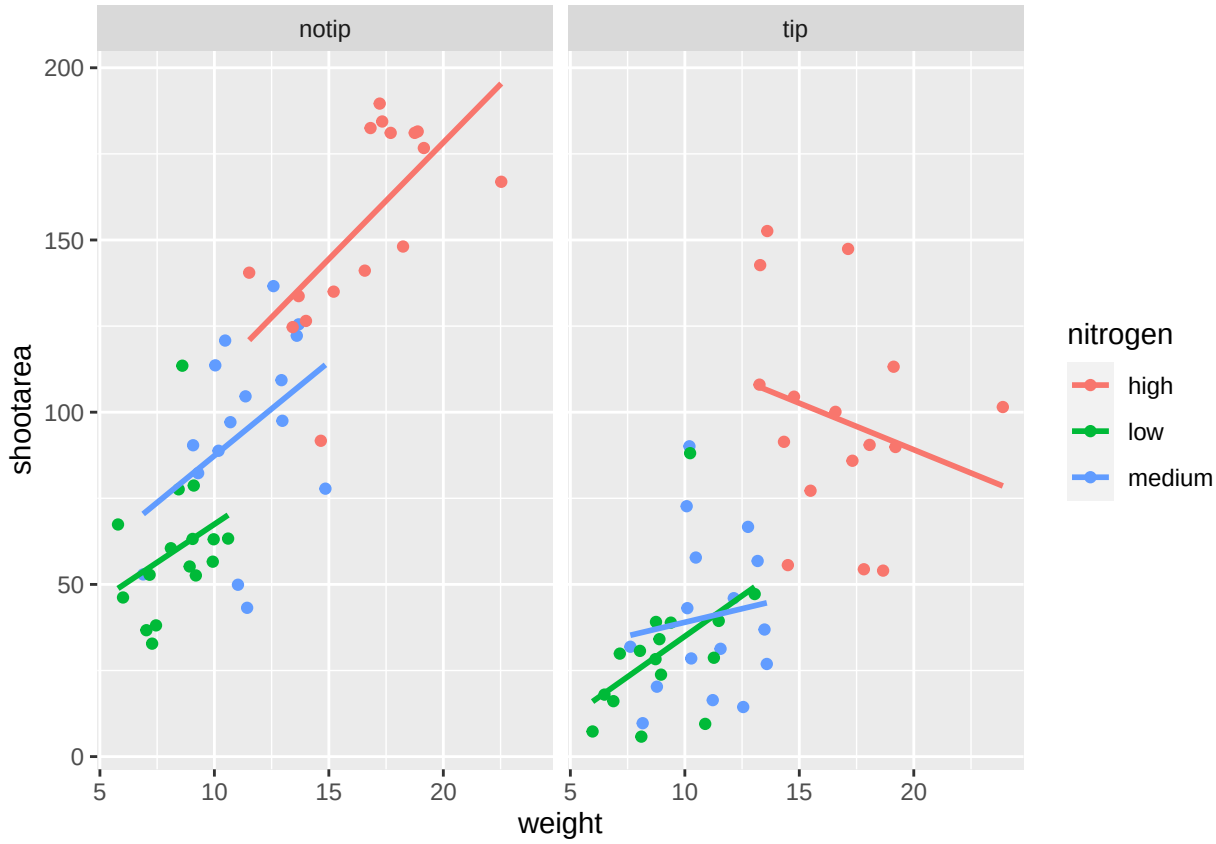
Having made our "pure" ggplot, the next big obstacle we're going to tackle is the grid like layout of the "final figure" where our main figure has been split according to the treat and block variables, with new trends shown for each combination Each of these panels (technically "multiples") are a great way to help other people understand what's going on in the data. This is especially true with large datasets which can obscure subtle trends simply because so much data is overlaid on top of each other. When we split a single figure into multiples, the same axes are used for all multiples which serve to highlight shifts in the data (data in some multiples may have inherently higher or lower values for instance).

ggplot2 includes options for specifying the layout of plots using the 'facets' layer. We'll start off by using facet_wrap() to show what this does. For facet_wrap() to work we need to specify a formula for how the facets will be defined (see ?facet_wrap for more details and also how to define facets without using a formula). In our example we want to use the factor treat to determine the layout so our formula would look like ~ treat. You can read ~ treat as saying "according to treatment". Let's see how it works:

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
```

```
  # Splitting the single figure into multiple depending on treatment
  facet_wrap(~ treat)
```

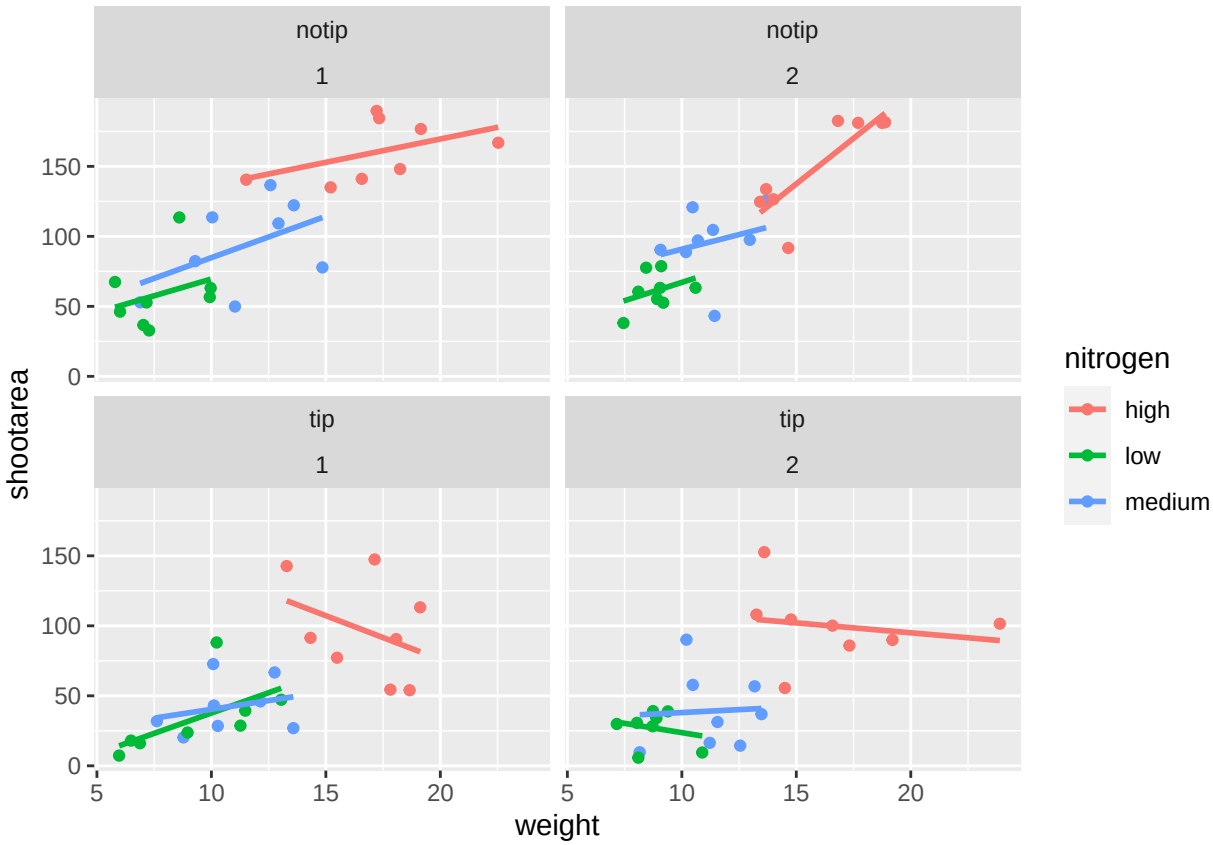
```
## `geom_smooth()` using formula = 'y ~ x'
```



That's pretty good. Notice how we can see the impact that the tip treatment has on shoot area now (generally lowering shoot area), where in the previous figure this was much more difficult to see? While this looks pretty good, we are still missing information showing any potential effect of the different blocks. Given that facet_wrap() can use a formula, maybe we could simply include block in the formula? Remember that the block variable refers to the region in the greenhouse where the plants were grown. Let's try it and see what happens.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  # Adding "block" to formula
  facet_wrap(~ treat + block)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



This facet layout is almost exactly what we want. Close but no cigar. In this case we actually want to be using facet_grid(), an alternative to facet_wrap(), which should put us back on track to make the "final figure".

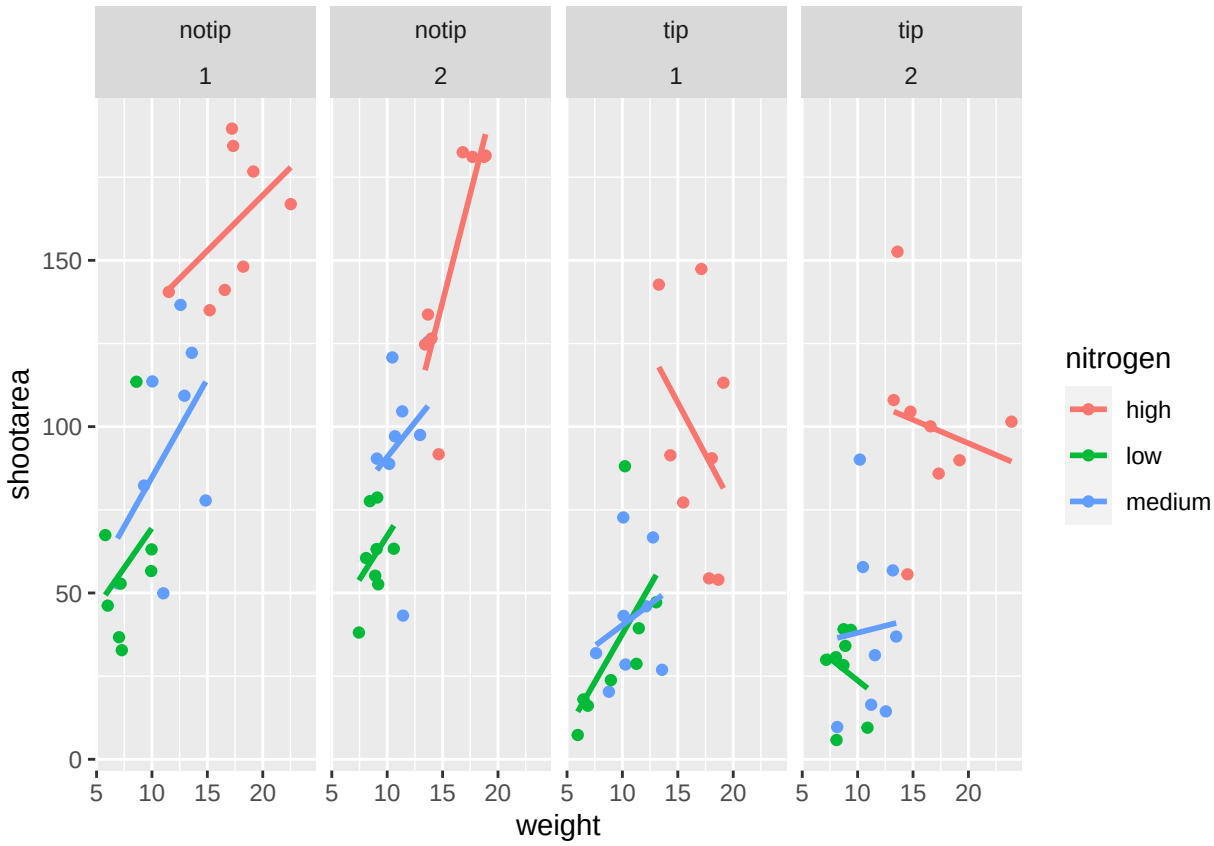
facet_grid

Play around: Try changing the formula to see what happens. Something like ~ treat + flowers or even ~ treat + block + flowers. The important thing to remember here is that facet_wrap() will create a new figure for each value in a variable. So when you wrap using a continuous variable like flowers, it makes a plot for every unique number of flowers counted. Be aware of what it is that you are doing, but never be scared to experiment. Mistakes are easily fixed in R - it's not like a point and click programme where you'd have to go back through all those clicks to get the same figure produced. Made a mistake? Easy, change it back and rerun the code (see Chapter 9 for version control which takes this to the next level).

Let's try using facet_grid instead of facet_wrap to produce the following plot.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  # Changing to facet_grid
  facet_grid(~ treat + block)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

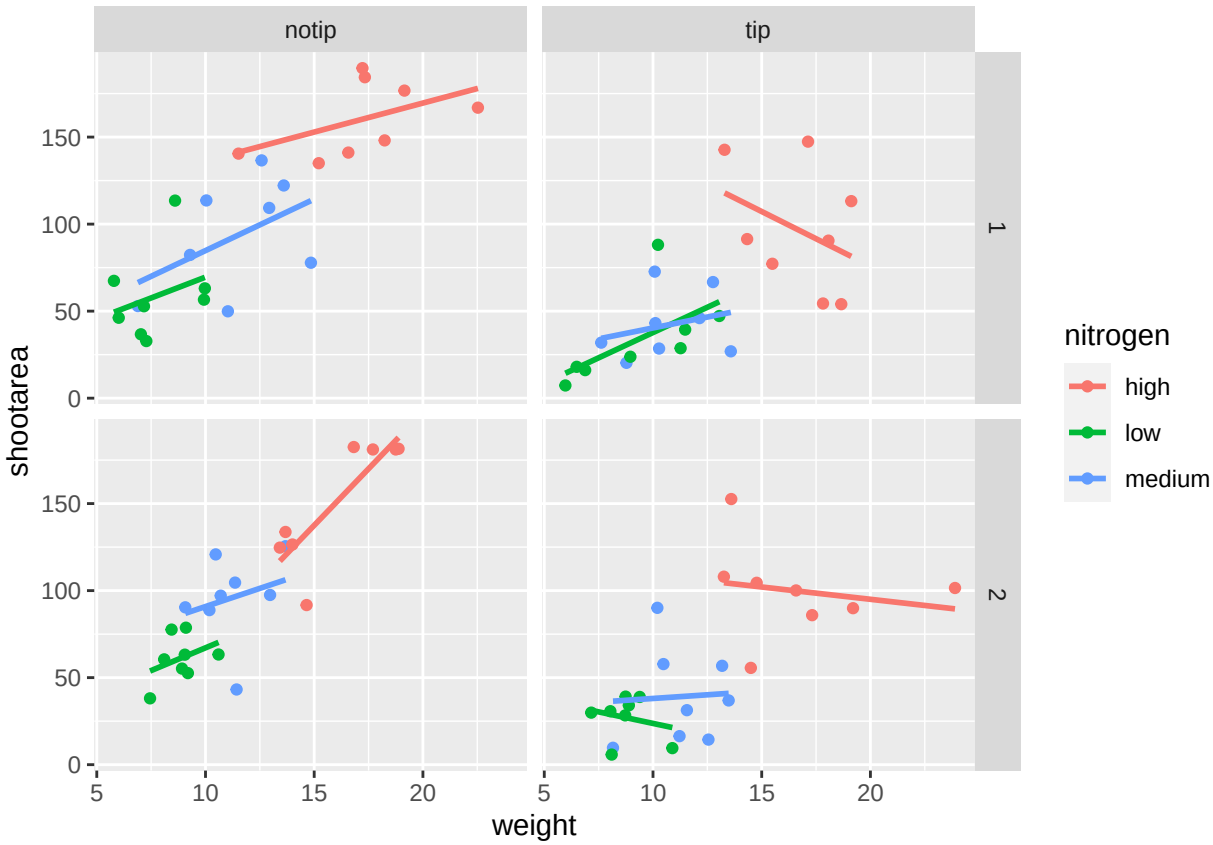


Disappointing

That's disappointing. It's pretty much the same as what we had before and is no closer to the "final figure". To fix this we need to do to rearrange our formula so that we say that it is block in relation to treatment (not in combination with).

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  # Rearranging formula, block in relation to treatment
  facet_grid(block ~ treat)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



And we're there. Although the styling is not the same as the "final figure" this is showing the same core fundamental information.

Customizing figure

While we already have a great figure showing the main aspects of our data, it uses many default layer options. Whilst the default options are fine we may want to change them to get our plot looking exactly how we want it. Maybe we're going to use this figure in a presentation and we want to make sure someone in the very back of the room can easily read the figure. Maybe we want to use our own colour scheme. Maybe we want to change the grey background to a nice bright neon pink. In essence, maybe we want to decide things for ourselves.

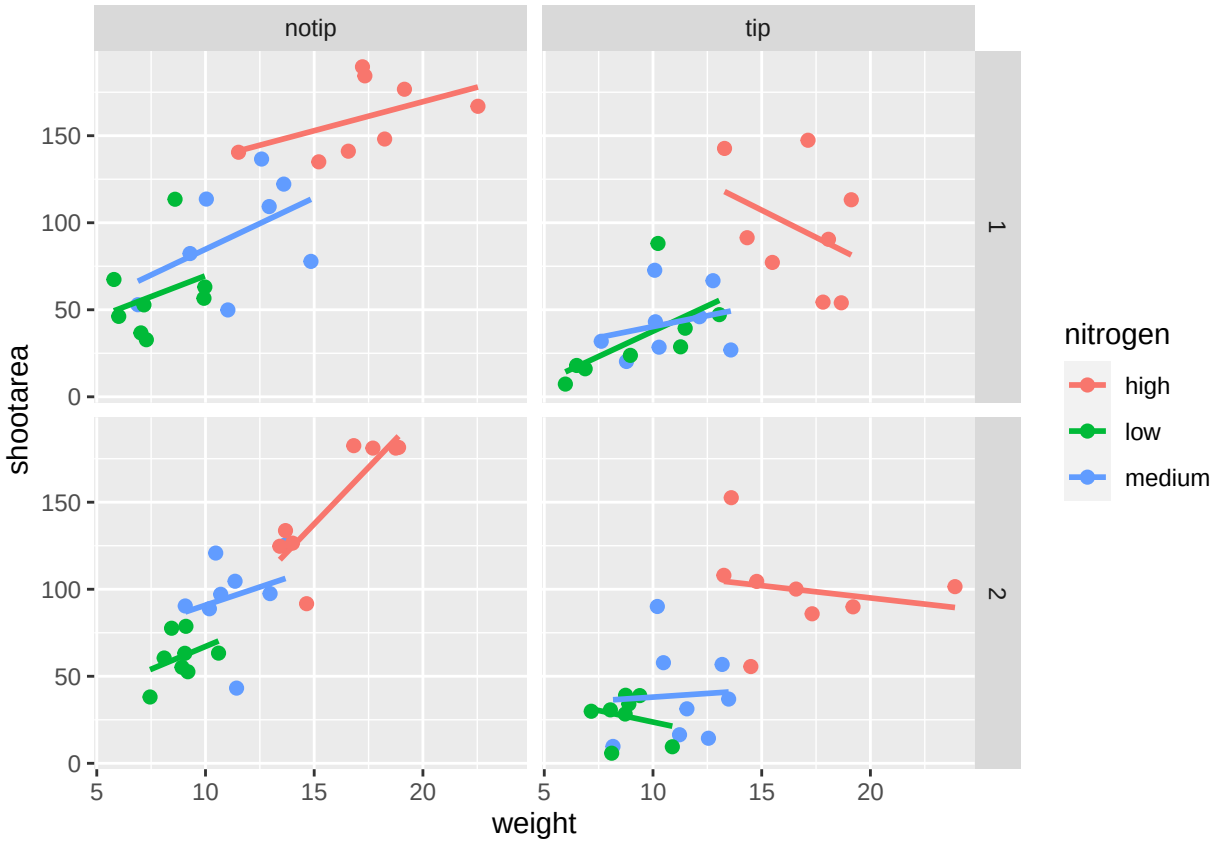
This next section will go through how to customise the appearance of our figure.

Let's start with the easier stuff, namely changing the size of the plotting symbols using the size = argument. Before we do, have a think about where we'd include this argument? Should it be in main call to ggplot() or in the geom_point() geom? Does size depend on a variable in our dataset and is therefore something we want displayed on the figure (meaning we should include it within aes())? Or is it merely changing the appearance of information?

Let's include it in the geom_point geom

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  # Including size argument to change the size of the points
  geom_point(size = 2) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat)
```

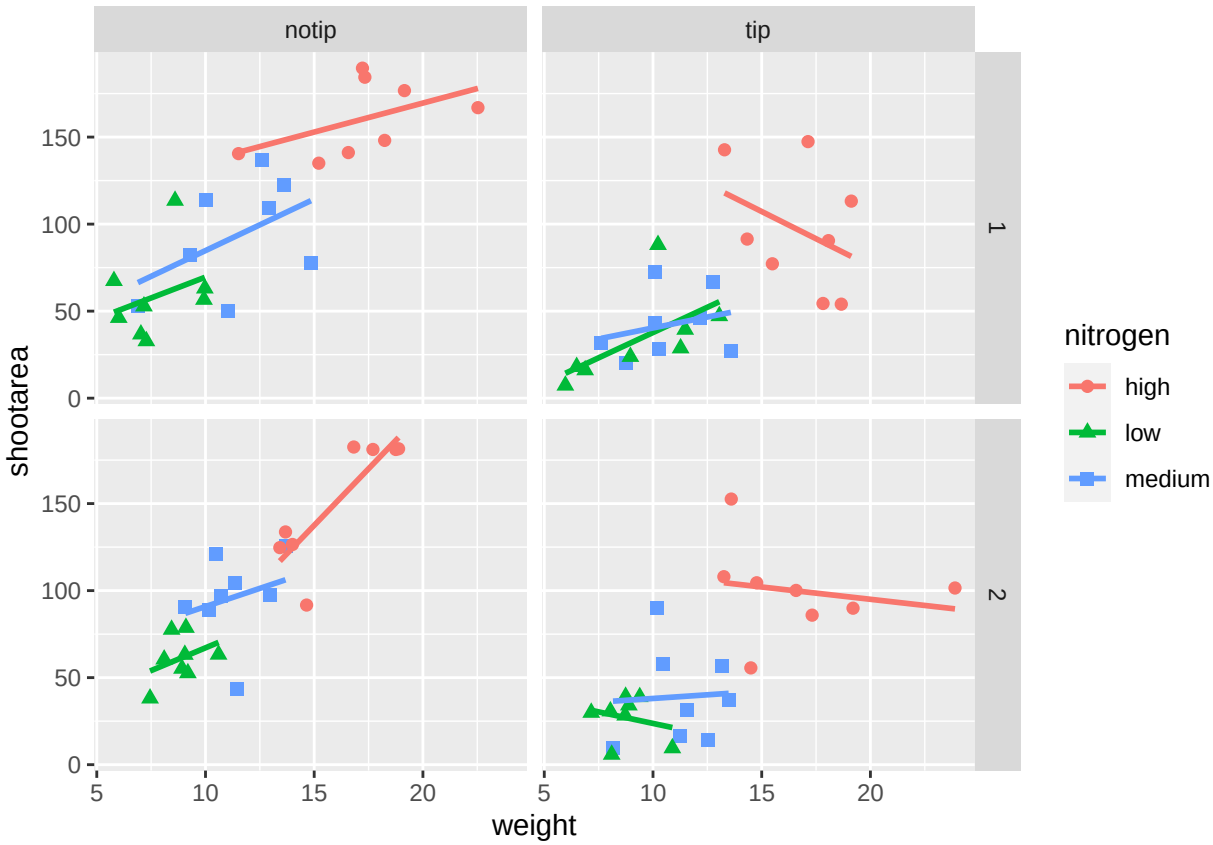
```
## `geom_smooth()` using formula = 'y ~ x'
```



If we wanted to change the shape of the plotting symbols to reflect the different nitrogen concentrations (low, high, medium), how do you think we'd do that? We'd use the shape = argument, but this time we need to include an aes() within geom_point() because we want to include specific information to be displayed on the figure.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  # Including shape argument to change the shape of the points
  geom_point(aes(shape = nitrogen), size = 2) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

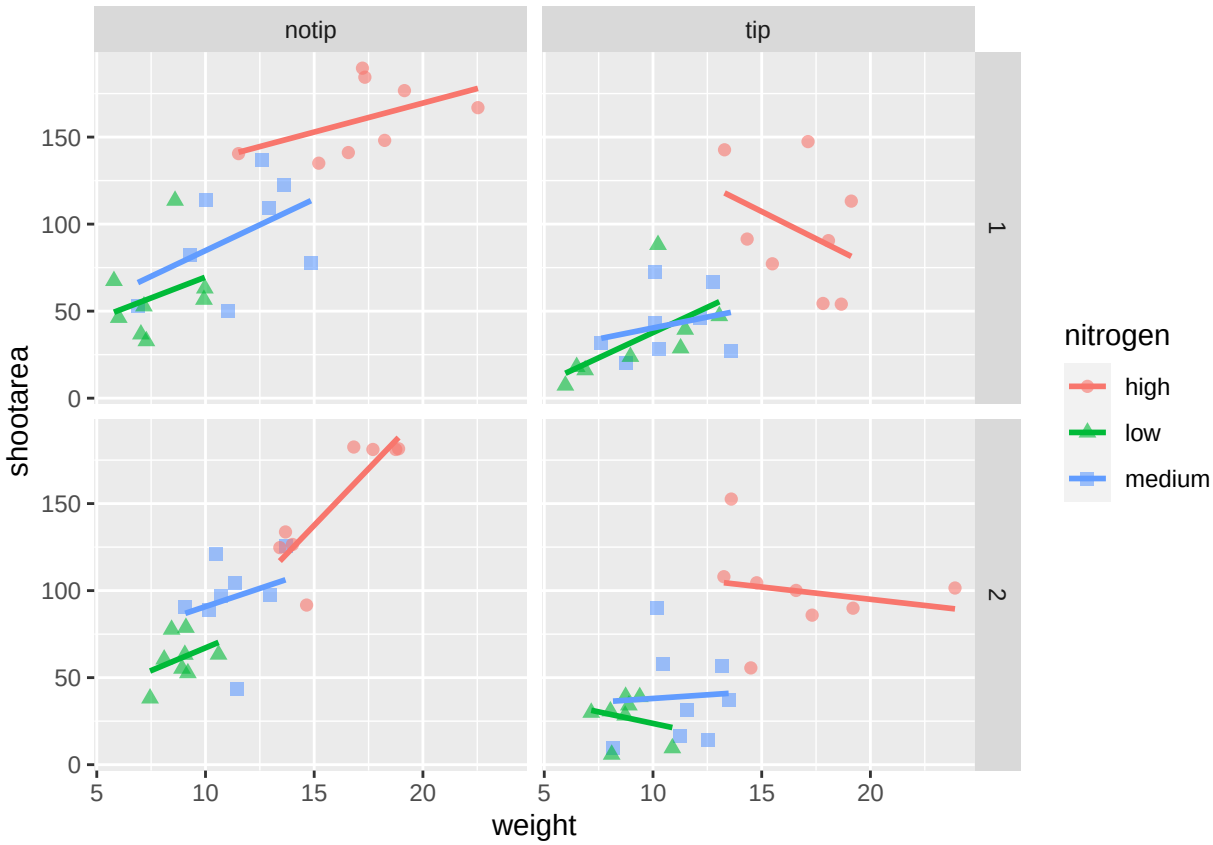


Aplha argument = Transparency

We're edging our way closer to our "final figure". Another thing we may want to be able to do is change the transparency of the points. While it's not actually that useful here, changing the transparency of points is really valuable when you have lots of data resulting in clusters of points obscuring information. Doing this is easily accomplished using the alpha = argument. Again, ask yourself where you think the alpha = argument should be included (hint: you should put it in the geom_point geom!).

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  # Including alpha argument to change the transparency of the points
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat)
```

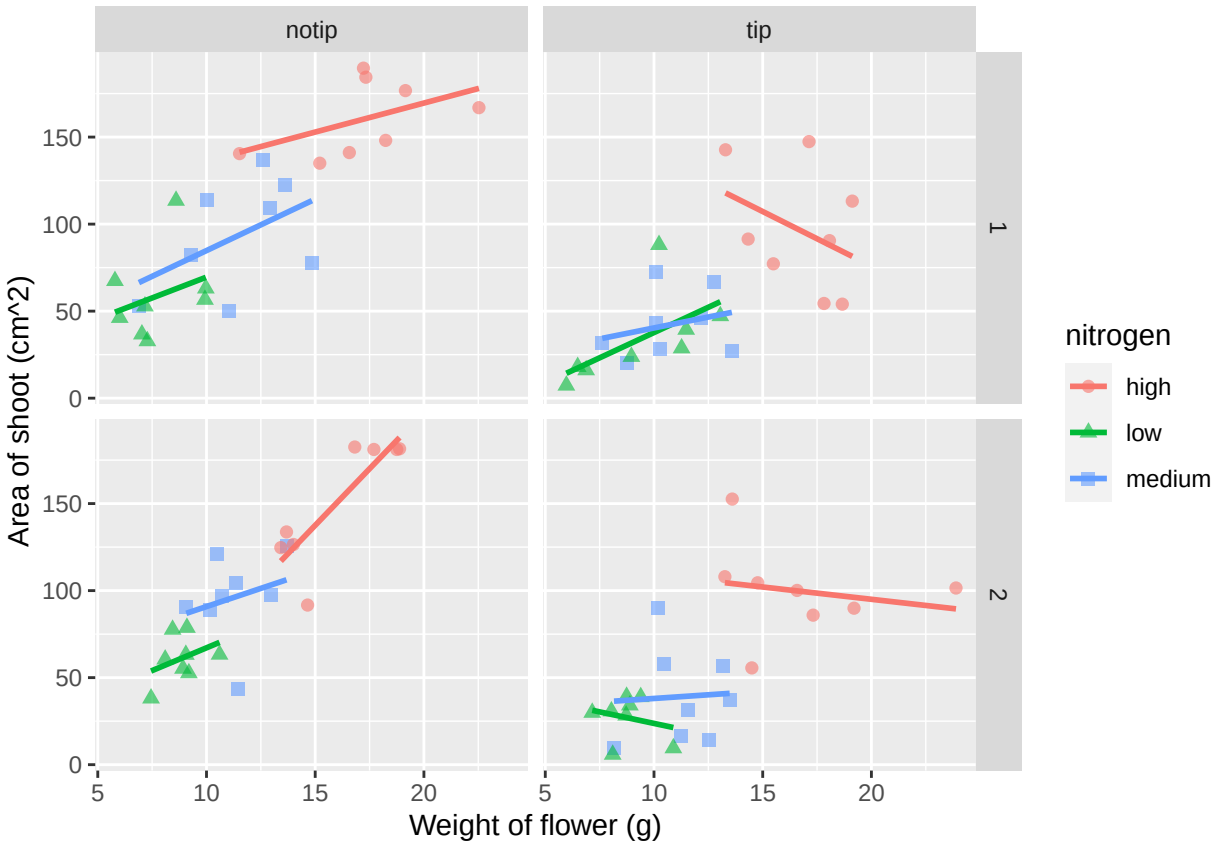
```
## `geom_smooth()` using formula = 'y ~ x'
```



We can also include user defined labels for the x and y axis. There are a couple of ways to do this, but a more familiar way may be to use the same syntax as used in base R figures; using xlab() and ylab(). We'll specify that these belong to the ggplot by using the + symbol.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  # Adding layers for x and y labels
  xlab("Weight of flower (g)") +
  ylab("Area of shoot (cm^2)")
```

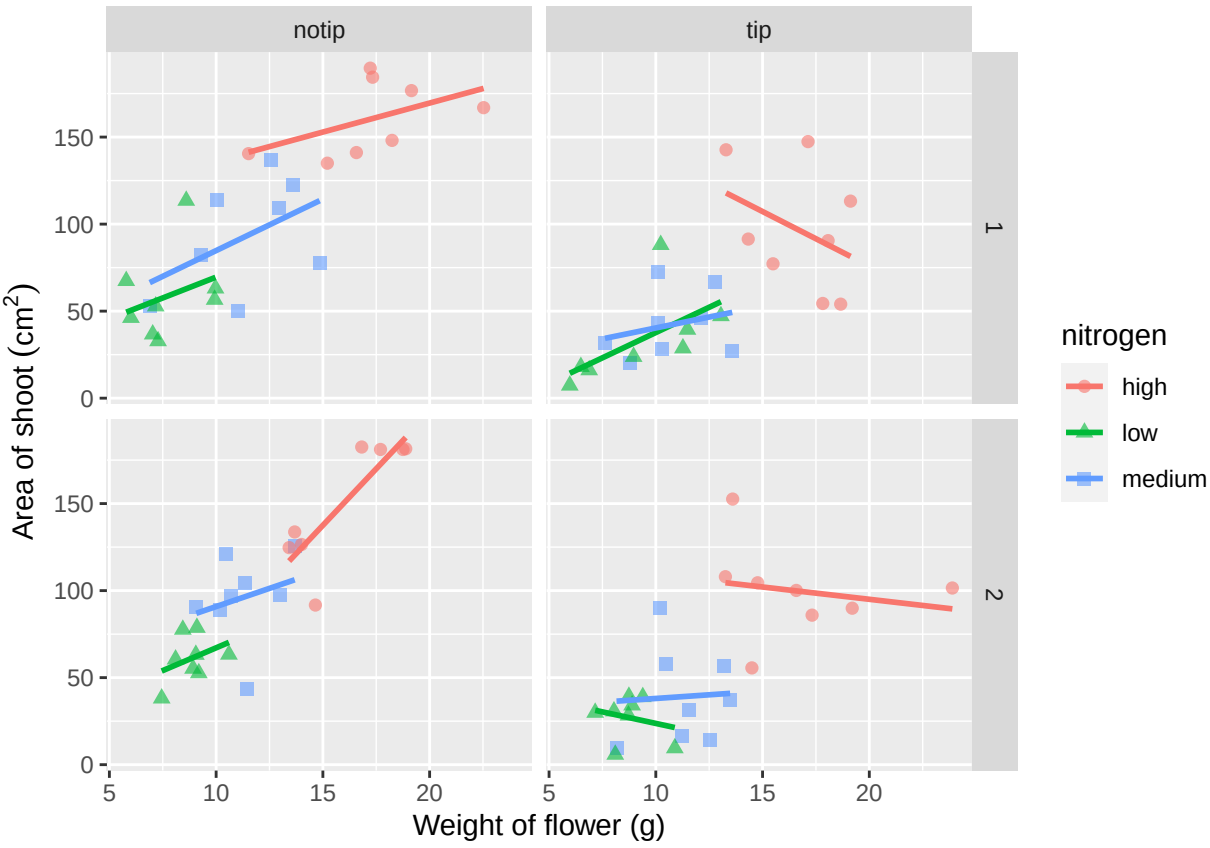
```
## `geom_smooth()` using formula = 'y ~ x'
```



Great. Just as we wanted, though getting the "(cm^2)" to show the square as a superscript would be ideal. Here, we're going to accomplish that using a function which is part of base R called bquote() which allows for special characters to be shown.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  # Using bquote to get mathematically correct formatting
  ylab(bquote("Area of shoot"~(cm^2)))
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

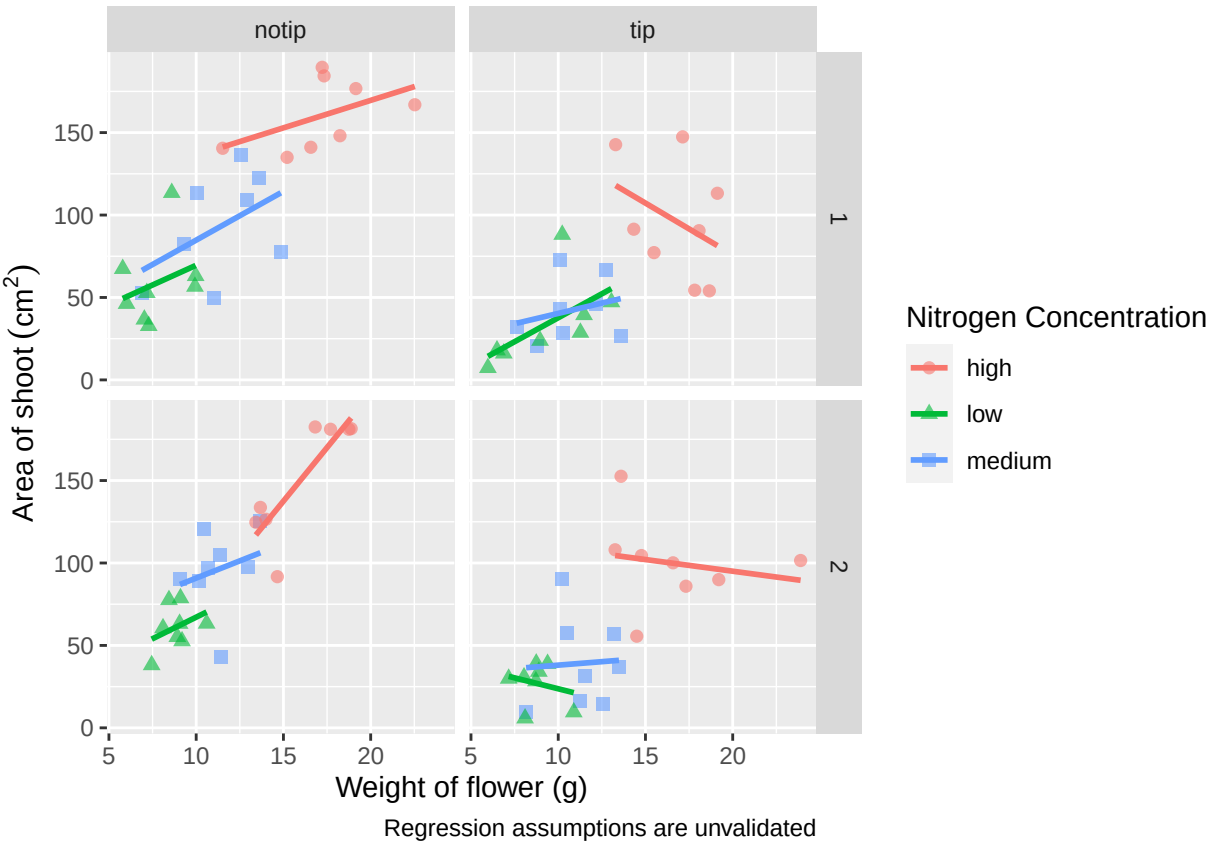


Legend and Caption

Let's now work on the legend title while also including a caption to warn people looking at the figure to treat the trend lines with caution. We'll use a new layer called labs(), short for labels, which we could have also used for specifying the x and y axes labels (we didn't only for demonstration purposes, but give it a shot). labs() is a fairly straightforward function. Have a look at the help file (using ?labs) to see which arguments are available. We'll be using caption = argument for our caption, but notice that there isn't a single simple argument for legend =? That's because the legend actually contains multiple pieces of information; such as the colour and shape of the symbols. So instead of legend = we'll use colour = and shape =. Here's how we do it:

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  # Adding labels for shape, colour and a caption
  labs(shape = "Nitrogen Concentration", colour = "Nitrogen Concentration",
       caption = "Regression assumptions are unvalidated")
```

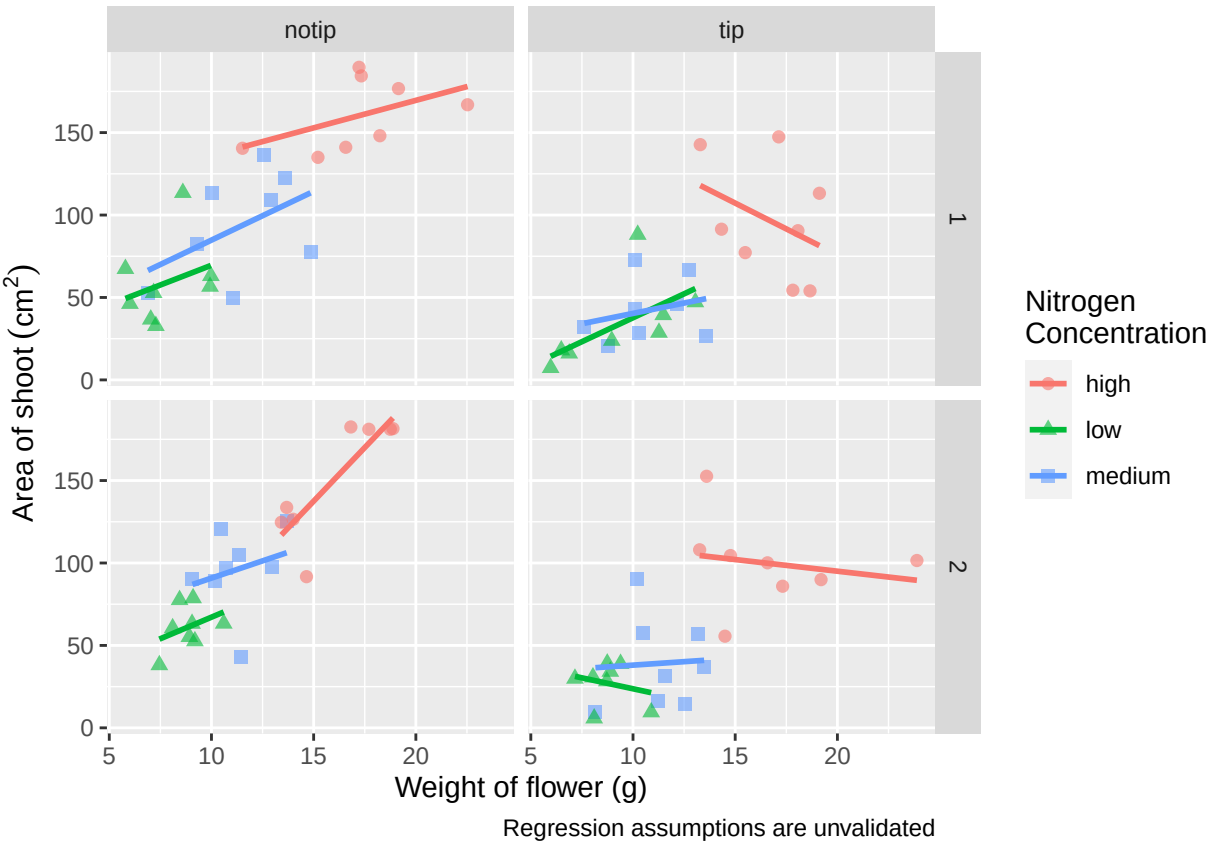
```
## `geom_smooth()` using formula = 'y ~ x'
```



Now's a good time to introduce the \n. This is a base R feature that tells R that a string should be continued on a new line. We can use that with "Nitrogen Concentration" so that the legend title becomes more compact.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  # Including \n to split legend title over two lines
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Settting the theme

Themes control the general style of a ggplot (things like the background colour, size of text etc.) and comes with a whole bunch of predefined themes. Let's play around with themes using some skills we've already learnt; assigning plots to an object and plotting multiple ggplots in a single figure using patchwork. We assign themes by creating a new layer with the general notation - theme_NameOfTheme(). For example, to use the theme_classic, theme_bw, theme_minimal and theme_light themes.

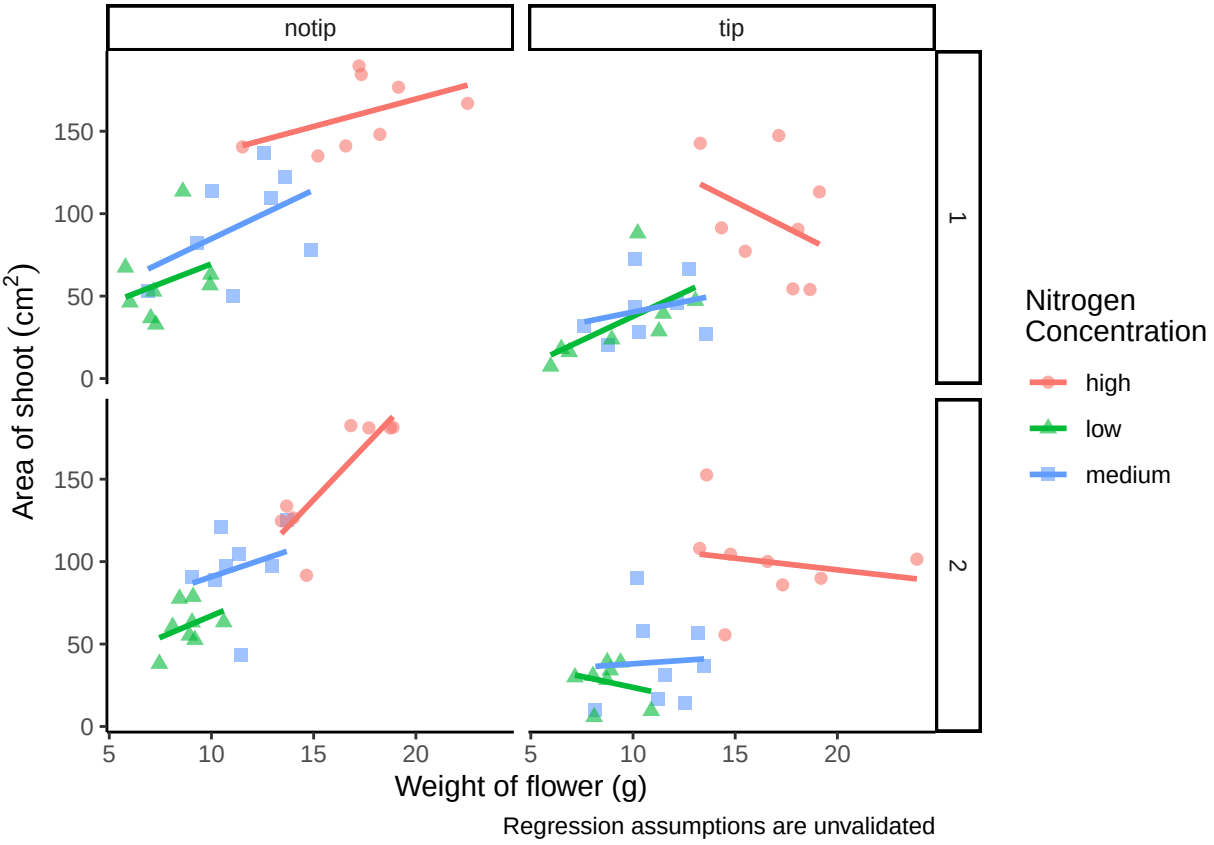
1. Classic theme

```
classic <- ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") + theme_classic()



#To use a them write the name of the object (that has our ggplot) + theme name
classic + theme_classic()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

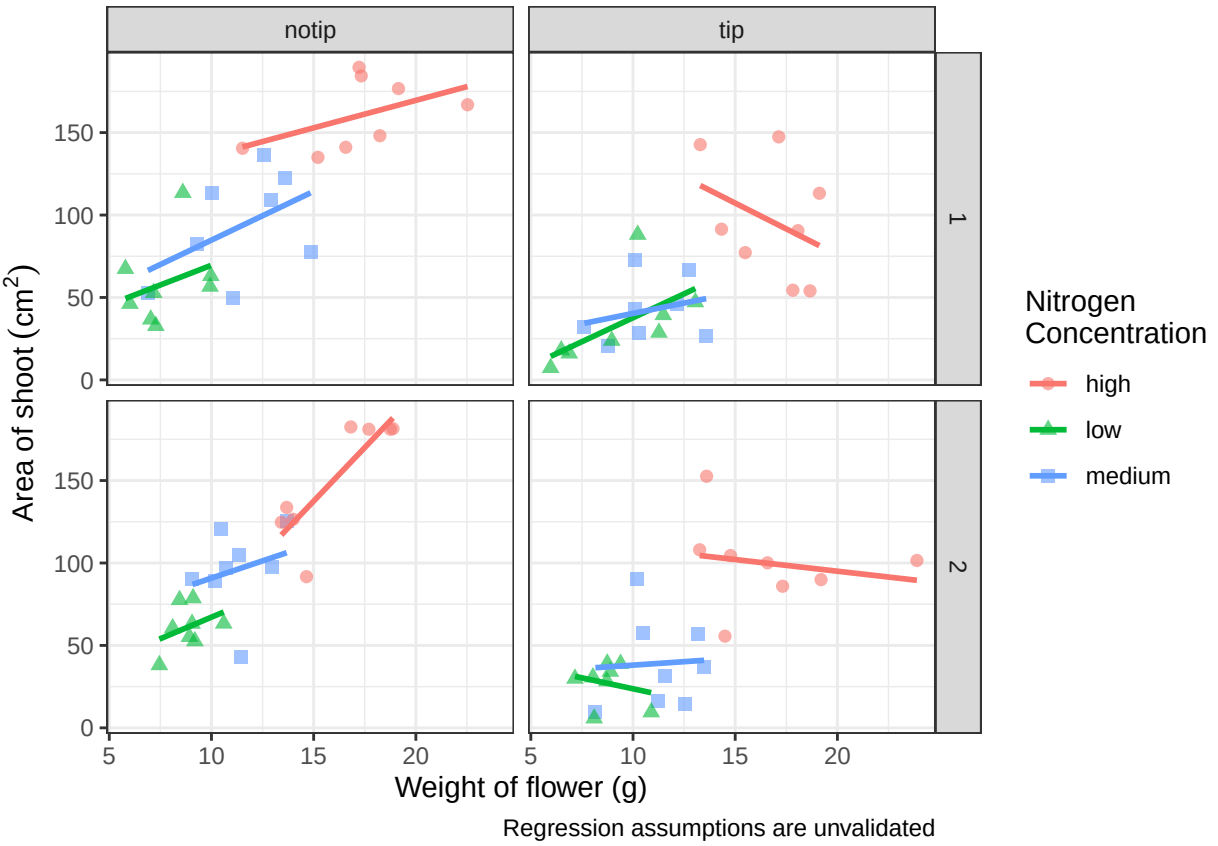


2. Black and white theme

```
bw <- ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") + theme_bw()


bw + theme_bw()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

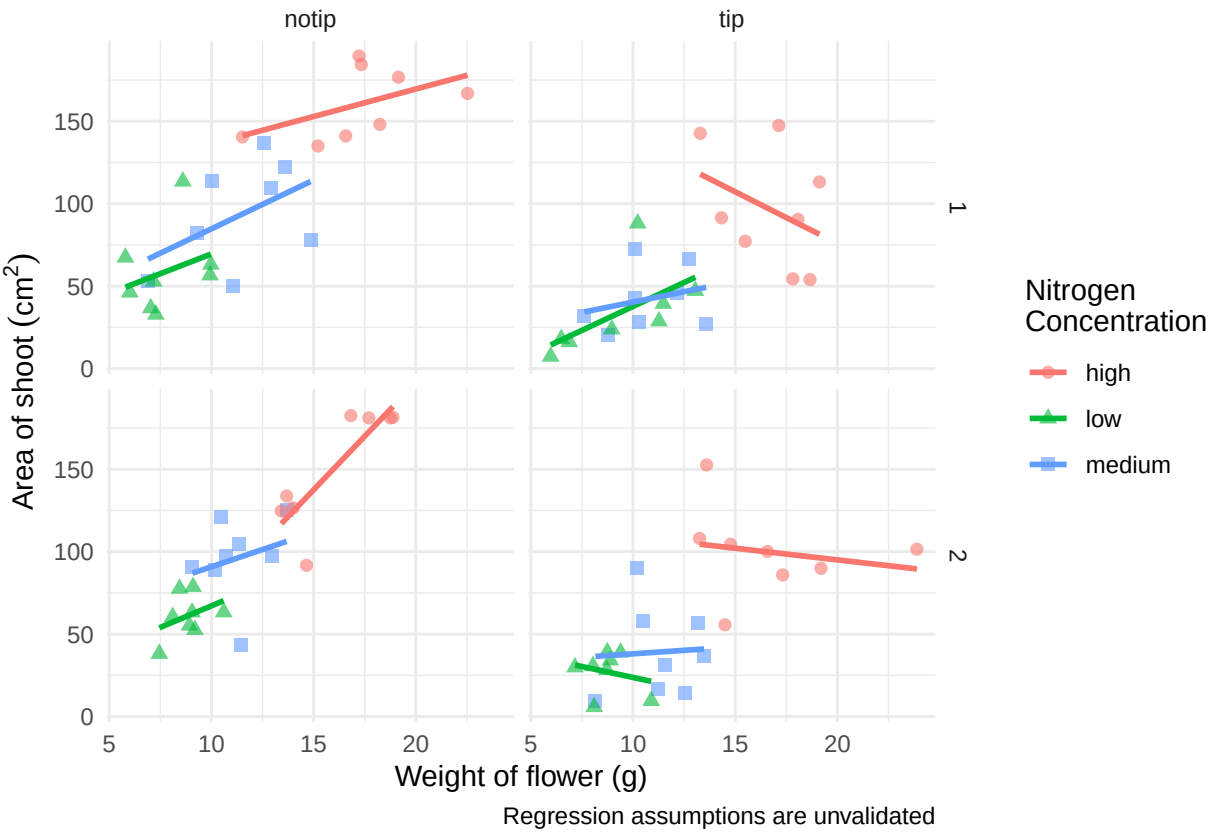


3. Minimal theme

```
minimal <- ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") + theme_minimal()


minimal + theme_minimal()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



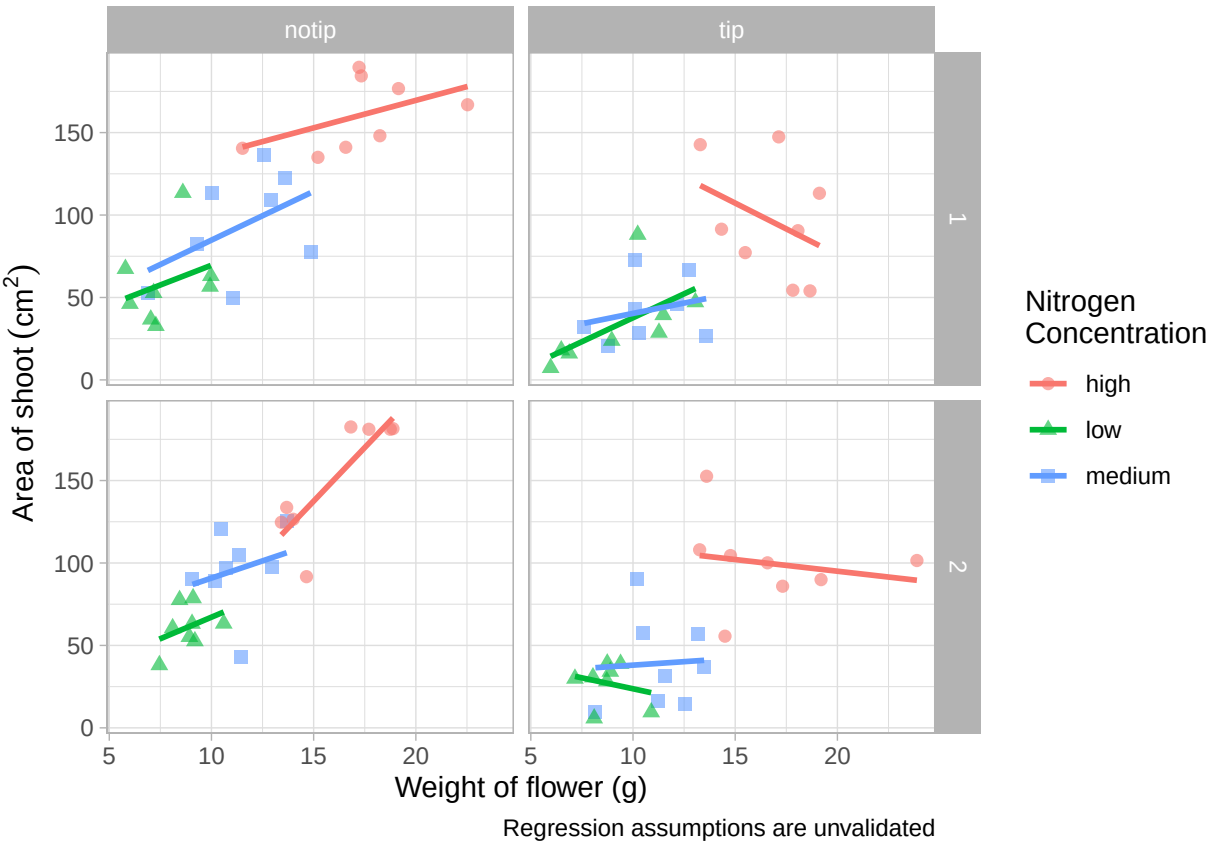
4. Light theme

```
light <- ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  theme_light()



light + theme_light()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



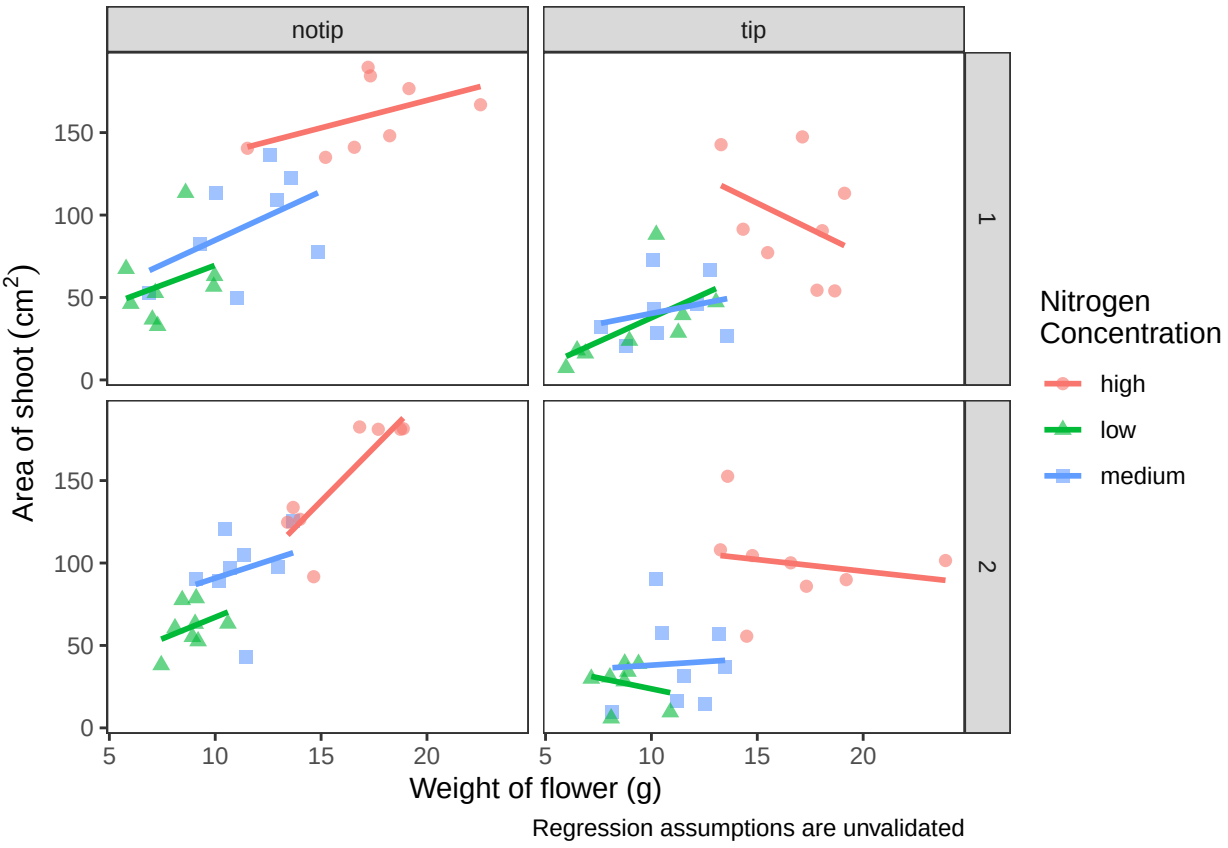
5. Test theme

```
test <- ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  theme_test()



test + theme_test()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



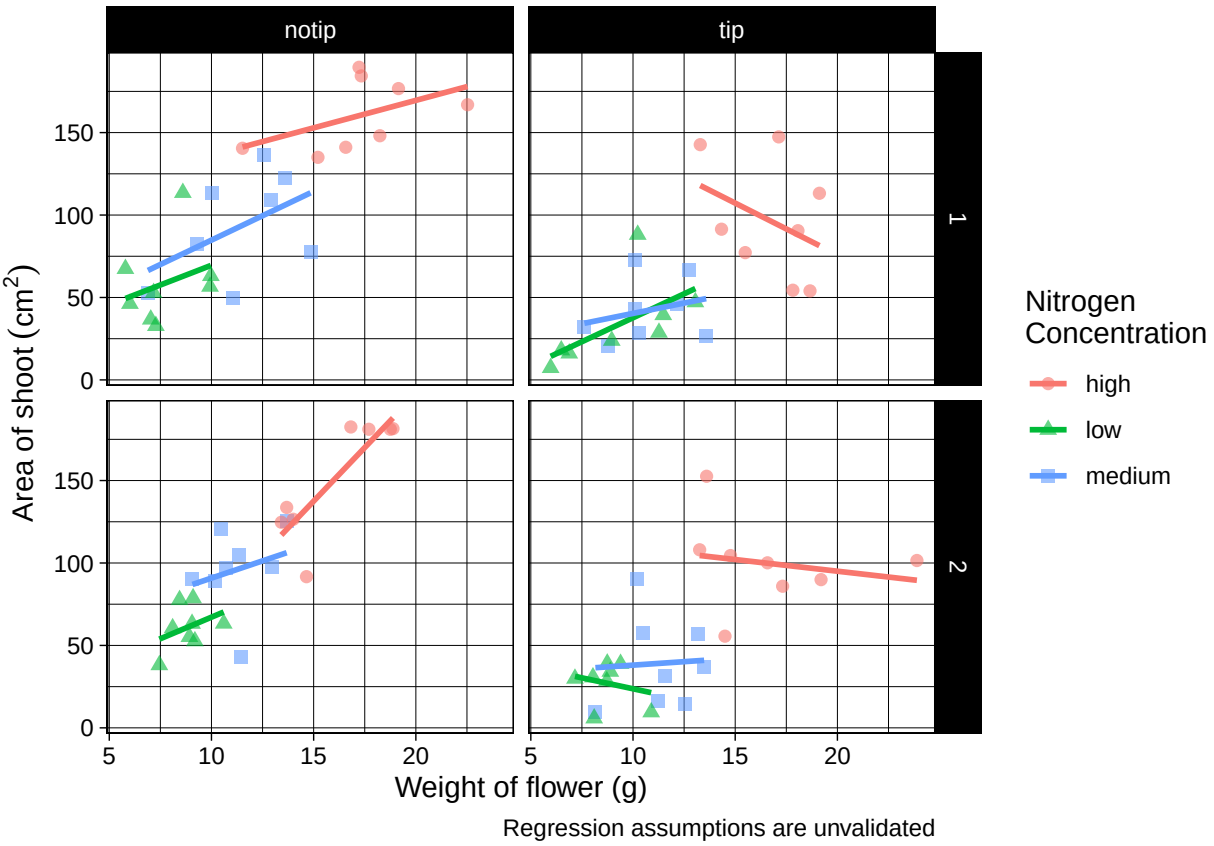
6. Line draw

```
linedraw <- ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  theme_linedraw()



linedraw + theme_linedraw()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Making your own theme

In terms of finding a theme that most closely matches our "final figure", it's probably going to be theme_classic(). There are additional themes available to you, and even more available online. ggthemes is a package which contains many more themes for you to use. The BBC even have their own ggplot2 theme called "BBplot" which they use when making their own figures (while good, we don't like it too much for scientific figures). Indeed, you can even make your own theme which is what we'll work on next. To begin with, we'll have a look to see how theme_classic() was coded. We can do that easily enough by just writing the function name without the parentheses (see Chapter 7 for a bit more on this).

Let's use this code as the basis for our own theme and modify it according to our needs. We'll call the theme, theme_rbook. Not all of the options will immediately make sense, but don't worry about this too much for now. Just know that the settings we're putting in place are: • Font size for axis titles = 13 • Font size for x axis text = 10 • Font size for y axis text = 10 • Font for caption = 10 and italics • Background colour = white • Background border = black • Axis lines = black • Strip colour (for facets) = light blue • Strip text colour (for facets) = black • Legend box colours = No colour This is by no means an exhaustive list of features you can specify in your own theme, but this will get you started. Of course, there's no need to use a personalised theme as the pre-built options are perfectly suitable.

```
theme_rbook <- function(base_size = 13, base_family = "", base_line_size = base_size/22,
                        base_rect_size = base_size/22) {
  theme(
    axis.title = element_text(size = 13),
    axis.text.x = element_text(size = 10),
    axis.text.y = element_text(size = 10),
    plot.caption = element_text(size = 10, face = "italic"),
```

```
    panel.background = element_rect(fill="white"),
    axis.line = element_line(size = 1, colour = "black"),
    strip.background =element_rect(fill = "#cddcdd"),
    panel.border = element_rect(colour = "black", fill=NA, size=0.5),
    strip.text = element_text(colour = "black"),
    legend.key=element_blank()
  )
}
```

theme_rbook() is now available for us to use just like any other theme.

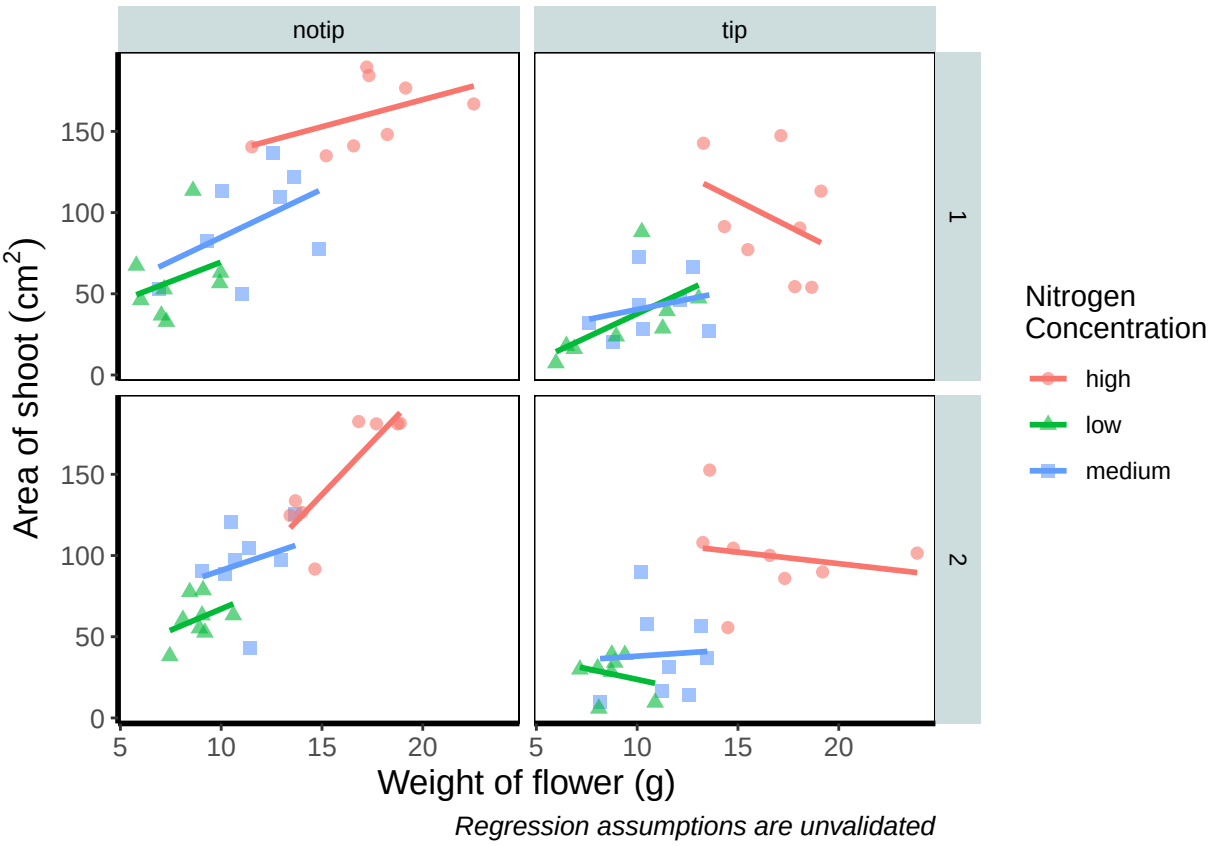
Let's try remaking our figure using our new theme.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  # Updated theme to our theme_rbook
  theme_rbook() # use our new theme
```

```
## Warning: The ‘size‘ argument of ‘element_line()‘ is deprecated as of ggplot2 3.4.0.
## i Please use the ‘linewidth‘ argument instead.
```

```
## Warning: The ‘size‘ argument of ‘element_rect()‘ is deprecated as of ggplot2 3.4.0.
## i Please use the ‘linewidth‘ argument instead.
```

```
## ‘geom_smooth()‘ using formula = ’y ~ x’
```



Prettification

We've pretty much replicated our "final figure". We just have a few final adjustments to make, and we'll do so in order of difficulty. Let's remind ourselves of what that "final figure" looked like. Remember, since we've previously stored the figure as an object called final_figure we can just type that into the console and pull up the figure

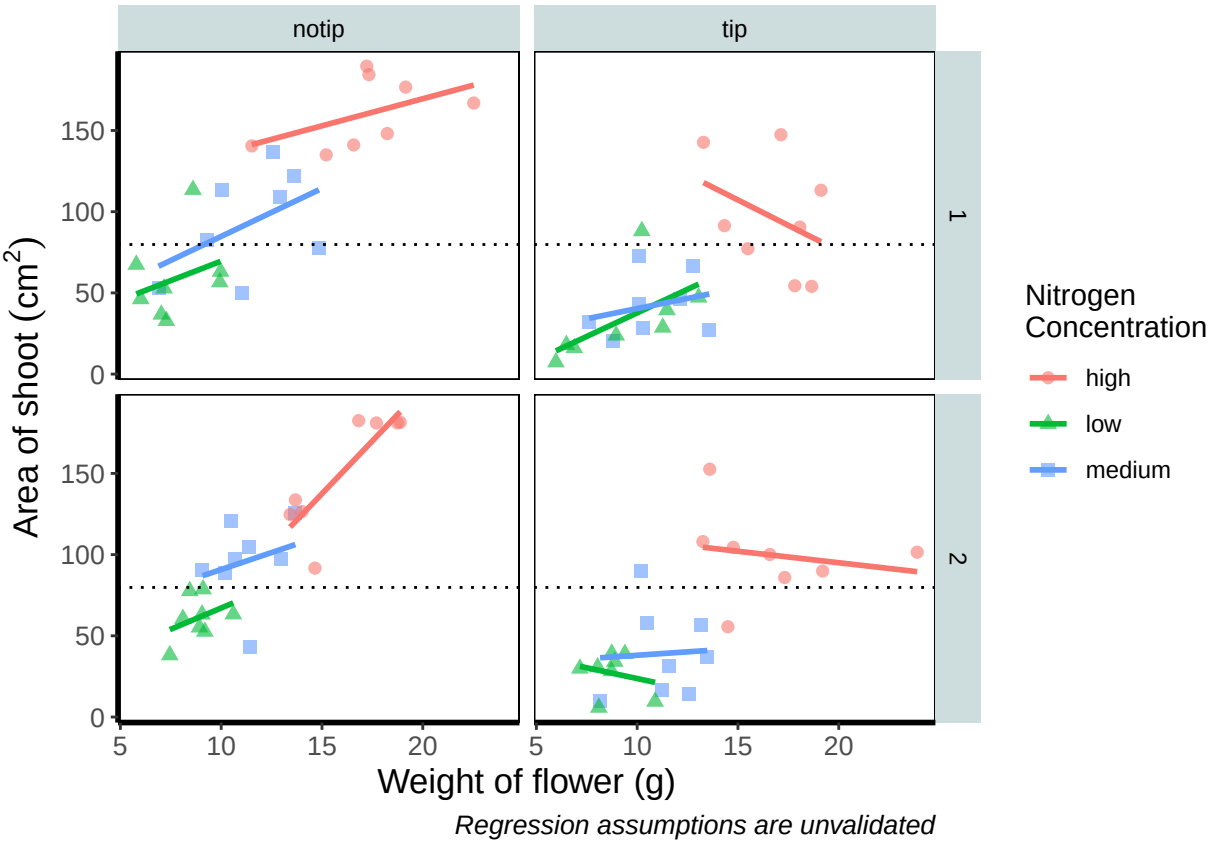
Let's begin the final push by including that dashed horizontal line at the average shoot area, at about 80, on our y axis. This represents the overall mean area of a shoot, regardless of nitrogen concentration, treatment, or block. To draw a horizontal line we use a geom called geom_hline(), and the most important thing we need to specify is the y intercept value (in this case the mean area of a shoot). We can also change the type of line using the argument linetype = and also the colour (as we did before). Let's see how it works.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  # Added a horizontal line using geom_hline
  geom_hline(aes(yintercept = mean(shootarea)), size = 0.5, colour = "black", linetype = 3) +
  theme_rbook()
```

```
## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0.
```

```
## i Please use ‘linewidth‘ instead.
```

```
## ‘geom_smooth()‘ using formula = ’y ~ x’
```



Notice how we included the function mean(shootarea) within the geom_hline() function? We could also do that externally to the ggplot2 code and get the same result.

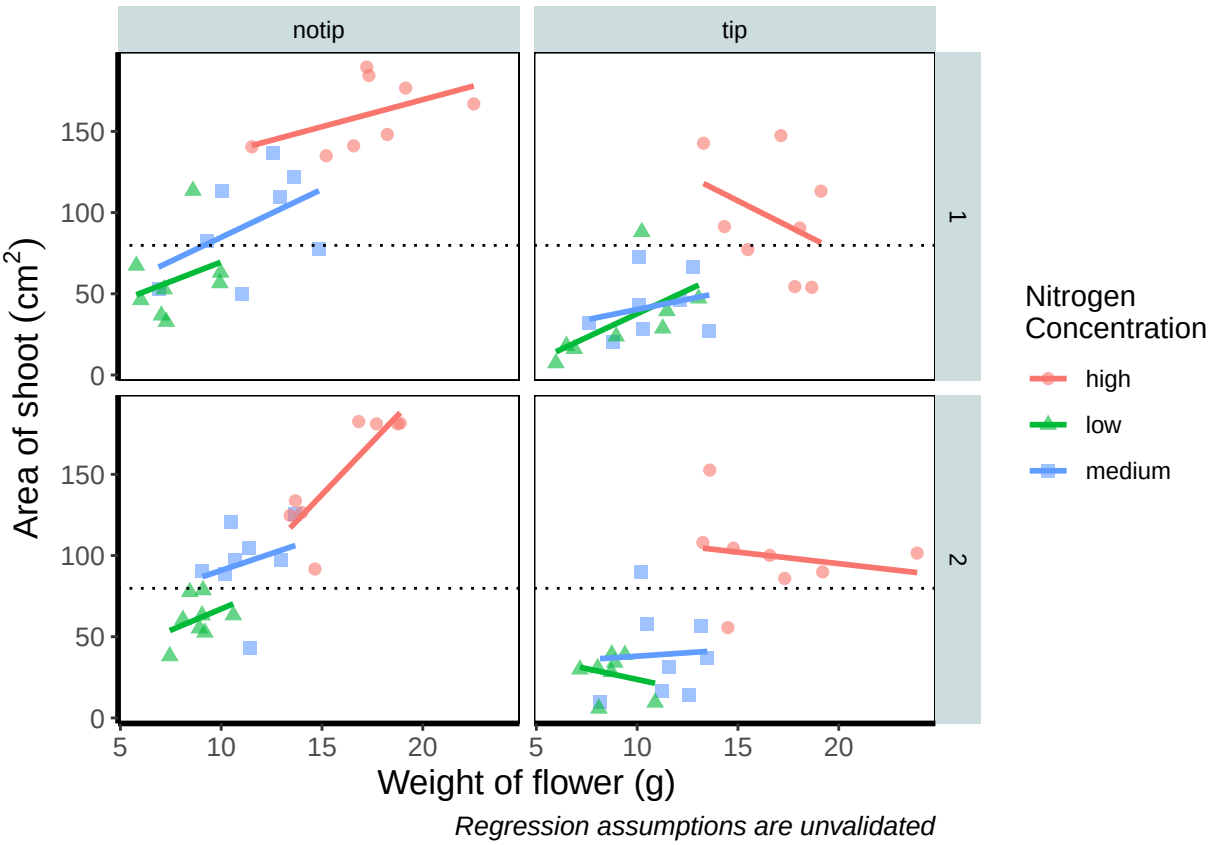
```
mean(flowergg$shootarea)
```

```
## [1] 79.78333
```

```
## [1] 79.78333
```

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  # Manually entering mean value
  geom_hline(aes(yintercept = 79.8), size = 0.5, colour = "black", linetype = 3) +
  theme_rbook()
```

```
## ‘geom_smooth()‘ using formula = ’y ~ x’
```



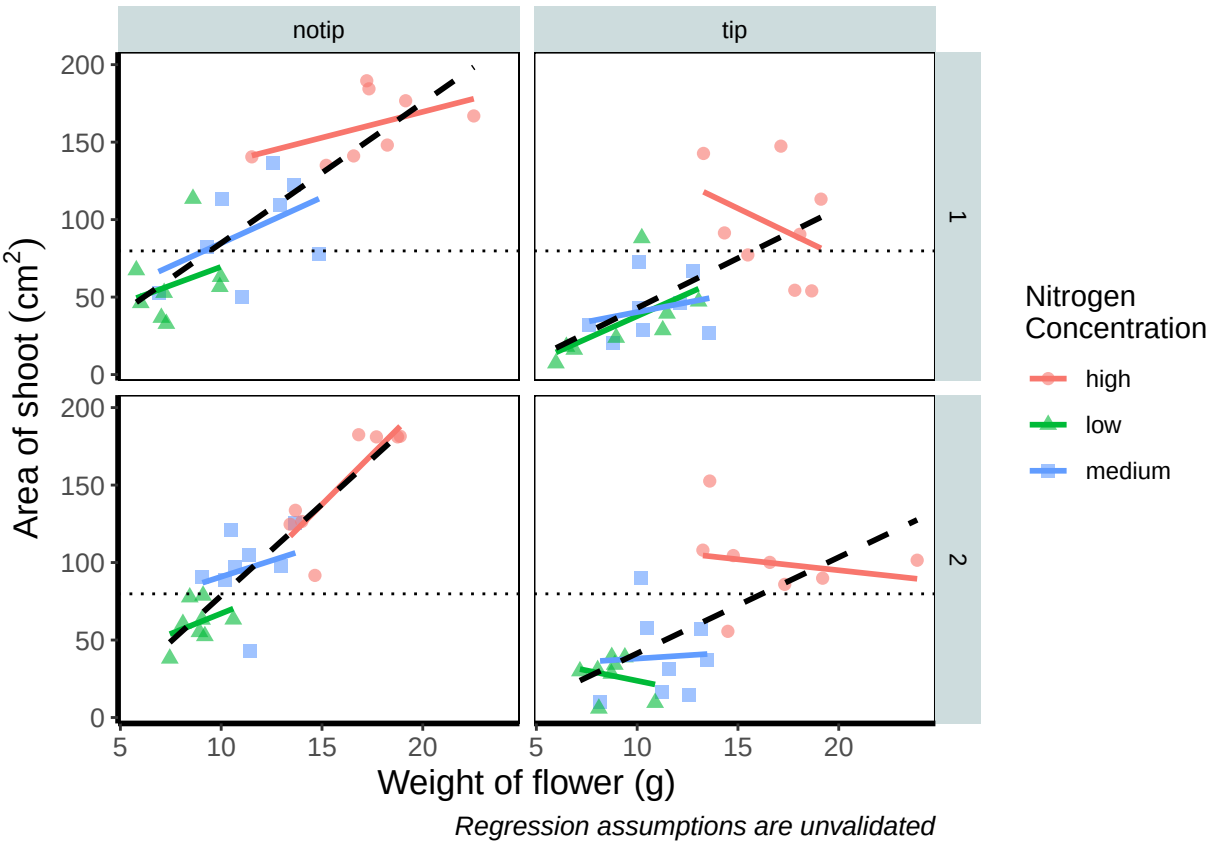
Exactly the same figure but produced in a slightly different way (the point being that there are always multiple ways to get what you want). Now let's tackle that "overall" nitrogen effect. This overall line is effectively the figure we produced much earlier when we learnt how to include a line of best fit from a linear model. However, we are already using `geom_smooth()`, surely we can't use it again?

This may shock and/or surprise you so please ensure you are seated. You can use `geom_smooth()`again. In fact you can use it as many times as you want. You can use any layer as many times as you want! Isn't the world full of wonderful miracles? ... Anyway, here's the code...

Overall nitrogen effect

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  # Adding a SECOND geom_smooth :O
  geom_smooth(method = "lm", se = FALSE, linetype = 2, alpha = 0.6, colour = "black") +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  geom_hline(aes(yintercept = 79.8), size = 0.5, colour = "black", linetype = 3) +
  theme_rbook()
```

```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```



that's great! But you should be asking yourself why that worked. Why when we specified the first `geom_smooth()` did it draw 3 lines, whereas the second time we used `geom_smooth()` it just drew a single line? The secret lies in a "conflict" (it isn't actually a conflict but that's what we'll call it) between the colour specified in the main call to `ggplot()` and the colour specified in the second `geom_smooth()`. Notice how in the second we've specifically told ggplot2 that the colour will be black, while prior to this it drew lines based on the number of groups (or colours) in nitrogen? In "overriding" the universal `ggplot()` with a geom specific argument we're able to get ggplot2 to plot what we want.

the only things left to do are to change the colour and the shape of the points to something of our choosing and include information on the "overall" trend line in the legend. we'll begin with the former; changing colour and shape to something we specifically want.

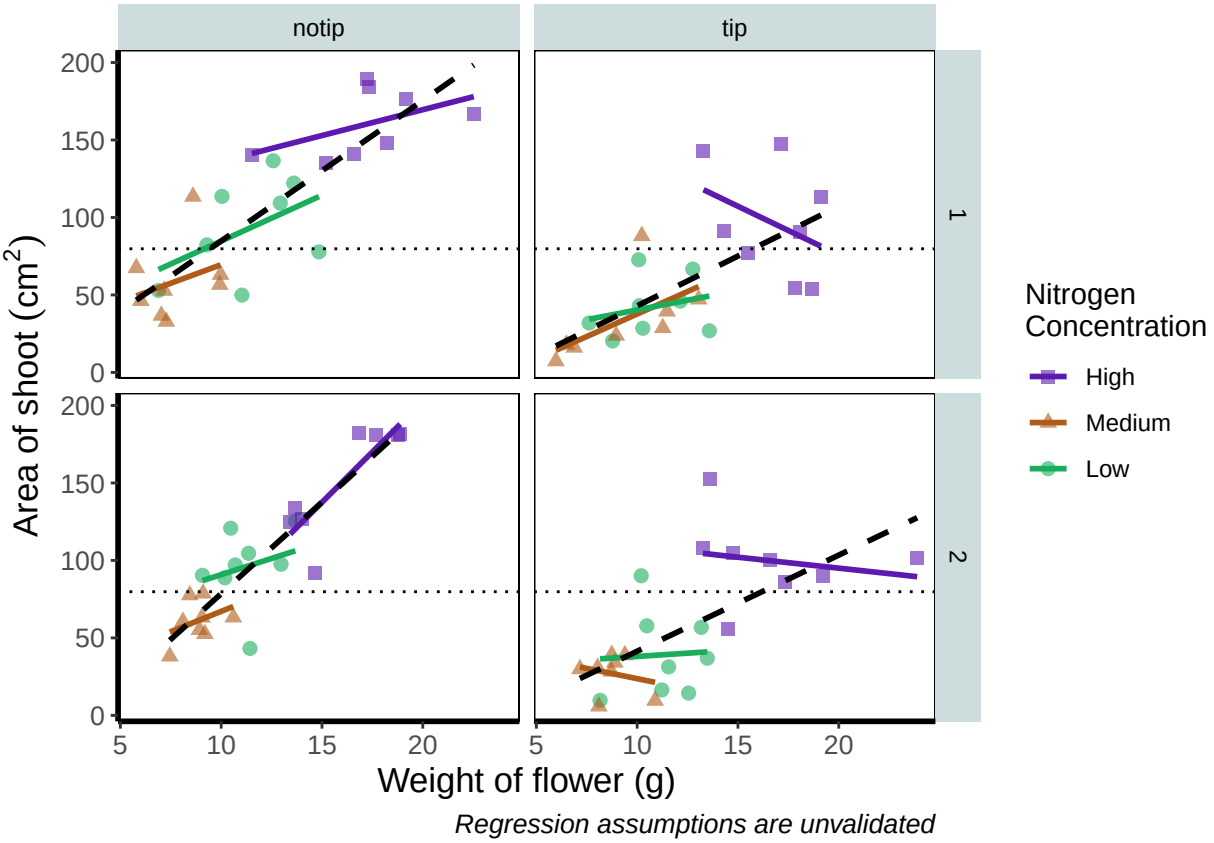
When we first started using ggplot2 this was the thing which caused us the most difficulty. We think the reason is, that to manually change the colours actually requires an additional layer, where we assumed this would be done in either the main call to `ggplot()` or in a geom.

Instead of doing this within the specific geom, we'll use scale_colour_manual() as well as`scale_shape_manual()`. Doing it this way will allow us to do two things at once; change the shape and colour to our choosing, and assign labels to these (much like what we did with xlab() and ylab()). Doing so is not too complex but will require nesting a function (c()) within our scale_colour_manual and scale_shape_manual functions (see Chapter 2 for reminder on the concatenate function (c()) if you've forgotten).

Choosing colours can be fiddly. We've found using a colour wheel helps with this step. you can always use Google to find an interactive colour wheel, or use Google's Colour picker. Any decent website should give you a HEX code, something like: #5C1AAE which is a "code" representation of a colour. Alternatively, there are colour names which R and ggplot2 will also understand (e.g. "firebrick4"). Having chosen our colours using whichever means, let's see how we can do it:

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  geom_smooth(method = "lm", se = FALSE, linetype = 2, alpha = 0.6, colour = "black") +
  facet_grid(block ~ treat) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  geom_hline(aes(yintercept = 79.8), size = 0.5, colour = "black", linetype = 3) +
  # Setting colour and associated labels
  scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                      labels = c("High", "Medium", "Low")) +
  # Setting shape and associated labels
  scale_shape_manual(values = c(15,17,19),
                     labels = c("High", "Medium", "Low")) +
  theme_rbook()
```

```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```



To make sense of that code (or any code for that matter) try running it piece by piece. For instance in the above code, if we run c("#5C1AAE", "#AE5C1A", "#1AAE5C") we'll get a list of those strings. That list is then passed on to scale_colour_manual() as the colours we wish to use. Since we only have three nitrogen concentrations, it will use these three colours. Try including an additional colour in the list and see what

happens (if you place the new colour at the end of the list, nothing will happen since it will use the first three colours of the list - try adding it to the start of the list). The same is true for scale_shape_manual().

But if you're paying close attention you'll notice that there's a mistake with the figure now. What should be labelled "Low" is actually labelled "Medium" (the green points and line are our low nitrogen concentration, but ggplot2 is saying that it's purple). ggplot2 hasn't made a mistake here, we have. Remember that code is purely logical. It will do explicitly what it is told to do, and in this case we've told it to call the labels High, Medium and Low. We could have just as easily told ggplot2 to call them Pretoria, Tokyo, and Copenhagen. The lesson here is to always be critical of what your outputs are. Double check everything you do.

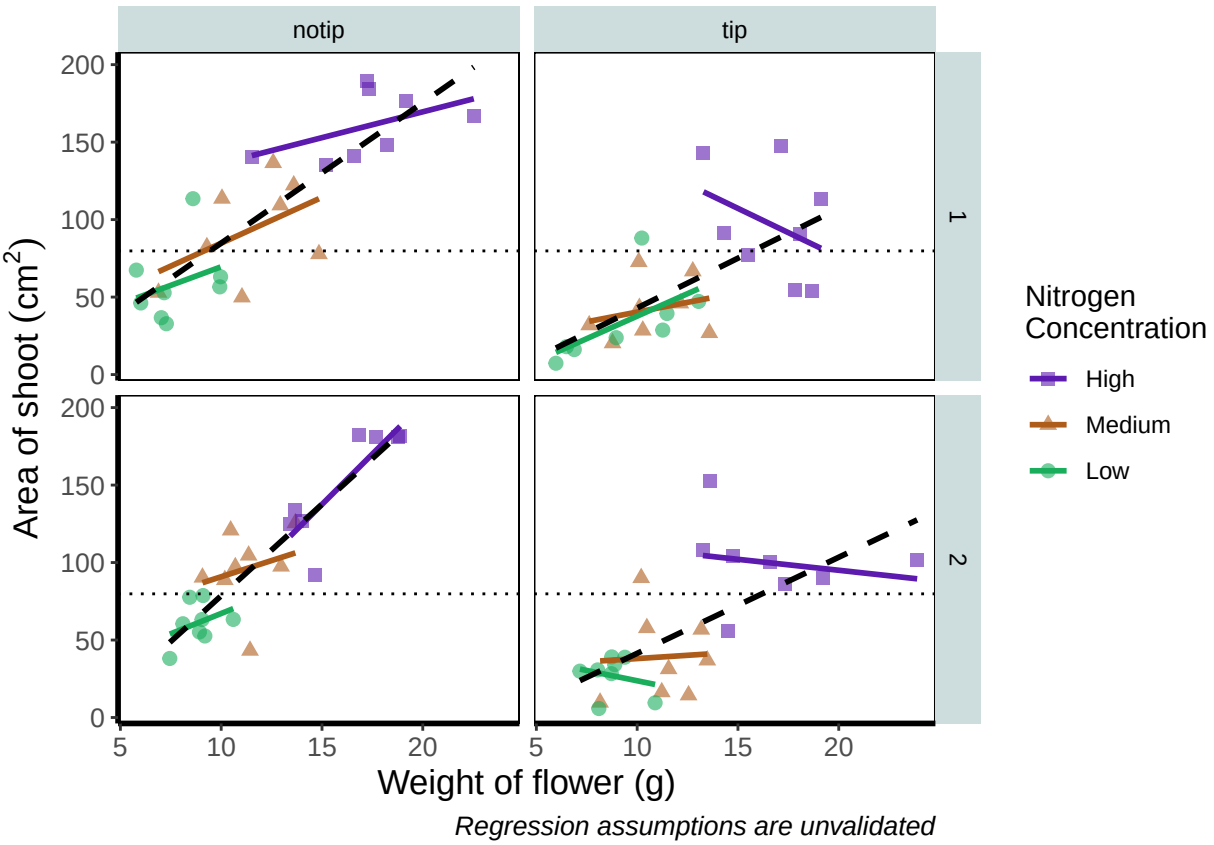
So how do we fix this? We need to do a little data manipulation to rearrange our factors so that the order goes High, Medium, Low. Let's do that:

```
flowergg$nitrogen <- factor(flowergg$nitrogen, levels = c("high", "medium", "low"))
```

With that done, we can re-run our above code to get a correct figure and assign it the name "rbook_figure".

```
rbook_figure <- ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
    geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
    geom_smooth(method = "lm", se = FALSE) +
    geom_smooth(method = "lm", se = FALSE, linetype = 2, alpha = 0.6, colour = "black") +
    facet_grid(block ~ treat) +
    xlab("Weight of flower (g)") +
    ylab(bquote("Area of shoot"~(cm^2))) +
    labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
         caption = "Regression assumptions are unvalidated") +
    geom_hline(aes(yintercept = 79.8), size = 0.5, colour = "black", linetype = 3) +
    scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                        labels = c("High", "Medium", "Low")) +
    scale_shape_manual(values = c(15,17,19),
                       labels = c("High", "Medium", "Low")) +
    theme_rbook()
  rbook_figure
```

```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```



Words of wisdom

Here are two final parting words of wisdom!.

1. First, as we've said before, don't fall into the trap of thinking your figures are superior to those who don't use ggplot2. As we've mentioned previously, equivalent figures are possible in both base R and ggplot2. The only difference is how you get to those figures.
2. Secondly, don't overcomplicate your figures. With regards to the final figure we produced here, we've gone back and forth as to whether we are guilty of this. The figure does contain a lot of information, drawing on information from five different variables, with one of those being presented in three different ways. We would be reluctant, for example, to include this in a presentation as it would likely be too much for an audience to fully appreciate in the 30 seconds to 1 minute that they'll see it. In the end we decided it was worth the risk as it served as a nice demonstration. Fortunately, or unfortunately depending on your view, there are no hard and fast rules when it comes to making figures. Much of it will be at your discretion, so please ensure you give it some thought.

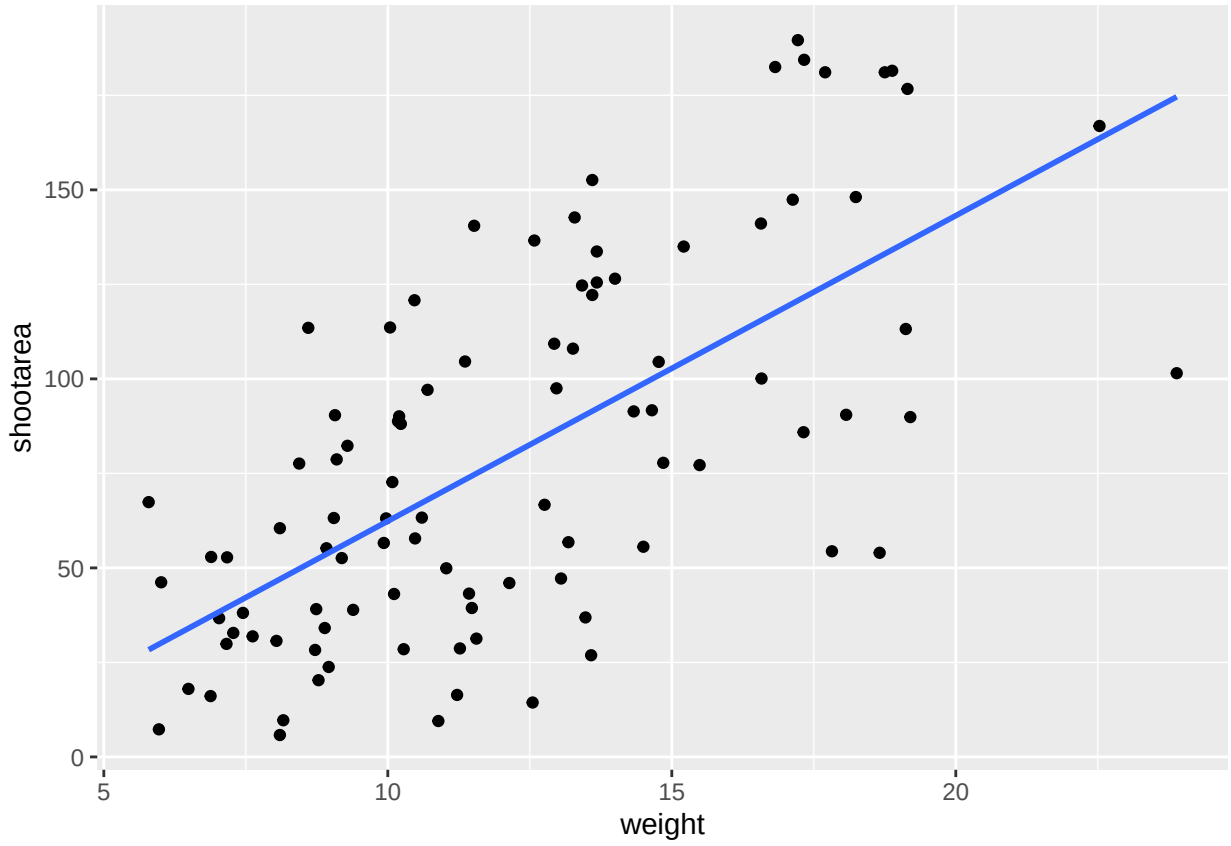
Tips and tricks

1. Statistics layer:

The statistics layer is often ignored in favour of working solely with the geometry layer, as we've done above. The two are largely interchangeable, though the relative rareness of online help and discussions on the statistics layer seems to have relegated it to almost a state of anonymity. There is real value in at least understanding what the statistics layer is doing, even if you don't ever need to make direct use of it. It is perhaps most clear what the statistical layer is doing in the early `geom_smooth()` figure we made.

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



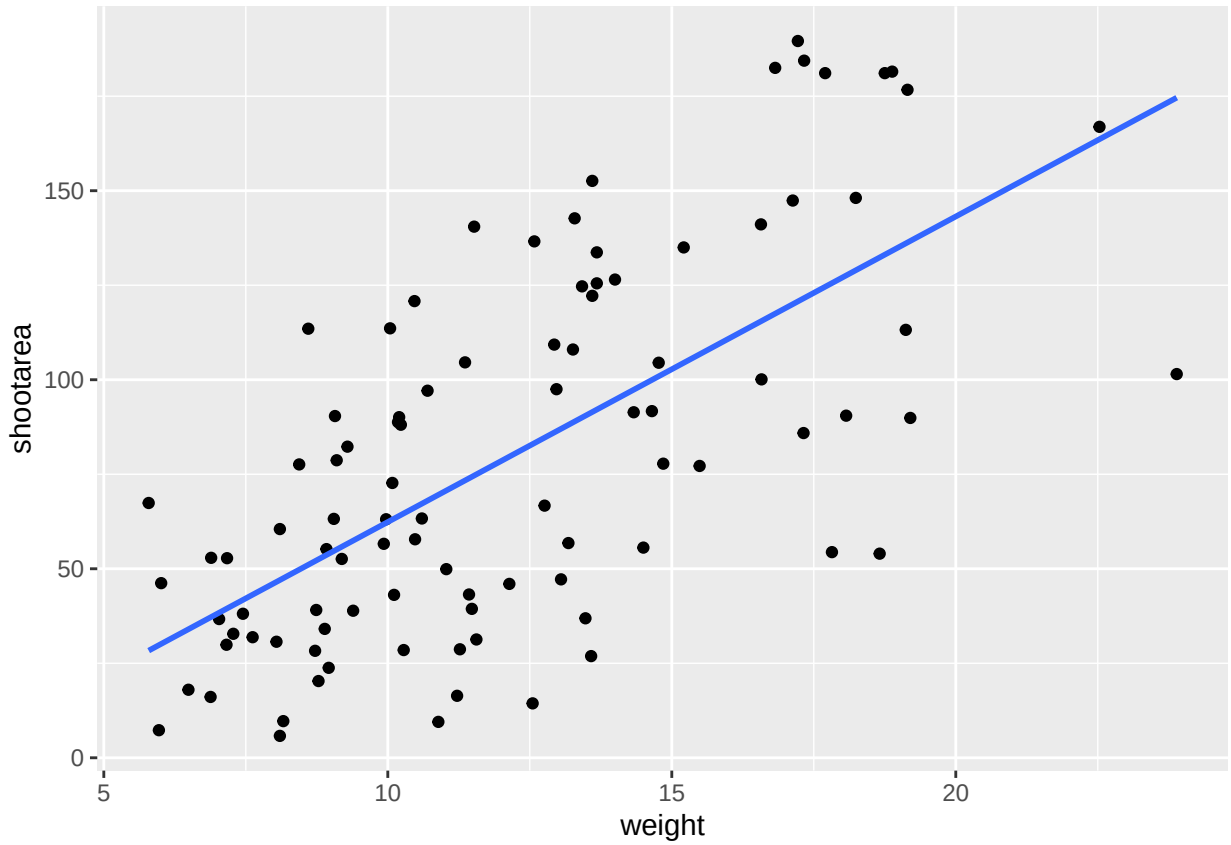

```
## `geom_smooth()` using formula 'y ~ x'
```

Nowhere in our dataset are there columns for either the y-intercept or the gradient needed to draw the straight line, yet we've managed to draw one. The statistics layer calculates these based on our data, without us necessarily knowing what we've done. It's also the engine behind converting your data into counts for producing a bar chart, or densities for violin plots, or summary statistics for boxplots and so on. It's entirely possible that you'll be able to use ggplot2 for the vast majority of you plotting without ever consulting the statistics layer in any more detail than we have here (simply by "calling" - unknowingly - to it via the geometry layer), but be aware that it exists.

If we wanted to recreate the above figure using the statistics layer we would do it like this:

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point() +
  # using stat_smooth instead of geom_smooth
  stat_smooth(geom = "smooth", method = "lm", se = FALSE)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



While in this example it doesn't make a difference which we use, in other cases we may want to use the calculated statistics in alternative ways. We won't get into it, but see ?after_stat if you are interested.

2. Axis limits and zooms: `coord_cartesian()` better

Fairly often, you may want to limit the range of your axes. Maybe you want to focus a particular part of the data to really tease apart any patterns occurring there. Whatever the reason, it's a useful skill, and with most things code related, there's a couple of ways to do this. We'll show two here; `xlim()` and `ylim()`, and `coord_cartesian()`. Using both of these we'll set the x axis to only show data between 10 and 15 g and the y axis to only show the area of the shoot between 50 and 150 mm2. We'll start with limiting the axes.

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point(aes(colour = nitrogen, shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(colour = "black", method = "lm", se = FALSE, linetype = 2, alpha = 0.6) +
  geom_smooth(aes(colour = nitrogen), method = "lm", se = FALSE, size = 1.2) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  geom_hline(aes(yintercept = 79.7833), size = 0.5, colour = "black", linetype = 3) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                      labels = c("High", "Medium", "Low")) +
  scale_shape_manual(values = c(15,17,19,21),
                     labels = c("High", "Medium", "Low")) +
  theme_rbook() +
  # New x and y limits
```

```
  xlim(c(10, 15)) +
  ylim(c(50, 150))
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

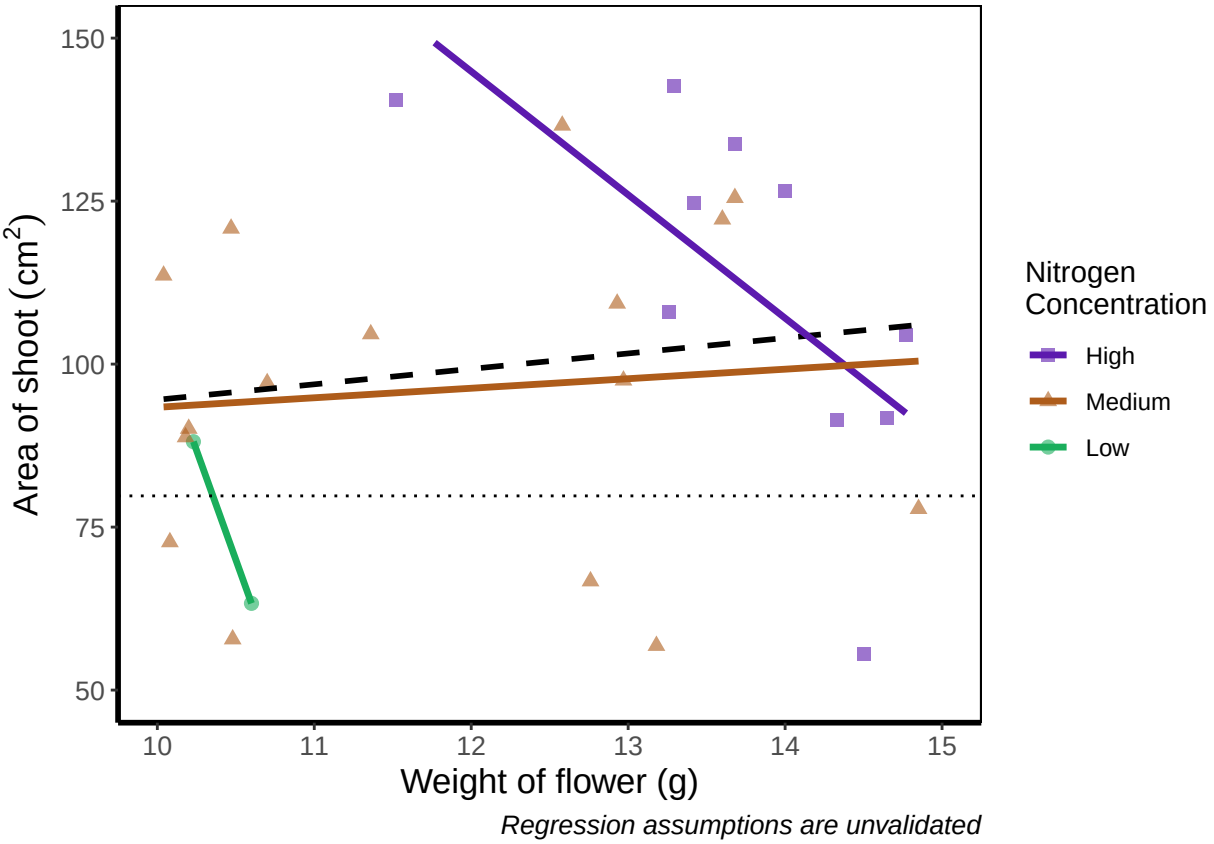
```
## Warning: Removed 68 rows containing non-finite values (`stat_smooth()`).
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## Warning: Removed 68 rows containing non-finite values (`stat_smooth()`).
```

```
## Warning: Removed 68 rows containing missing values (`geom_point()`).
```

```
## Warning: Removed 6 rows containing missing values (`geom_smooth()`).
```



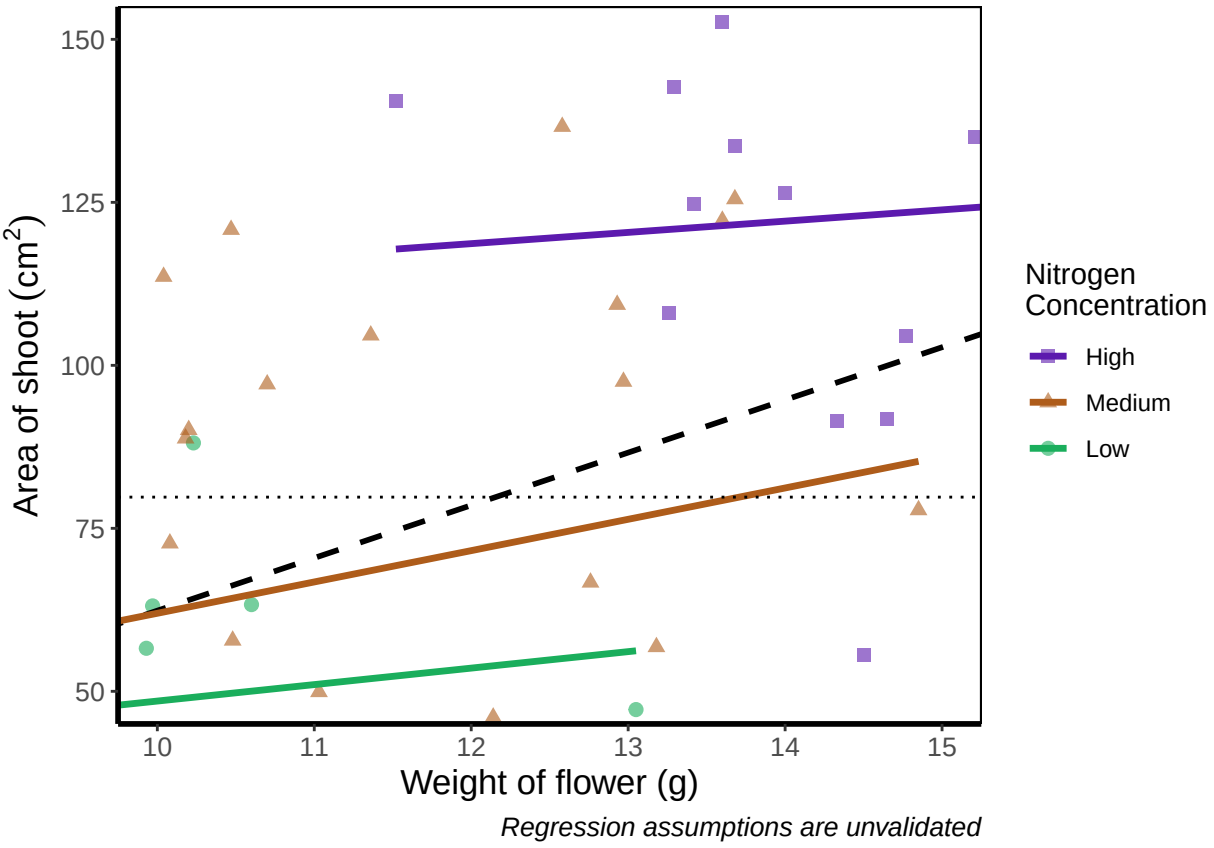
If you run this yourself you'll see warning messages telling us that n rows contain either missing or non-finite values? That's because we've essentially chopped out a huge part of our data using this method (everything outside of the ranges that we specified is "removed" from the data). As a result of doing this our lines have now completely changed direction. Notice that for low nitrogen concentration, the line is being drawn using only two points? This may, or may not be a problem depending on the aim we have, but we can use an alternative method; `coord_cartesian()`.

Warning messages: 1: Removed 68 rows containing non-finite values (`stat_smooth()`). 2: Removed 68 rows containing non-finite values (`stat_smooth()`). 3: Removed 68 rows containing missing values (`geom_point()`). 4: Removed 6 rows containing missing values (`geom_smooth()`).

coord_cartesian() works in much the same way, but instead of chopping out data, it instead zooms in. Doing so means that the entire dataset is maintained (and any trends are maintained).

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point(aes(colour = nitrogen, shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(colour = "black", method = "lm", se = FALSE, linetype = 2, alpha = 0.6) +
  geom_smooth(aes(colour = nitrogen), method = "lm", se = FALSE, size = 1.2) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  geom_hline(aes(yintercept = 79.7833), size = 0.5, colour = "black", linetype = 3) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                      labels = c("High", "Medium", "Low")) +
  scale_shape_manual(values = c(15,17,19,21),
                     labels = c("High", "Medium", "Low")) +
  theme_rbook() +
  # Zooming in rather than chopping out
  coord_cartesian(xlim = c(10, 15), ylim = c(50, 150))
```

```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```



Notice now that the trends are maintained (as the lines are being informed by data which are off-screen). We would generally advise using `coord_cartesian()` as it protects you against possible misinterpretations.

3. Layering layers

THE ORDER OF LAYERS MATTER. SELECT AND THEN PRESS AND HOLD ALT + UP OR DOWN ARROW

The layers are read and "painted" in order of their appearance in the code. If `geom_point()` comes before `geom_col()`, then your points may well end up being hidden.

To fix this is easy, we simply need to move the layers up or down in the code. A useful tip for those using Rstudio, is that you can move lines of code especially easily. Simply click on a line of code, hold down Alt and then press either the up or down arrows, and the entire line will move up or down as well. For multiple lines of code, simply highlight all those lines you want to move and press Alt + Up/Down arrow.

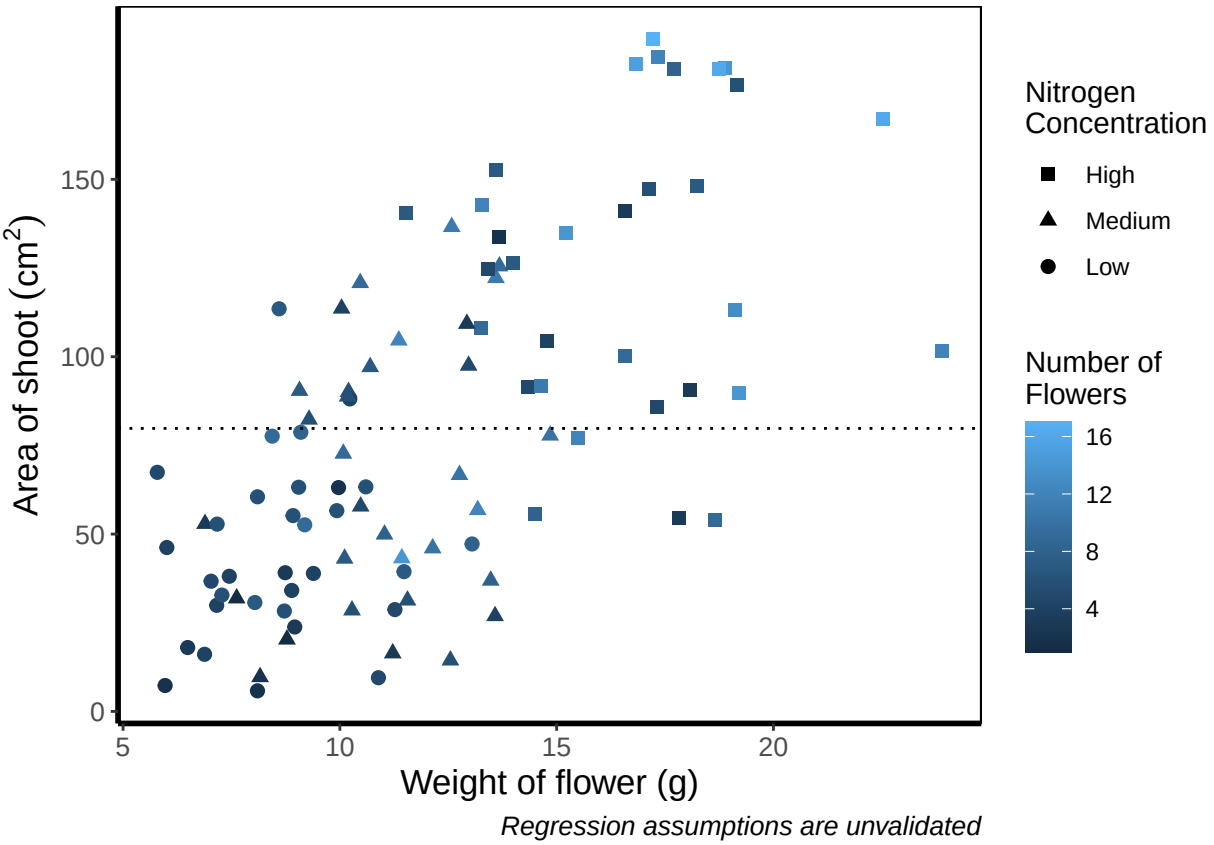
4. Continuous colours

Instead of categorical colours, such as we've used for nitrogen concentration, what if instead we wanted a gradient? To illustrate this, we'll remove the trend lines to highlight the changes we make. We'll also be using the flowers variable (i.e. number of flowers) to specify the colour that points should be coloured.

We have three options that we'll use here; the default colour scheme, the `scale_colour_gradient()` scheme, and an alternative `schemescale_colour_gradient2()`. Remember that we'll also need to change our label for the legend.

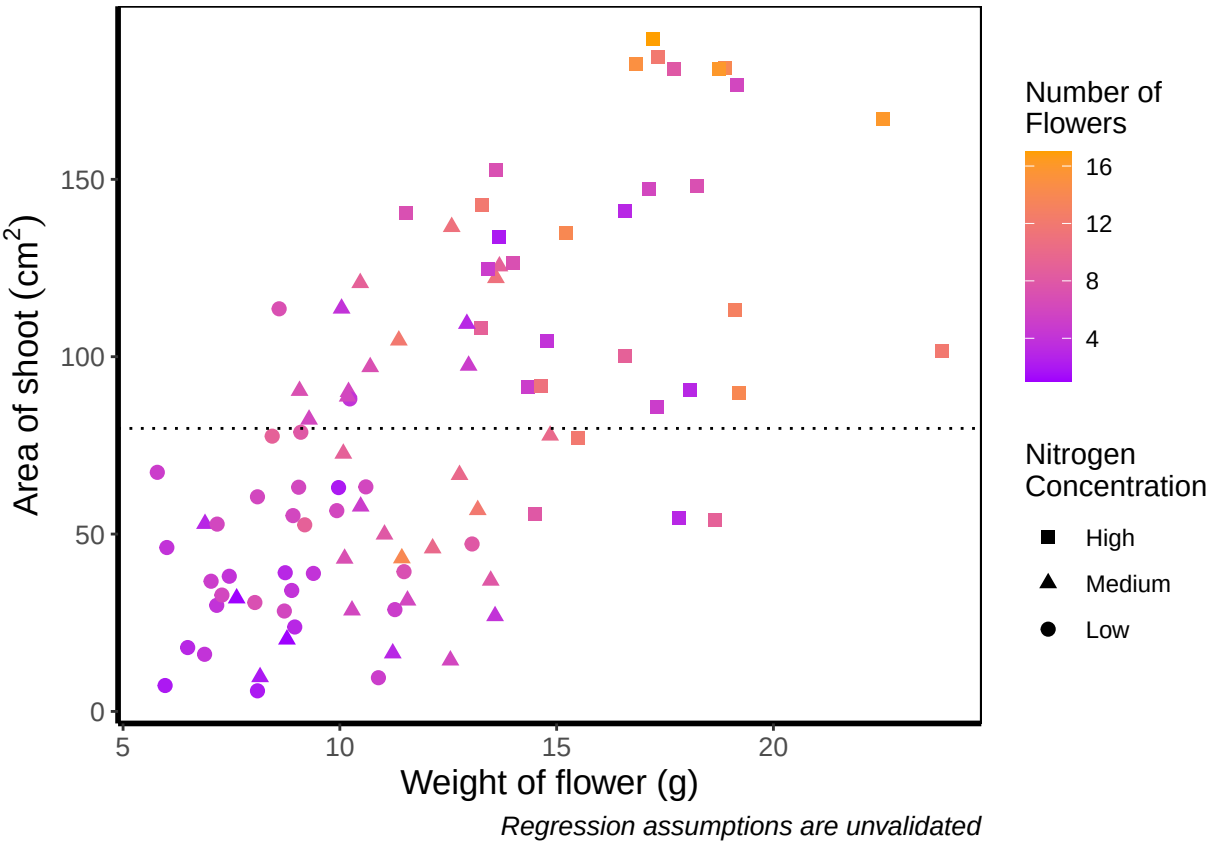
We'll start with the default option. Here we only need to change nitrogen (which is a factor) to flowers (which is continuous) in the colour = argument within `aes()`:

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  # Deleted geom_smooths for illustrative purposes only
  # (and also removed alpha argument from geom_point)
  geom_point(aes(colour = flowers, shape = nitrogen), size = 2) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  geom_hline(aes(yintercept = 79.7833), size = 0.5, colour = "black", linetype = 3) +
  # Changed colour argument label
  labs(shape = "Nitrogen\nConcentration", colour = "Number of\nFlowers",
       caption = "Regression assumptions are unvalidated") +
  scale_shape_manual(values = c(15,17,19,21),
                     labels = c("High", "Medium", "Low")) +
  theme_rbook()
```



It would help ourselves (and our audience), if we changed the colours to something more noticeably different, using `scale_colour_gradient()`. This works much as `scale_colour_manual()` except that this time we specify the low = and high = values using arguments.

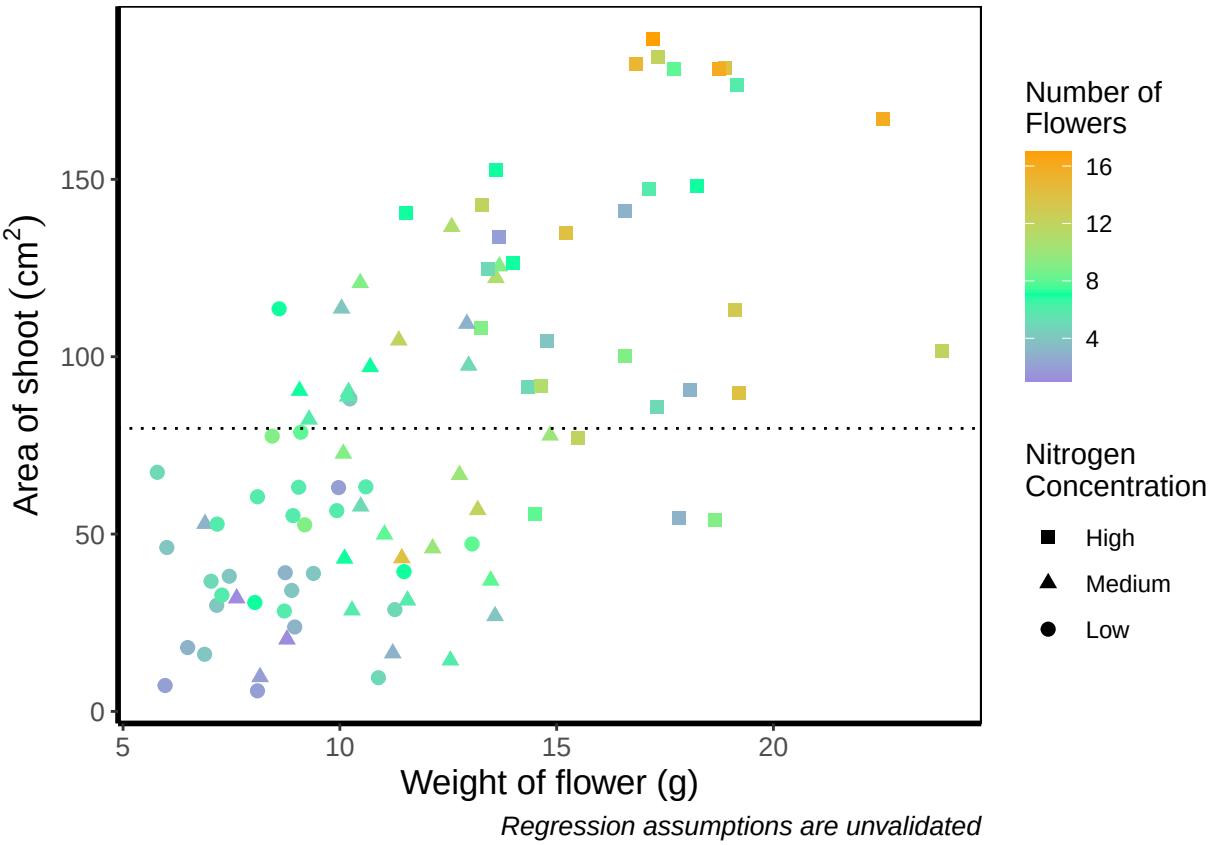
```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point(aes(colour = flowers, shape = nitrogen), size = 2) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  geom_hline(aes(yintercept = 79.7833), size = 0.5, colour = "black", linetype = 3) +
  # Updated legend name for colour
  labs(shape = "Nitrogen\nConcentration", colour = "Number of\nFlowers",
       caption = "Regression assumptions are unvalidated") +
  scale_shape_manual(values = c(15,17,19,21),
                     labels = c("High", "Medium", "Low")) +
  # Adding scale_colour_gradient
  scale_colour_gradient(low = "#9F00FF", high = "#FF9F00") +
  theme_rbook()
```



Although arguably better, we still struggle to spot the difference when there are between 5 and 12 flowers. Maybe having an additional colour would help those mid values stand out a bit more. The way we can do that here is to set a midpoint where the colours shift from green to blue to pink. Doing so might help us see the variation even more clearly.

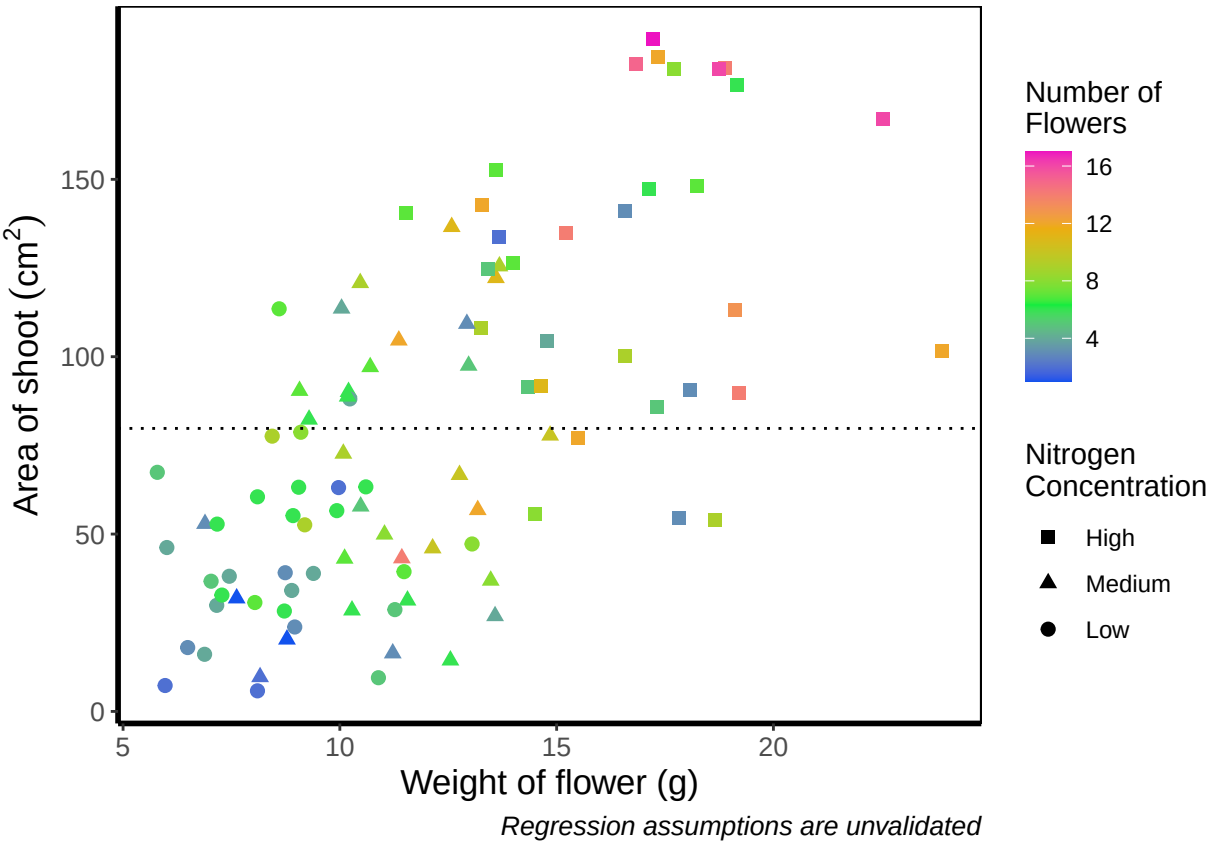
This is exactly what `scale_colour_gradient2()` allows. `scale_colour_gradient2()` works in much the same way as `scale_colour_gradient()` except that we have two additional arguments to worry about; midpoint = where we specify a value for the midpoint, and mid = where we state the colour the midpoint should take. We'll set the midpoint using mean()‘.

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point(aes(colour = flowers, shape = nitrogen), size = 2) +
  xlab("Weight of flower (g)") + ylab(bquote("Area of shoot"~(cm^2))) +
  geom_hline(aes(yintercept = 79.7833), size = 0.5, colour = "black", linetype = 3) +
  labs(shape = "Nitrogen\nConcentration", colour = "Number of\nFlowers",
       caption = "Regression assumptions are unvalidated") +
  scale_shape_manual(values = c(15,17,19,21),
                     labels = c("High", "Medium", "Low")) +
  # Adding scale_colour_gradient2
  scale_colour_gradient2(midpoint = mean(flowergg$flowers),
                         low = "#9F00FF", mid = "#00FF9F", high = "#FF9F00") +
  theme_rbook()
```



Definitely not our favourite figure. Perhaps if we add more colours, that will help things a bit (probably not but let's do it anyway). We now move onto using scale_colour_gradientn(), which diverges slightly. Instead of specifying colours for low, mid, and/or high, here we'll be specifying them using proportions within the values = argument. A common mistake with values =, within scale_colour_gradient(), is to assume (justifiably in our opinion) that we'd specify the actual numbers of flowers as our values. This is wrong. Try doing so and you'll likely see a grey colour bar and grey points. Instead values = represent the proportional ranges where we want the colour to occupy. In the code below, we use 0, 0.25, 0.5, 0.75 and 1 as our proportions, corresponding to 4 colours (note that we have one fewer colour than proportions given as the colours occupy a range and not a value).

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point(aes(colour = flowers, shape = nitrogen), size = 2) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  geom_hline(aes(yintercept = 79.7833), size = 0.5, colour = "black", linetype = 3) +
  labs(shape = "Nitrogen\nConcentration", colour = "Number of\nFlowers",
       caption = "Regression assumptions are unvalidated") +
  scale_shape_manual(values = c(15,17,19,21),
                     labels = c("High", "Medium", "Low")) +
  # Adding scale_colour_gradientn
  scale_colour_gradientn(colours = c("#1252ED", "#12ED3F", "#EDAD12", "#ED12C0"),
                         values = c(0, 0.25, 0.5, 0.75, 1)) +
  theme_rbook()
```



Slightly nauseating but it's doing what we wanted it to do, so we shouldn't really complain.

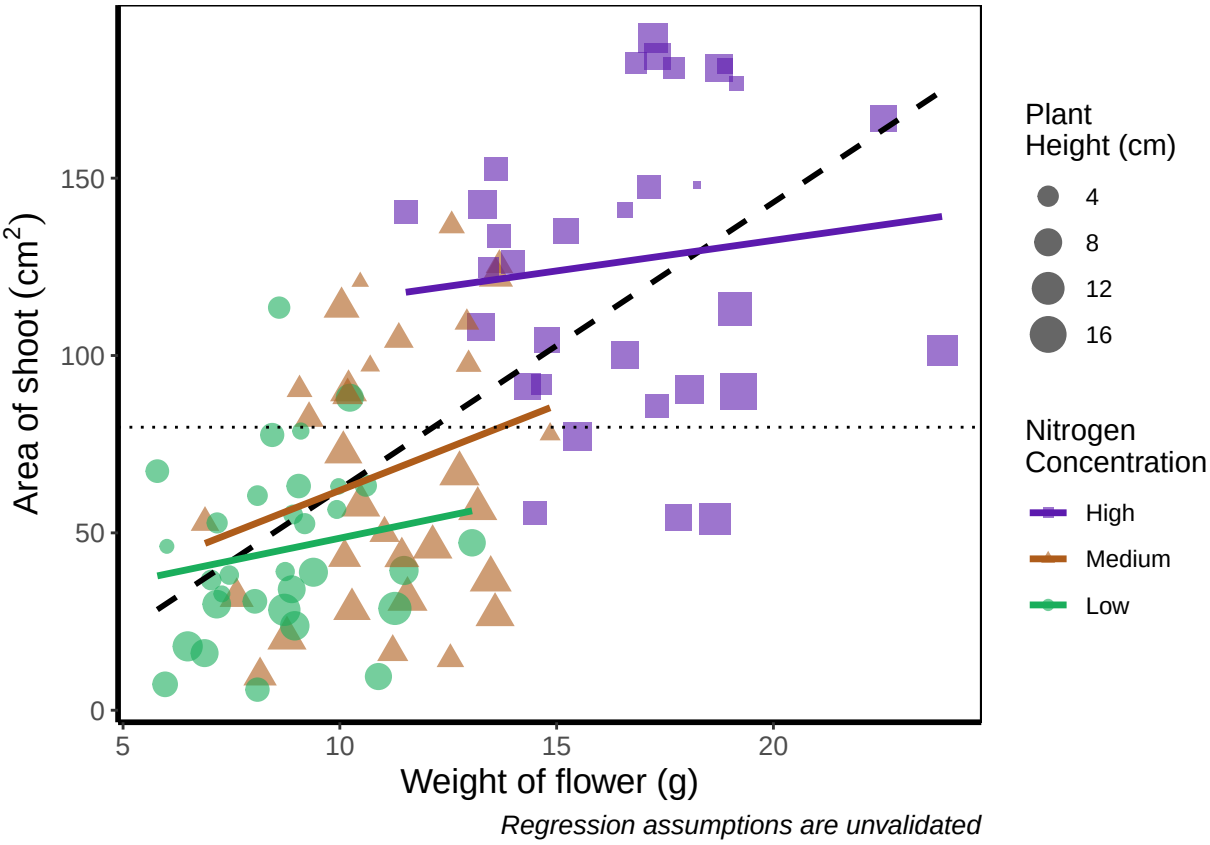
5. Size of points

Previously, we altered to size of points to be a constant number (e.g. size = 2). What if instead we wanted size to change according to a variable in our dataset? We can do this very easily by including a continuous variable with the size = argument.

```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  # Moving size into aes and changing to a continuous variable
  geom_point(aes(colour = nitrogen, shape = nitrogen, size = height), alpha = 0.6) +
  geom_smooth(colour = "black", method = "lm", se = FALSE, linetype = 2, alpha = 0.6) +
  geom_smooth(aes(colour = nitrogen), method = "lm", se = FALSE, size = 1.2) +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  geom_hline(aes(yintercept = 79.7833), size = 0.5, colour = "black", linetype = 3) +
  # Including size label
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated",
       size = "Plant\nHeight (cm)") +
  scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                      labels = c("High", "Medium", "Low")) +
  scale_shape_manual(values = c(15,17,19,21),
                     labels = c("High", "Medium", "Low")) +
  theme_rbook()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Now the sizes reflect the height of the plants, with bigger points representing taller plants and vice-versa.

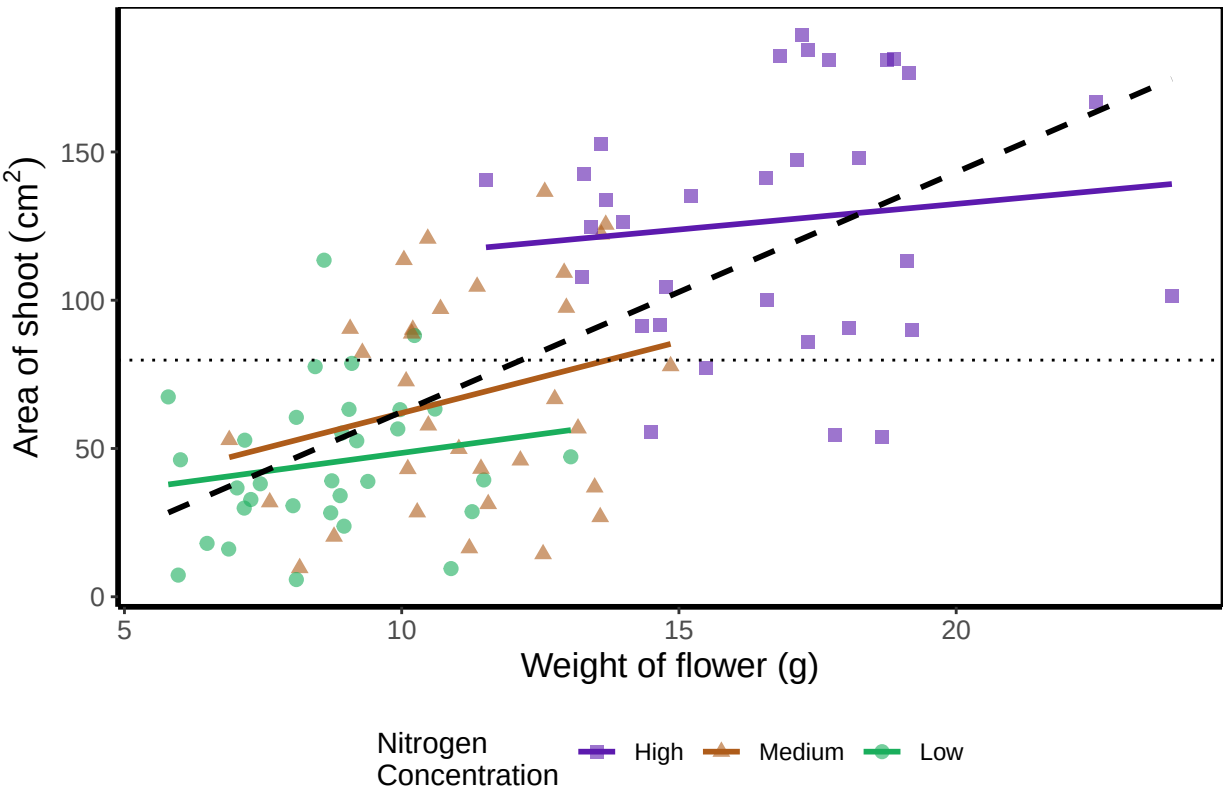
6. Moving the legend

To move the position of the legend requires tweaking the theme, just as we did before with theme_rbook(). But for legends we might not want this to be set in stone whenever we use the theme (i.e. coding this into theme_rbook()). Instead we can change it on the fly depending on the individual figure. To do so, we can use a theme() layer and the argument legend.position =, followed swiftly by another layer specifying that we still want to use theme_rbook().

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  geom_smooth(method = "lm", se = FALSE, linetype = 2, alpha = 0.6, colour = "black") +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  geom_hline(aes(yintercept = 79.8), size = 0.5, colour = "black", linetype = 3) +
  scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                      labels = c("High", "Medium", "Low")) +
  scale_shape_manual(values = c(15,17,19),
                     labels = c("High", "Medium", "Low")) +
  # Moving the legend
```

```
  theme(legend.position = "bottom") +
  theme_rbook()
```

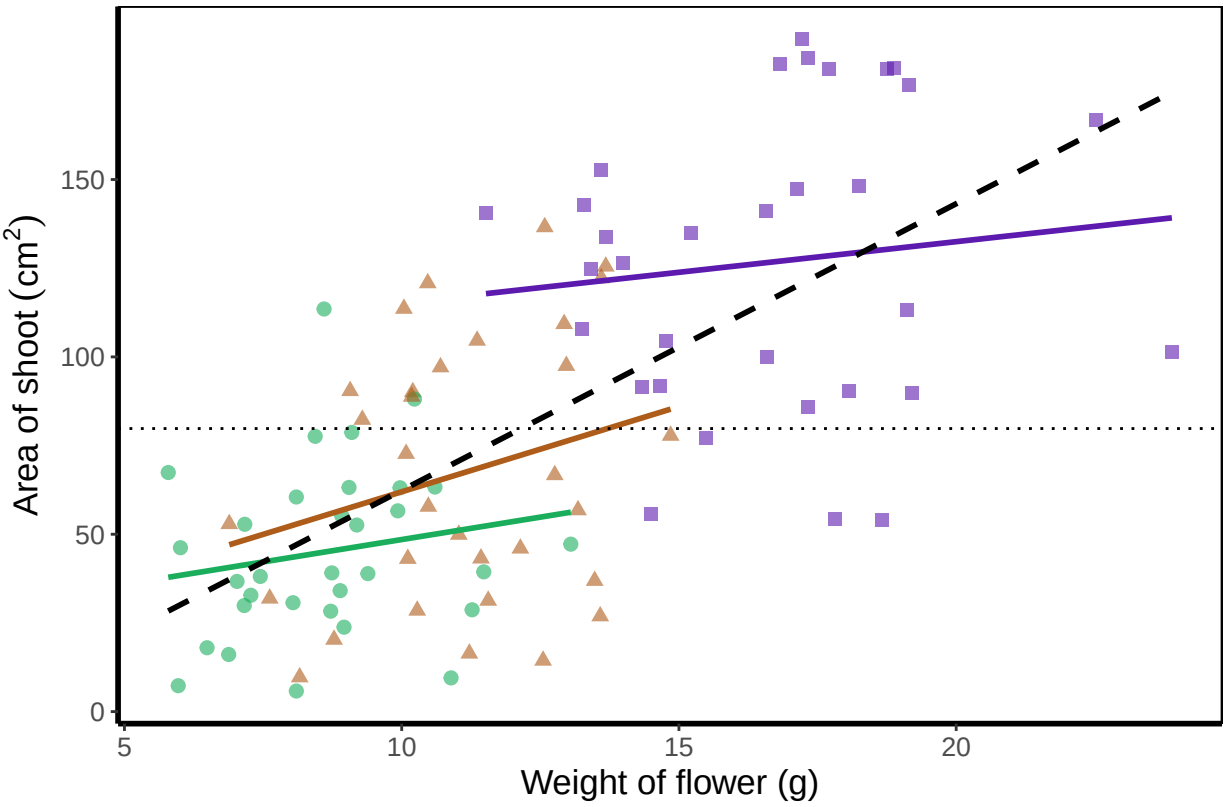
```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```



7. Hiding the legend

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  geom_smooth(method = "lm", se = FALSE, linetype = 2, alpha = 0.6, colour = "black") +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  geom_hline(aes(yintercept = 79.8), size = 0.5, colour = "black", linetype = 3) +
  scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                      labels = c("High", "Medium", "Low")) +
  scale_shape_manual(values = c(15,17,19),
                     labels = c("High", "Medium", "Low")) +
  # Hiding the legend
  theme(legend.position = "none") +
  theme_rbook()
```

```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```

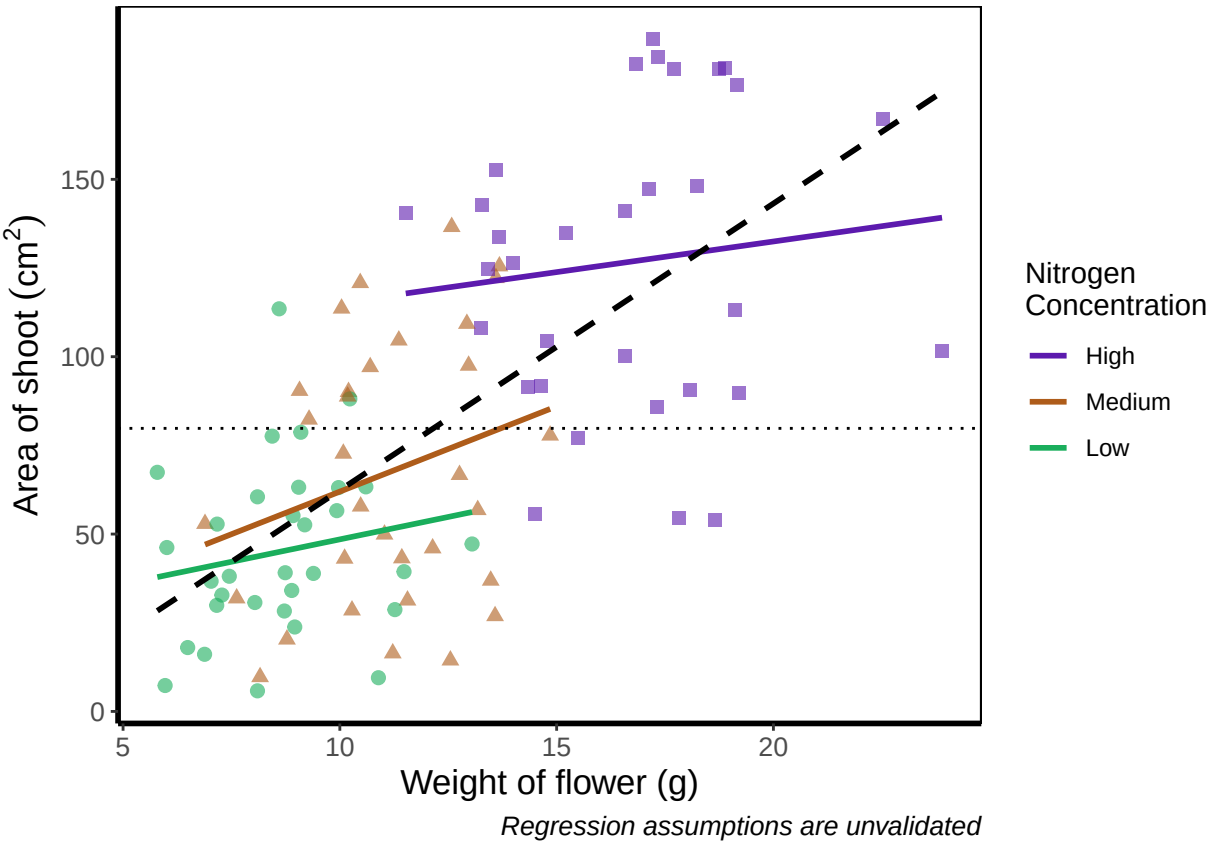


8. Hiding part of the legend

What if we really don't want points included in the legend? Instead of stating this using theme(), we'll include it within geom_point() using show.legend = FALSE.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  # Including show.legend = FALSE to prevent inclusion in legend
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6, show.legend = FALSE) +
  geom_smooth(method = "lm", se = FALSE) +
  geom_smooth(method = "lm", se = FALSE, linetype = 2, alpha = 0.6, colour = "black") +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  geom_hline(aes(yintercept = 79.8), size = 0.5, colour = "black", linetype = 3) +
  scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                      labels = c("High", "Medium", "Low")) +
  scale_shape_manual(values = c(15,17,19),
                     labels = c("High", "Medium", "Low")) +
  theme_rbook()
```

```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```



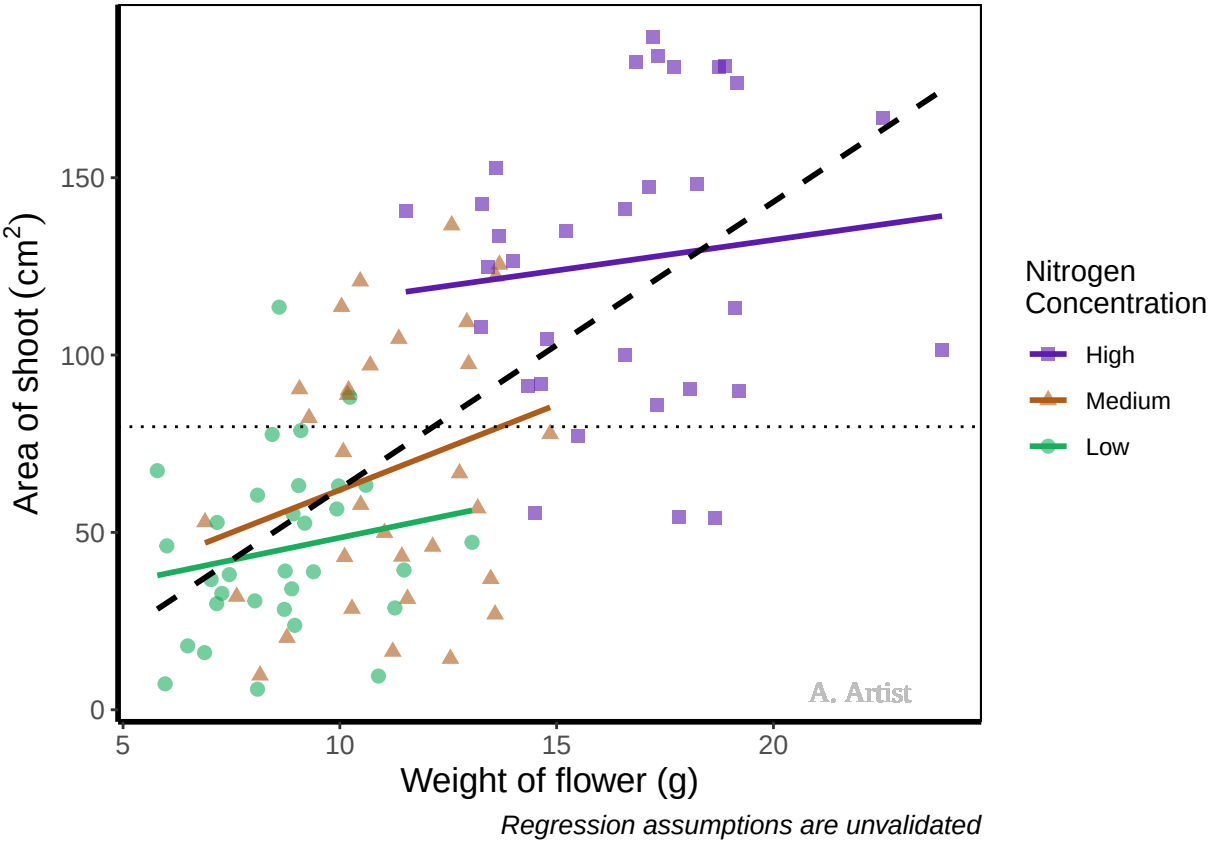
9. Writing on a figure

What if we were so utterly proud of our figure that we wanted to sign it (just like a painter signs their works of art)? We can do this using geom_text(). If we want to change the font, we need to check which ones are available for us to use. We can check this by running windowsFonts(). We'll use Times New Roman in this example, which is referred to as serif. Not happy with your font options? Check out the extrafont package which expands your 'fontage'.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  geom_smooth(method = "lm", se = FALSE, linetype = 2, alpha = 0.6, colour = "black") +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  geom_hline(aes(yintercept = 79.8), size = 0.5, colour = "black", linetype = 3) +
  scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                      labels = c("High", "Medium", "Low")) +
  scale_shape_manual(values = c(15,17,19),
                     labels = c("High", "Medium", "Low")) +
  # Including layer to display text
  geom_text(x = 22, y = 5, label = "A. Artist", colour = "grey", family = "serif") +
  theme_rbook()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



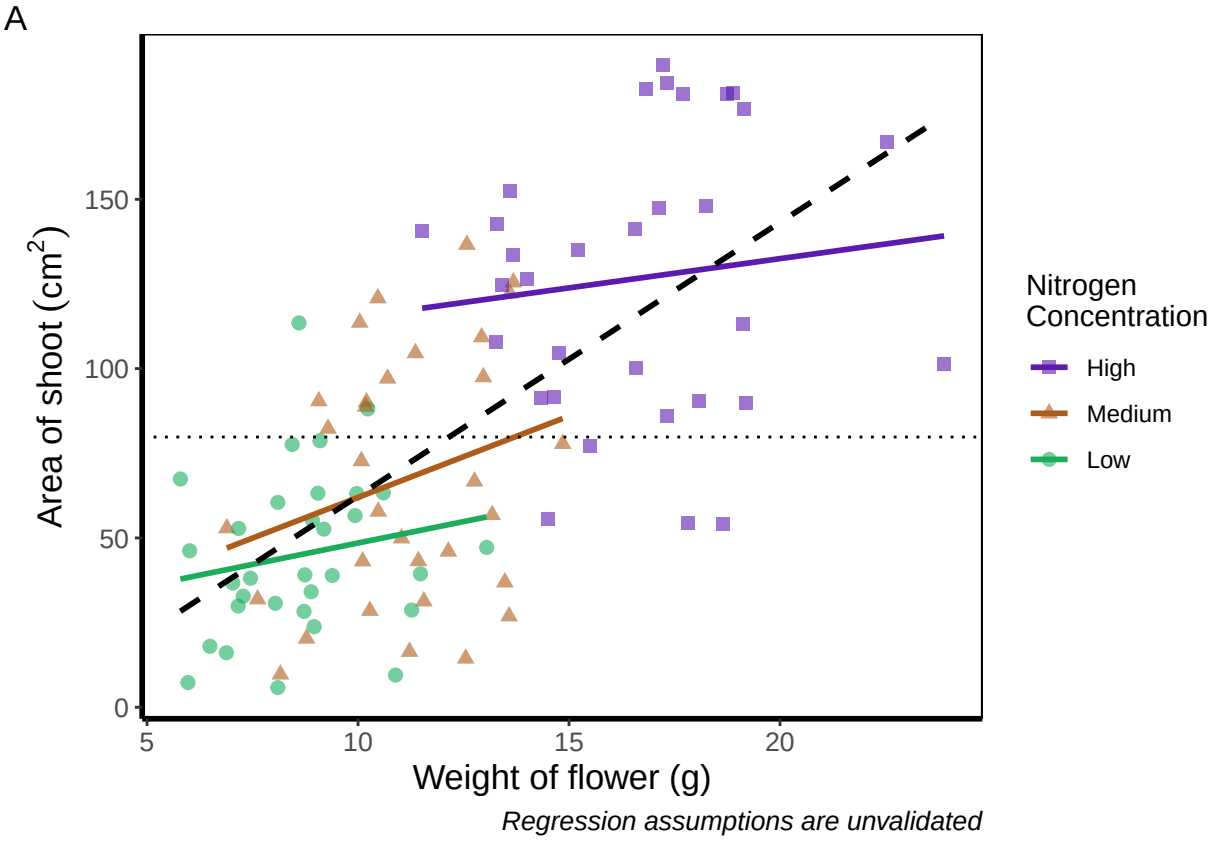
In reality there are more appropriate uses for geom_text() but whatever the reason, the mechanics remain the same. We specify what the x and y position are (on the scale of the axes), what we want written (using label =), the font (using family =). If you want to do more complex tasks with text and labels, check out ggrepel which extends the options available to you.

Similarly, if we want to include a tag for the figure, for instance we may want to refer to this figure as A we can do this using an additional argument in labs(). Let's see how that works

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  geom_smooth(method = "lm", se = FALSE, linetype = 2, alpha = 0.6, colour = "black") +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  # Including tag argument
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated", tag = "A") +
  geom_hline(aes(yintercept = 79.8), size = 0.5, colour = "black", linetype = 3) +
  scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                      labels = c("High", "Medium", "Low")) +
  scale_shape_manual(values = c(15,17,19),
                     labels = c("High", "Medium", "Low")) +
  theme_rbook()
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



Doing so we get an "A" at the top left of the figure. If we weren't happy with the position of the "A", we can always use geom_text() instead and position it ourselves.

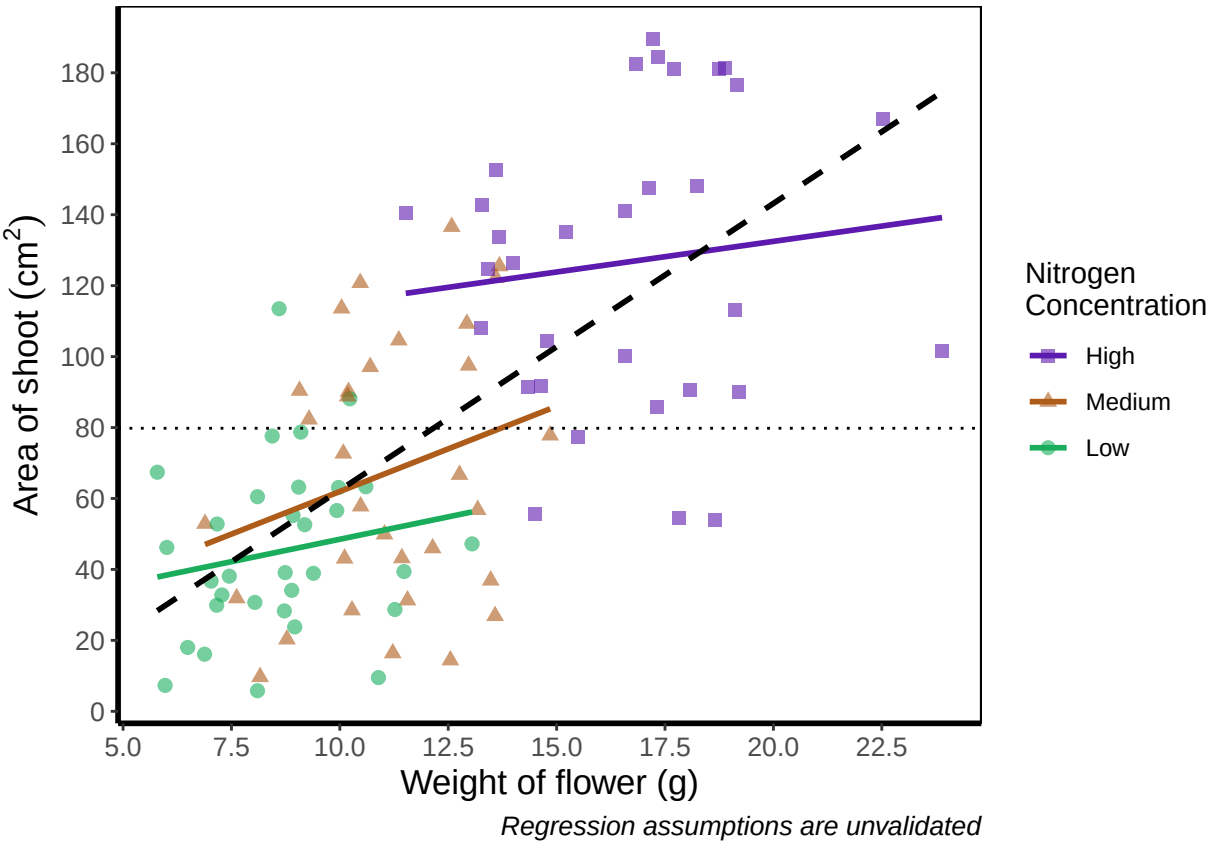
10. Axes tick marks and tick labels

What are we to do if we want more or fewer ticks on an axis? We can do this using the appropriate layers; scale_y_discrete() and scale_x_discrete() for discrete data (e.g. factors); and scale_y_continuous() and scale_x_continuous() for continuous data. Within these layers, the argument we want to use is called breaks =, though we need to use this in combination with seq() (see Chapter 2 for a reminder on how the seq() function works). We'll alter the x axis ticks in this example, with a tick label every 2.5 units.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  geom_smooth(method = "lm", se = FALSE, linetype = 2, alpha = 0.6, colour = "black") +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
       caption = "Regression assumptions are unvalidated") +
  geom_hline(aes(yintercept = 79.8), size = 0.5, colour = "black", linetype = 3) +
  scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                      labels = c("High", "Medium", "Low")) +
  scale_shape_manual(values = c(15,17,19),
                     labels = c("High", "Medium", "Low")) +
```

```
  # Adjusting breaks on x axis
  scale_x_continuous(breaks = seq(from = 5, to = 25, by = 2.5)) +
  scale_y_continuous(breaks = seq(from = 0, to = 200, by = 20))+
  theme_rbook()
```

```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```



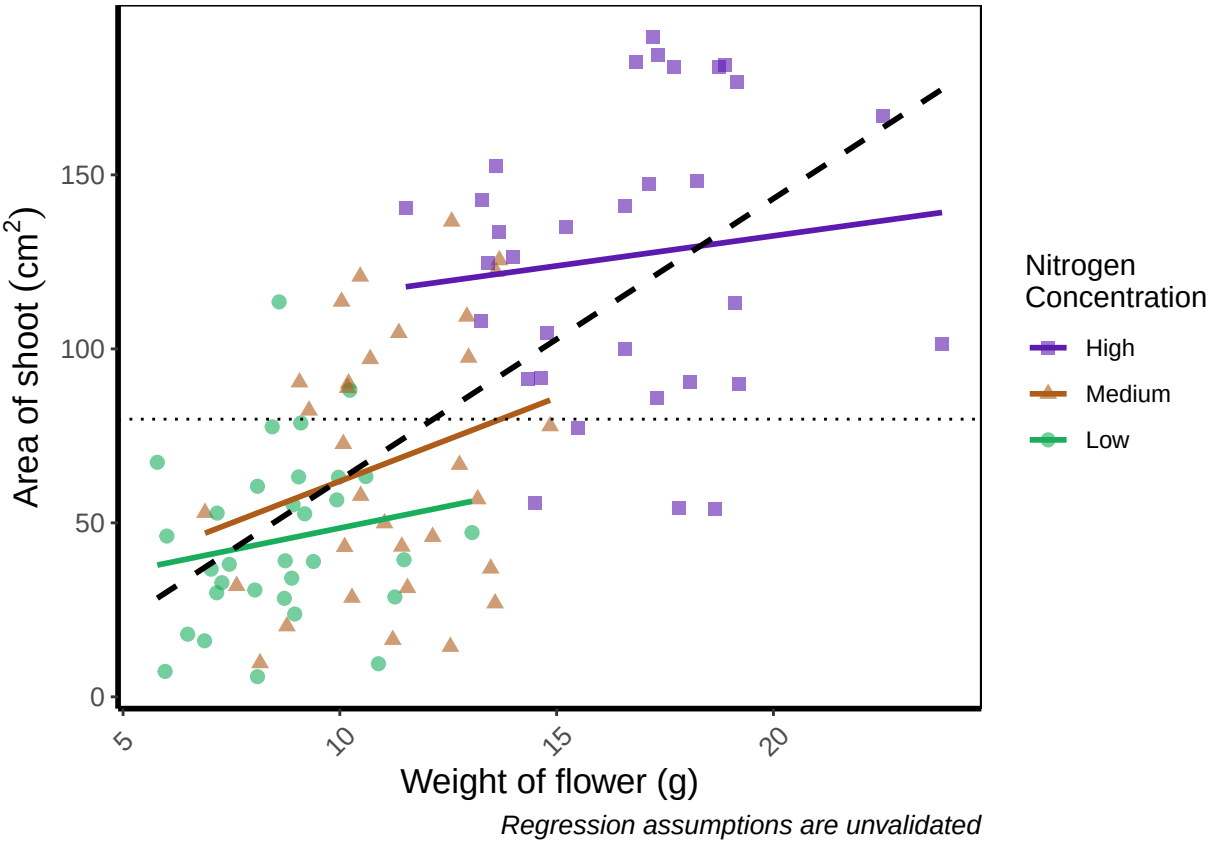
11. Rotating axes labels (for long scientific names):

Axis tick labels sometimes need to be rotated. If you've ever worked with data from multiple species (with those lovely long latin names) for example, you'll know that it can be a nightmare making figures. The names can end up overlapping to such an extent that your axis tick labels merge into a giant black blob of unreadable abstractionism. In such cases it's best to rotate the text to make it readable. Doing so isn't too much of a pain and we'll be using theme() again to set the text angle to 45 degrees in addition to a little vertical adjustment so that the text doesn't get too close or run too far away from the axis.

```
ggplot(aes(x = weight, y = shootarea, colour = nitrogen), data = flowergg) +
  geom_point(aes(shape = nitrogen), size = 2, alpha = 0.6) +
  geom_smooth(method = "lm", se = FALSE) +
  geom_smooth(method = "lm", se = FALSE, linetype = 2, alpha = 0.6, colour = "black") +
  xlab("Weight of flower (g)") +
  ylab(bquote("Area of shoot"~(cm^2))) +
  labs(shape = "Nitrogen\nConcentration", colour = "Nitrogen\nConcentration",
```

```
      caption = "Regression assumptions are unvalidated") +
  geom_hline(aes(yintercept = 79.8), size = 0.5, colour = "black", linetype = 3) +
  scale_colour_manual(values = c("#5C1AAE", "#AE5C1A", "#1AAE5C"),
                      labels = c("High", "Medium", "Low")) +
  scale_shape_manual(values = c(15,17,19),
                     labels = c("High", "Medium", "Low")) +
  # Changing the angle of the axis text
  theme(axis.text.x=element_text(angle = 45, vjust = 0.5)) +
  theme_rbook()
```

```
## `geom_smooth()` using formula = 'y ~ x'
## `geom_smooth()` using formula = 'y ~ x'
```

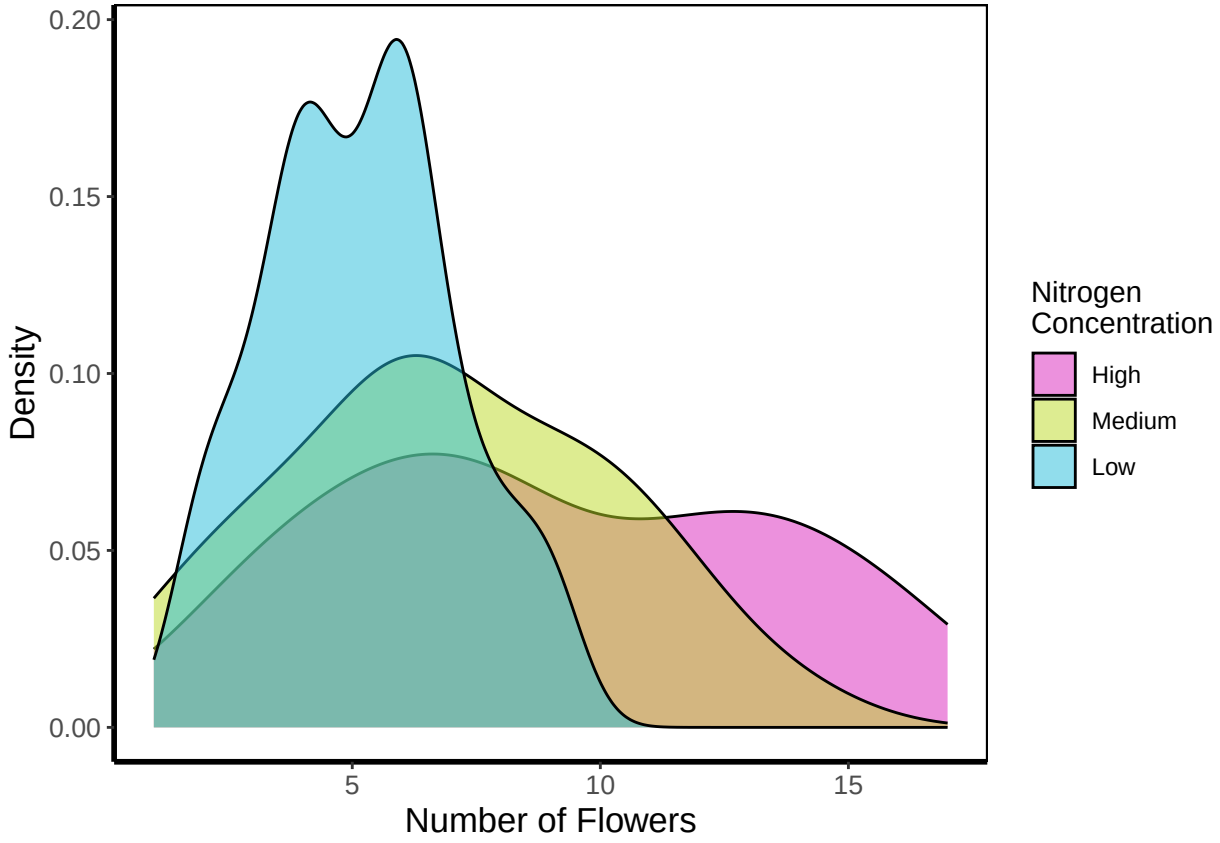


12. Common types of plots (A ggplot bestiary)

1. Density plot Below is a density plot which is much like a histogram. The x axis shows observations of given numbers of flowers, while the y axis is the density of observations (roughly equivalent to number of rows with that many flowers, calculated in the background by the statistics layer). Each density is coloured according to nitrogen concentration, though note that we're using fill = instead of colour =. Try using colour instead to see what happens.

Notice that we haven't used data = flower here and instead just used flower? When an object is not assigned with an argument, ggplot2 will assume that it is the dataset. We're using that here, but we actually prefer to explicitly state the argument name in our own work.

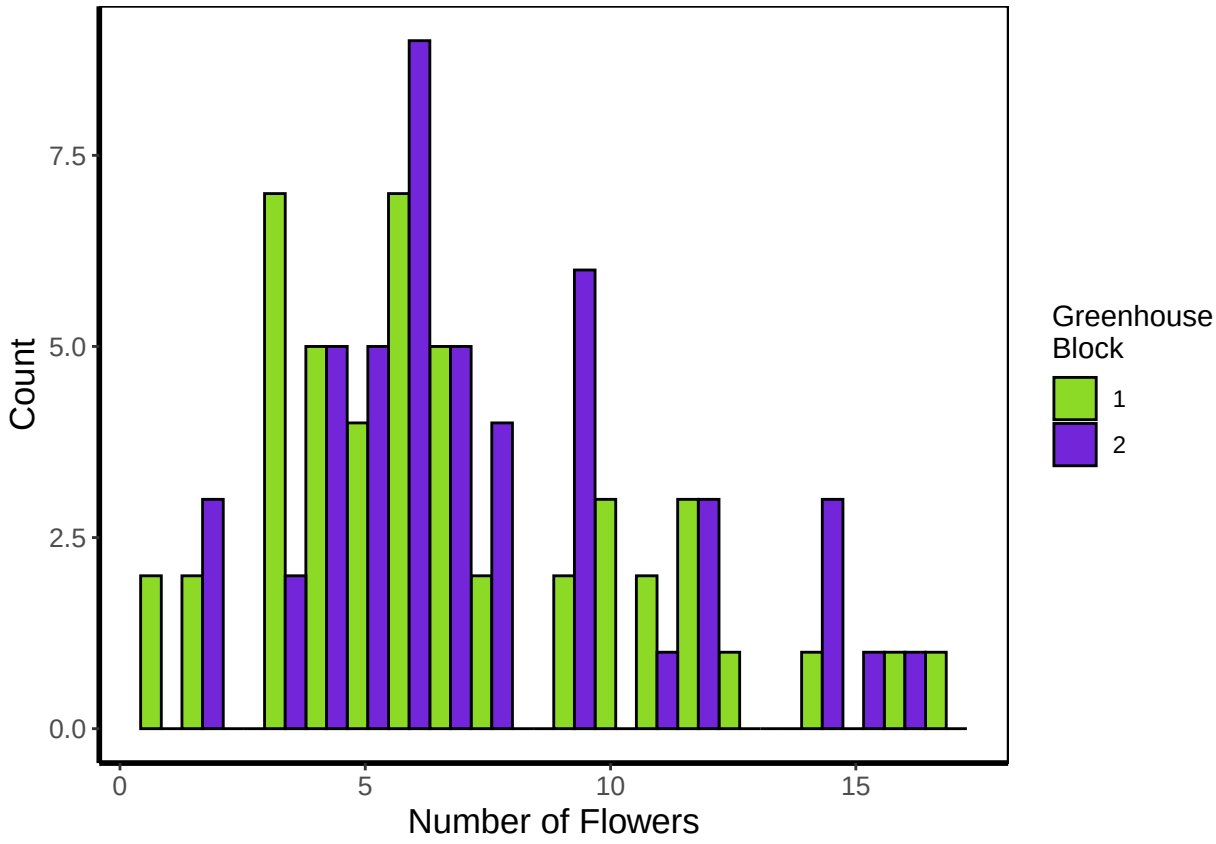
```
ggplot(flowergg) +
  geom_density(aes(x = flowers, fill = nitrogen), alpha = 0.5) +
  labs(y = "Density", x = "Number of Flowers", fill = "Nitrogen\nConcentration") +
  scale_fill_manual(labels = c("High", "Medium", "Low"),
                    values = c("#DB24BC", "#BCDB24", "#24BCDB")) +
  theme_rbook()
```



2. Histogram Next is a histogram (a much more traditional version of a density plot). There are a couple of things to take note of here. The first is that flower$block is numeric and not a factor. We can correct that here fairly easily using the factor() function to convert it from numeric to factor (though ideally we'd have done this before - see Chapter 3).

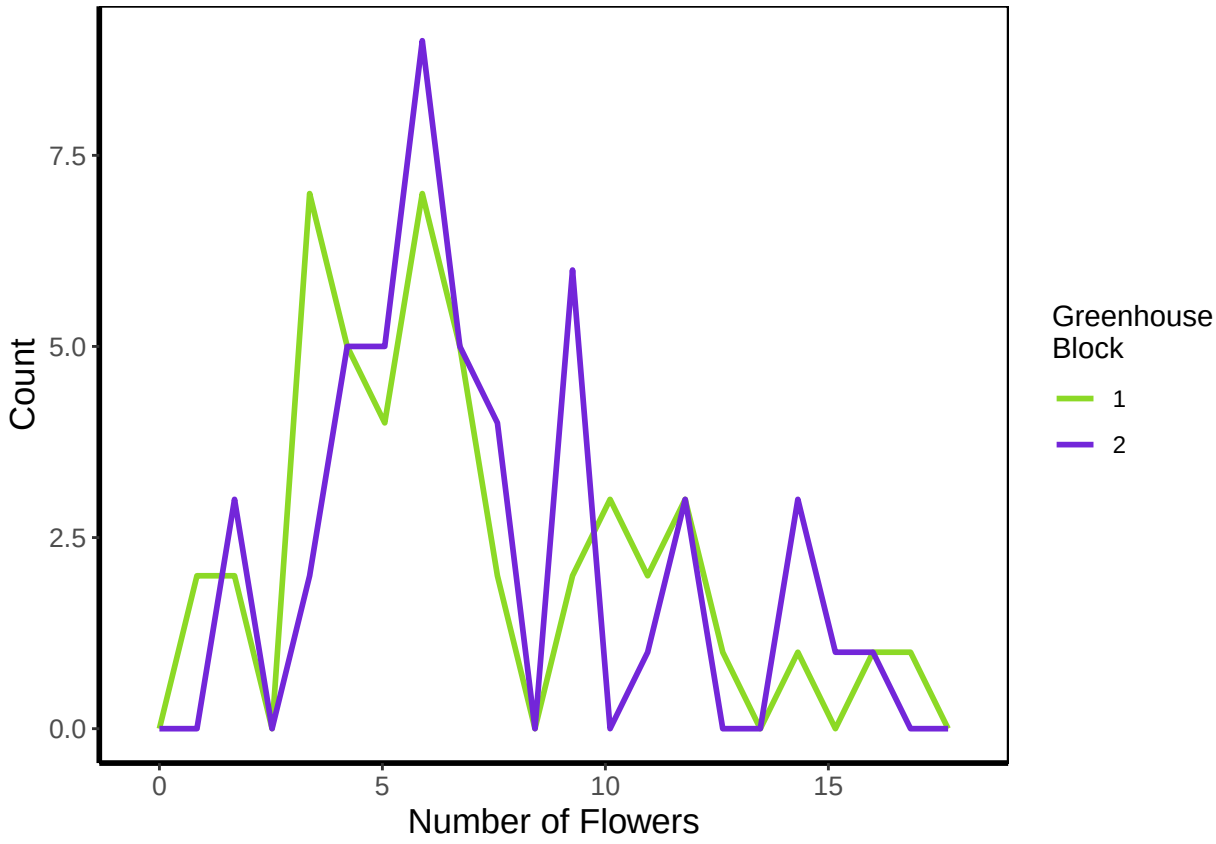
The other thing to take note of is that we've specified bins = 20. The number of bins control how many times the y-axis is broken up to show the data. Try increasing and decreasing to see the effect. The last is using the position = argument and stating that we do not want the bars to be stacked (the default position), instead we want them side-by-side, a.k.a. dodged.

```
ggplot(flowergg) +
  geom_histogram(aes(x = flowers, fill = factor(block)), colour = "black", bins = 20,
                 position = "dodge") +
  labs(y = "Count", x = "Number of Flowers", fill = "Greenhouse\nBlock") +
  scale_fill_manual(labels = c("1", "2"),
                    values = c("#8CD926", "#7326D9")) +
  theme_rbook()
```



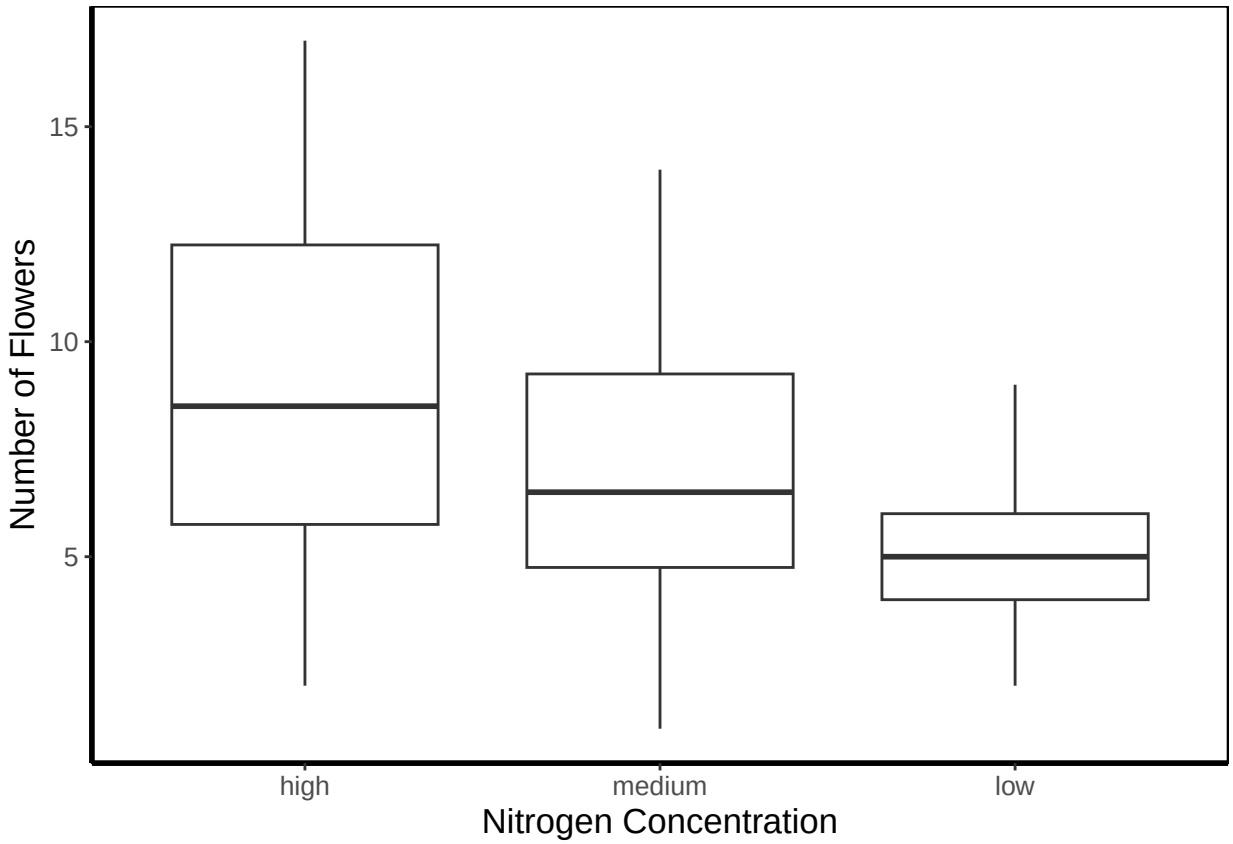
3. Frequency polygon A frequency polygon is yet another visualisation of the above two. The only difference here is that we are drawing a line to each value, instead of a density curve or bars.

```
ggplot(flowergg) +
  geom_freqpoly(aes(x = flowers, colour = factor(block)), size = 1, bins = 20) +
  labs(y = "Count", x = "Number of Flowers", colour = "Greenhouse\nBlock") +
  scale_colour_manual(labels = c("1", "2"),
                      values = c("#8CD926", "#7326D9")) +
  theme_rbook()
```



4. Boxplot Boxplots are a classic way to show to spread of data, and they're easy to make in ggplot2. The dark line in the middle of the box shows the median, the boxes show the 25th and 75th percentiles (which is different from the base R boxplot()), and the whiskers show 1.5 times the inter-quartile range (i.e. the distance between between the lower and upper quartiles).

```
ggplot(flowergg) +
  geom_boxplot(aes(y = flowers, x = nitrogen)) +
  labs(y = "Number of Flowers", x = "Nitrogen Concentration") +
  theme_rbook()
```

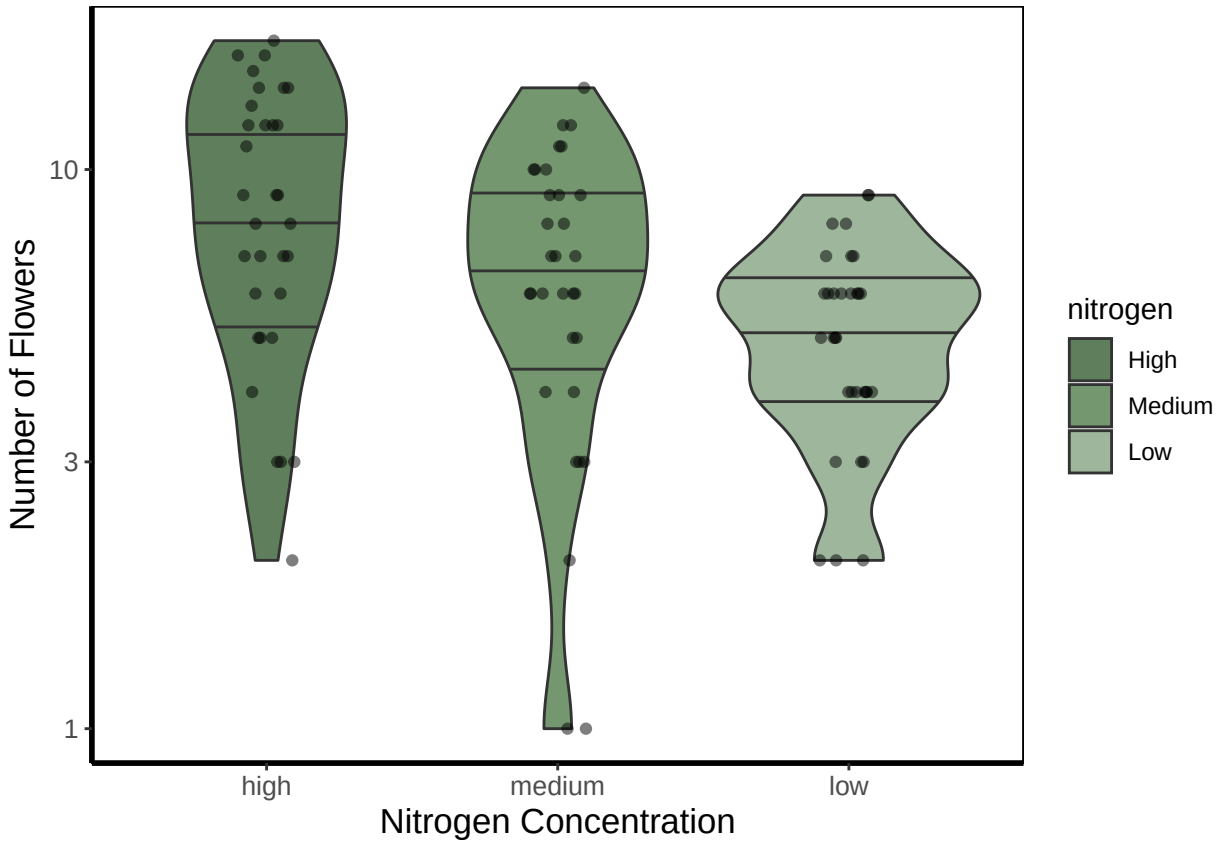


5. Violin plots Violin plots are an increasingly popular alternative to boxplots. They display much of the same information, as well as showing a version of the density plot above (imagine each violin plot, cut in half vertically and place on it's side, thus showing the overall distribution of the data). In the plot below the figure is slightly more complex than those above and so deserves some explanation.

Within geom_violin() we've included draw_quantiles = where we've specified we want quantile lines drawn at the 25, 50 and 75 quantiles (using the c() function). In combination with geom_violin() we've also included geom_jitter(). geom_jitter() is similar to geom_point() but induces a slight random spread of the points, often helpful when those points would otherwise be clustered. Within geom_jitter() we've also set height = 0, and width = 0.1 which specifies how much to jitter the points in a given dimension (here essentially telling ggplot2 not to jitter by height, and only to jitter width by a small amount).

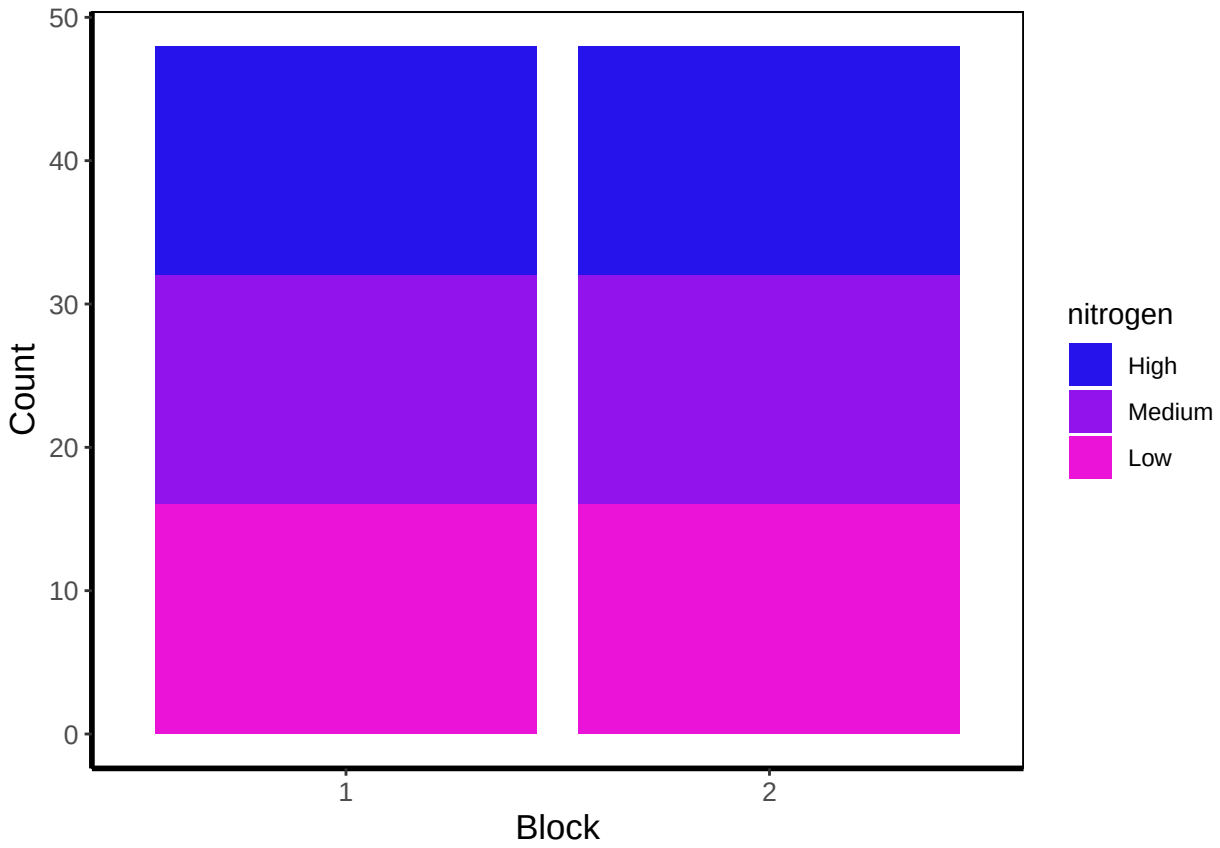
Finally, we're also using this plot to show scale_y_log10. Hopefully this is largely selfexplanatory (it converts the y-axis to the log_10_ scale). There are additional scaling options for axis (for instance scale_y_sqrt()). Please note that using a log scaled axis in this case is actually doing harm in terms of understanding the data, we'd actually be much better off not doing so in this particular case.

```
ggplot(flowergg) +
  geom_violin(aes(y = flowers, x = nitrogen, fill = nitrogen),
              draw_quantiles = c(0.25, 0.5, 0.75)) +
  geom_jitter(aes(y = flowers, x = nitrogen), colour = "black", height = 0,
              width = 0.1, alpha = 0.5) +
  scale_fill_manual(labels = c("High", "Medium", "Low"),
                    values = c("#5f7f5c", "#749770", "#9eb69b")) +
  labs(y = "Number of Flowers", x = "Nitrogen Concentration") +
  scale_y_log10() +
  theme_rbook()
```



6. Barchart Below is an example of barcharts. It is included here for completeness, but be aware that they are viewed with contention (with good reason). Briefly, barcharts can hide information, or imply there is data where there is none; ultimately misleading the reader. There are almost always better alternatives to use that better demonstrate the data.

```
ggplot(flowergg) +
  geom_bar(aes(x = factor(block), fill = nitrogen)) +
  scale_fill_manual(labels = c("High", "Medium", "Low"),
                    values = c("#2613EC", "#9313EC", "#EC13D9")) +
  labs(y = "Count", x = "Block") +
  theme_rbook()
```



The barchart shows the numbers of observations in each block, with each bar split according to the number of observations in each nitrogen concentration. In this case they are equal because the dataset (and experimental design) was balanced.

7. Quantile lines While we can draw a straight line, perhaps we would also like to include the descriptive nature of a boxplot, except using continuous data. We can use quantile lines in such cases. Note that for quantiles to be calculated ggplot2 requires the installation of the package quantreg.

```
library(quantreg)
```

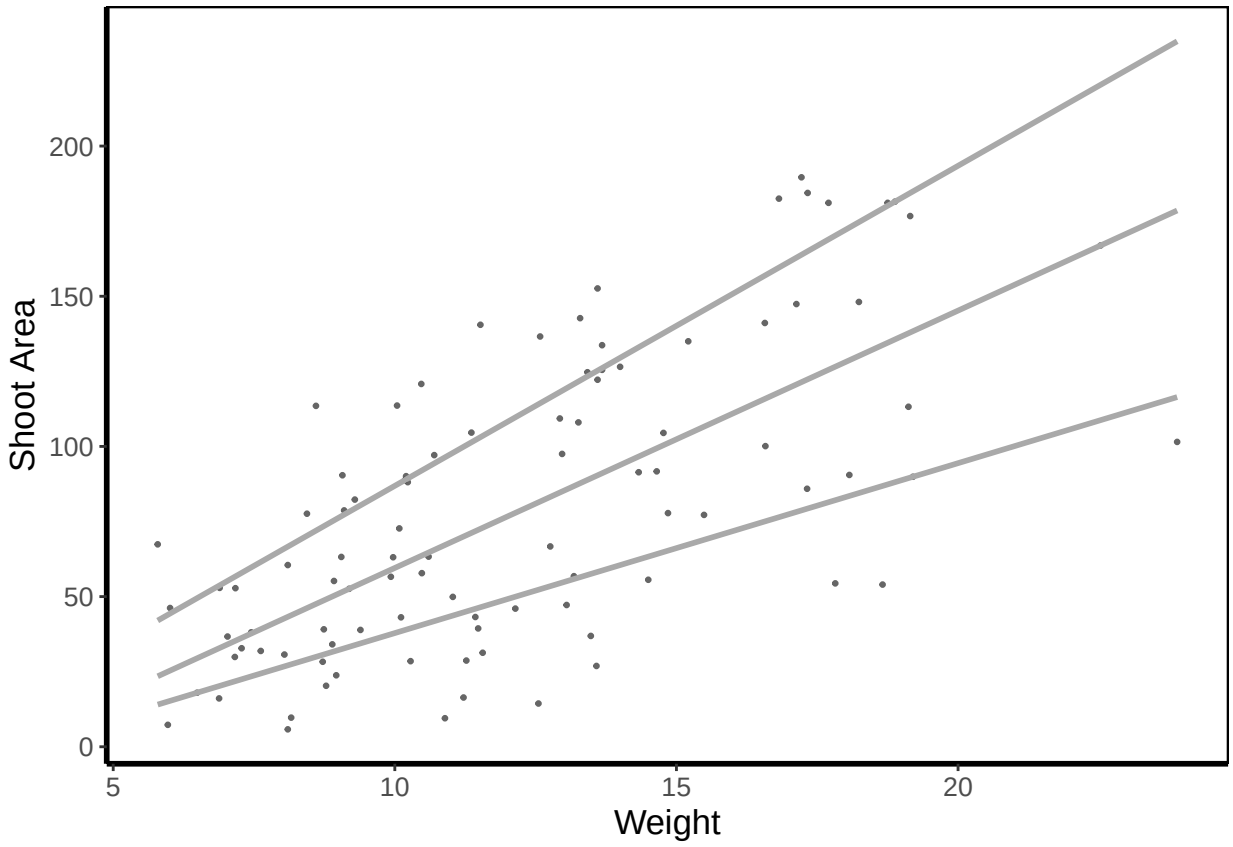
```
## Loading required package: SparseM
```

```
##
## Attaching package: 'SparseM'
```

```
## The following object is masked from 'package:base':
##
##     backsolve
```

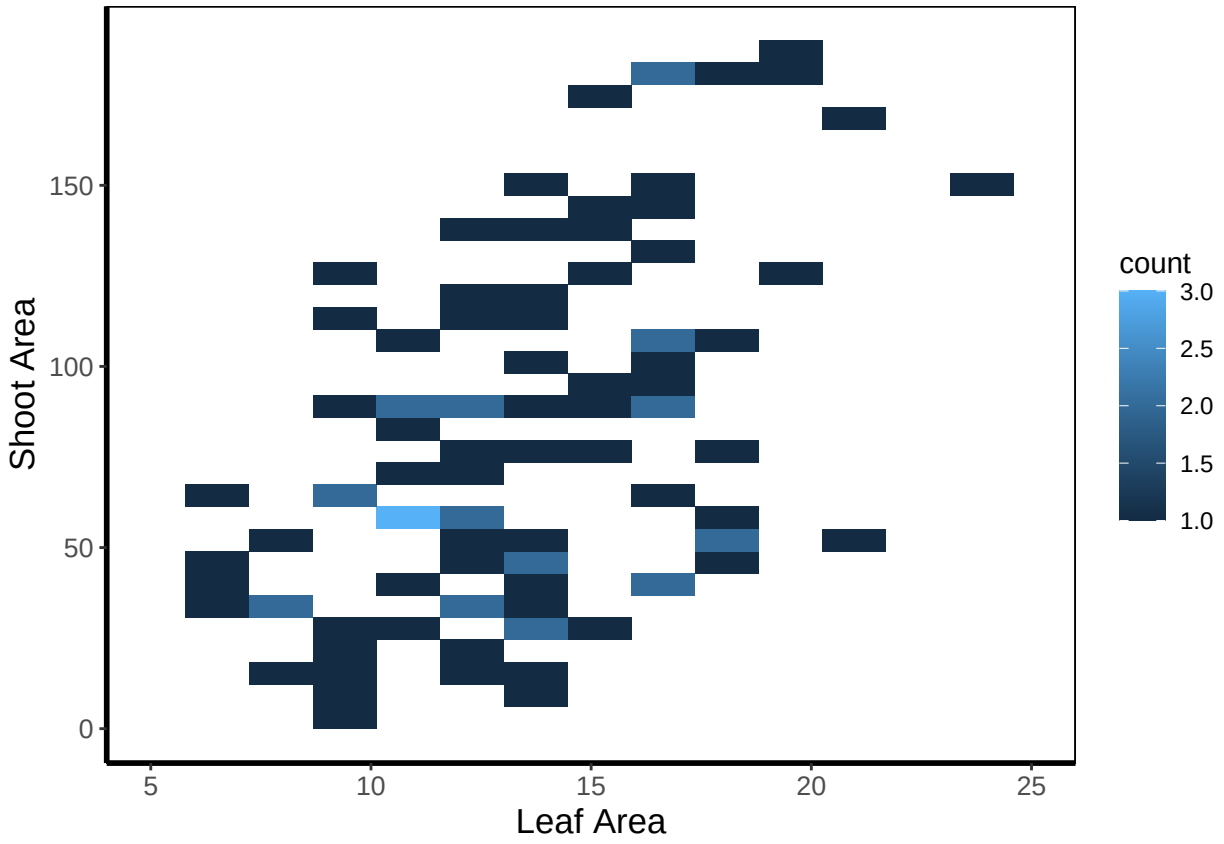
```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point(size = 0.5, alpha = 0.6) +
  geom_quantile(colour = "darkgrey", size = 1) +
  labs(y = "Shoot Area", x = "Weight") +
  theme_rbook()
```

```
## Smoothing formula not specified. Using: y ~ x
```



8. Heat map (BETTER FOR SPATIAL DISTRIBUTION) Heatmaps are a great tool to visualise spatial patterns. ggplot2 can easily handle such data using geom_bin2d() to allow us to see if our data is more (or less) clustered.

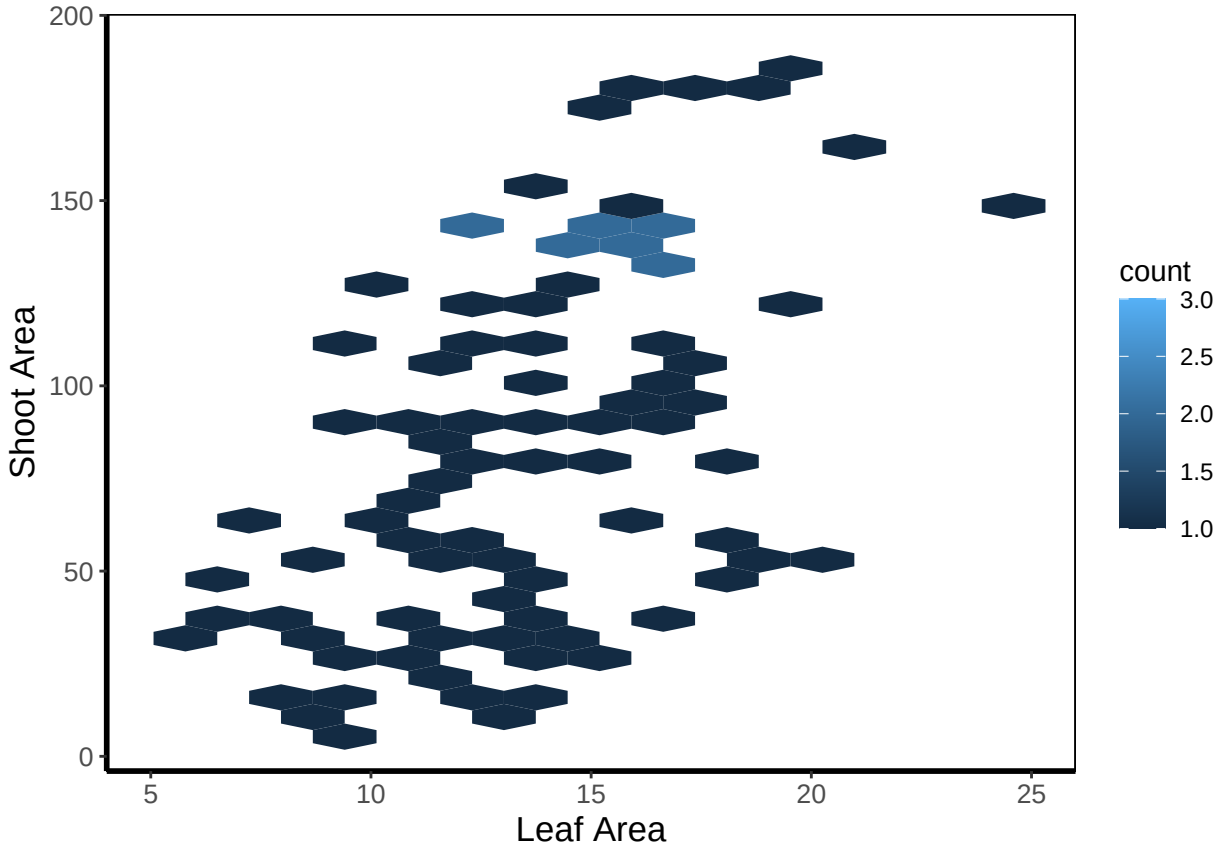
```
ggplot(aes(x = leafarea, y = shootarea), data = flowergg) +
  geom_bin2d() +
  labs(y = "Shoot Area", x = "Leaf Area") +
  coord_cartesian(xlim = c(5,25)) +
  theme_rbook()
```



In this example, lighter blue squares show combinations of leaf area and shoot area where we have more data, and dark blue shows the converse.

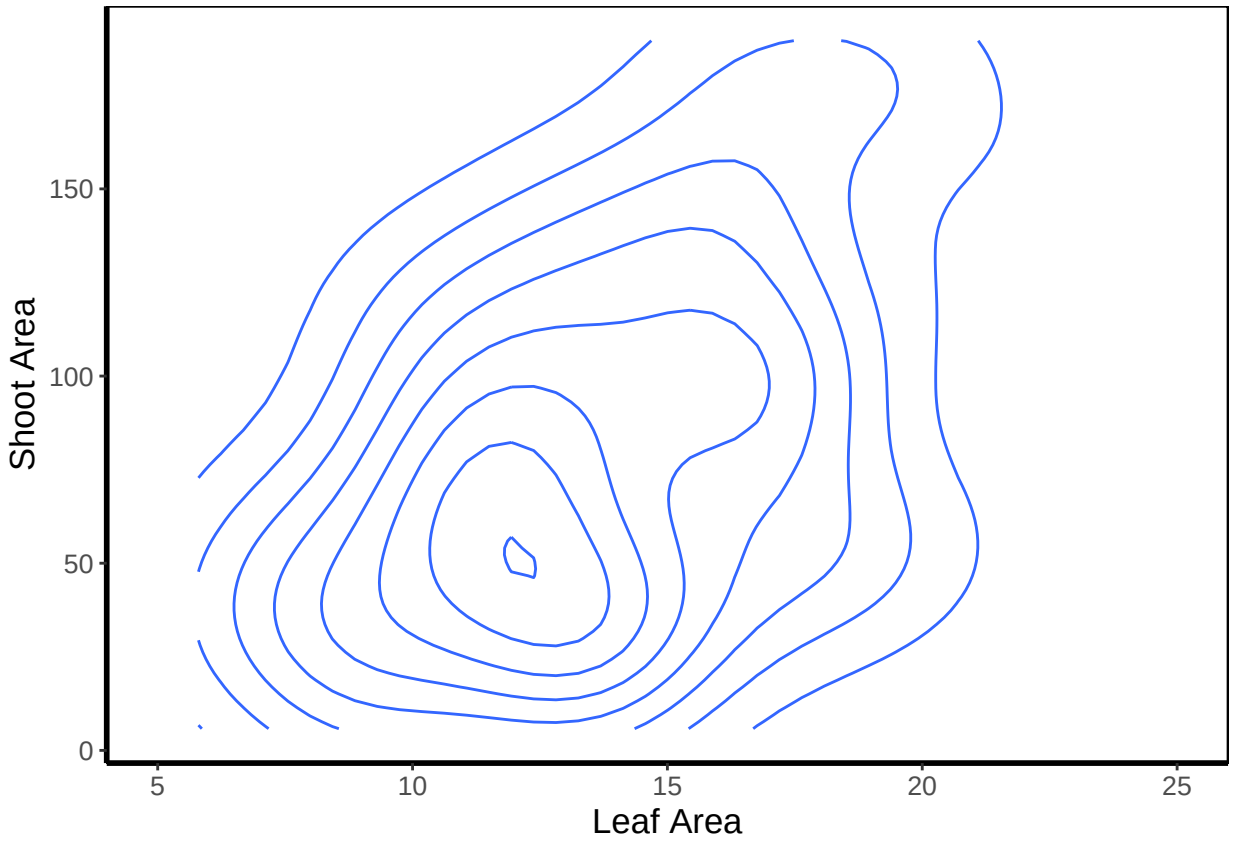
9. Hexmap A similar version to geom_density2d() is geom_hex(). The only difference between the two is that the squares are replaced with hexagons. Note that geom_hex() requires you to first install an additional package called hexbin.

```
library(hexbin)
ggplot(aes(x = leafarea, y = shootarea), data = flowergg) +
  geom_hex() +
  labs(y = "Shoot Area", x = "Leaf Area") +
  coord_cartesian(xlim = c(5,25)) +
  theme_rbook()
```



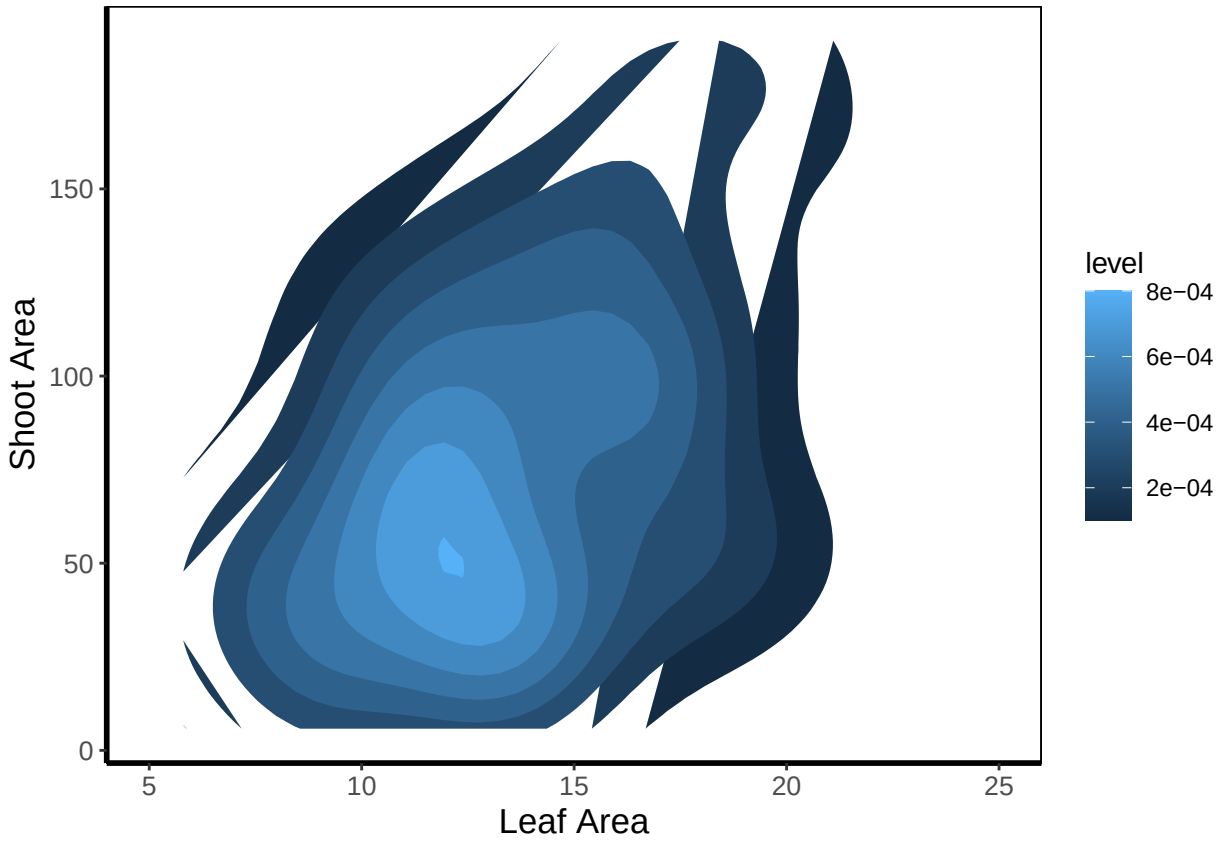
10. Contour map Similar to a heatmap we can make a contour map using geom_density_2d(). The way to read this figure is much the same way as you'd read a topographical map showing mountains or peaks. The central polygon represents the space (amongst shoot and leaf area) where there are most observations. As you "step" down this mountain to the next line, we step down in the number of counts. Think of this as showing where points are most clustered, as in geom_bin2d().

```
ggplot(aes(x = leafarea, y = shootarea), data = flowergg) +
  geom_density2d() +
  labs(y = "Shoot Area", x = "Leaf Area") +
  coord_cartesian(xlim = c(5,25)) +
  theme_rbook()
```



We can then expand on this using the statistics layer, via stat_nameOfStatistic. For instance, we can use the calculated "level" (representing the height of contour) to fill in our figure. To do so, we'll swap out geom_density_2d() for stat_density_2d() which will allow us to colour in the contour map.

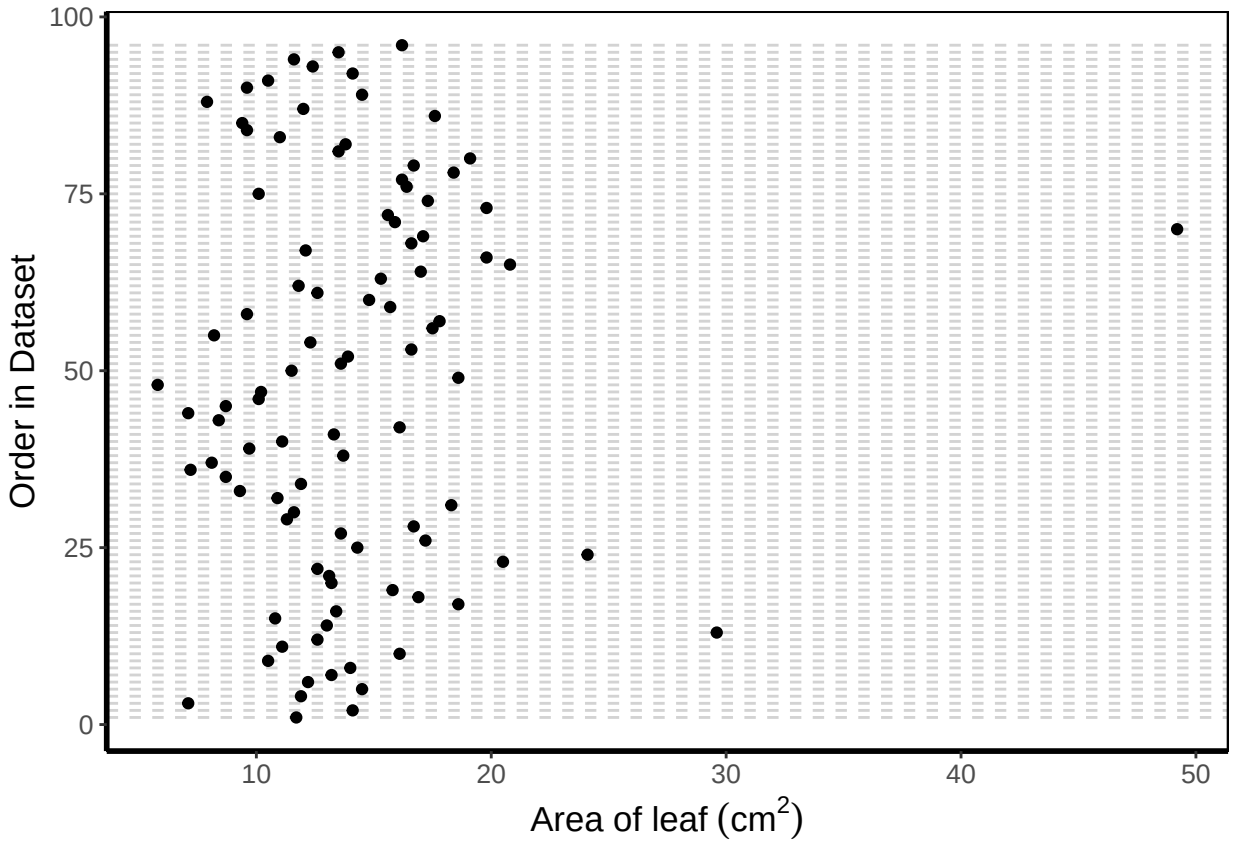
```
ggplot(aes(x = leafarea, y = shootarea), data = flowergg) +
  stat_density_2d(aes(fill = after_stat(level)), geom = "polygon") +
  labs(y = "Shoot Area", x = "Leaf Area") +
  coord_cartesian(xlim = c(5,25)) +
  theme_rbook()
```



11. cleveland dotplot The cleveland dotplot is a figure well suited to detect unusual oberservations (outliers?) in our data. The y axis is simply the order in which the data appears in the dataset. The x axis is our variable of interest. Points far to the left or far to the right are indicative of outliers. ggplot2 does not have a geom specifically designed for a cleveland dotplot, though because of the grammar of graphics framework, we can build it ourselves. We do this by first using the function rownames().

This function returns the row name of each row. In most data frames, the row names are simply numbers. Once we have this information, we can convert this to numbers using as.numeric(). After doing this we have a vector of numbers from 1 to 96. Keep in mind that such techniques can be used for any sort of figure we want to make. We'll use the same technique to add horiztonal lines for each row of data to replicate the traditional look of a dotchart.

```
ggplot(flowergg) +
  geom_hline(aes(yintercept = as.numeric(rownames(flowergg))), linetype = 2,
             colour = "lightgrey") +
  geom_point(aes(x = leafarea, y = as.numeric(rownames(flowergg)))) +
  labs(y = "Order in Dataset", x = bquote("Area of leaf"~(cm^2))) +
  theme_rbook()
```



12. Pairs plot For the final figure we will need an additional package, called GGally. Within GGally is a function called ggpairs() which is equivalent to pairs() (part of base R). Both functions produce a scatterplot matrix of all variables of interest. Running diagonally down from left to right are plots showing distributions; either as stacked barcharts or as density plots, in this case coloured according to nitrogen concentration. The bottom plots show the plotted relationships, with variables on the top as the x axis, and the variables on the right plotted as the y axis. For example, the very bottom left plots shows the relationship between number of flowers on the y axis and treatment on the x axis, coloured according to nitrogen concentration. Conversely, the upper plots show either the correlation between variables, when both variables are continuous and the correlation can be calculated, boxplots when the plot is of a factor variable and a continuous variable, or as a stacked barchart when both variables are factors.

Such figures are a fantastic way to quickly show relationships in the dataset. They can of course be used to plot only part of the dataset, for instance using flowers[,1:5] to plot the first five columns of the dataset.

We've included two additional arguments in the code below. cardinality_threshold = forces GGally to plot all of the variables in our dataset (where it normally wants fewer variables) as well as progress = to avoid a progress bar appearing when we run the code.

```
library(GGally)
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

```
flowergg$block <- factor(flowergg$block)
ggpairs(flowergg, aes(colour = nitrogen), cardinality_threshold = NULL, progress = FALSE) +
  theme_rbook()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
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## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
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```

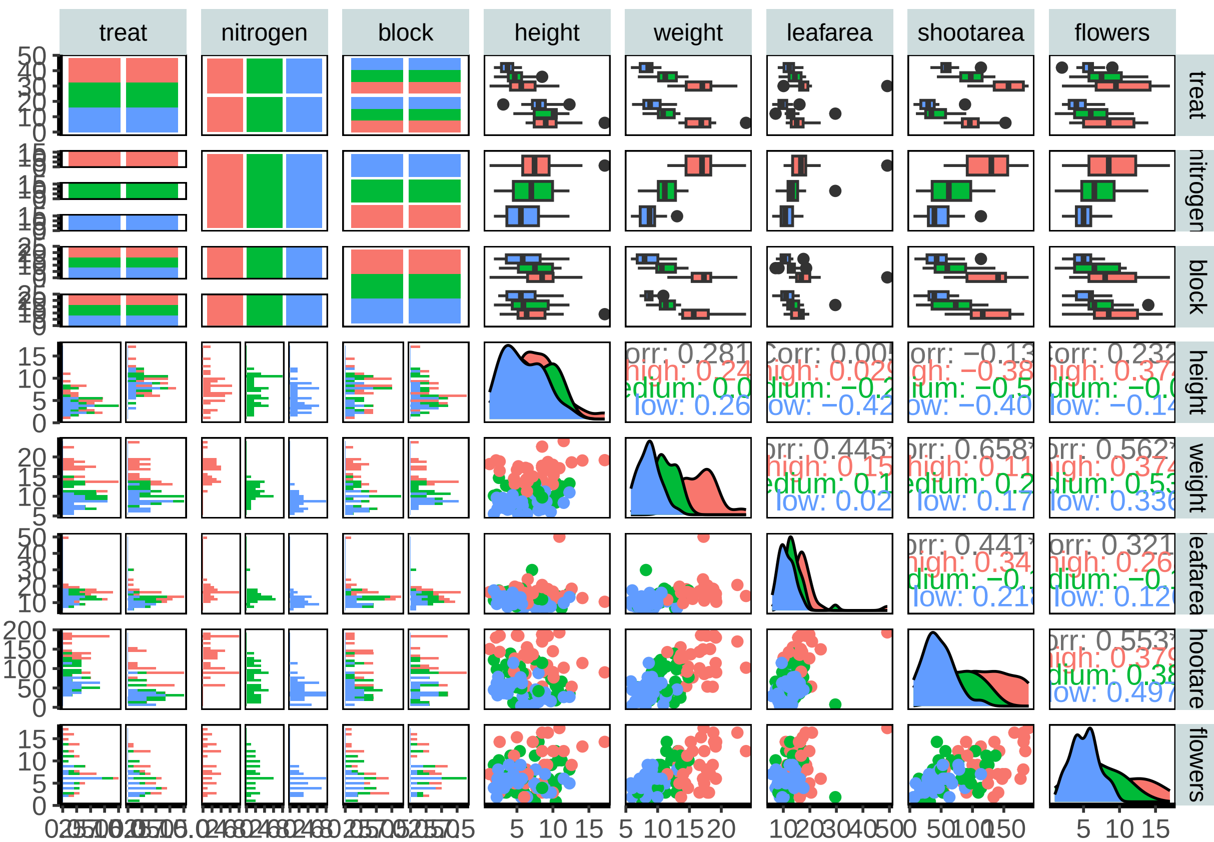


```
sessionInfo()
```

```
## R version 4.2.2 (2022-10-31)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Big Sur ... 10.16
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRlapack.dylib
```

```
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] GGally_2.1.2  hexbin_1.28.2 quantreg_5.94 SparseM_1.81  ggplot2_3.4.0
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.9         plyr_1.8.8         RColorBrewer_1.1-3 pillar_1.8.1
##  [5] compiler_4.2.2     highr_0.10         tools_4.2.2        digest_0.6.31
##  [9] lattice_0.20-45    nlme_3.1-161       evaluate_0.19      lifecycle_1.0.3
## [13] tibble_3.1.8       gtable_0.3.1       mgcv_1.8-41        pkgconfig_2.0.3
## [17] rlang_1.0.6        Matrix_1.5-3       cli_3.5.0          yaml_2.3.6
## [21] xfun_0.36          fastmap_1.1.0      withr_2.5.0        stringr_1.5.0
## [25] dplyr_1.0.10       knitr_1.41         MatrixModels_0.5-1 generics_0.1.3
## [29] vctrs_0.5.1        isoband_0.2.7      grid_4.2.2         tidyselect_1.2.0
## [33] reshape_0.8.9      glue_1.6.2         R6_2.5.1           fansi_1.0.3
## [37] survival_3.4-0     rmarkdown_2.19     farver_2.1.1       magrittr_2.0.3
## [41] MASS_7.3-58.1      scales_1.2.1       htmltools_0.5.4    splines_4.2.2
## [45] colorspace_2.0-3   labeling_0.4.2     utf8_1.2.2         stringi_1.7.8
## [49] munsell_0.5.0
```