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

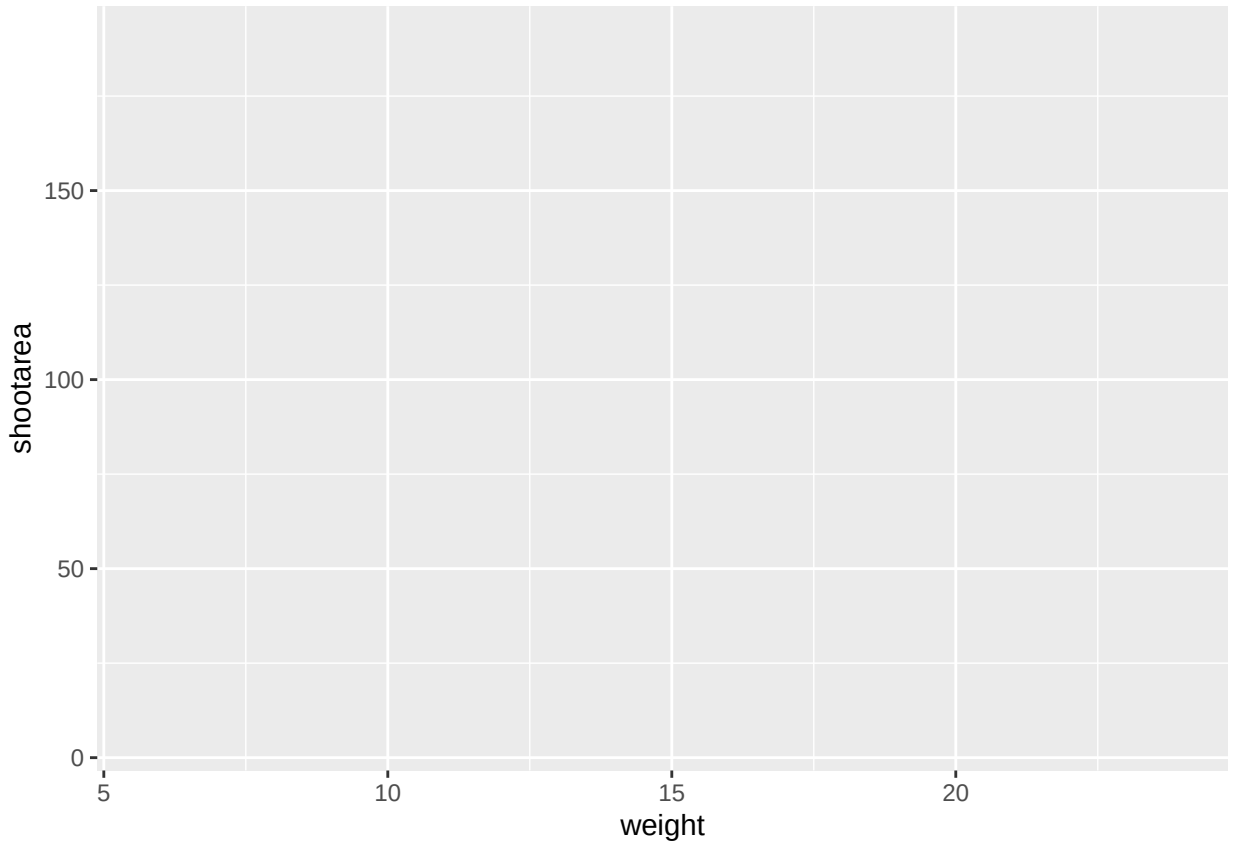
To do this in ggplot2 we need to make use of the aes() function and also add a data = argument.

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,

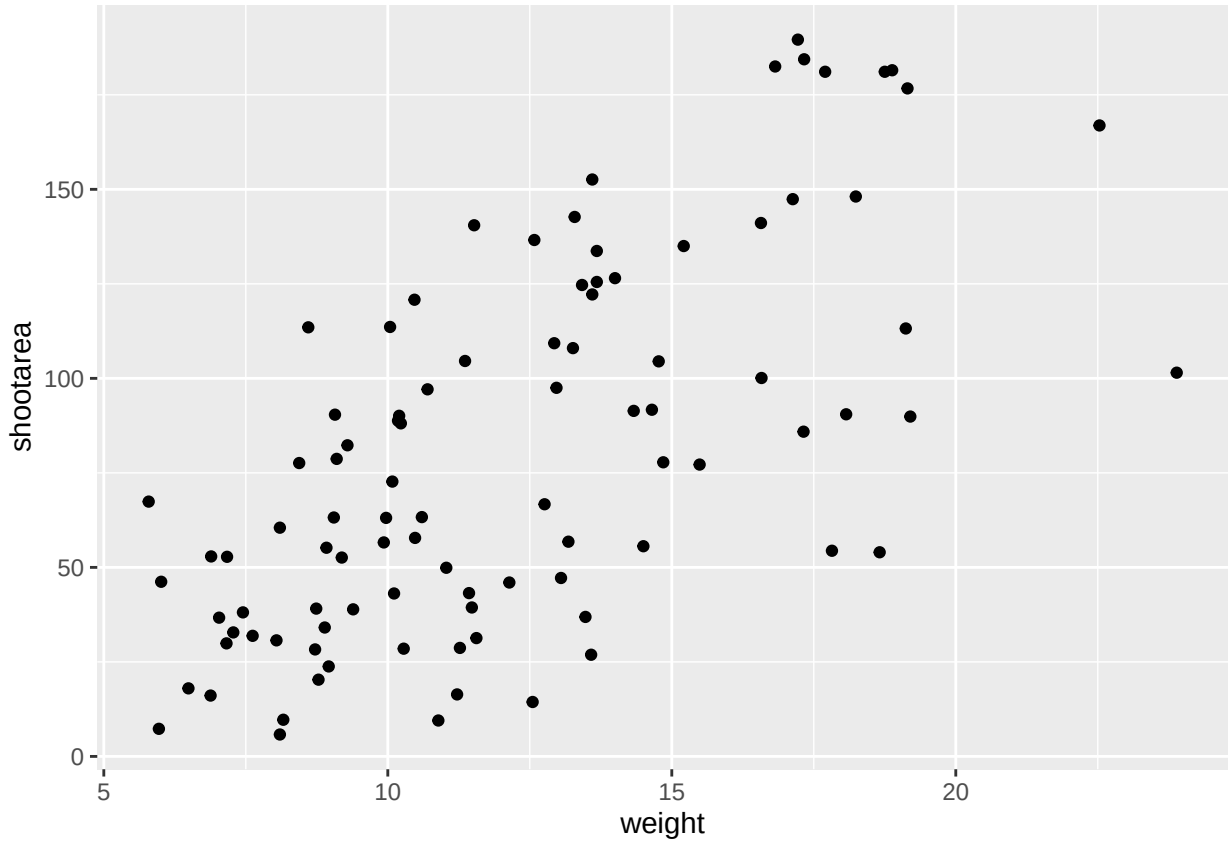
```
geom_point()
```

```
## 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:

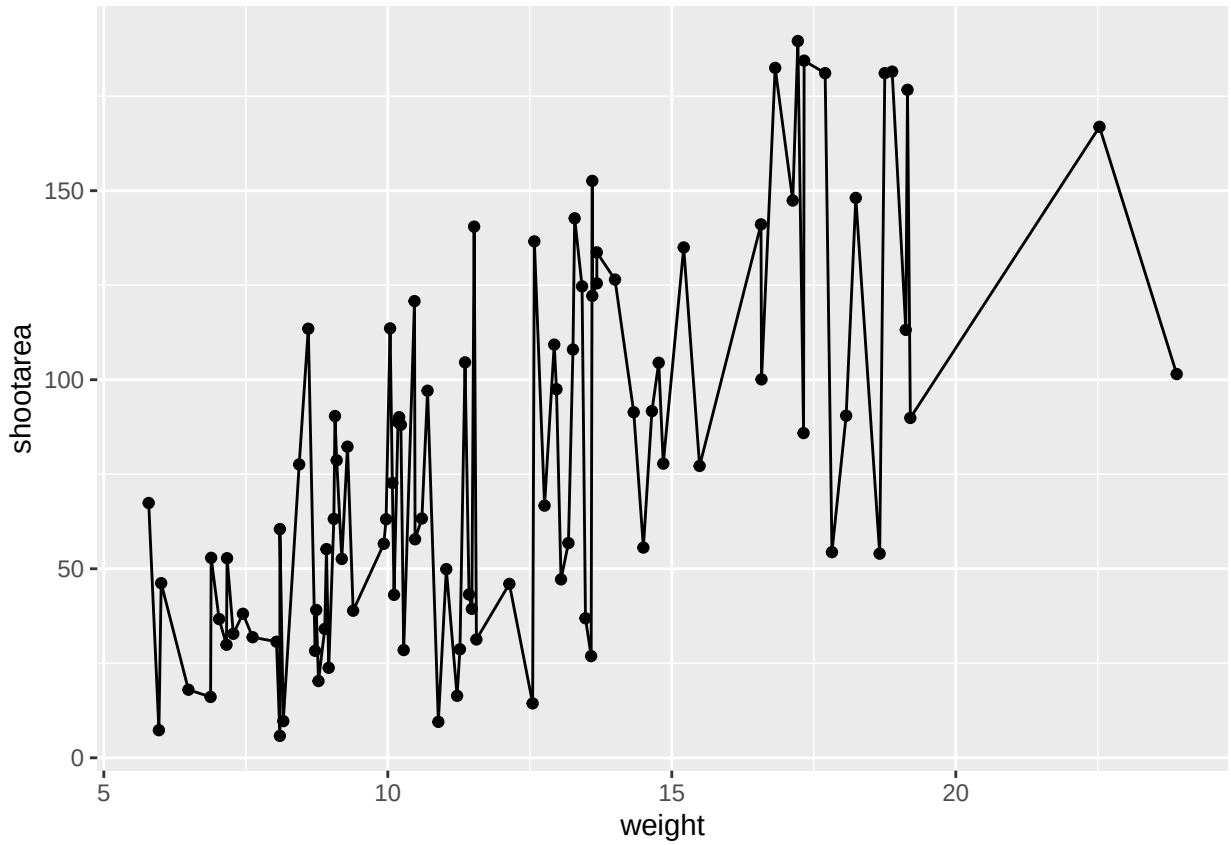
1. Data - the information we want to plot
2. Mapping - which variables we want displayed and where
3. Geometry - how we want that data displayed

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

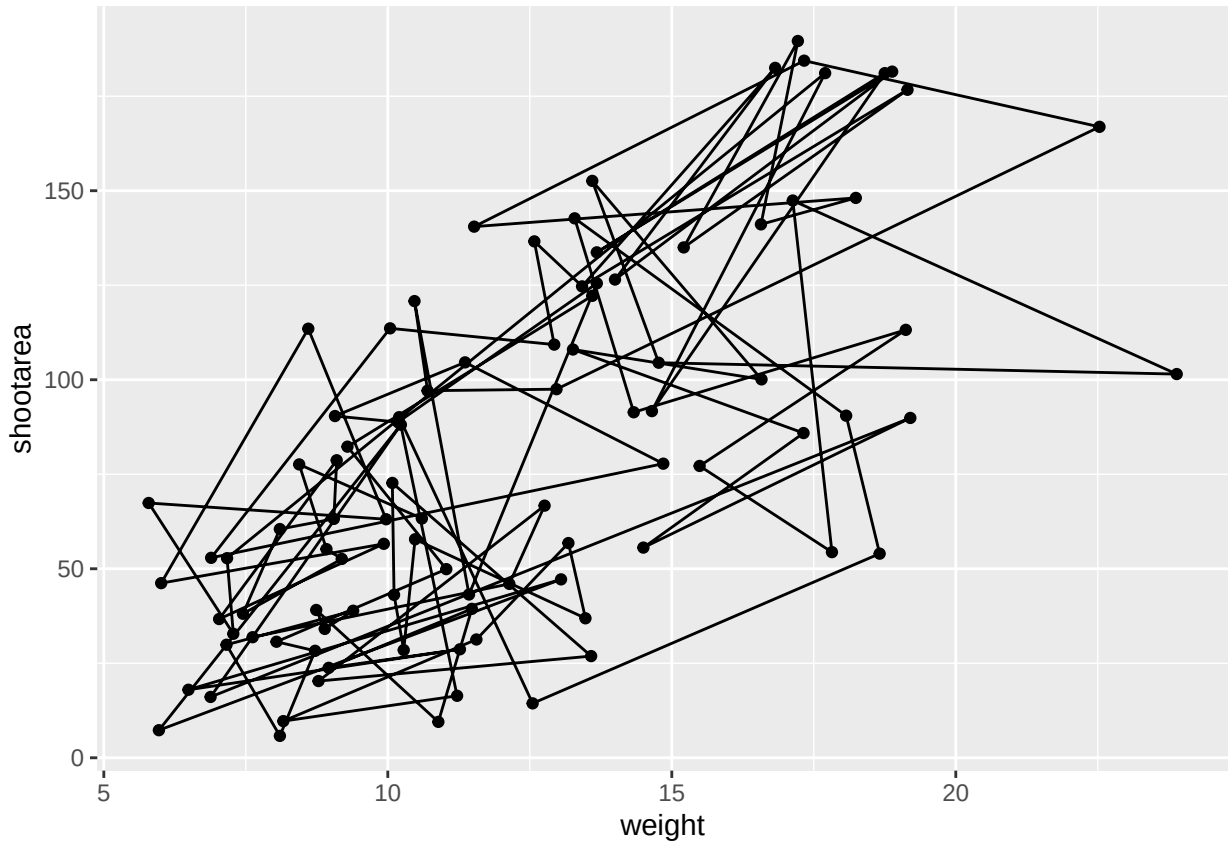
However, for showing to other people we might want something a bit more developed. If we glance back to our "final figure" we can see that we have lines representing the different nitrogen concentrations. We can include lines using a geom. If you have a quick look through the available geoms here, you 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,

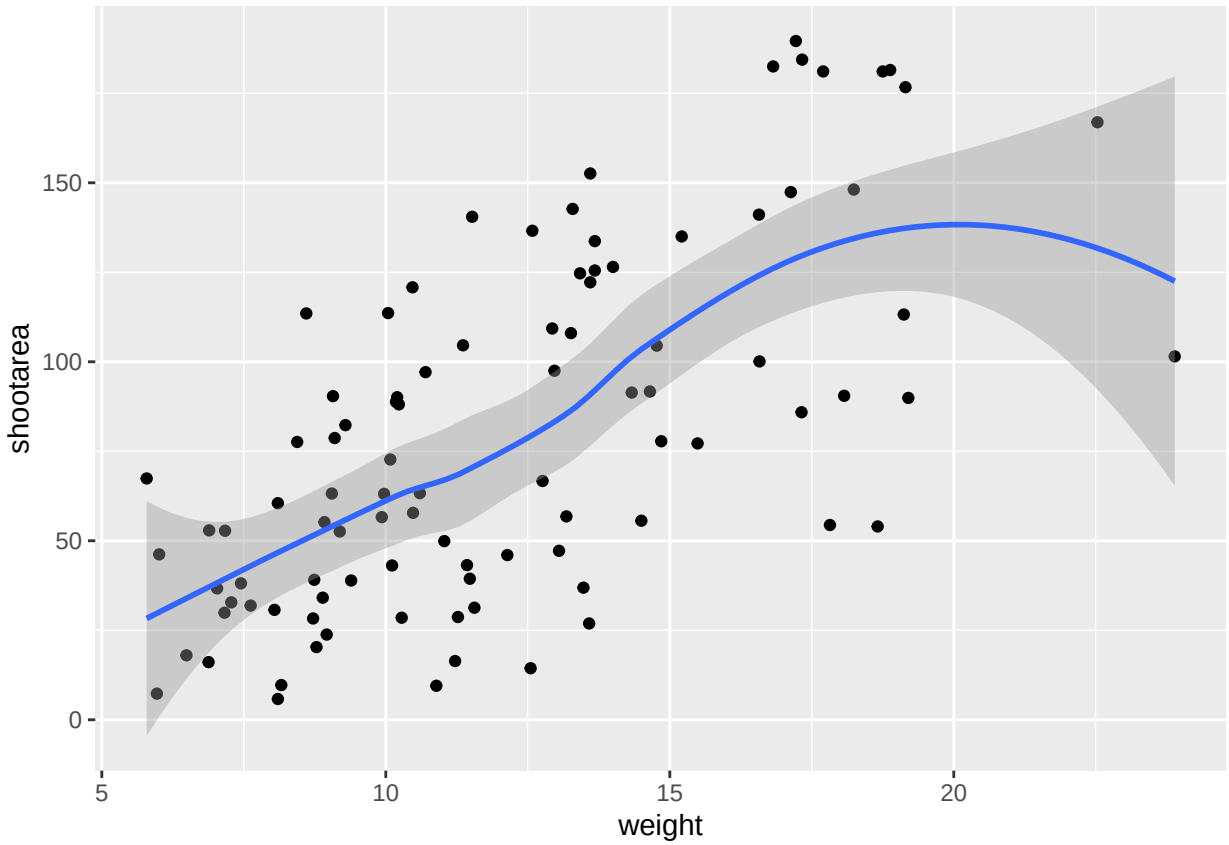
```
ggplot(aes(x = weight, y = shootarea), data = flowergg) +
  geom_point() +
  geom_path()
```



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'
```

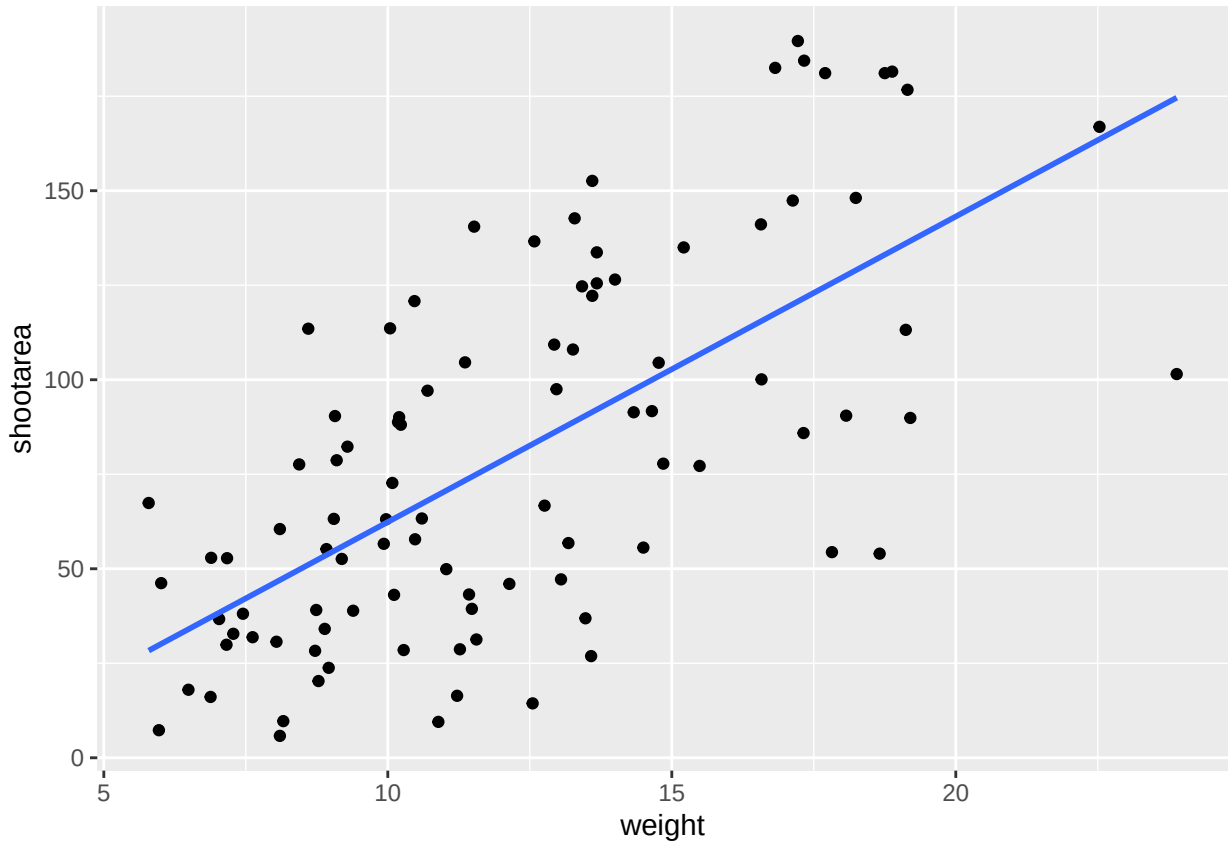


Better, but still not what we wanted. The challenge here is that drawing a line is actually somewhat complicated. The way our line above was drawn was by using a method called "LOESS" (locally estimated scatterplot smoothing) which gives something very close to a moving average; useful in some cases, 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".

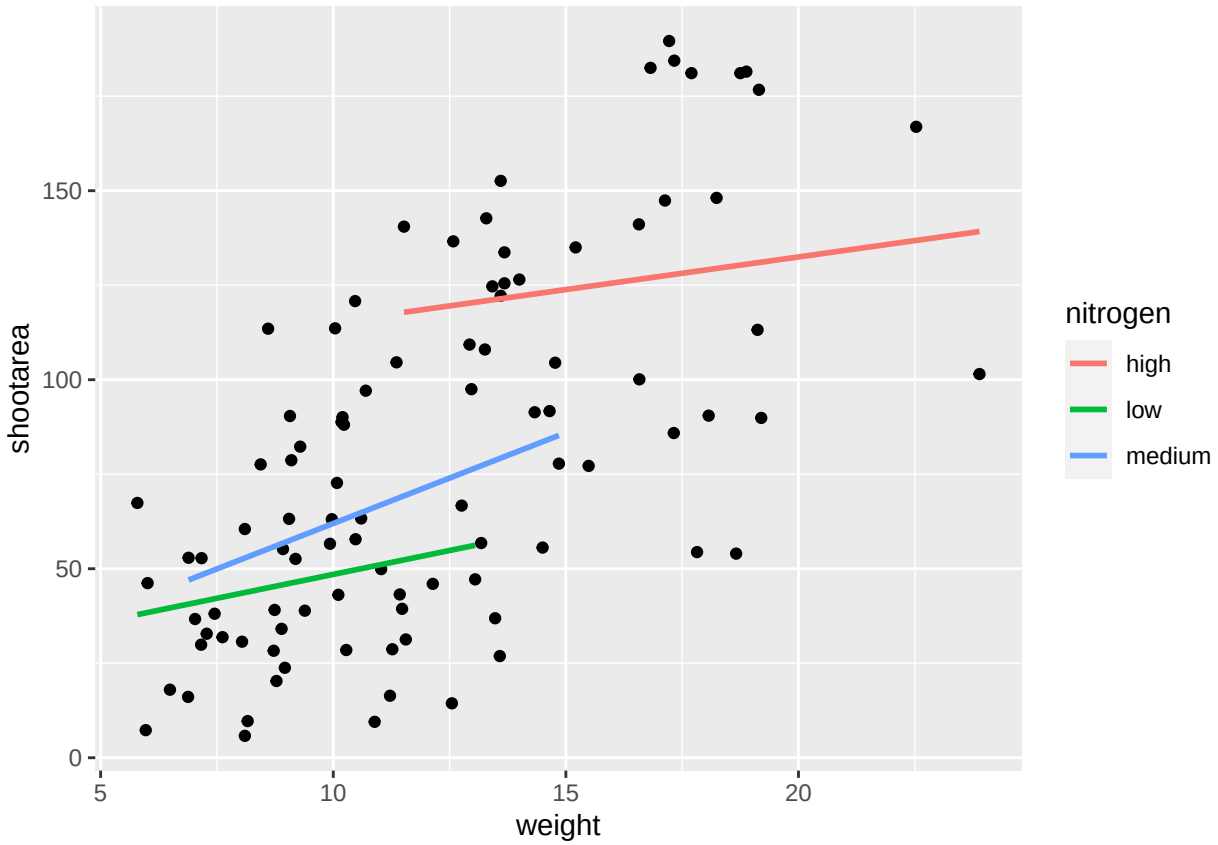
We need to alter geom_smooth() so that it draws lines for each level of nitrogen concentration. Getting ggplot2 to do that is pretty straightforward

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.

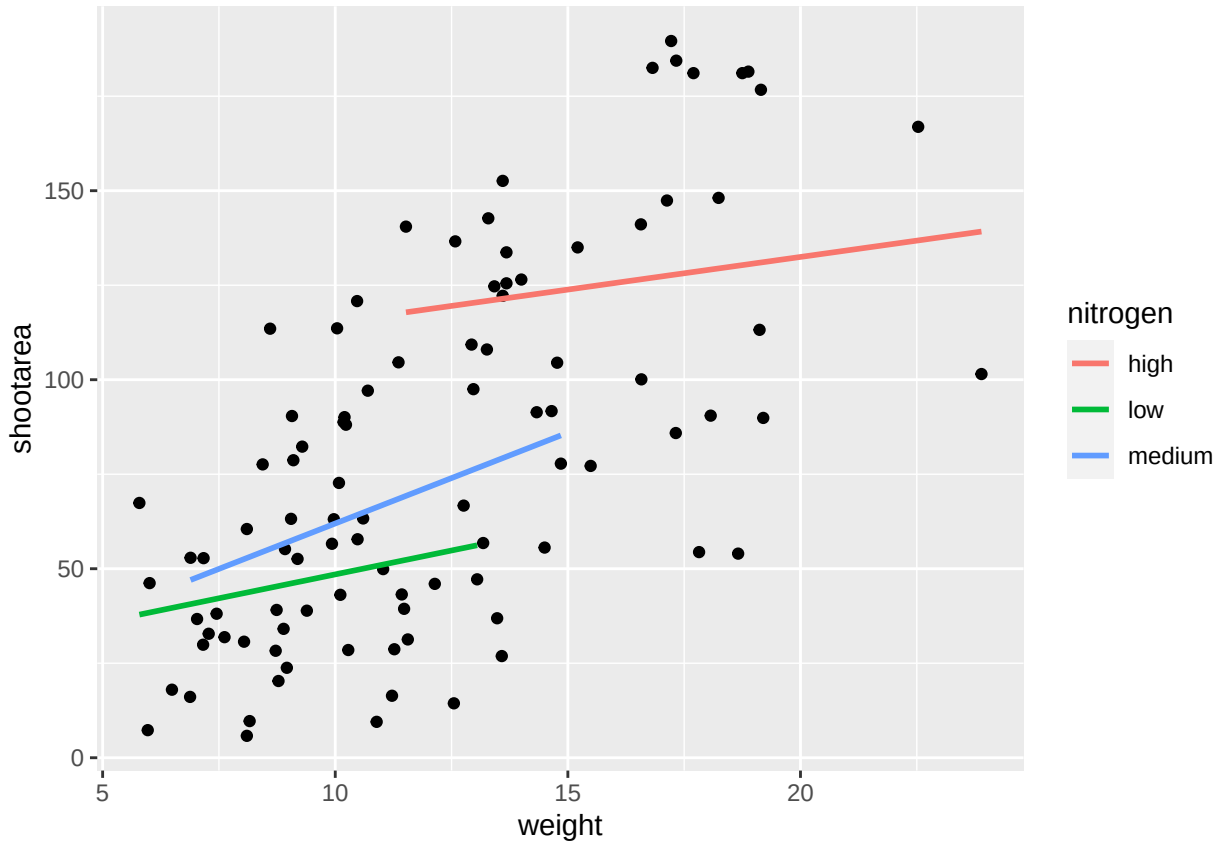
Where to include information

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!).

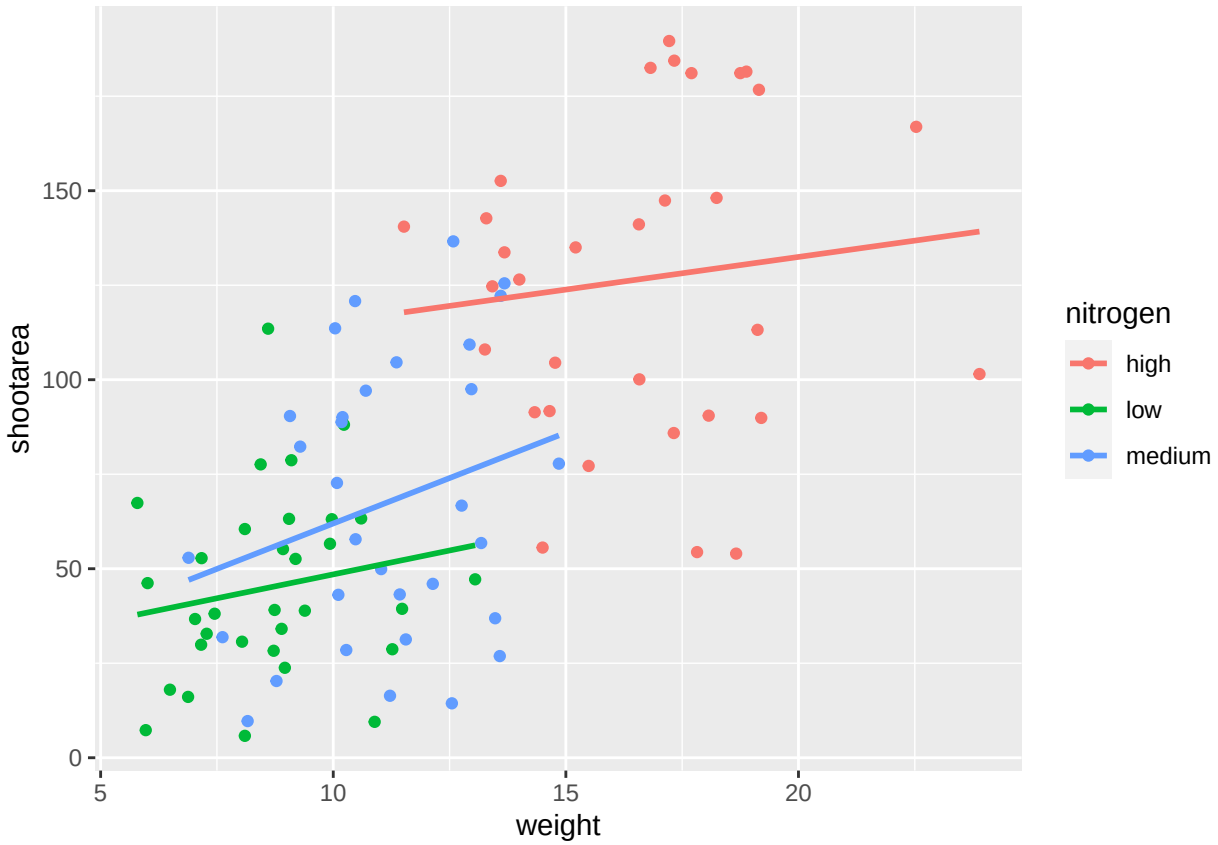
It can allow different geoms to display different (albeit similar) information (see more on this later). For this worked example, we'll move the same information back to the universal ggplot(),#

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)

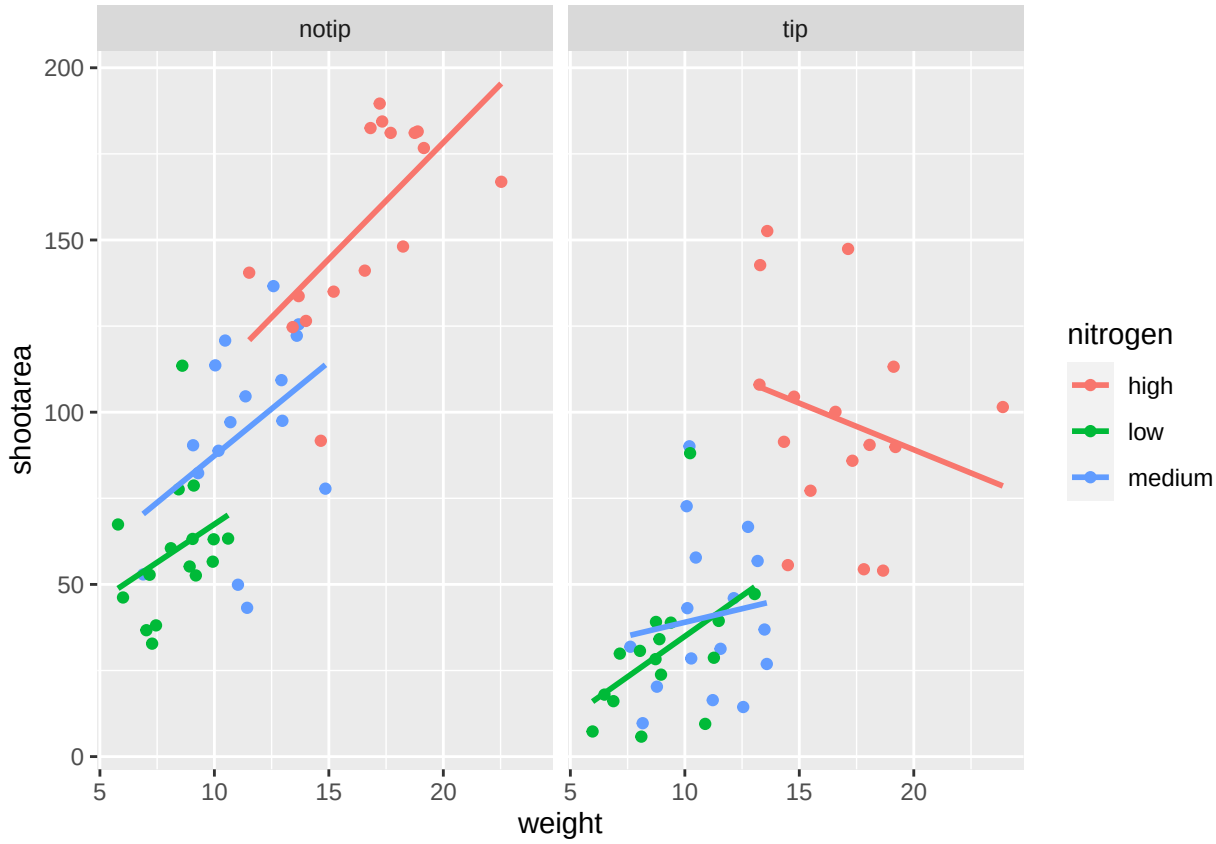
Having made our "pure" ggplot, the next big obstacle we're going to tackle is the grid like layout of the "final figure" where our main figure has been split according to the treat and block variables, with new trends shown for each combination Each of these panels (technically "multiples") are a great 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)
```

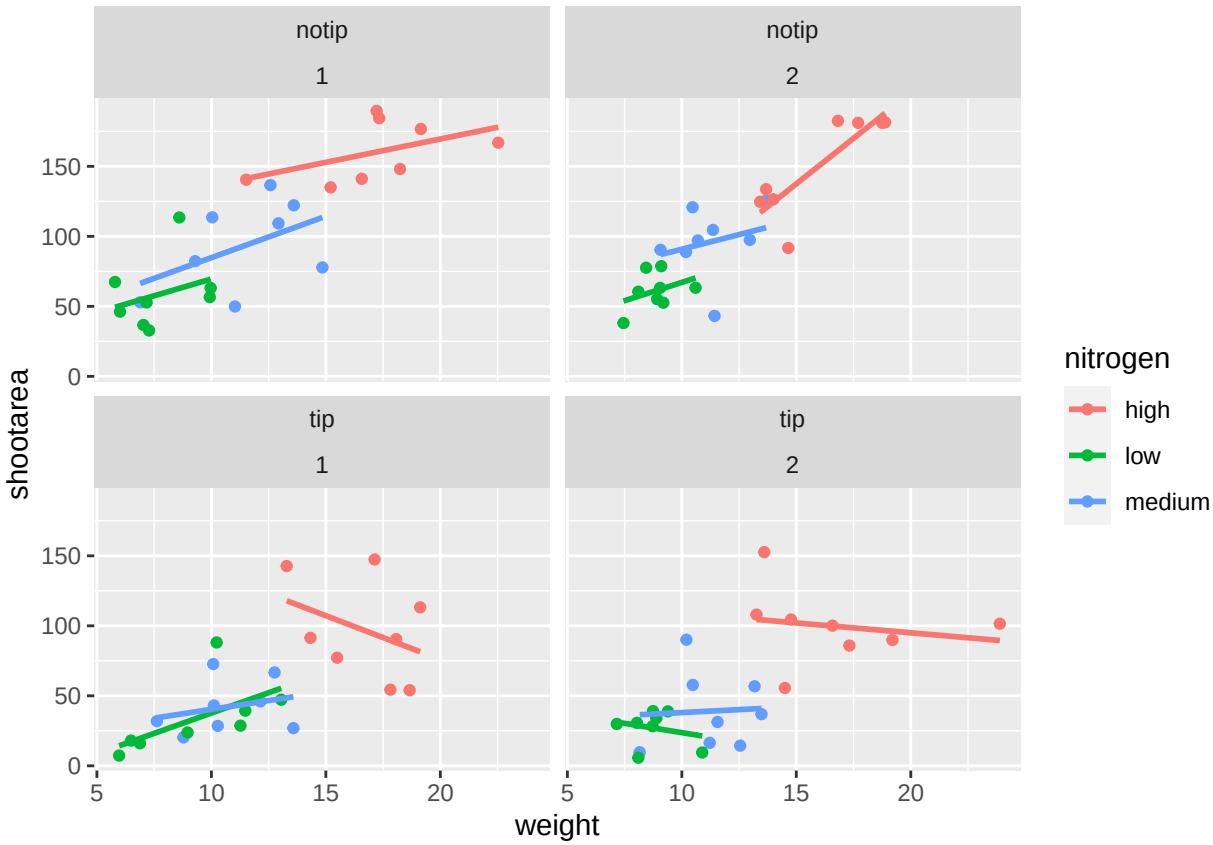
```
## `geom_smooth()` using formula = 'y ~ x'
```



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".

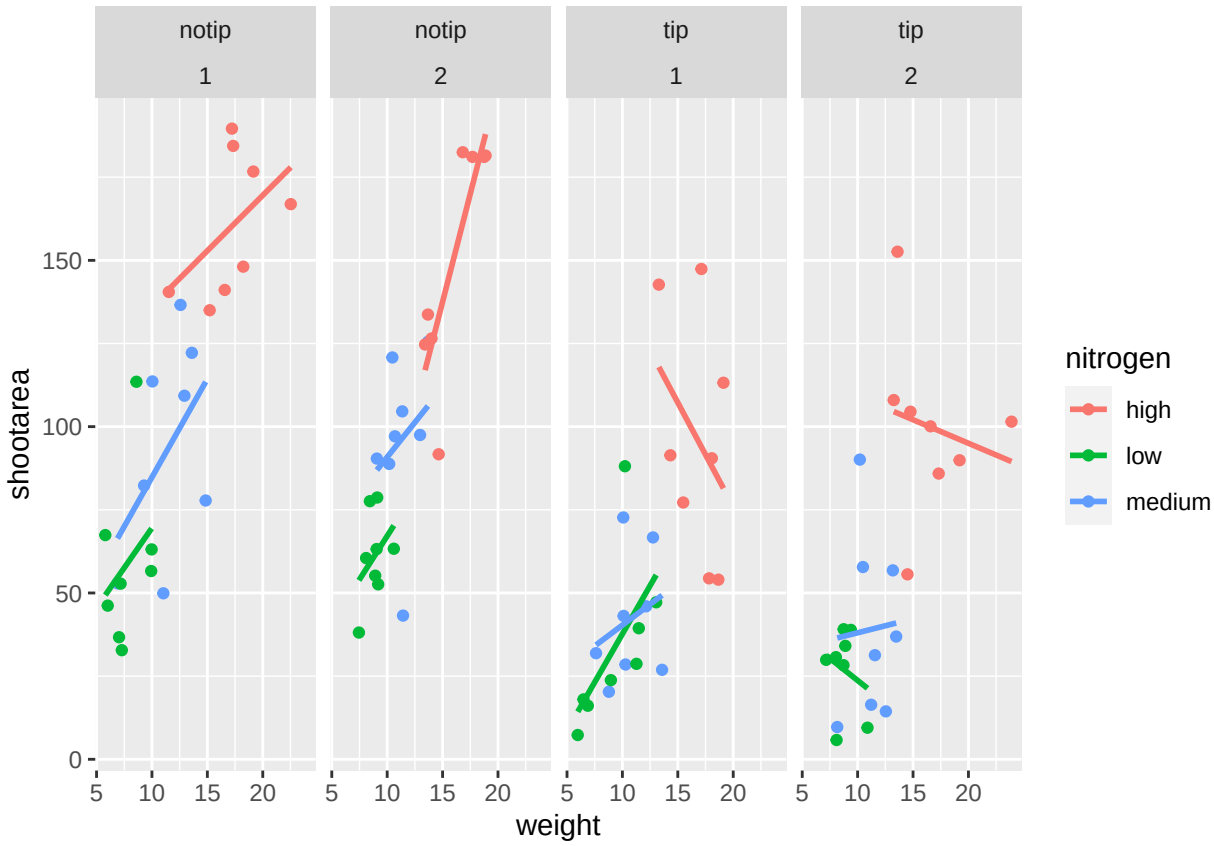
facet_grid

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'
```

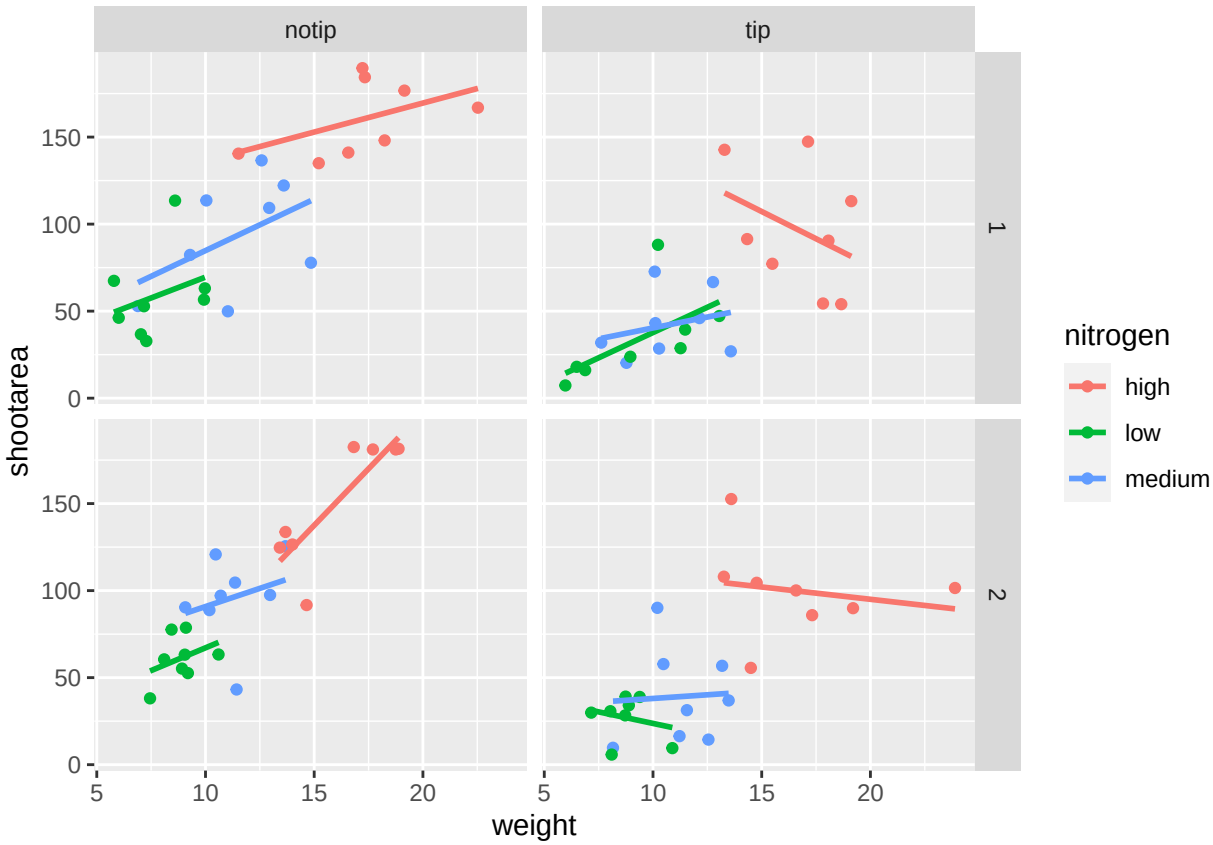


Disappointing

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.

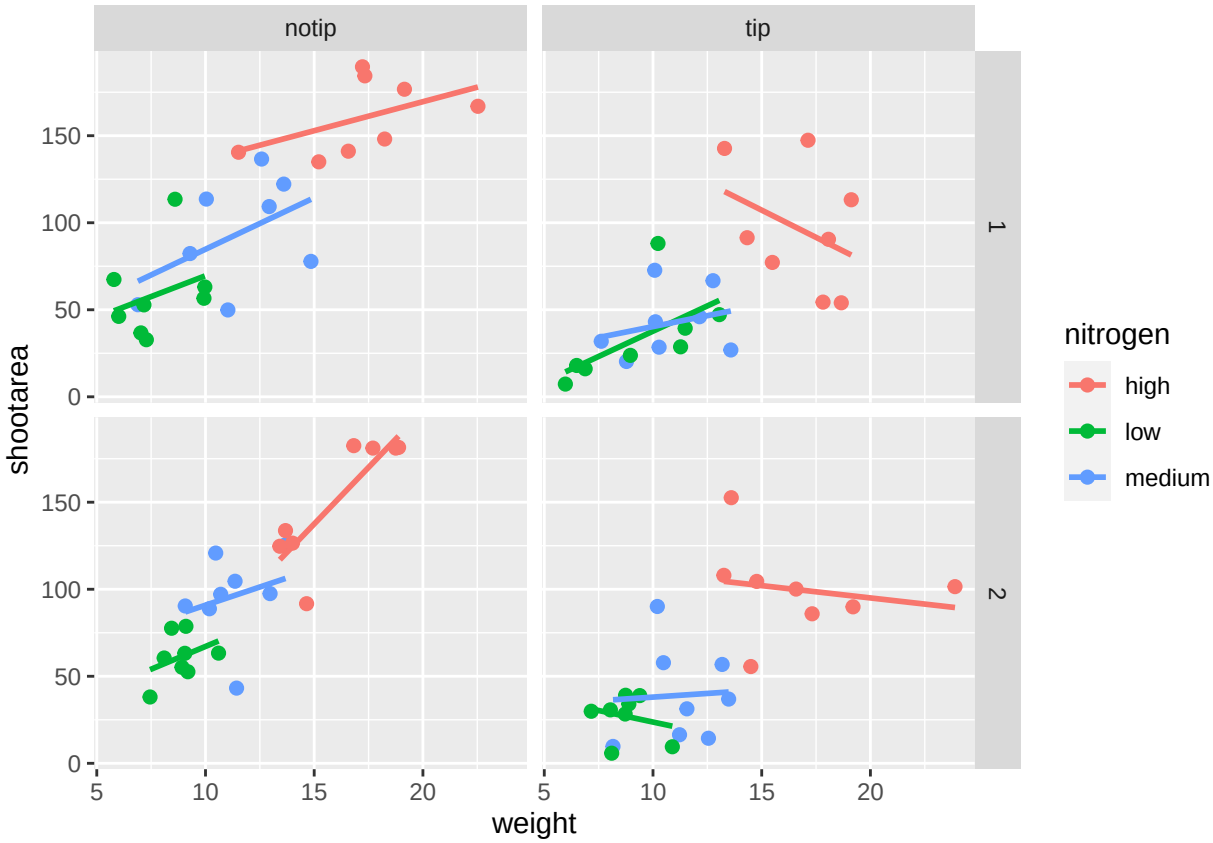
This next section will go through how to customise the appearance of our figure.

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)
```

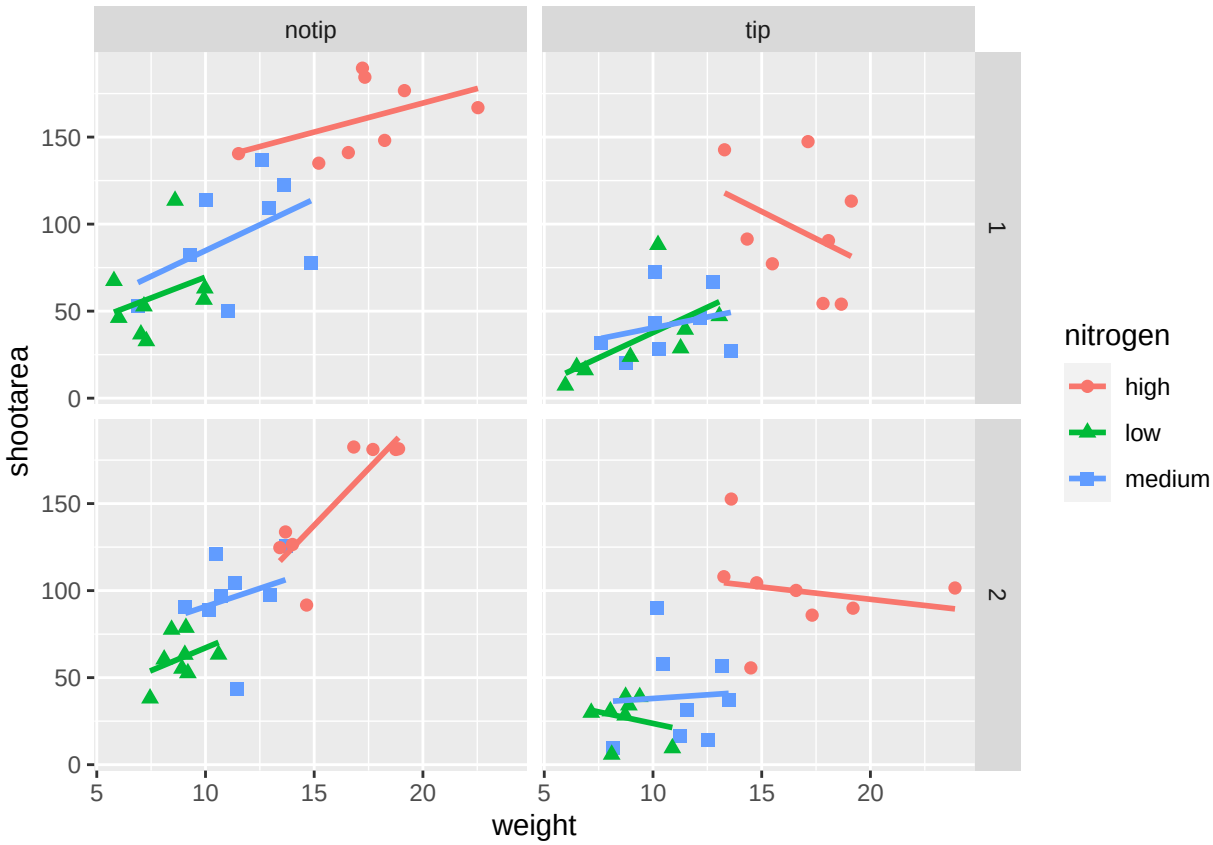
```
## `geom_smooth()` using formula = 'y ~ x'
```



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'
```

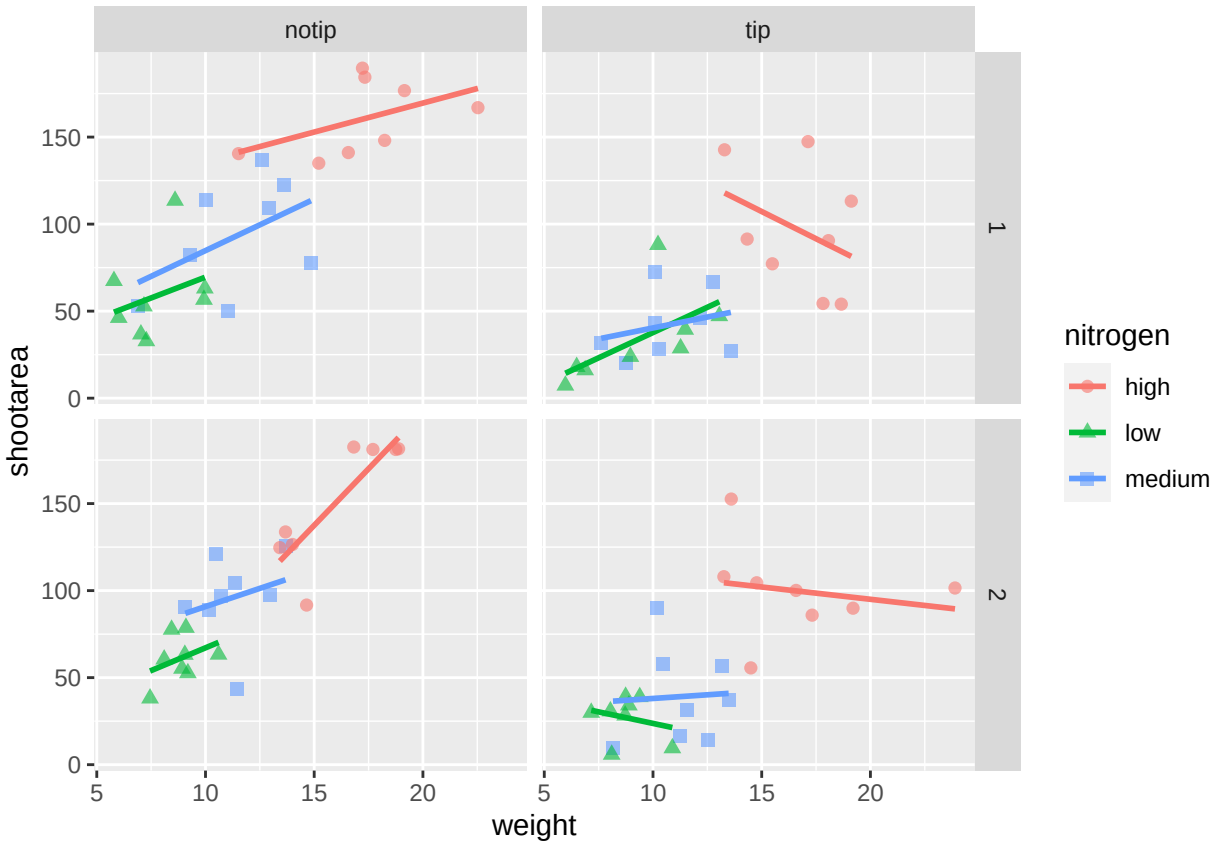


Aplha argument = Transparency

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)
```

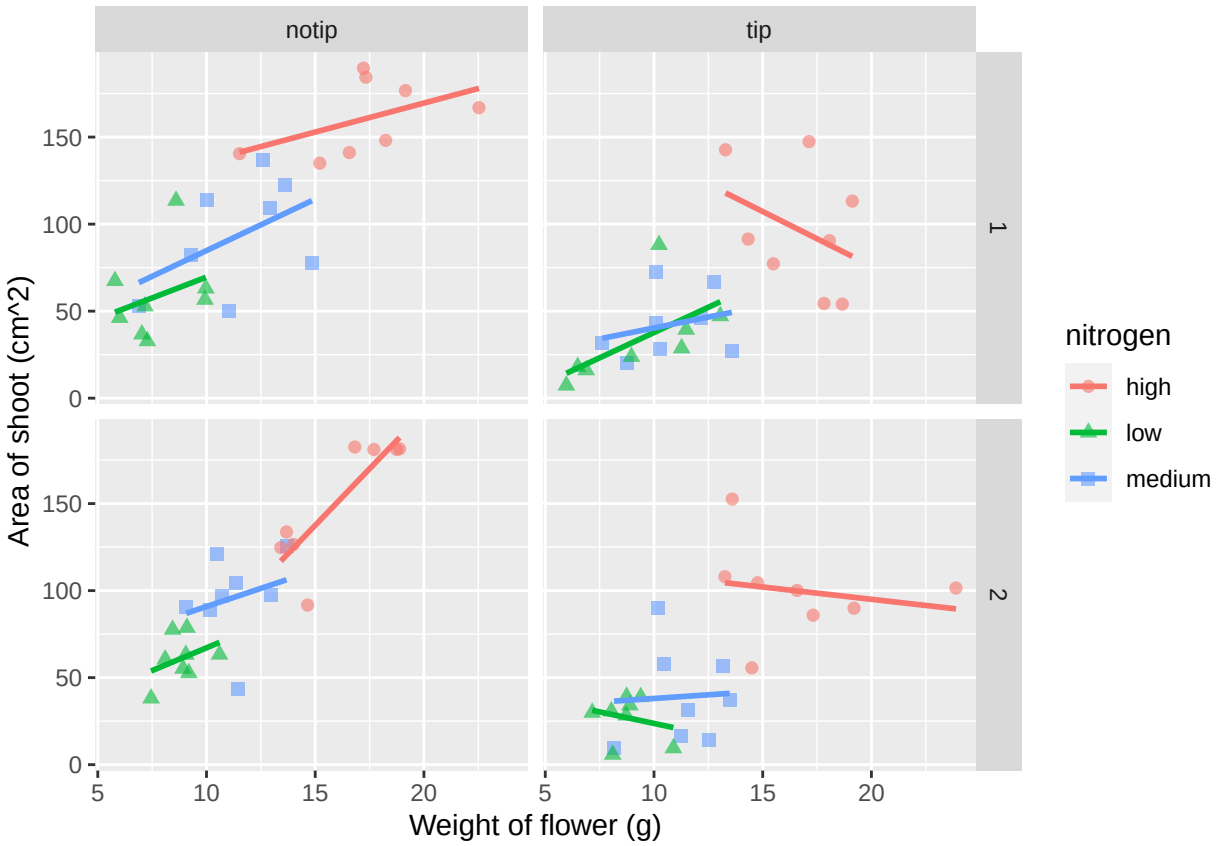
```
## `geom_smooth()` using formula = 'y ~ x'
```



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)")
```

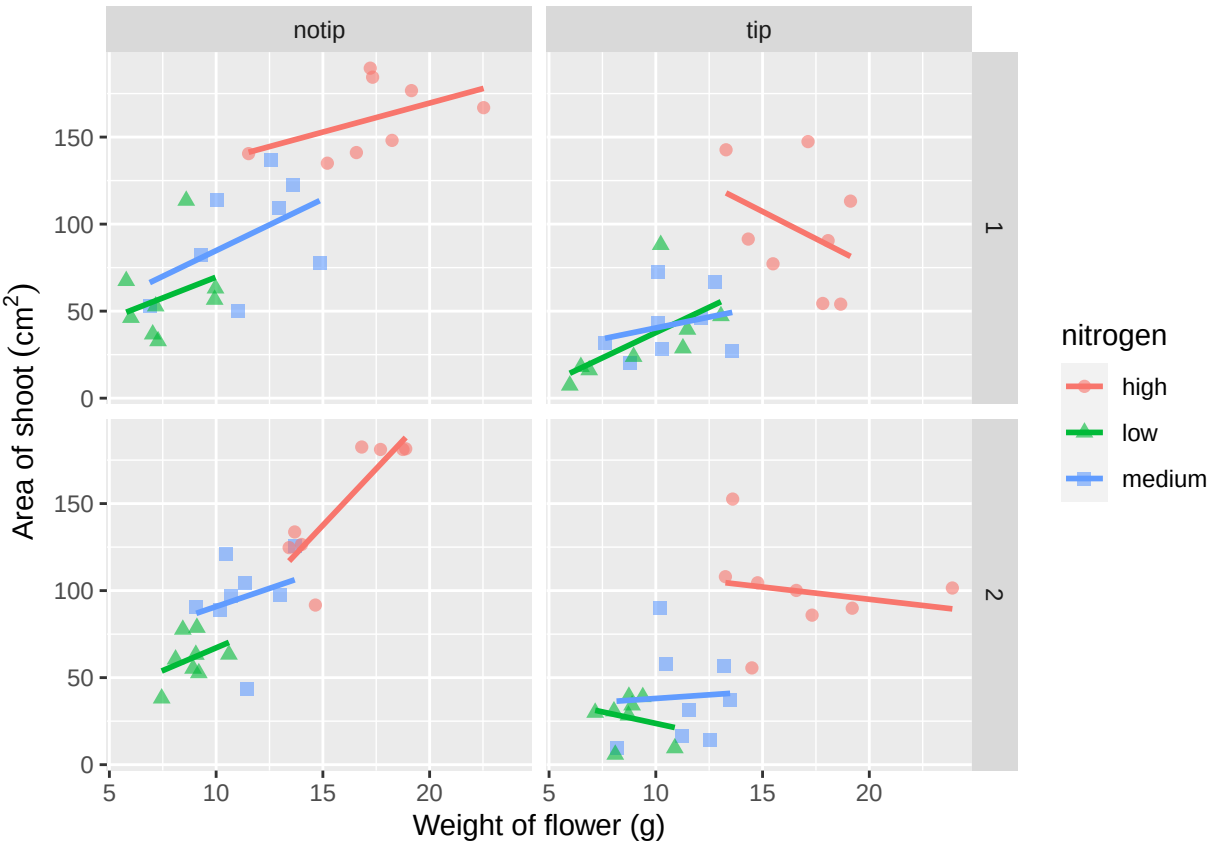
```
## `geom_smooth()` using formula = 'y ~ x'
```



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'
```

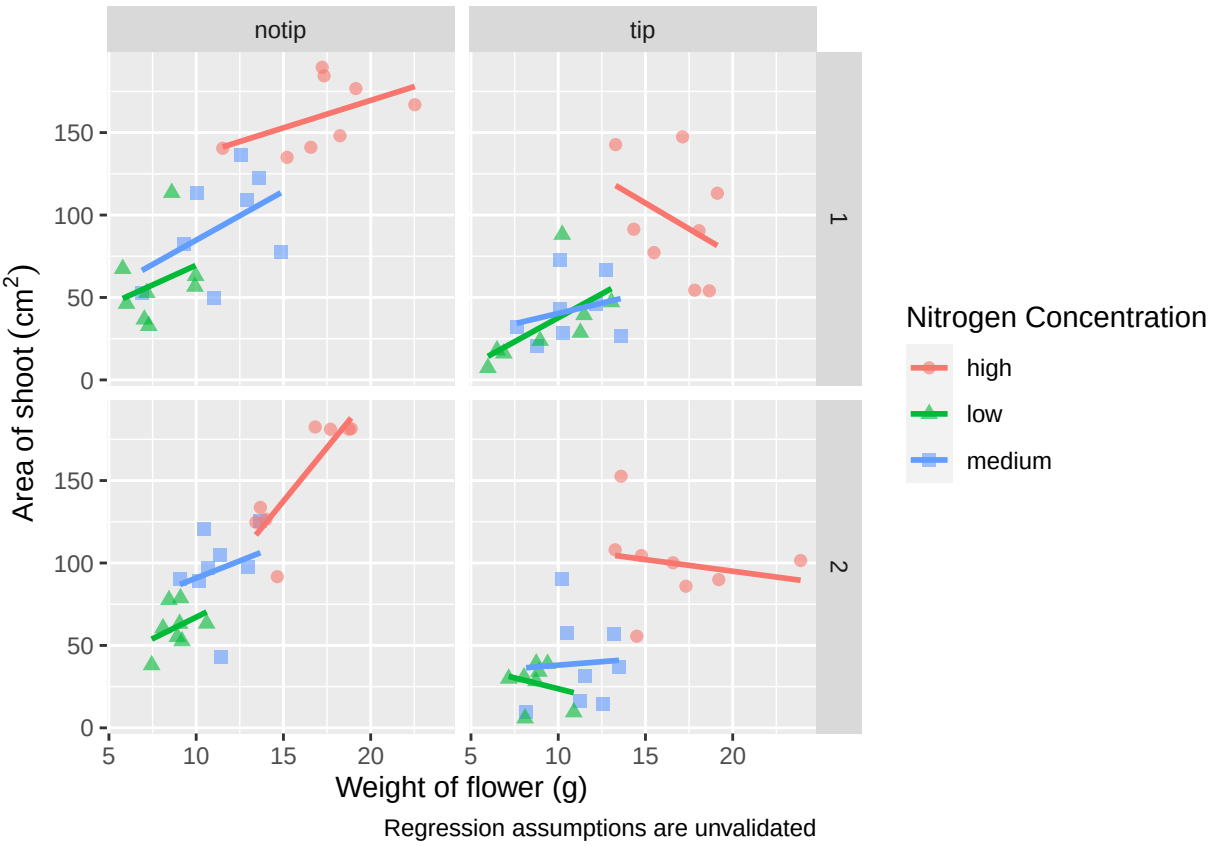


Legend and Caption

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")
```

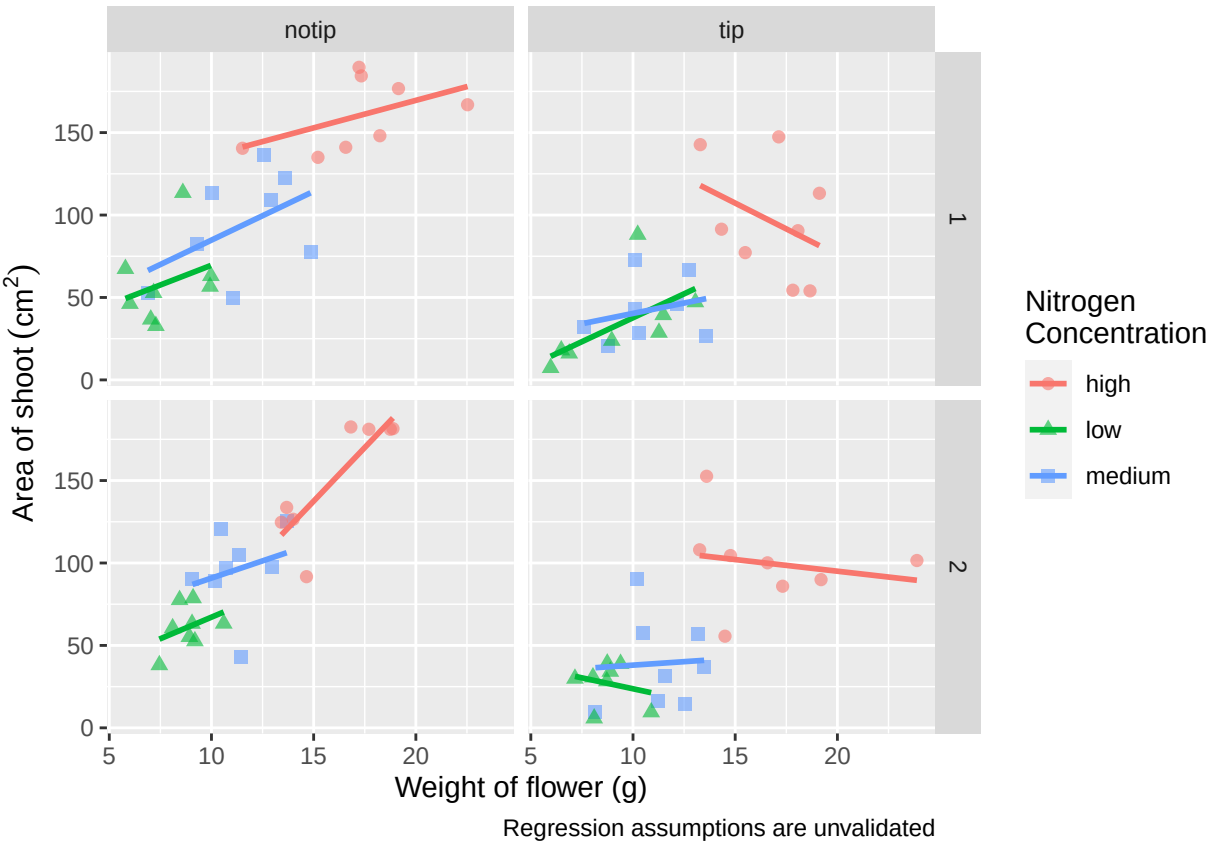
```
## `geom_smooth()` using formula = 'y ~ x'
```



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.

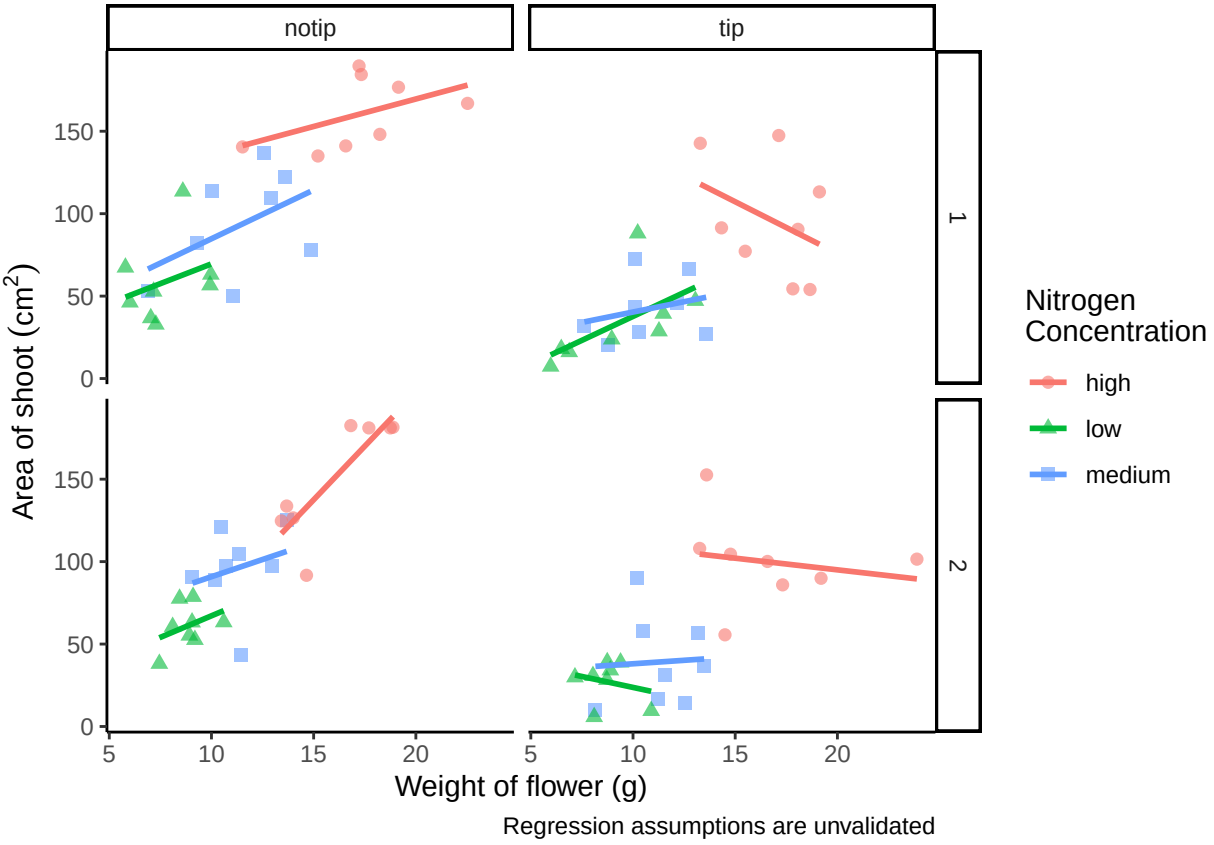
1. Classic theme

```
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'
```

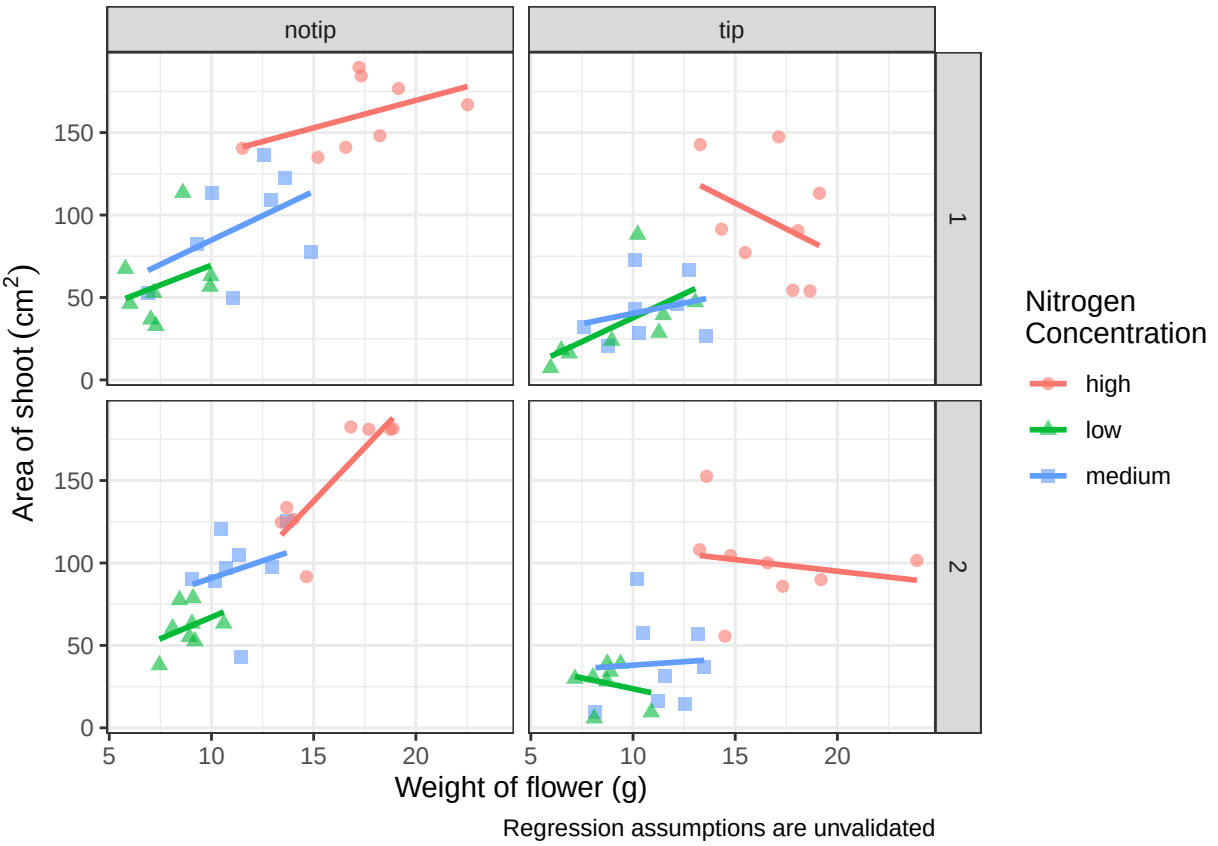


2. Black and white theme

```
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'
```

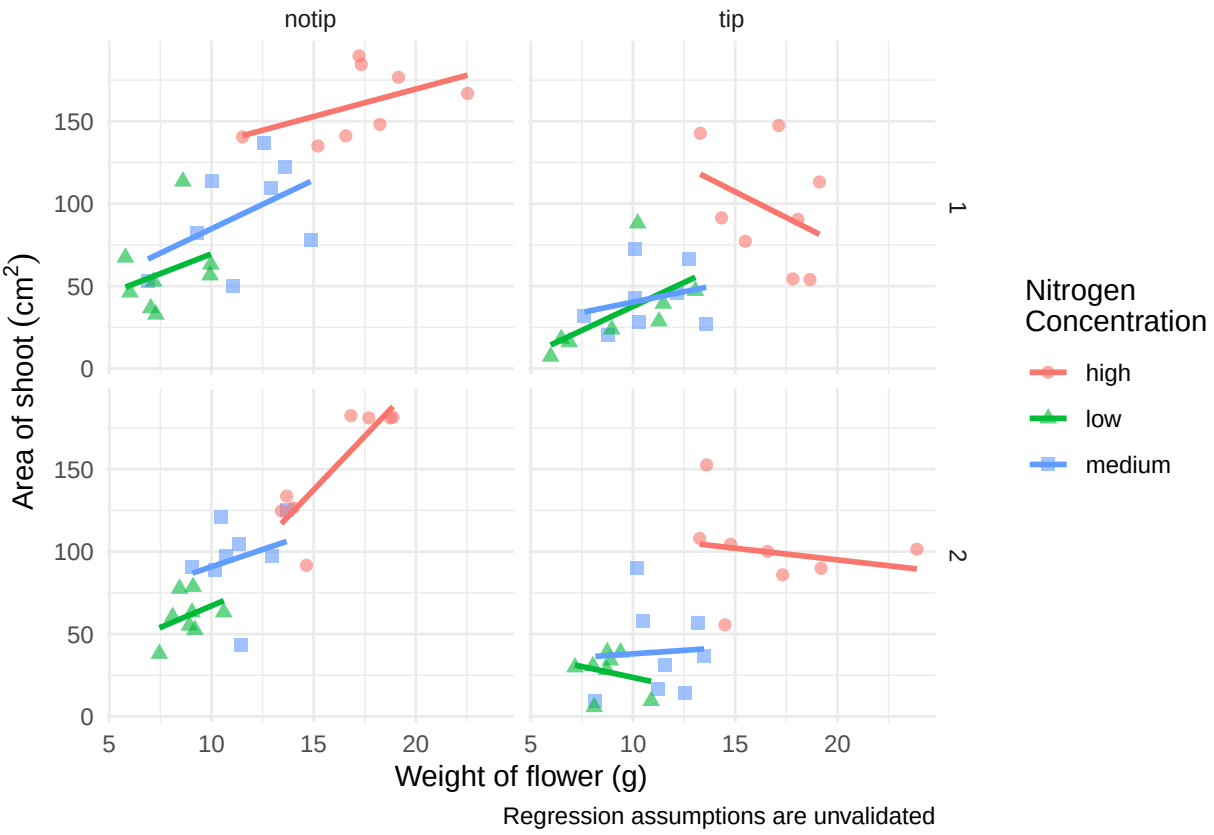


3. Minimal theme

```
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'
```



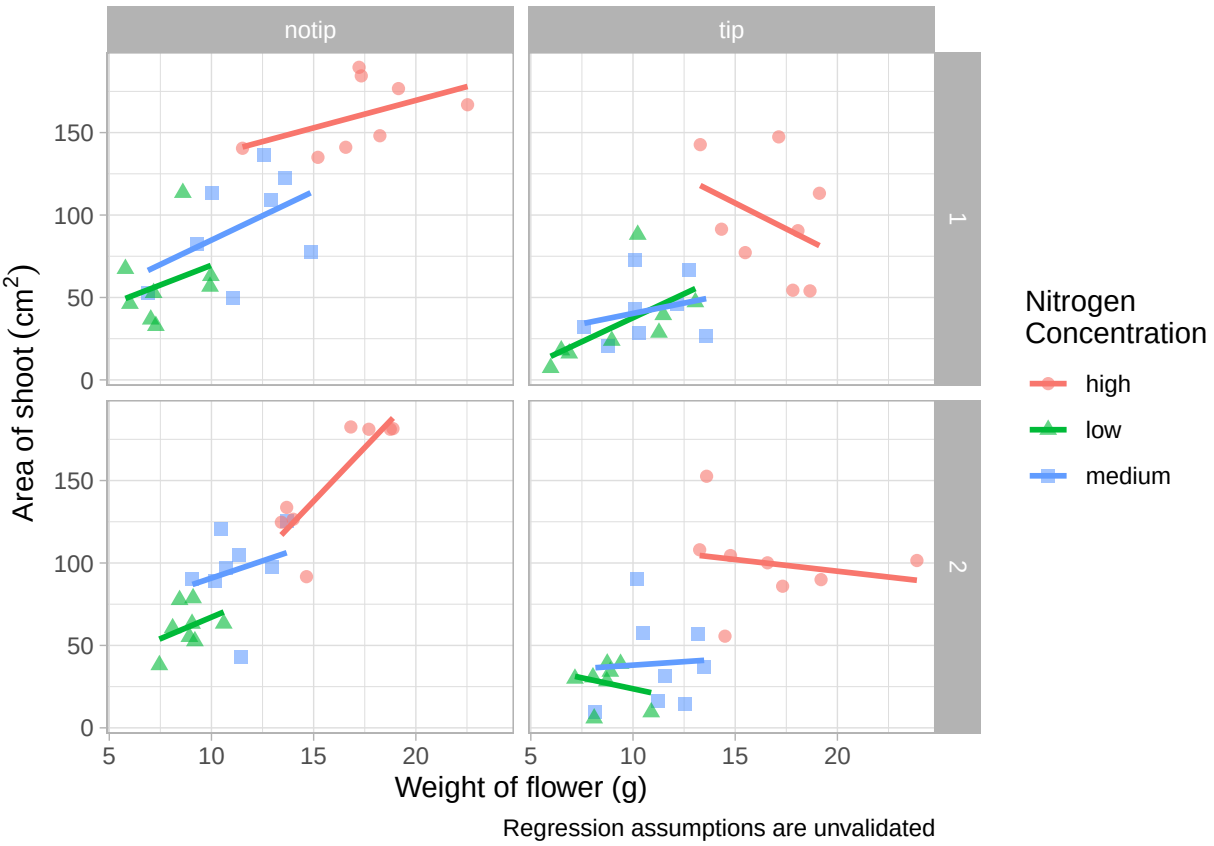
4. Light theme

```
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'
```



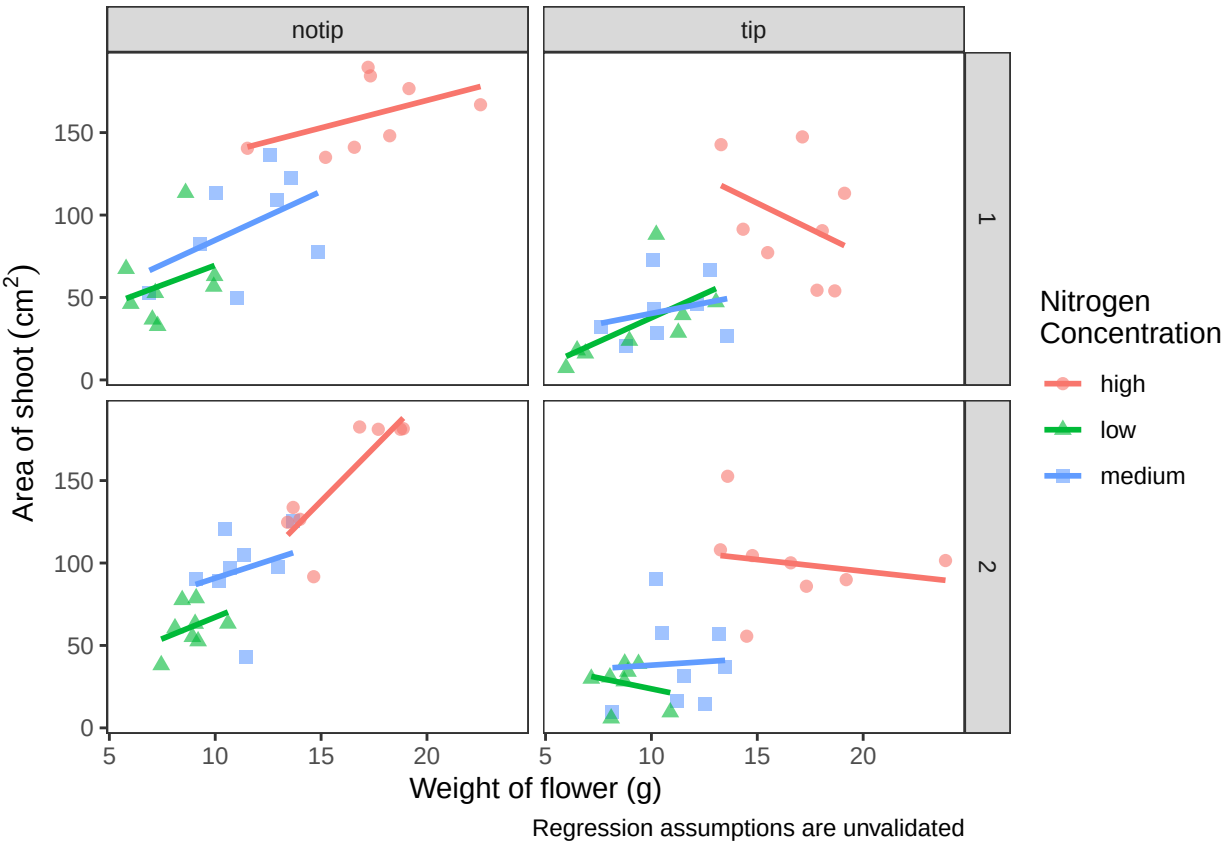
5. Test theme

```
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'
```



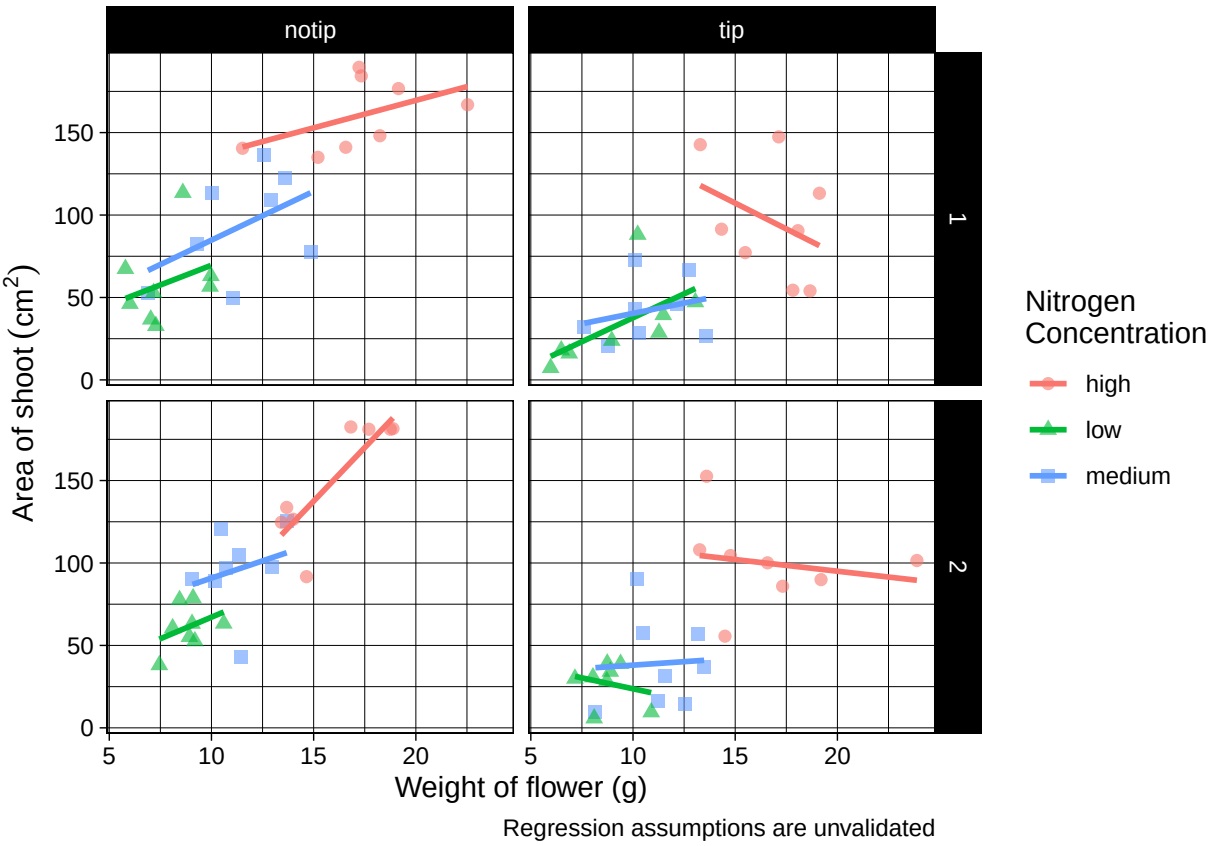
6. Line draw

```
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.

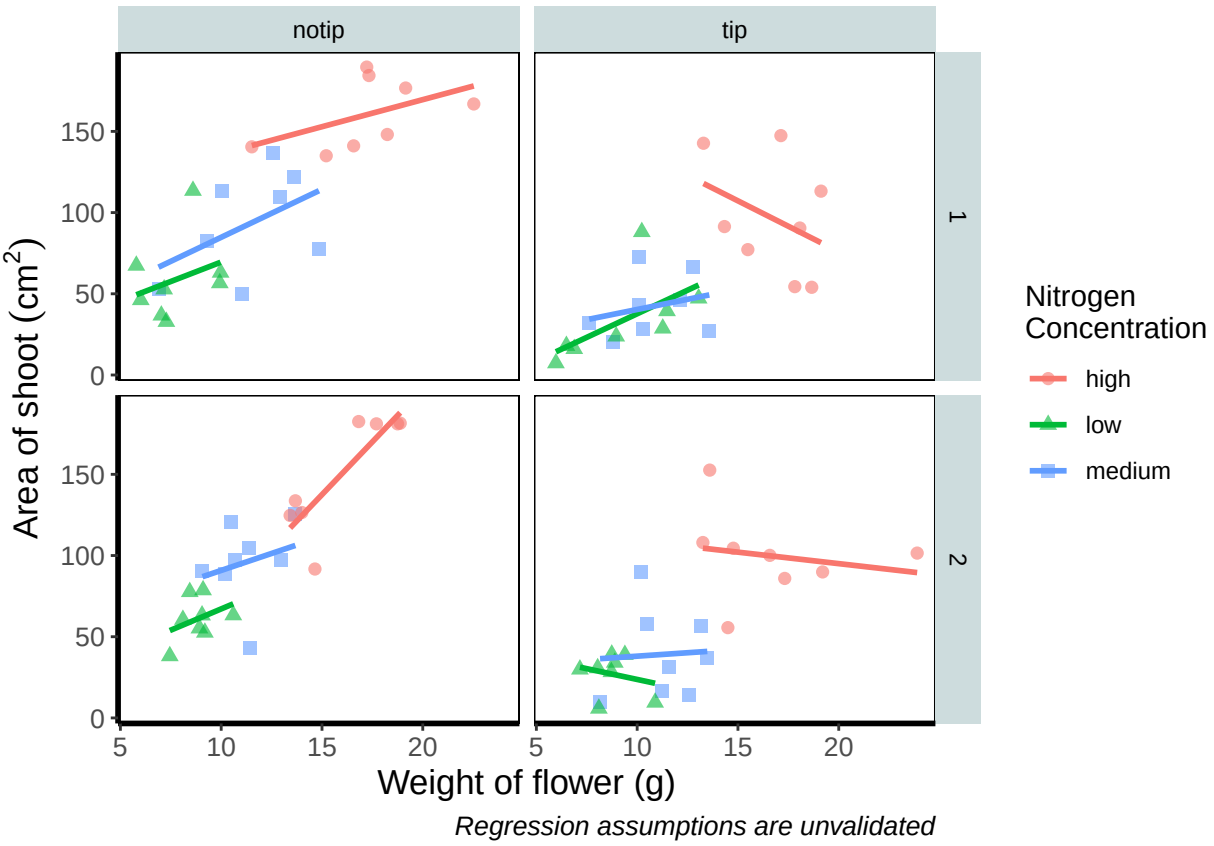
Let's try remaking our figure using our new theme.

```
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

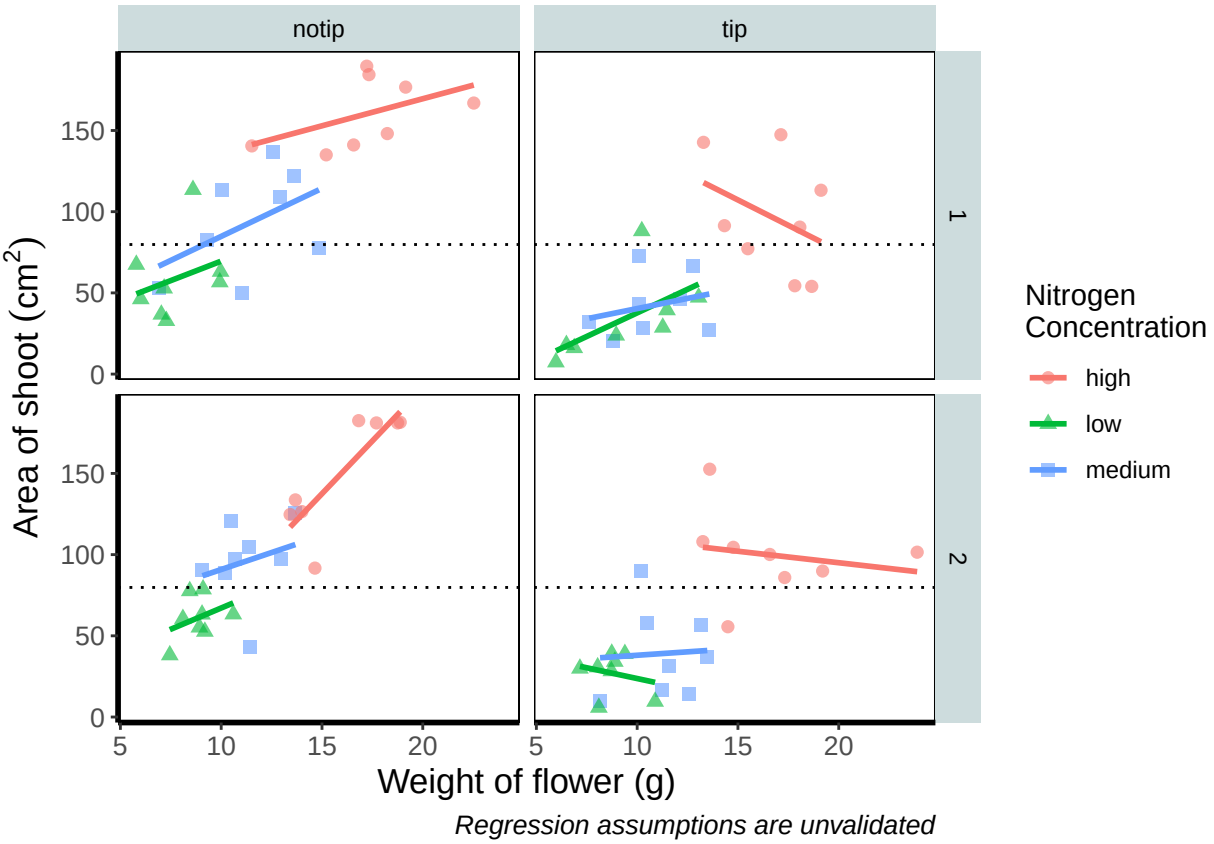
Let's begin the final push by including that dashed horizontal line at the average shoot area, at about 80, on our y axis. This represents the overall mean area of a shoot, regardless of nitrogen concentration, treatment, or block. To draw a horizontal line we use a geom called geom_hline(), and the 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.

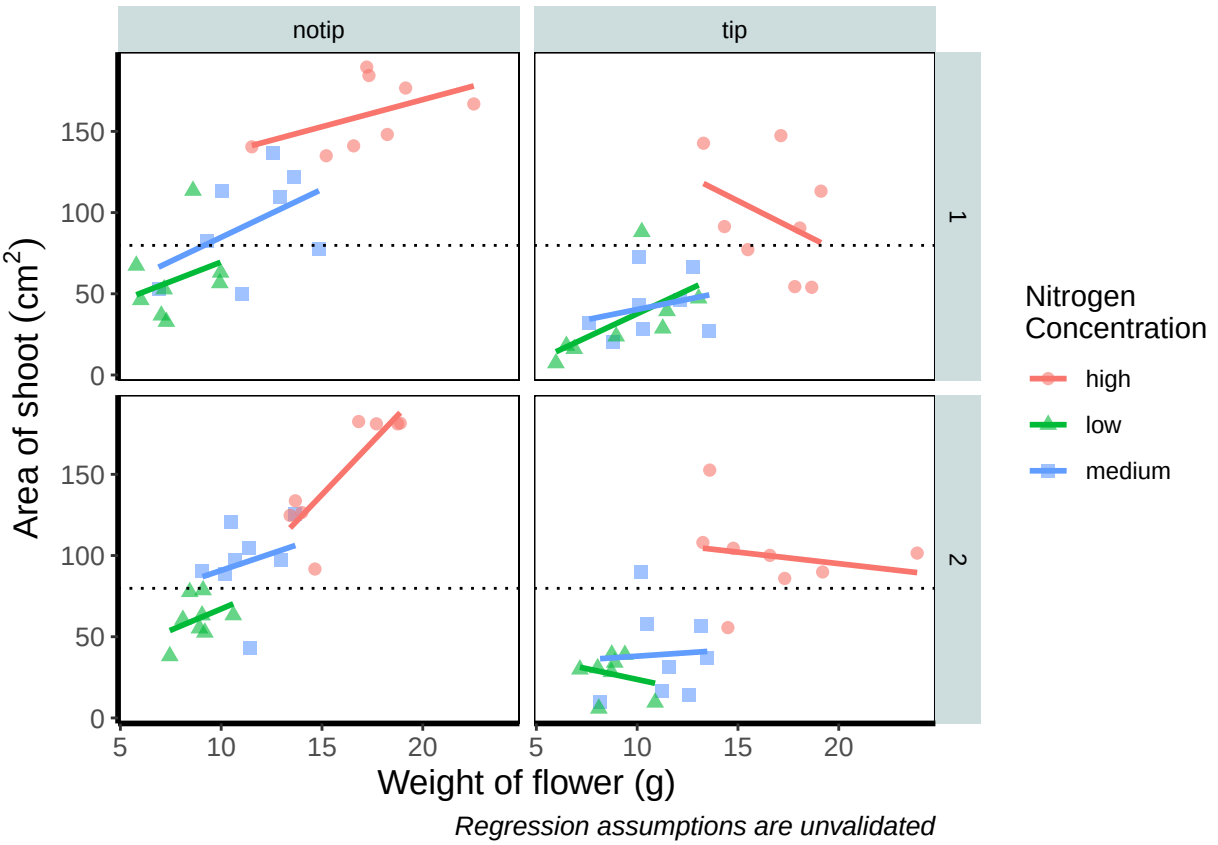
```
mean(flowergg$shootarea)
```

```
## [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’
```



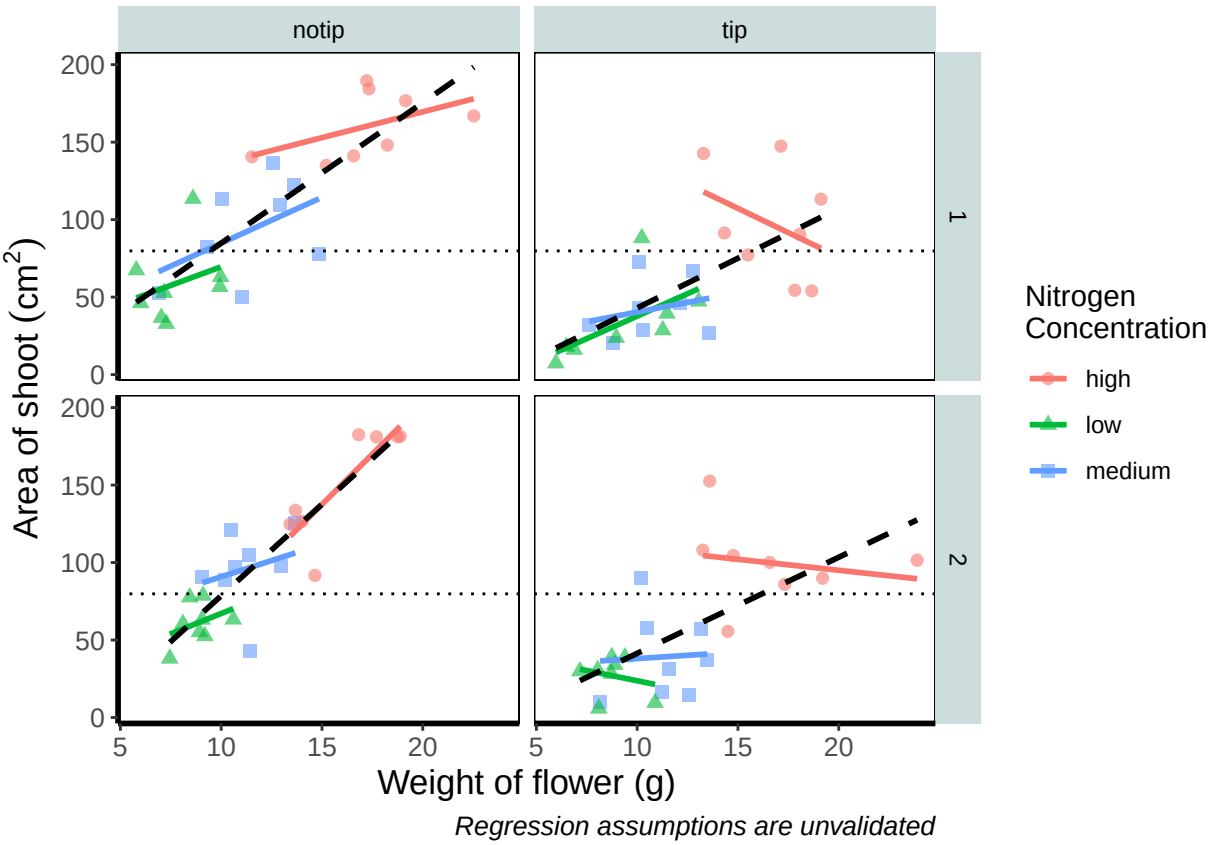
Exactly the same figure but produced in a slightly different way (the point being that there are always multiple ways to get what you want). Now let's tackle that "overall" nitrogen effect. This overall line is effectively the figure we produced much earlier when we learnt how to include a line of best 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.

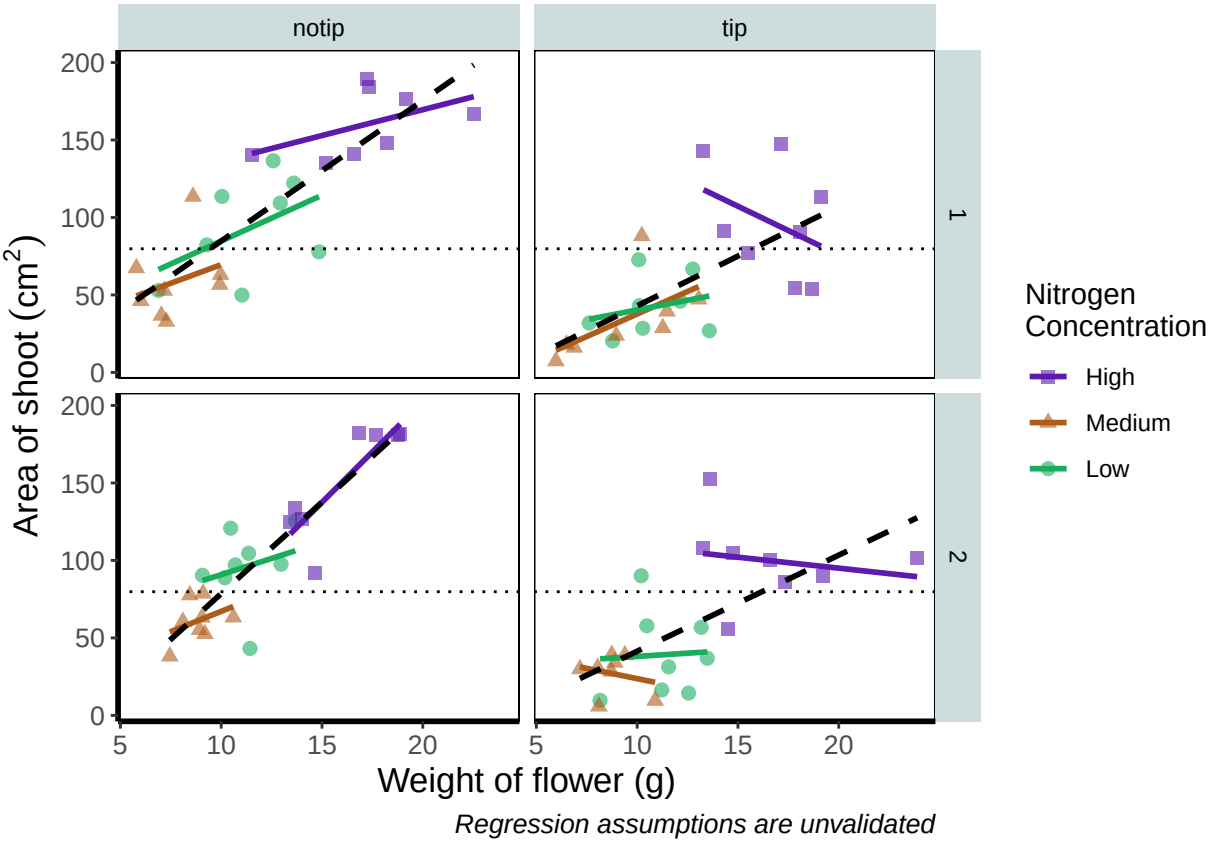
When we first started using ggplot2 this was the thing which caused us the most difficulty. We think the reason is, that to manually change the colours actually requires an additional layer, where we assumed this would be done in either the main call to `ggplot()` or in a geom.

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.

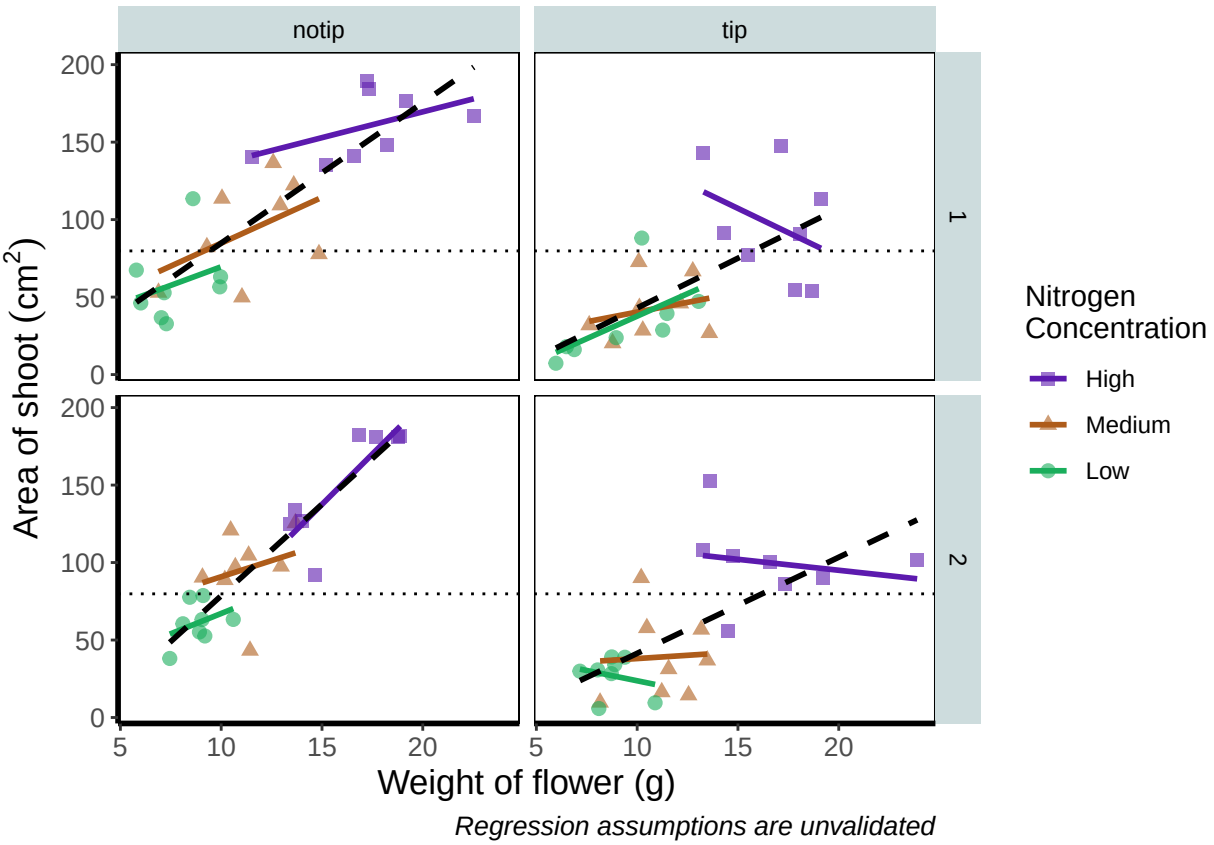
So how do we fix this? We need to do a little data manipulation to rearrange our factors so that the order goes High, Medium, Low. Let's do that:

```
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.