Lecture 3

Advanced Data Visualization with ggplot2

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20 February, 2025

Section 1

Introduction

Introduction

- This **ggplot2** course builds on your knowledge from the introductory course to produce meaningful explanatory plots.
- **Statistics** will be calculated on the fly and you'll see how **Coordinates** and **Facets** aid in communication.

Introduction

- You'll also explore details of data visualization best practices with ggplot2 to help make sure you have a sound understanding of what works and why.
- By the end of the course, you'll have all the tools needed to make a custom plotting function to explore a large data set, combining statistics and excellent visuals.

Statistics

- A picture paints a thousand words, which is why R ggplot2 is such a powerful tool for graphical data analysis.
- In this section, you'll progress from simply plotting data to applying a variety of statistical methods.

Statistics

- These include a variety of linear models, descriptive and inferential statistics (mean, standard deviation and confidence intervals) and custom functions.
- **Stats** with **geoms** Smoothing To practice on the remaining layers (statistics, coordinates and facets), we'll continue working on several datasets from the first lecture.

Statistics

- The **mtcars** dataset contains information for 32 cars from Motor Trends magazine from 1974.
- This dataset is small, intuitive, and contains a variety of continuous and categorical (both nominal and ordinal) variables.

Statistics

- In the previous lecture you learned how to effectively use some basic geometries, such as point, bar and line.
- Now you'll explore statistics associated with specific geoms, for example, smoothing and lines.

Statistics

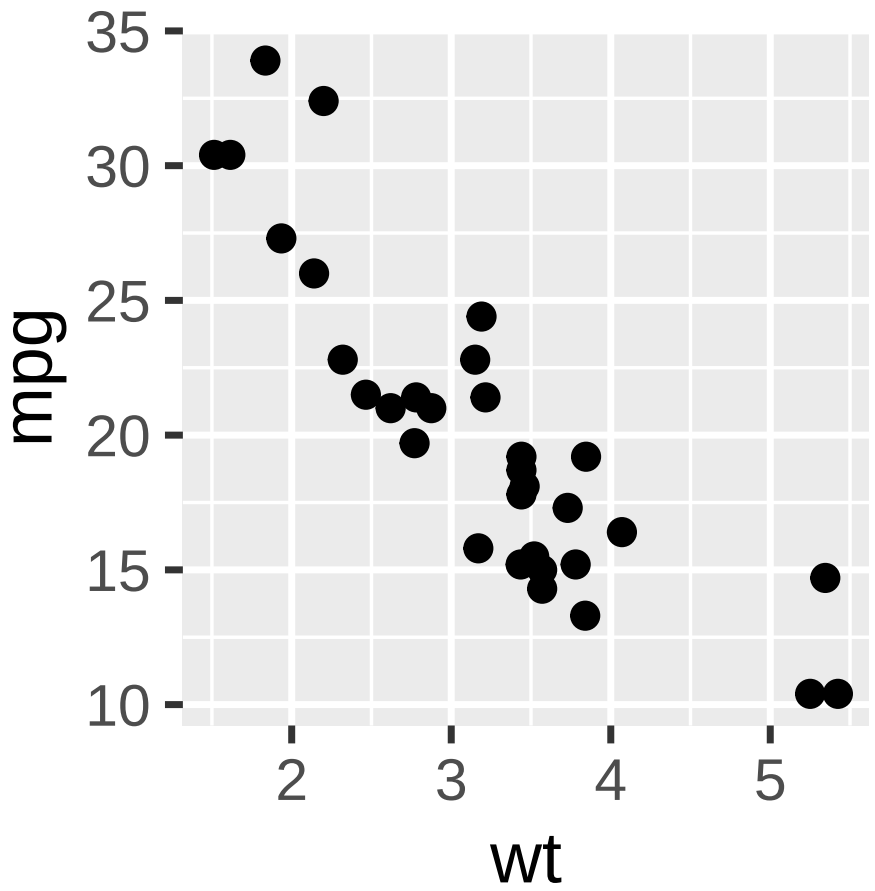
Look at the structure of mtcars. Using mtcars

```
library(tidyverse)
# View the structure of mtcars
str(mtcars)
```

```
'data.frame':   32 obs. of  11 variables:
 $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ..
 $ cyl : num  6 6 4 6 8 6 8 4 4 6 ...
 $ disp: num  160 160 108 258 360 ...
 $ hp  : num  110 110 93 110 175 105 245 62 95 123 ...
 $ drat: num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92
 $ wt  : num  2.62 2.88 2.32 3.21 3.44 ...
 $ qsec: num  16.5 17 18.6 19.4 17 ...
 $ vs  : num  0 0 1 1 0 1 0 1 1 1 ...
 $ am  : num  1 1 1 0 0 0 0 0 0 0 ...
 $ gear: num  4 4 4 3 3 3 3 4 4 4 ...
 $ carb: num  4 4 1 1 2 1 4 2 2 4 ...
```

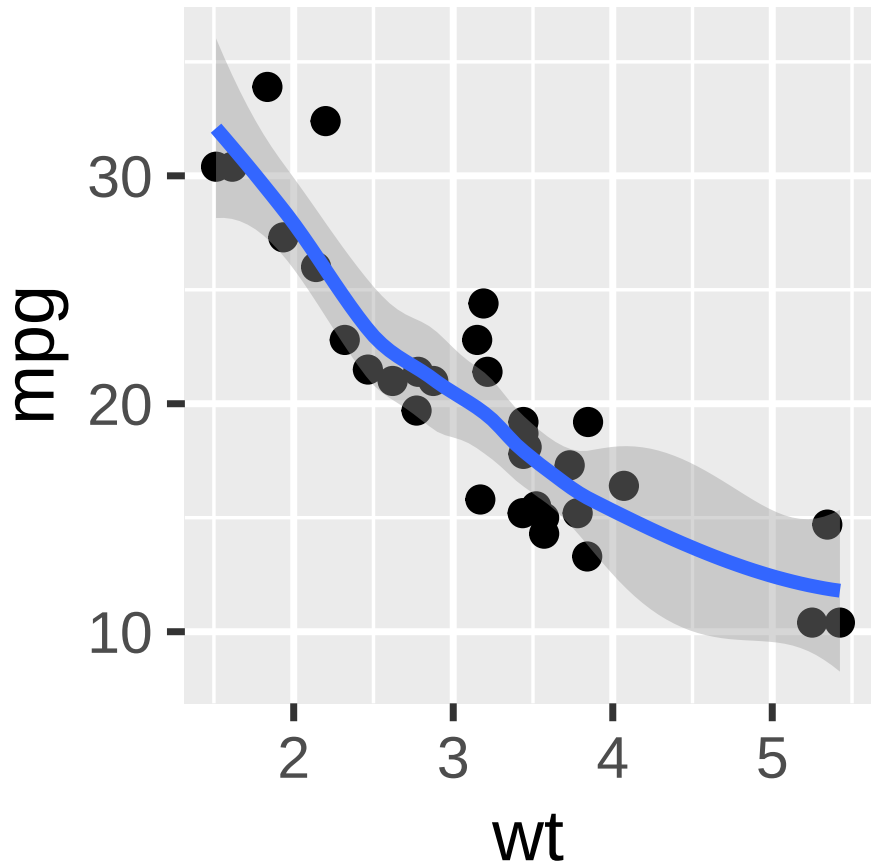
Draw a scatter plot of mpg vs. wt.

```
# Using mtcars, draw a scatter plot of mpg vs. wt
ggplot(mtcars, aes(x = wt, y = mpg)) + geom_point()
```



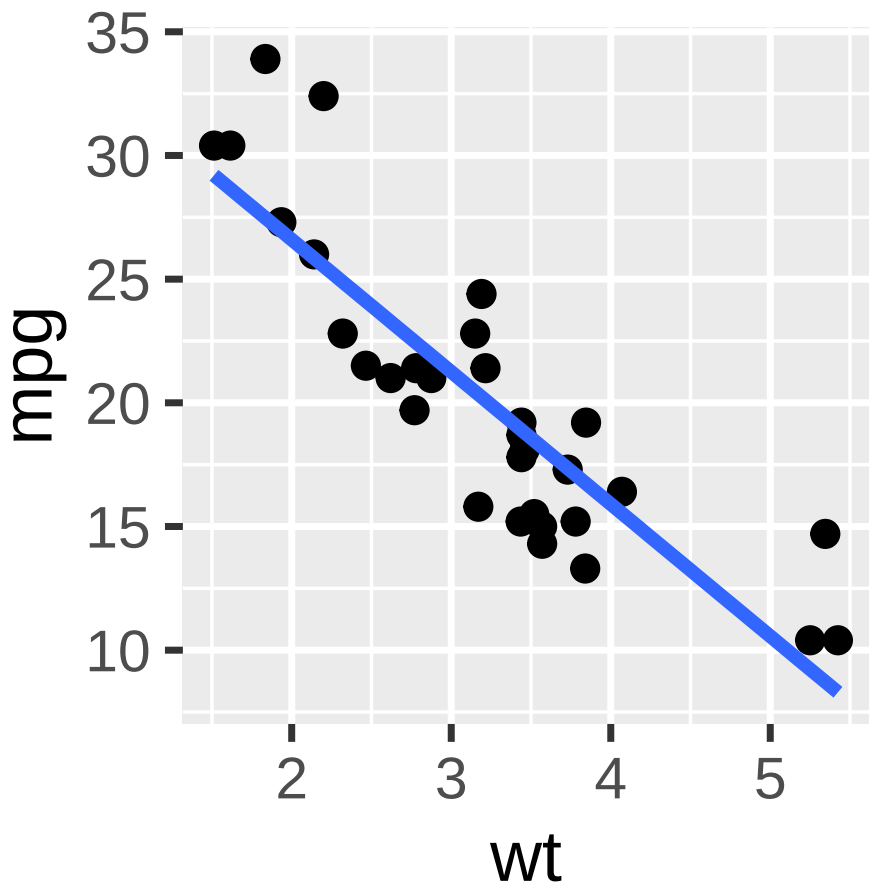
Update the plot to add a smooth trend line. Use the default method, which uses the LOESS model to fit the curve.

```
# Amend the plot to add a smooth layer
ggplot(mtcars, aes(x = wt, y = mpg)) + geom_point() + geom_smooth()
```



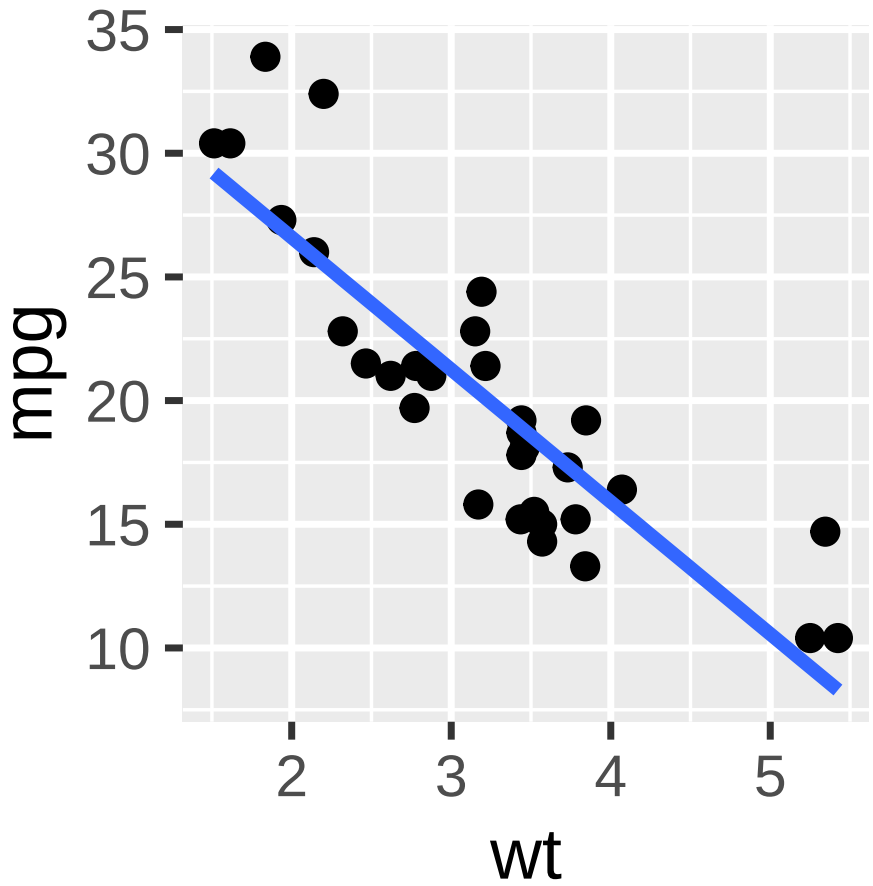
Update the smooth layer.

```
# Amend the plot. Use lin. reg. smoothing; turn off std err
# ribbon
ggplot(mtcars, aes(x = wt, y = mpg)) + geom_point() + geom_smooth(method = "lm",
    se = FALSE)
```



Draw the same plot again, swapping geom_smooth() for stat_smooth().

```
# Amend the plot. Swap geom_smooth() for stat_smooth().
ggplot(mtcars, aes(x = wt, y = mpg)) + geom_point() + stat_smooth(method = "lm",
    se = FALSE)
```



Grouping variables

- We'll continue with the previous exercise by considering the situation of looking at sub-groups in our dataset.
- For this we'll encounter the invisible group aesthetic.

Grouping variables

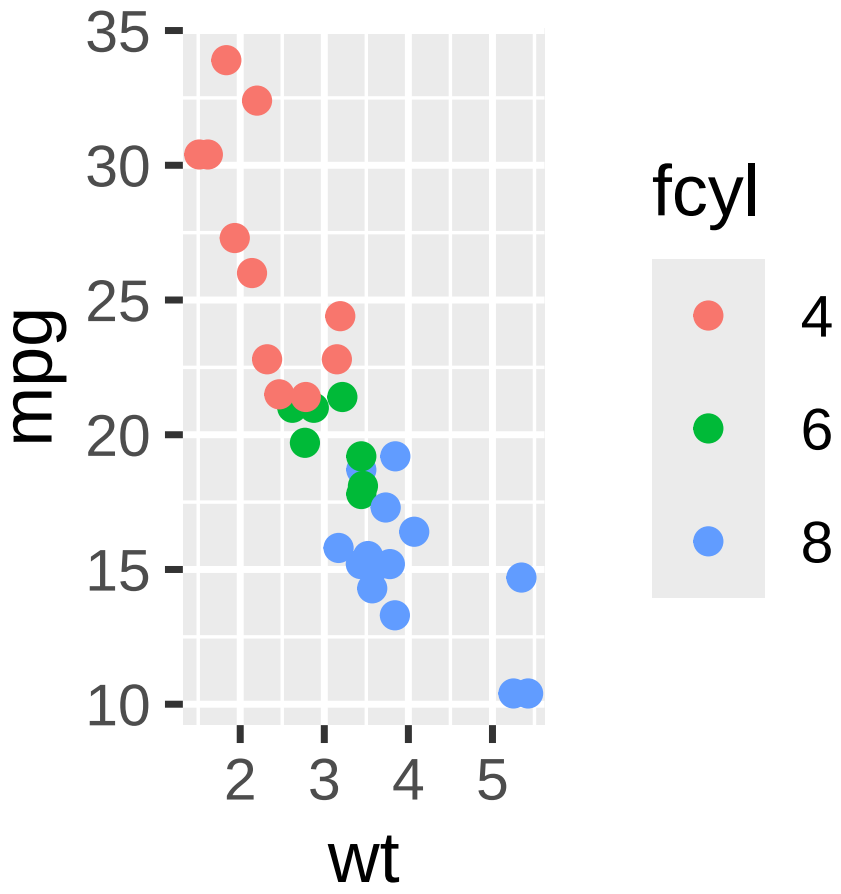
mtcars has been given an extra column, fcyl, that is the cyl column converted to a proper factor variable.

```
mtcars <- mtcars %>%
    mutate(fcyl = as.factor(cyl), fam = as.factor(am))
```

Grouping variables

Using mtcars, plot mpg vs. wt, colored by fcyl, add a point layer.

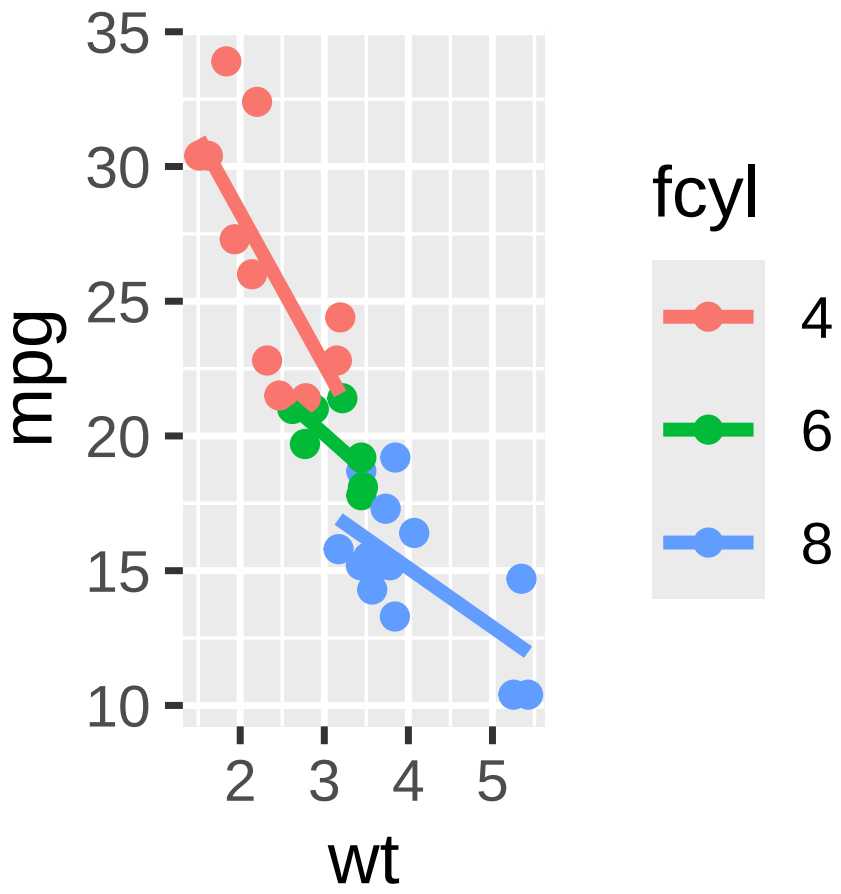
```
ggplot(mtcars, aes(x = wt, y = mpg, color = fcyl)) + geom_point()
```



Grouping variables

Add a smooth stat using a linear model, and don't show the se ribbon.

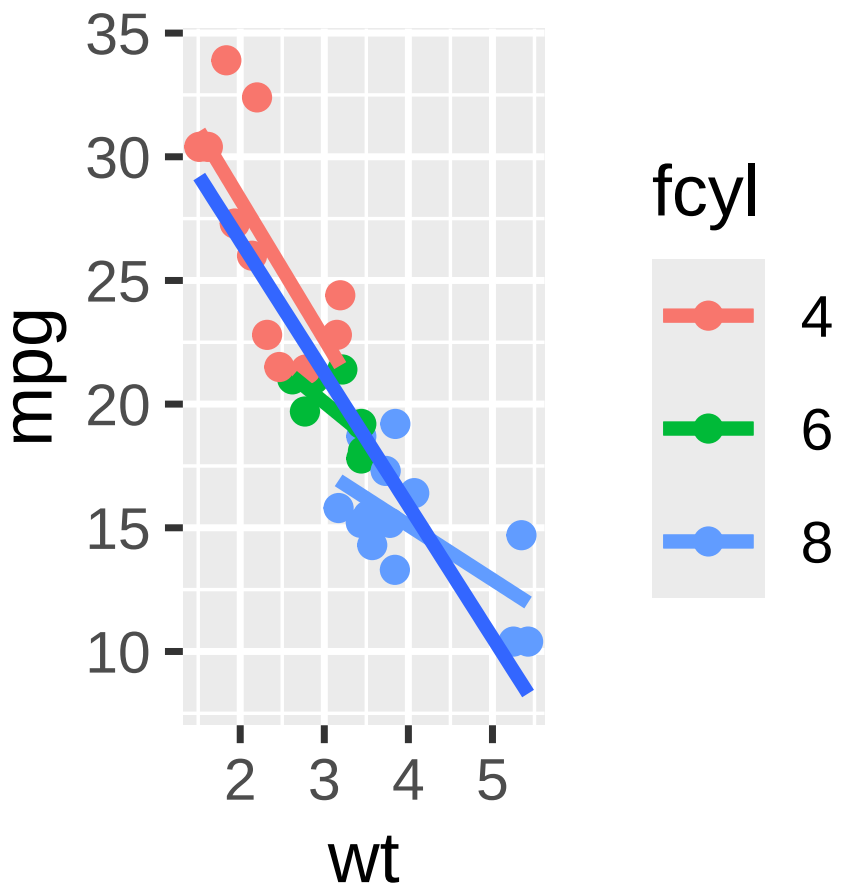
```
# Using mtcars, plot mpg vs. wt, colored by fcyl
ggplot(mtcars, aes(x = wt, y = mpg, color = fcyl)) + geom_point() +
    stat_smooth(method = "lm", se = FALSE)
```



Grouping variables

Update the plot to add a second smooth stat.

```
# Amend the plot to add another smooth layer with dummy
# grouping
ggplot(mtcars, aes(x = wt, y = mpg, color = fcyl)) + geom_point() +
    stat_smooth(method = "lm", se = FALSE) + stat_smooth(aes(group = 1),
    method = "lm", se = FALSE)
```



Grouping variables

- In the previous exercise we used se = FALSE in *stat_smooth*() to remove the 95% Confidence Interval.
- Here we'll consider another argument, **span**, used in LOESS smoothing, and we'll take a look at a nice scenario of properly mapping different models.

Grouping variables

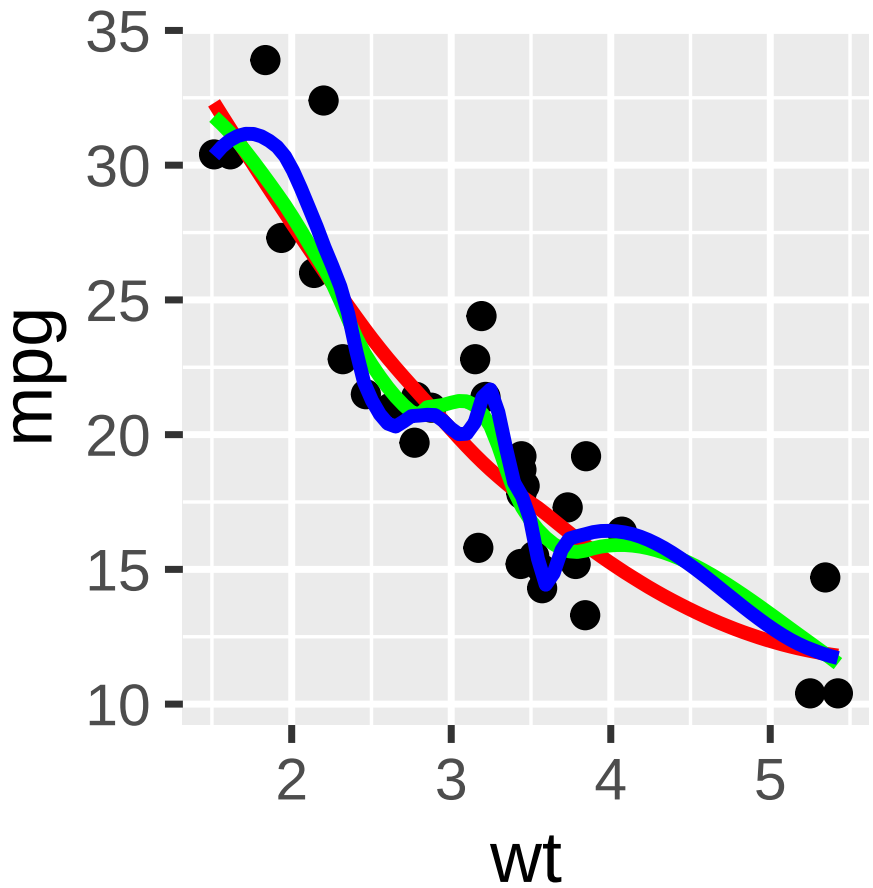
- Explore the effect of the span argument on LOESS curves.
- Add three smooth LOESS stats, each without the standard error ribbon.

Grouping variables

- Color the 1st one “red”; set its span to 0.9.
- Color the 2nd one “green”; set its span to 0.6.
- Color the 3rd one “blue”; set its span to 0.3.

Grouping variables

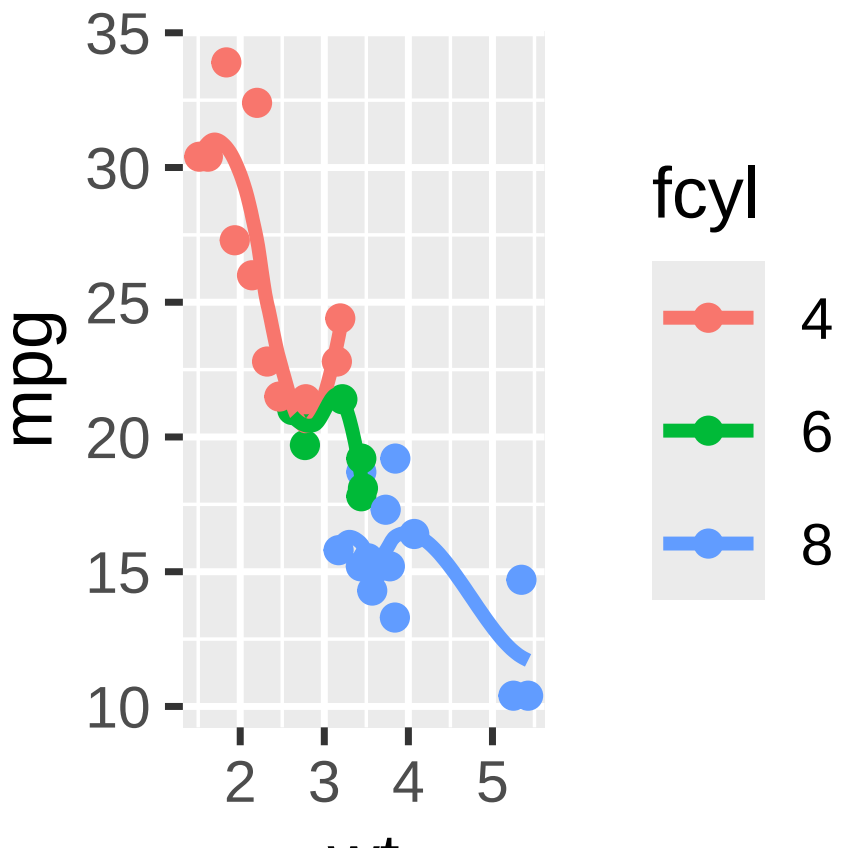
```
ggplot(mtcars, aes(x = wt, y = mpg)) + geom_point() + stat_smooth(se = FALSE,
    color = "red", span = 0.9) + stat_smooth(se = FALSE, color = "green",
    span = 0.6) + stat_smooth(se = FALSE, color = "blue", span = 0.3)
```



Compare LOESS and linear regression smoothing on small regions of data.

- Add a smooth LOESS stat, without the standard error ribbon.

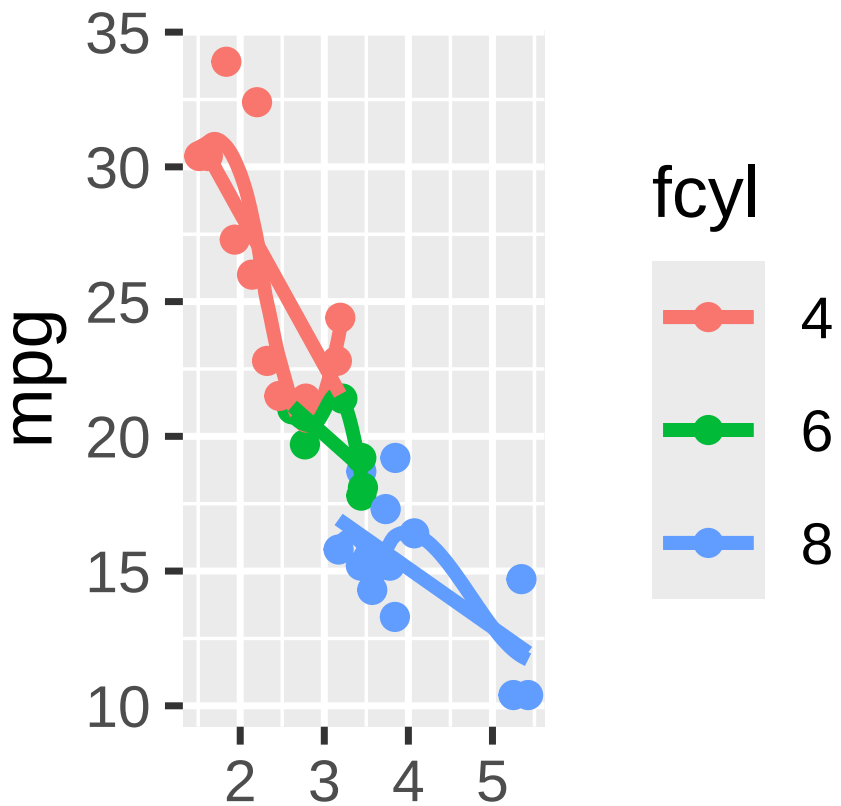
```
# Amend the plot to color by fcyl
ggplot(mtcars, aes(x = wt, y = mpg, color = fcyl)) + geom_point() +
    # Add a smooth LOESS stat, no ribbon
stat_smooth(se = FALSE)
```



Compare LOESS and linear regression smoothing on small regions of data.

Add a smooth linear regression stat, again without the standard error ribbon.

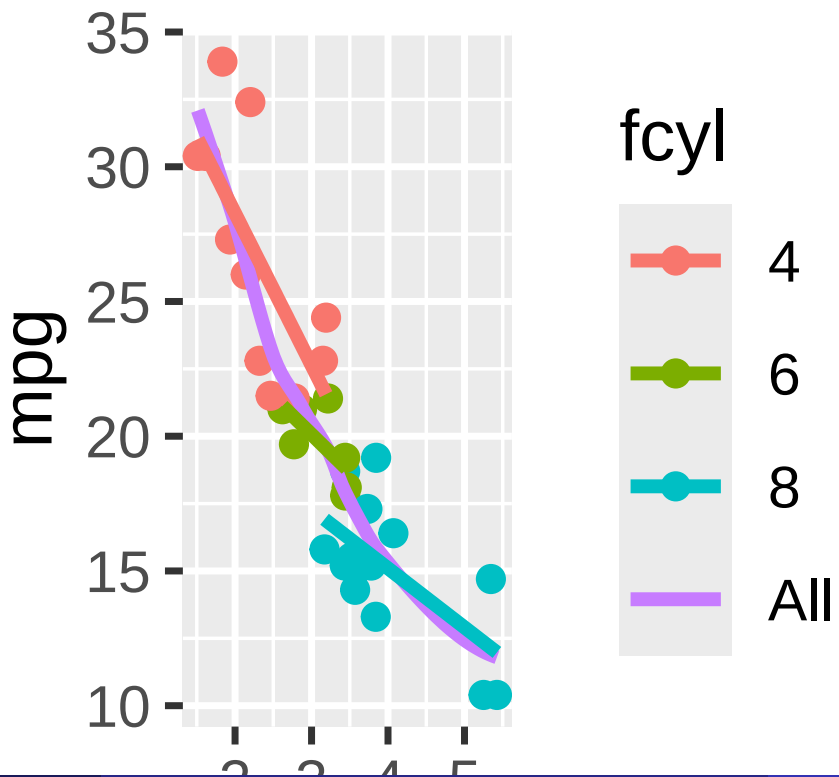
```
# Amend the plot to color by fcyl
ggplot(mtcars, aes(x = wt, y = mpg, color = fcyl)) + geom_point() +
    stat_smooth(se = FALSE) + stat_smooth(method = "lm", se = FALSE)  # Add a smooth lin. reg. stat, no ribbon
```



Compare LOESS and linear regression smoothing on small regions of data.

- Amend the smooth LOESS stat to map color to a dummy variable, "All".

```
# Amend the plot
ggplot(mtcars, aes(x = wt, y = mpg, color = fcyl)) + geom_point() +
    stat_smooth(aes(color = "All"), se = FALSE) + stat_smooth(method = "lm",
    se = FALSE)
```



Modifying stat_smooth (2)

- In this exercise we'll take a look at the standard error ribbons, which show the 95% confidence interval of smoothing models.
- ggplot2 and the Vocab data frame are already loaded for you.

Modifying stat_smooth (2)

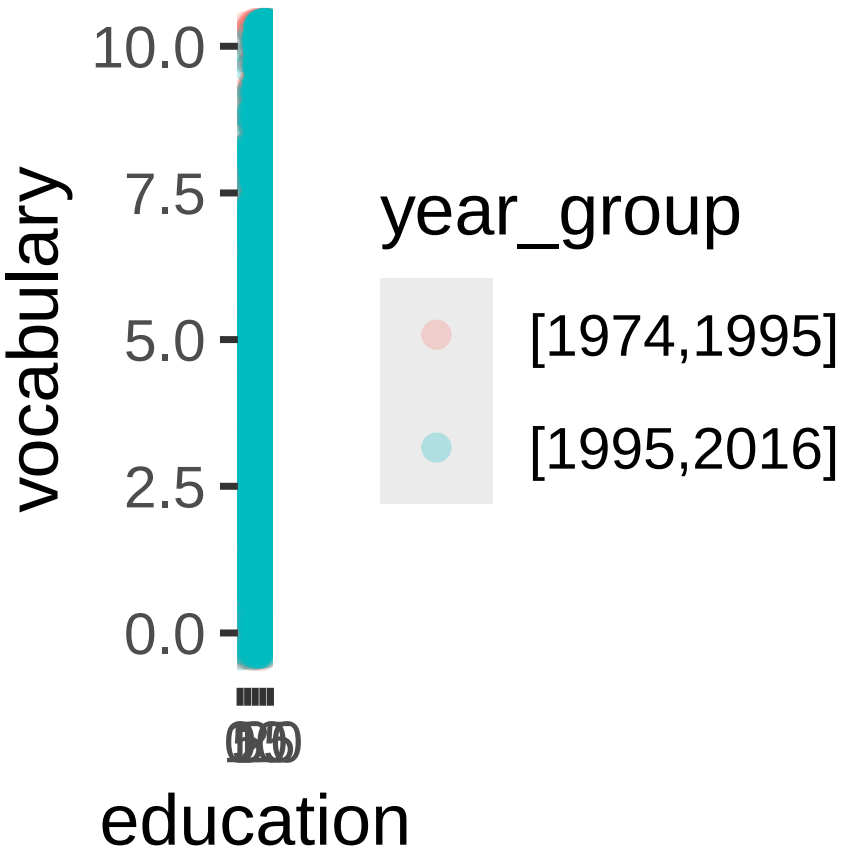
- Vocab has been given an extra column, *year_group*, splitting the dates into before and after 1995.

```
library(carData)
Vocab <- Vocab %>%
    mutate(year_group = as.factor(ifelse(year < 1995, "[1974,1995]",
        "[1995,2016]")))
```

Modifying stat_smooth (2)

Using Vocab, plot vocabulary vs. education, colored by year_group. Use geom_jitter() to add jittered points with transparency 0.25.

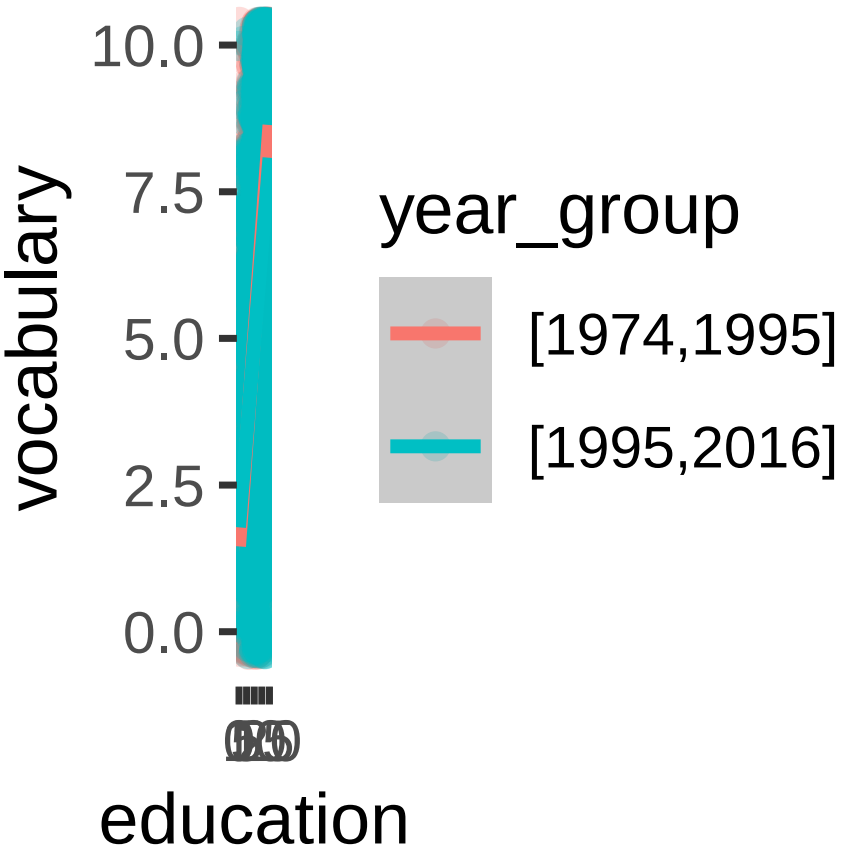
```
# Plot vocabulary vs. education, colored by year_group
ggplot(Vocab, aes(x = education, y = vocabulary, color = year_group)) +
    geom_jitter(alpha = 0.25)
```



Modifying stat_smooth (2)

Add a smooth linear regression stat (with the standard error ribbon).

```
# Plot vocabulary vs. education, colored by year_group
ggplot(Vocab, aes(x = education, y = vocabulary, color = year_group)) +
    geom_jitter(alpha = 0.25) + stat_smooth(method = "lm")
```

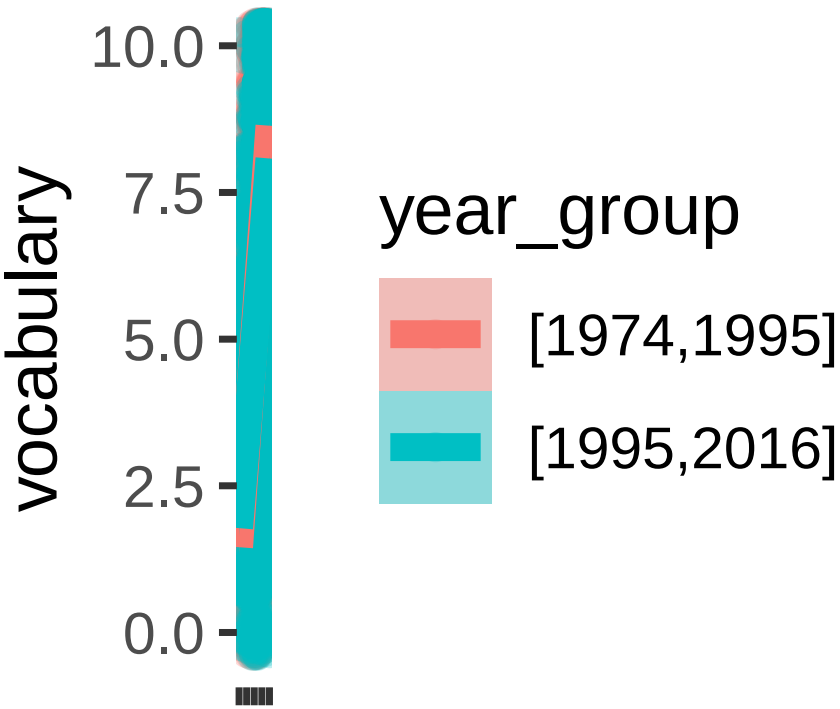


Modifying stat_smooth (2)

It's easier to read the plot if the standard error ribbons match the lines, and the lines have more emphasis.

Update the smooth stat. Map the fill color to *year_group*.

```
# Amend the plot
ggplot(Vocab, aes(x = education, y = vocabulary, color = year_group)) +
    geom_jitter(alpha = 0.25) + stat_smooth(aes(fill = year_group),
    method = "lm", size = 2)  # Map the fill color to year_group, set the line size to 2
```



Quantiles

Here, we'll continue with the **Vocab** dataset and use *stat_quantile*() to apply a quantile regression.

Quantiles

Linear regression predicts the mean response from the explanatory variables, quantile regression predicts a quantile response (e.g. the median) from the explanatory variables. Specific quantiles can be specified with the quantiles argument.

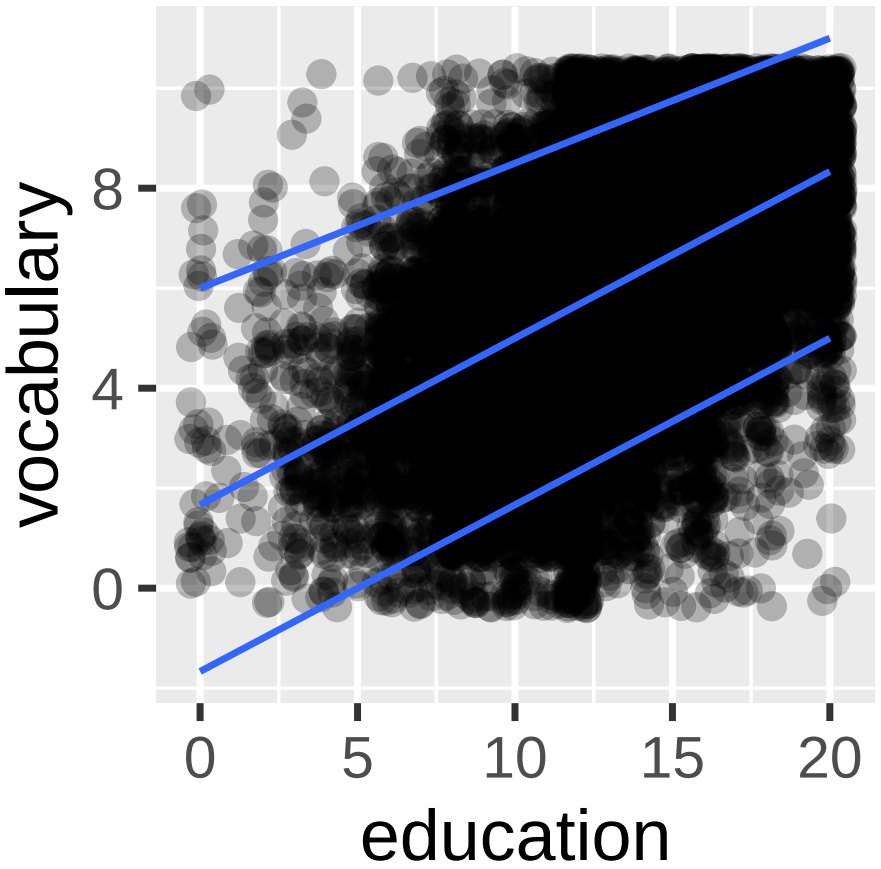
Quantiles

- Specifying many quantiles and color your models according to year can make plots too busy.
- We'll explore ways of dealing with this in the next chapter.

Quantiles

Update the plot to add a quantile regression stat, at quantiles 0.05, 0.5, and 0.95.

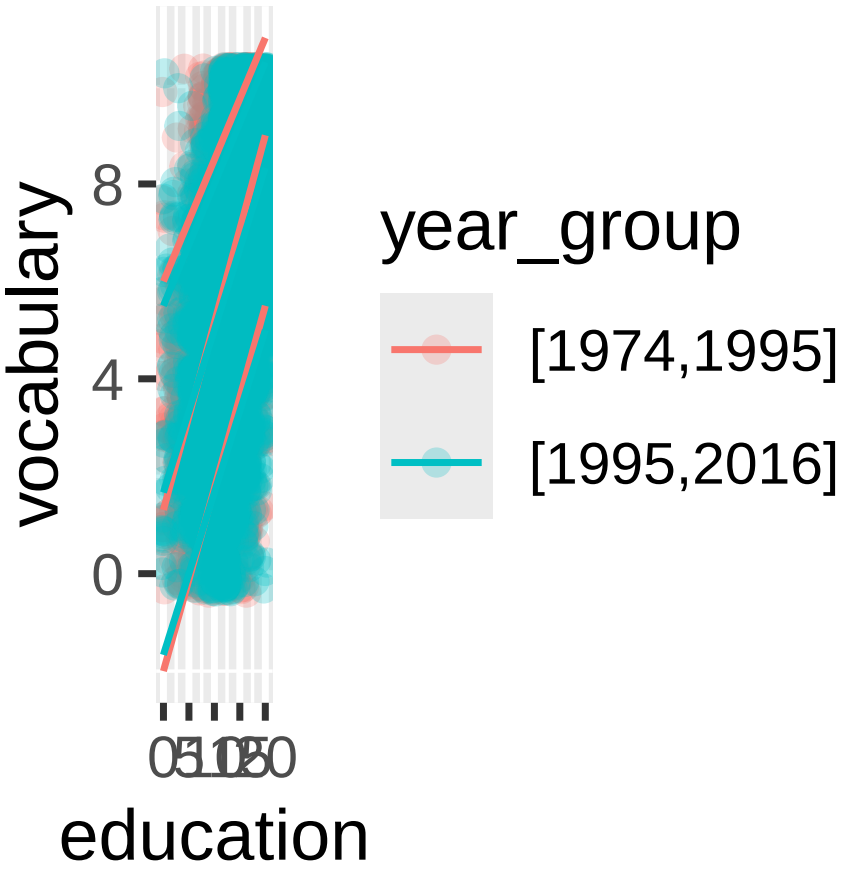
```
ggplot(Vocab, aes(x = education, y = vocabulary)) + geom_jitter(alpha = 0.25) +
    stat_quantile(quantiles = c(0.05, 0.5, 0.95))  # Add a quantile stat, at 0.05, 0.5, and 0.95
```



Quantiles

Amend the plot to color according to *year_group*.

```
# Amend the plot to color by year_group
ggplot(Vocab, aes(x = education, y = vocabulary, color = year_group)) +
    geom_jitter(alpha = 0.25) + stat_quantile(quantiles = c(0.05,
    0.5, 0.95))
```



Using *stat_sum()*

- In the first course, you saw that this is one of the four causes of overplotting.
- You'd get a single point at each intersection between the two variables.

Using *stat_sum()*

- One solution, shown in the step 1, is jittering with transparency.
- Another solution is to use *stat_sum()*, which calculates the total number of overlapping observations and maps that onto the size aesthetic.

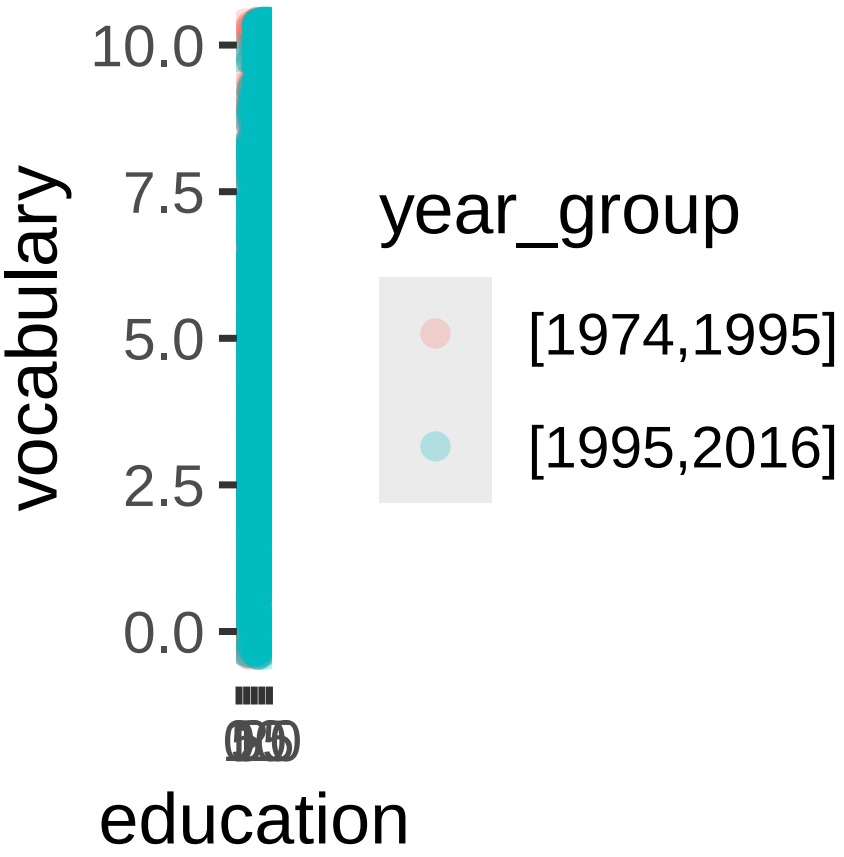
Using *stat_sum()*

Using *stat_sum()* allows a special variable, prop.., to show the proportion of values within the dataset.

Using *stat_sum()*

Run the code to see how jittering & transparency solves overplotting.

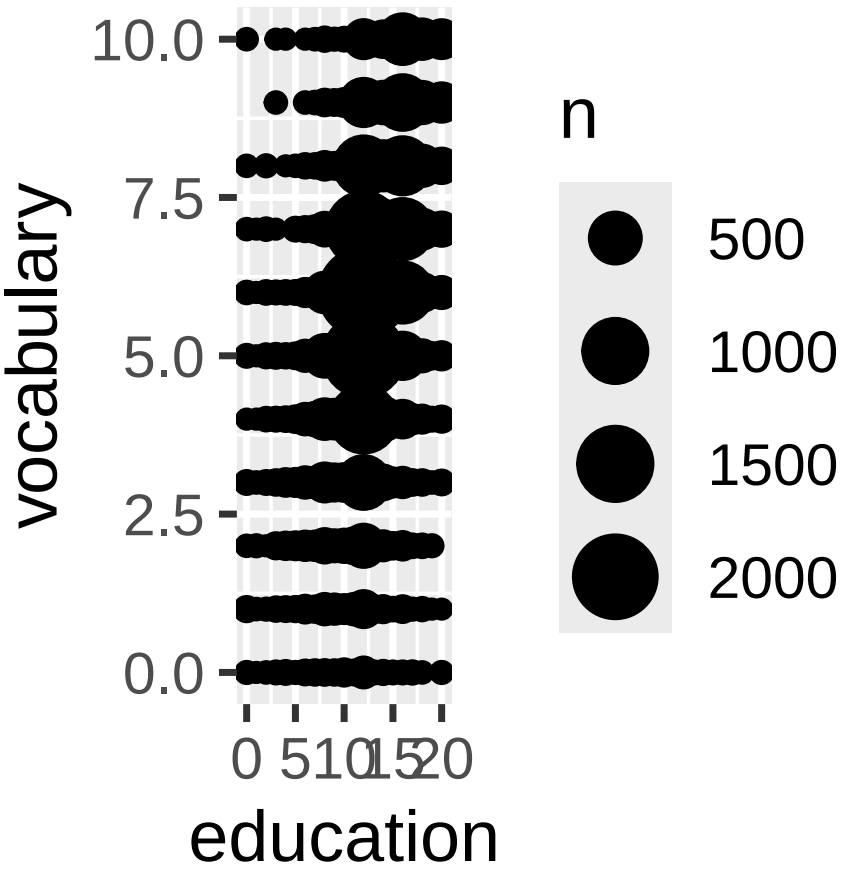
```
# Plot vocabulary vs. education, colored by year_group
ggplot(Vocab, aes(x = education, y = vocabulary, color = year_group)) +
    geom_jitter(alpha = 0.25)  # Add jittered points with transparency 0.25
```



Using *stat_sum()*

Replace the jittered points with a sum stat, using stat_sum().

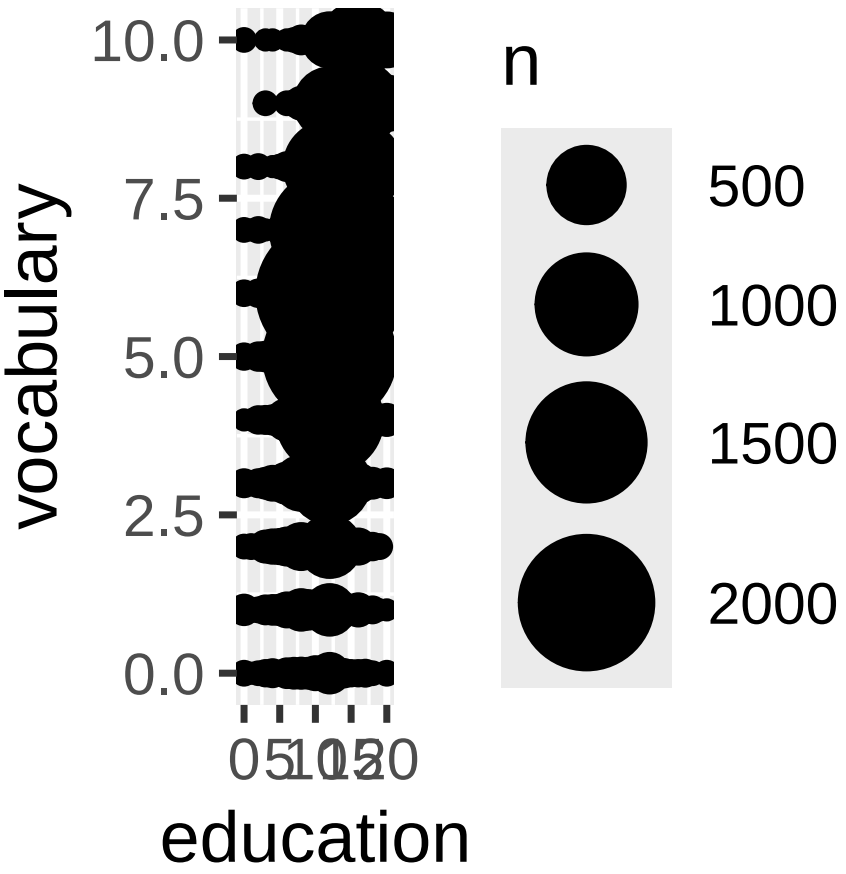
```
ggplot(Vocab, aes(x = education, y = vocabulary)) + stat_sum()
```



Using *stat_sum()*

Modify the size aesthetic with the appropriate scale function.

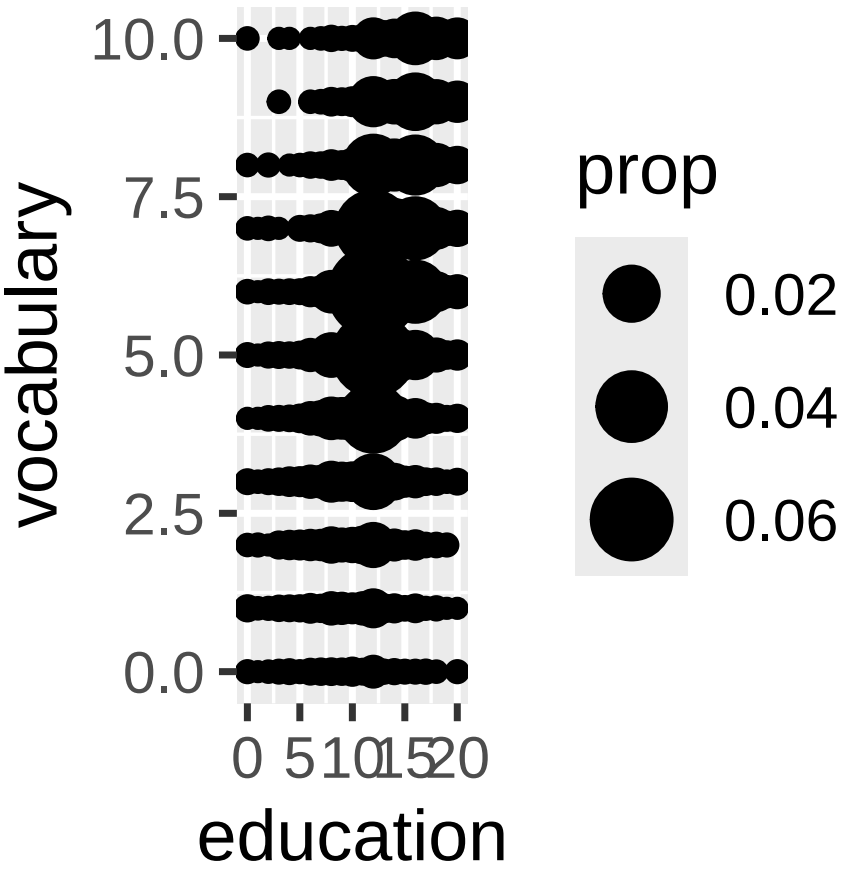
```
ggplot(Vocab, aes(x = education, y = vocabulary)) + stat_sum() +
    # Add a size scale, from 1 to 10
scale_size(range = c(1, 10))
```



Using *stat_sum()*

Inside *stat_sum()* , set **size** to ..prop.. so circle size represents the proportion of the whole dataset.

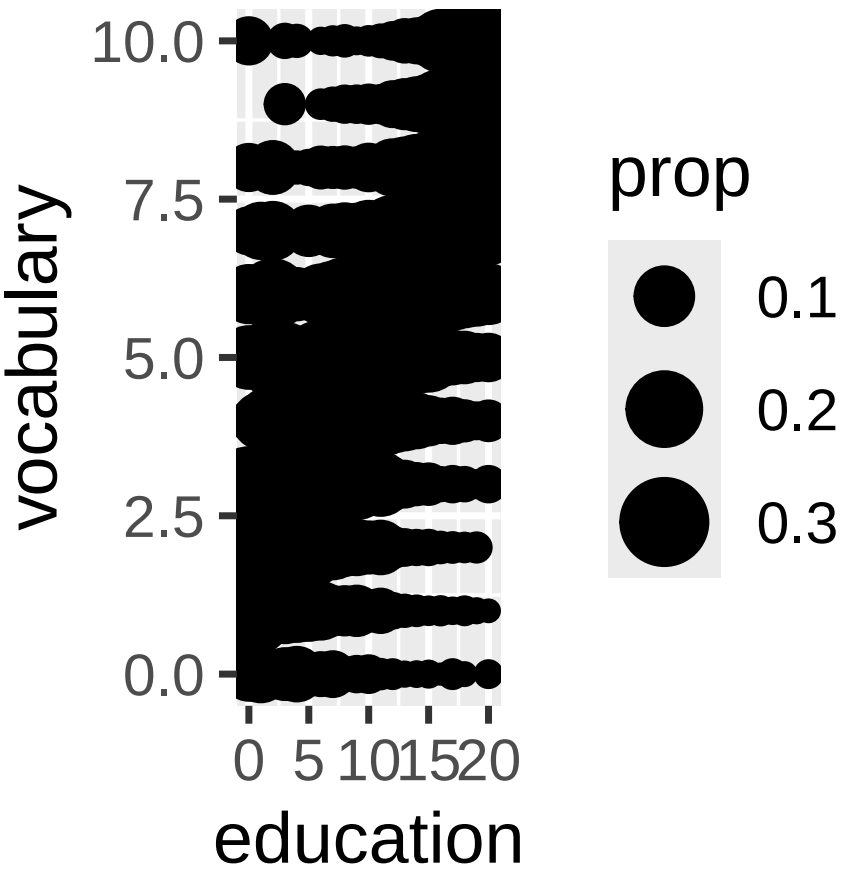
```
# Amend the stat to use proportion sizes
ggplot(Vocab, aes(x = education, y = vocabulary)) + stat_sum(aes(size = ..prop..))
```



Using *stat_sum()*

Update the plot to group by education, so that circle size represents the proportion of the group.

```
# Amend the plot to group by education
ggplot(Vocab, aes(x = education, y = vocabulary, group = education)) +
    stat_sum(aes(size = ..prop..))
```



Stats outside geoms

- Preparations In the following exercises, we'll aim to make the plot shown in the viewer.
- Here, we'll establish our positions and base layer of the plot.
- Establishing these items as independent objects will allow us to recycle them easily in many layers, or plots.

Stats outside geoms

position_jitter() adds jittering (e.g. for points).

position_dodge() dodges geoms, (e.g. bar, col, boxplot, violin, errorbar, pointrange).

position_jitterdodge() jitters and dodges geoms, (e.g. points).

Stats outside geoms

As before, we'll use **mtcars**, where **fcyl** and **fam** are proper factor variables of the original cyl and am variables.

Stats outside geoms

Using these three functions, define these position objects:

- *posn_j* : will jitter with a width of 0.2.

```
# Define position objects 1. Jitter with width 0.2
posn_j <- position_jitter(width = 0.2)

# 2. Dodge with width 0.1
posn_d <- position_dodge(width = 0.1)

# 3. Jitter-dodge with jitter.width 0.2 and dodge.width 0.1
posn_jd <- position_jitterdodge(jitter.width = 0.2, dodge.width = 0.1)
```

Stats outside geoms

Using these three functions, define these position objects:

- *posn_d* : will dodge with a width of 0.1.

```
# Define position objects 1. Jitter with width 0.2
posn_j <- position_jitter(width = 0.2)

# 2. Dodge with width 0.1
posn_d <- position_dodge(width = 0.1)

# 3. Jitter-dodge with jitter.width 0.2 and dodge.width 0.1
posn_jd <- position_jitterdodge(jitter.width = 0.2, dodge.width = 0.1)
```

Stats outside geoms

Using these three functions, define these position objects:

- *posn_jd* will jitter and dodge with a jitter.width of 0.2 and a dodge.width of 0.1.

```
# Define position objects 1. Jitter with width 0.2
posn_j <- position_jitter(width = 0.2)

# 2. Dodge with width 0.1
posn_d <- position_dodge(width = 0.1)

# 3. Jitter-dodge with jitter.width 0.2 and dodge.width 0.1
posn_jd <- position_jitterdodge(jitter.width = 0.2, dodge.width = 0.1)
```

Stats outside geoms

Plot wt vs. fcyl, colored by fam.

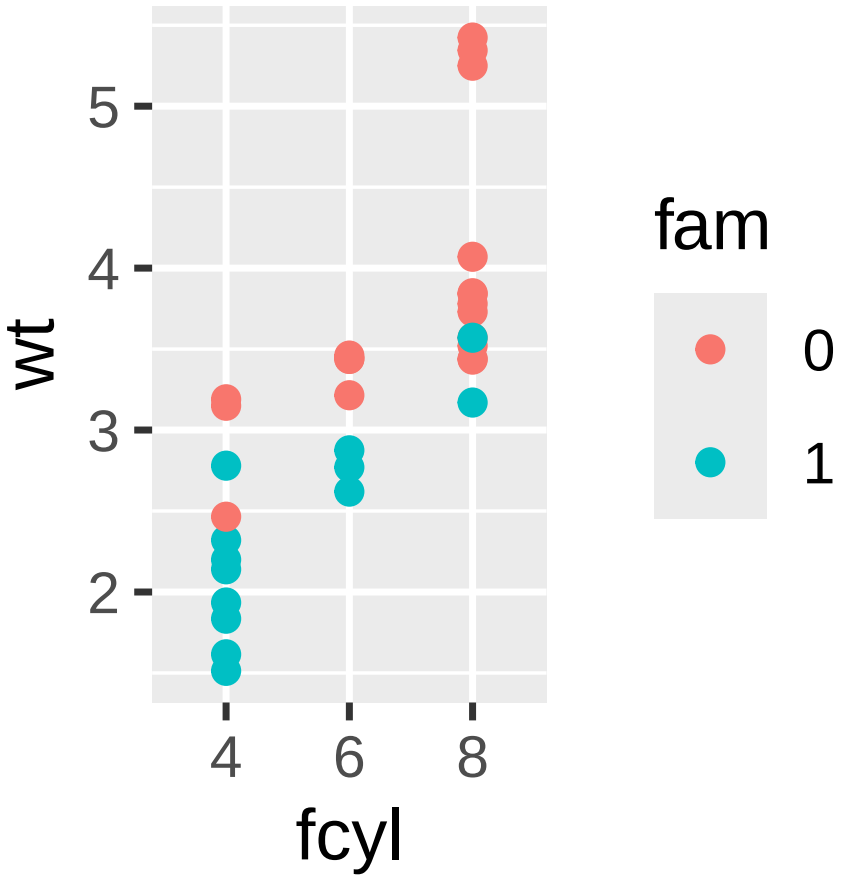
```
# Create the plot base: wt vs. fcyl, colored by fam
p_wt_vs_fcyl_by_fam <- ggplot(mtcars, aes(x = fcyl, y = wt, color = fam))
```

Assign this base layer to $p\_wt\_vs\_fcyl\_by\_fam$.

Stats outside geoms

Plot the data using *geom_point()*.

```
# Add a point layer
p_wt_vs_fcyl_by_fam + geom_point()
```



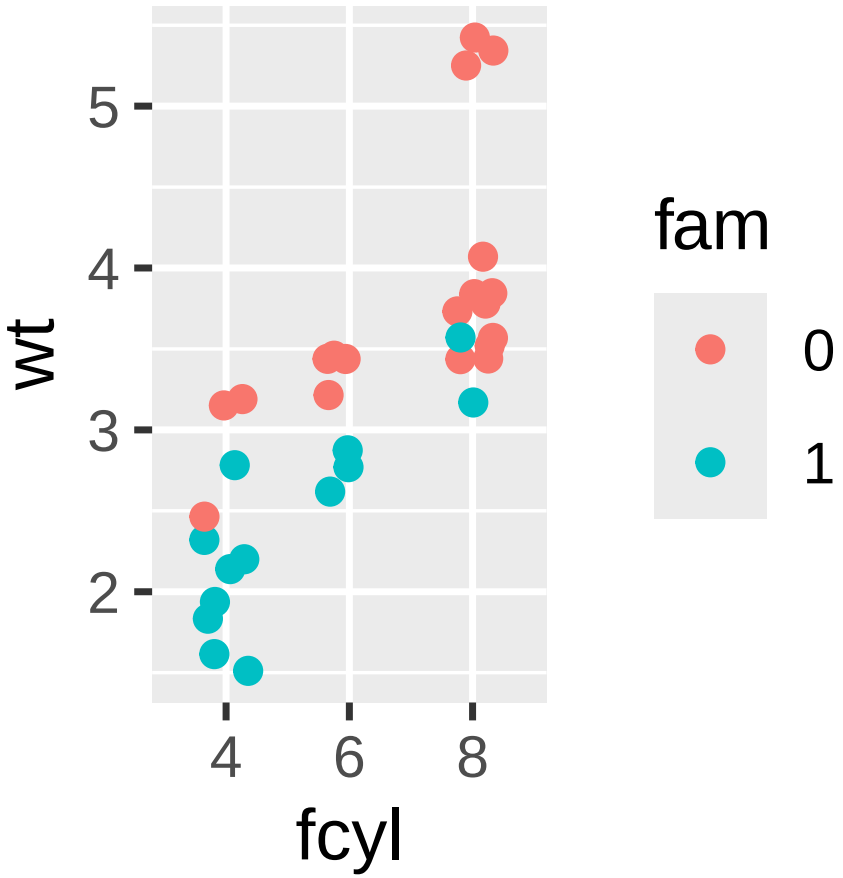
Using position objects

- Now that the position objects have been created, you can apply them to the base plot to see their effects.
- You do this by adding a point geom and setting the position argument to the position object.

Using position objects

Apply the jitter position, *posn_j*, to the base plot.

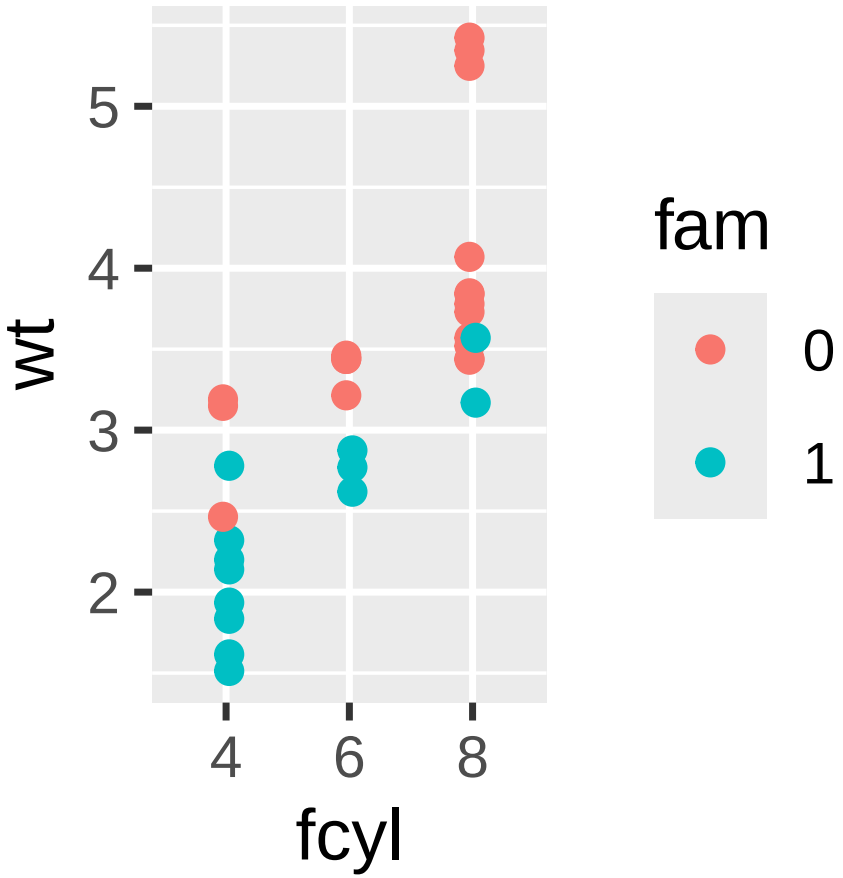
```
# Add jittering only
p_wt_vs_fcyl_by_fam + geom_point(position = posn_j)
```



Using position objects

Apply the dodge position, *posn_d*, to the base plot.

```
# Add dodging only
p_wt_vs_fcyl_by_fam + geom_point(position = posn_d)
```



stat_summary()

Summary statistics refers to a combination of location (mean or median) and spread (standard deviation or confidence interval).

These metrics are calculated in *stat_summary()* by passing a function to the fun.data argument.

stat_summary()

mean_sdl(), calculates multiples of the standard deviation and *mean_cl_normal*() calculates the t-corrected 95% CI.

Arguments to the data function are passed to stat_summary()'s fun.args argument as a list.

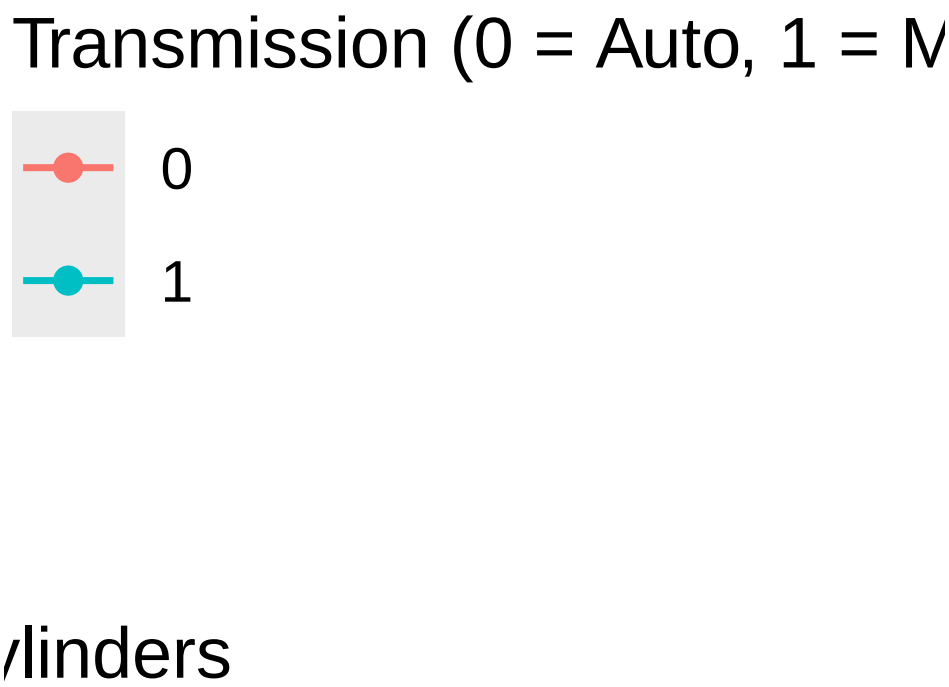
Let's start with basic plot

```
# Example dataset
data(mtcars)
# Define position dodge
posn_d <- position_dodge(width = 0.2)
# Base plot
p_wt_vs_fcyl_by_fam <- ggplot(mtcars, aes(x = factor(cyl), y = wt,
    color = factor(am))) + geom_point(position = posn_d) + labs(x = "Number of Cylinders",
    y = "Weight", color = "Transmission (0 = Auto, 1 = Manual)")
```

stat_summary()

Add error bars representing the standard deviation.

```
# Plot with standard deviation error bars
p_wt_vs_fcyl_by_fam + stat_summary(geom = "errorbar", position = posn_d,
    width = 0.2)
```

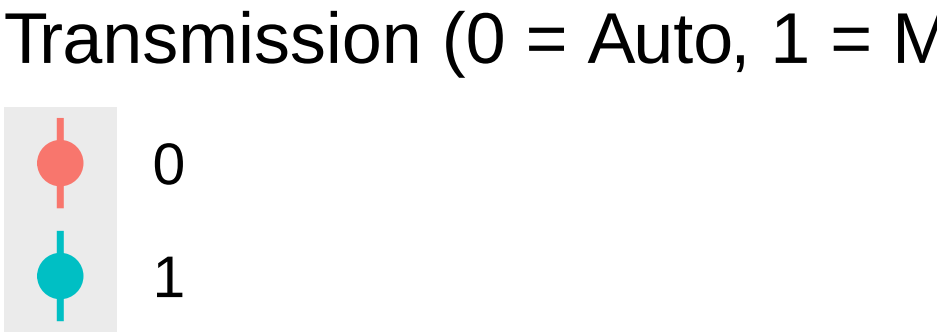


stat_summary()

Set the data function to *mean_sdl* (without parentheses).

Draw 1 standard deviation each side of the mean, pass arguments to the *mean_sdl* function by assigning them to fun.args in the form of a list.

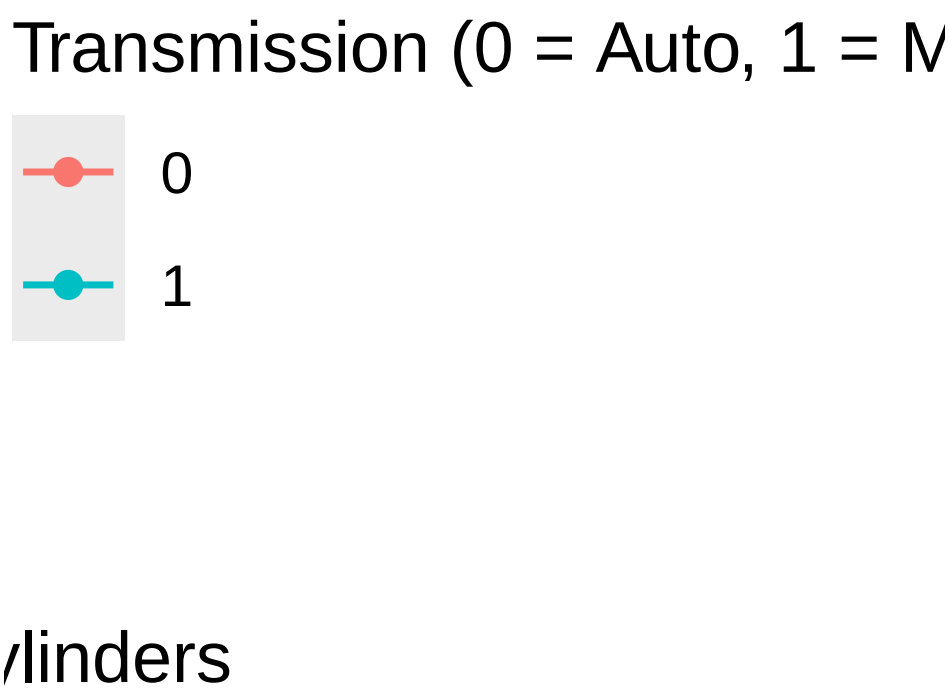
```
p_wt_vs_fcyl_by_fam + stat_summary(fun.data = mean_sdl, fun.args = list(mult = 1),
    position = posn_d)
```



stat_summary()

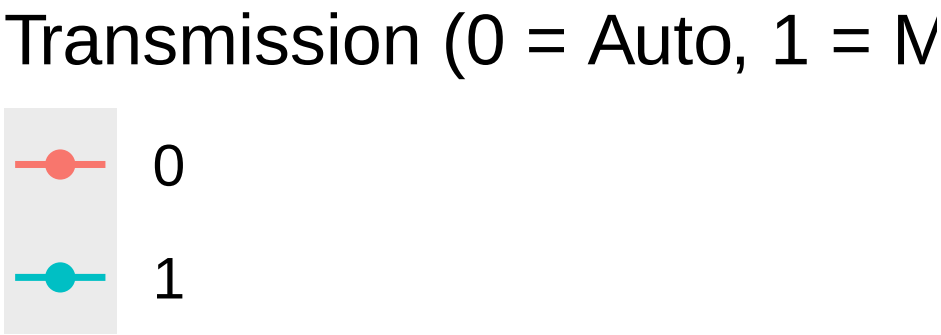
- Update the summary stat to use an "errorbar" geom by assigning it to the geom argument.

```
p_wt_vs_fcyl_by_fam + stat_summary(fun.data = mean_sdl, geom = "errorbar",
    fun.args = list(mult = 1), position = posn_d)
```



stat_summary()

```r
# Define position dodge
posn_d <- position_dodge(width = 0.2)
# Add summary stat with 95% confidence limits using mean_cl_normal
p_wt_vs_fcyl_by_fam +
  stat_summary(
    fun.data = mean_cl_normal,  # Compute 95% confidence limits
    geom = "errorbar",          # Use error bars
    position = posn_d,          # Apply dodge position
    width = 0.2                 # Set width of error bars
  )
```



Section 2

Coordinates

Coordinates

The Coordinates layers offer specific and very useful tools for efficiently and accurately communicating data.

Coordinates

Here we'll look at the various ways of effectively using these layers, so you can clearly visualize lognormal datasets, variables with units, and periodic data.

Coordinates

Coordinates Zooming In In the video, you saw different ways of using the coordinates layer to zoom in.

In this exercise, we'll compare zooming by changing scales and by changing coordinates.

Coordinates

The big difference is that the scale functions change the underlying dataset, which affects calculations made by computed geoms (like histograms or smooth trend lines), whereas coordinate functions make no changes to the dataset.

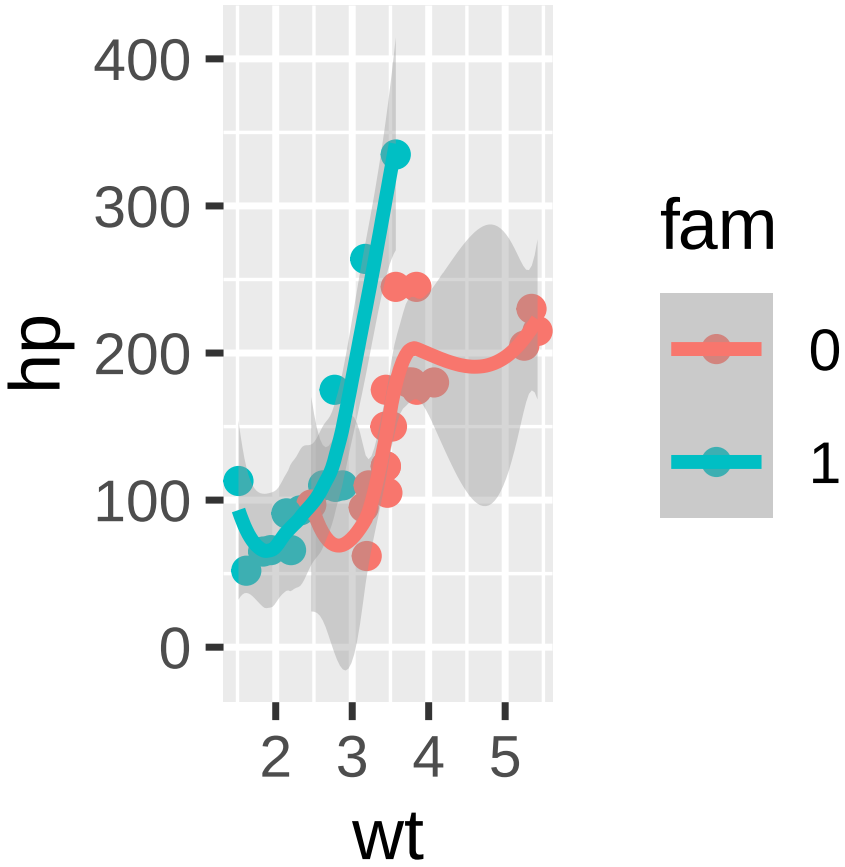
Coordinates

A scatter plot using mtcars with a LOESS smoothed trend line is provided. Take a look at this before updating it.

```
mtcars <- mtcars %>%
    mutate(fcyl = as.factor(cyl), fam = as.factor(am))
```

Coordinates

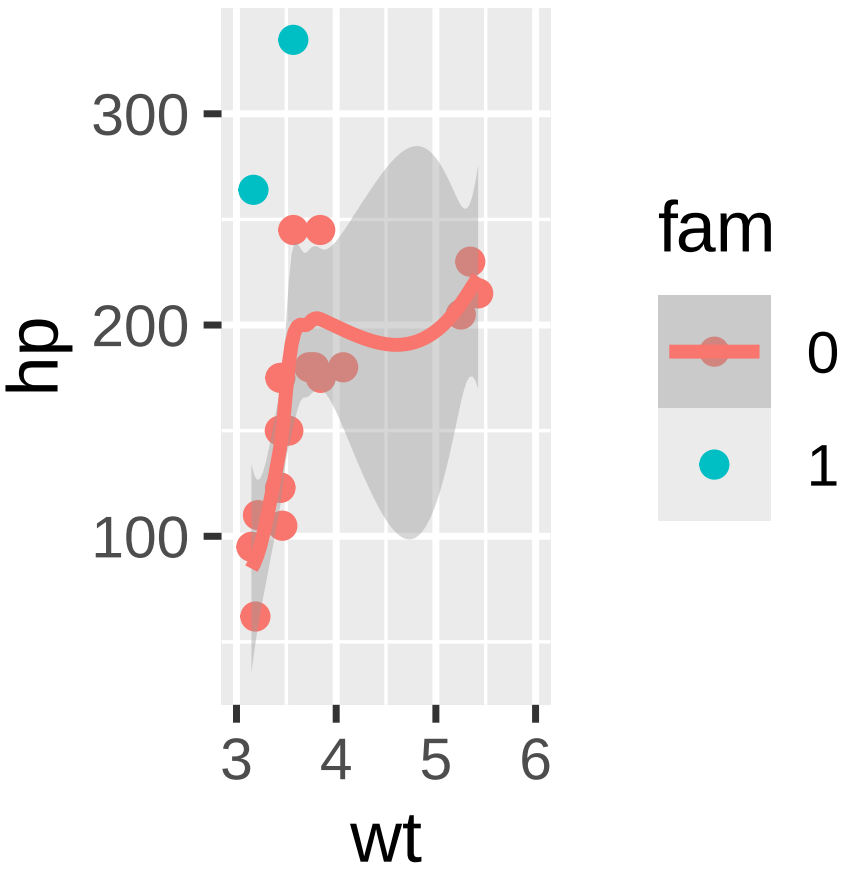
```
# Run the code, view the plot, then update it
ggplot(mtcars, aes(x = wt, y = hp, color = fam)) + geom_point() +
    geom_smooth()
```



Coordinates

Update the plot by adding (+) a continuous x scale with limits from 3 to 6. Spoiler: this will cause a problem!

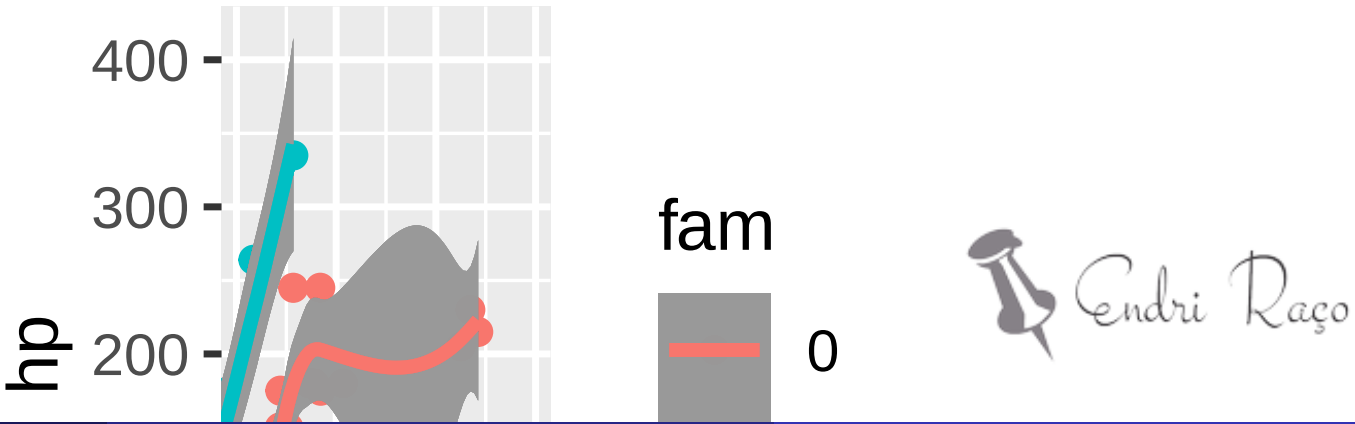
```
# Run the code, view the plot, then update it
ggplot(mtcars, aes(x = wt, y = hp, color = fam)) + geom_point() +
    geom_smooth() + scale_x_continuous(limits = c(3, 6))  # Add a continuous x scale with x limits from 3 to 6
```



Coordinates

Update the plot by adding a Cartesian coordinate system with x limits, xlim, from 3 to 6.

```
ggplot(mtcars, aes(x = wt, y = hp, color = fam)) + geom_point() +
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 geom_smooth()
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 +
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 #
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 Add
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 Cartesian
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 coordinates
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 with
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 x
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 limits
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 from
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 3
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 to
    geom_smooth() + # Add Cartesian coordinates with x limits from 3 to 6 6
coord_cartesian(xlim = c(3, 6))
```



Coordinates

We can set the aspect ratio of a plot with $coord\_fixed()$, which uses $ratio = 1$ as a default.

A $1:1$ aspect ratio is most appropriate when two continuous variables are on the same scale, as with the iris dataset.

Coordinates

All variables are measured in centimeters, so it only makes sense that one unit on the plot should be the same physical distance on each axis.

This gives a more truthful depiction of the relationship between the two variables since the aspect ratio can change the angle of our smoothing line.

Coordinates

This would give an erroneous impression of the data. Of course the underlying linear models don't change, but our perception can be influenced by the angle drawn.

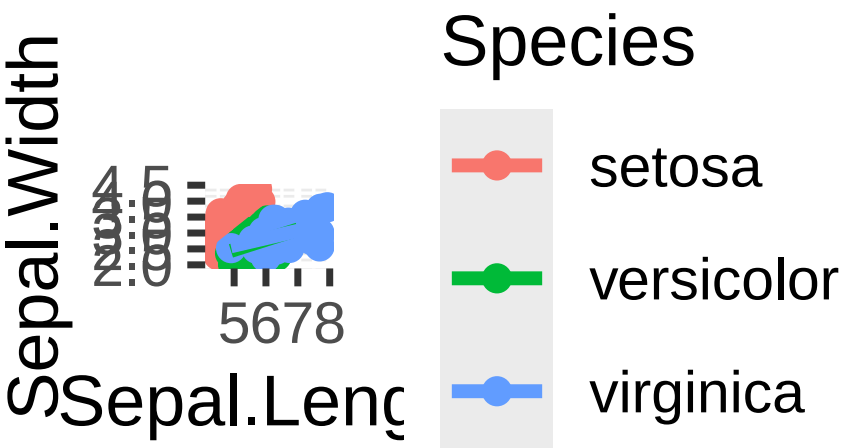
Coordinates

A plot using the iris dataset, of **sepal width** vs. **sepal length** colored by species, is shown in the viewer.

Aspect ratio I: 1:1 ratios

Add a fixed coordinate layer to force a 1:1 aspect ratio.

```
ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, color = Species)) +
    geom_jitter() + geom_smooth(method = "lm", se = FALSE) +
    coord_fixed()  # Fix the coordinate ratio
```



Aspect ratio II

- setting ratios When values are not on the same scale it can be a bit tricky to set an appropriate aspect ratio.
- A classic William Cleveland (inventor of dot plots) example is the sunspots data set. We have 3200 observations from 1750 to 2016.

Aspect ratio II

- *sun_plot* is a plot without any set aspect ratio.

```
library(reshape2)
library(zoo)
sunspots.m <- data.frame(year = index(sunspot.month), value = melt(sunspot.month)$value)
sun_plot <- ggplot(sunspots.m, aes(x = year, y = value)) + geom_line()
```

- It fills up the graphics device.

Aspect ratio II

- To make aspect ratios clear, we've drawn an orange box that is 75 units high and 75 years wide.

```
library(reshape2)
library(zoo)
sunspots.m <- data.frame(year = index(sunspot.month), value = melt(sunspot.month)$value)
sun_plot <- ggplot(sunspots.m, aes(x = year, y = value)) + geom_line() +
    coord_fixed()
```

- Using a $1:1$ aspect ratio would make the box square.

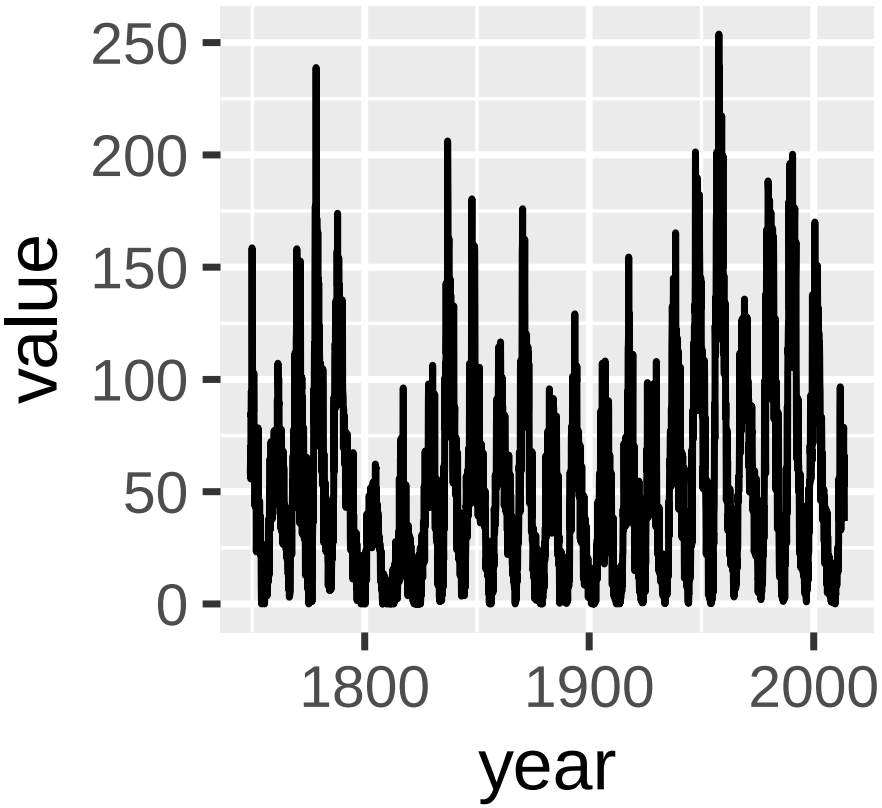
Aspect ratio II

That aspect ratio would make things harder to see the oscillations: it is better to force a wider ratio.

Aspect ratio II

Fix the coordinates to a 1:1 aspect ratio. The y axis is now unreadably small. Make it bigger!

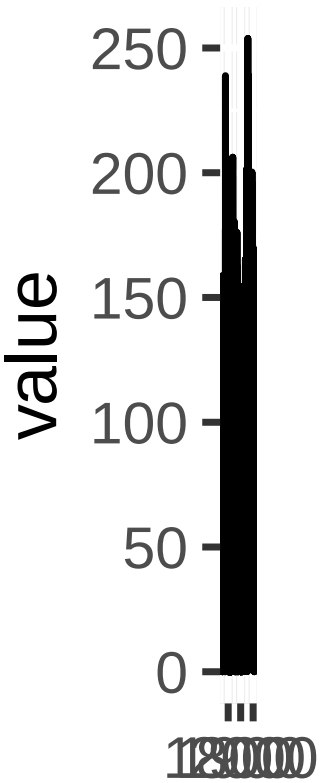
```
# Fix the aspect ratio to 1:1
sun_plot + coord_fixed()
```



Aspect ratio II

- Change the aspect ratio to 20 : 1.
- This is the aspect ratio recommended by Cleveland to help make the trend among oscillations easiest to see. # Fix the aspect ratio to 1:1

```
# Change the aspect ratio to 20:1
sun_plot + coord_fixed(ratio = 20)
```



Expand and clip

The $coord\_\star()$ layer functions offer two useful arguments that work well together: expand and clip.

Expand and clip

expand sets a buffer margin around the plot, so data and axes don't overlap.

Setting expand to 0 draws the axes to the limits of the data.

Expand and clip

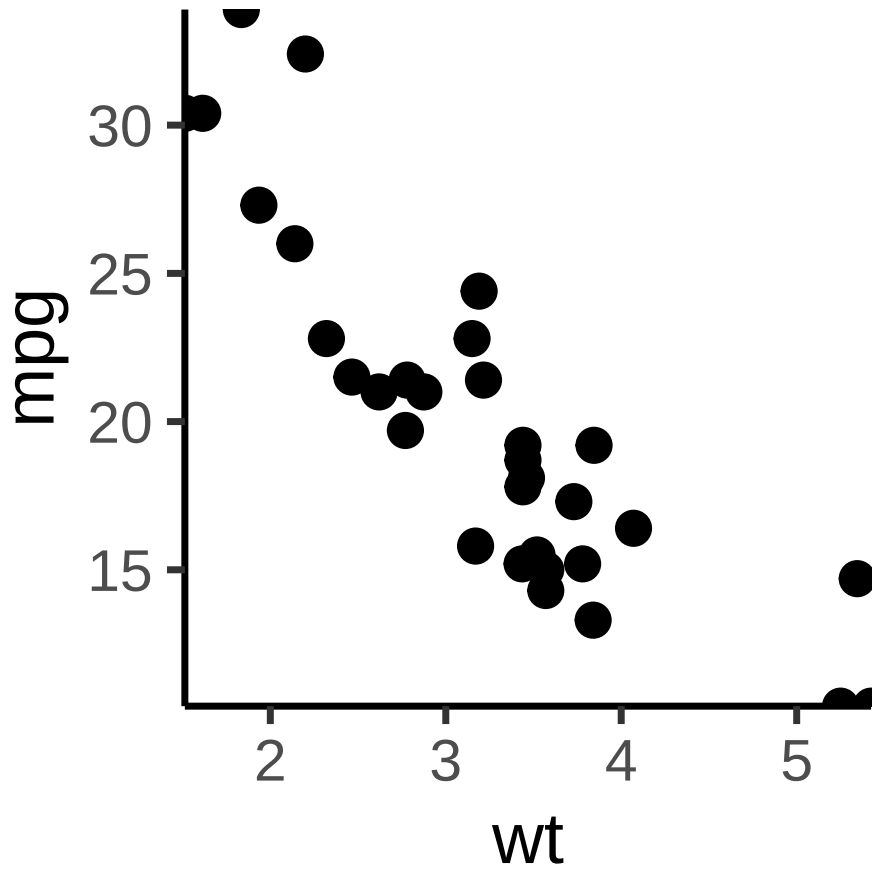
clip decides whether plot elements that would lie outside the plot panel are displayed or ignored ("clipped").

When done properly this can make a great visual effect! We'll use theme_classic() and modify the axis lines in this example.

Expand and clip

Add Cartesian coordinates with zero expansion, to remove all buffer margins on both the x and y axes.

```
ggplot(mtcars, aes(wt, mpg)) + geom_point(size = 2) + theme_classic() +
    coord_cartesian(expand = 0)
```

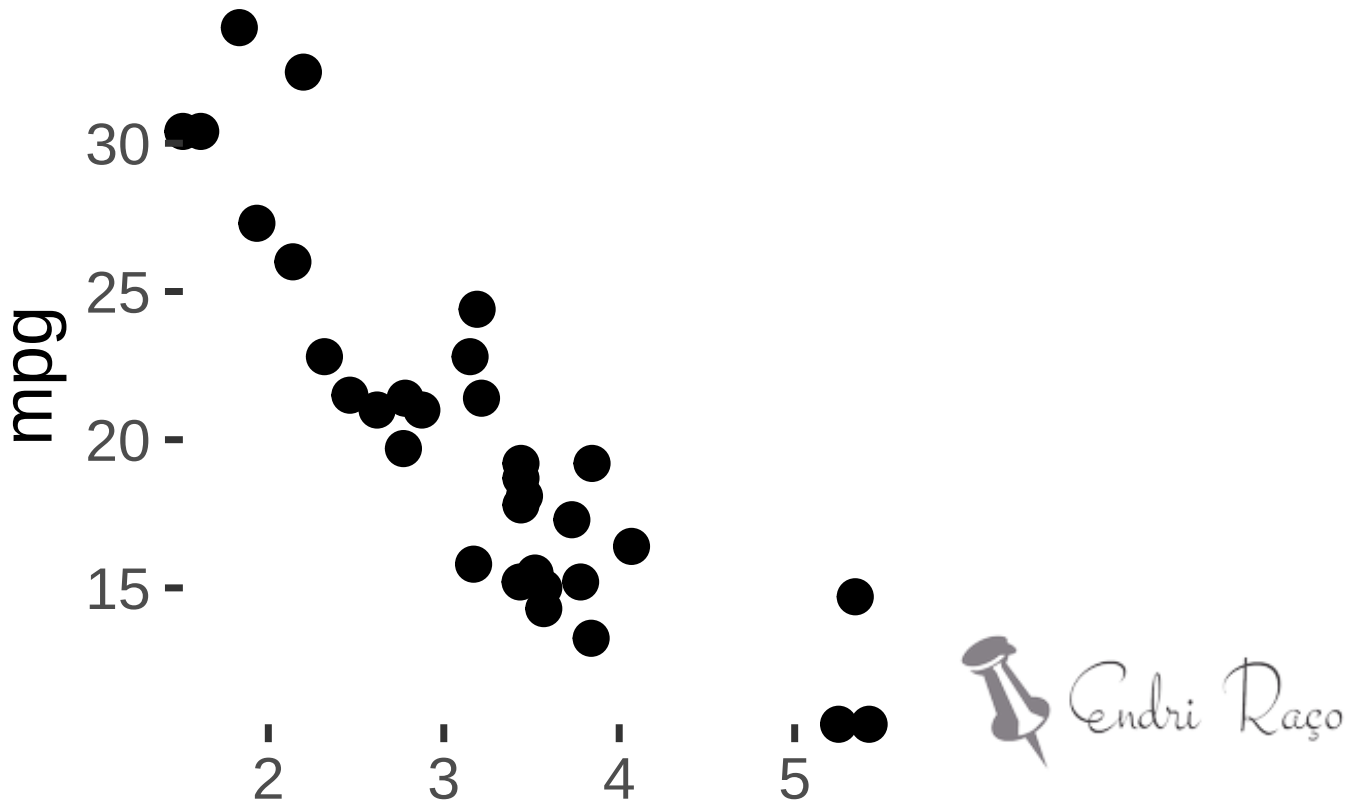


Expand and clip

Set the clip argument to “off” to prevent this.

Remove the axis lines by setting the axis.line argument to element_blank() in the theme() layer function.

```
ggplot(mtcars, aes(wt, mpg)) + geom_point(size = 2) + coord_cartesian(expand = 0,
    clip = "off") + theme_classic() + theme(axis.line = element_blank())  # Remove axis lines
```



Coordinates vs. scales

Log-transforming scales Using $scale\_y\_log10()$ and $scale\_x\_log10()$ is equivalent to transforming our actual dataset before getting to ggplot2.

Coordinates vs. scales

Using $coord\_trans()$, setting $x = "log10"$ and/or $y = "log10"$ arguments, transforms the data after statistics have been calculated.

Coordinates vs. scales

The plot will look the same as with using $scale\_y\_log10()$, but the scales will be different, meaning that we'll see the original values on our log10 transformed axes.

Coordinates vs. scales

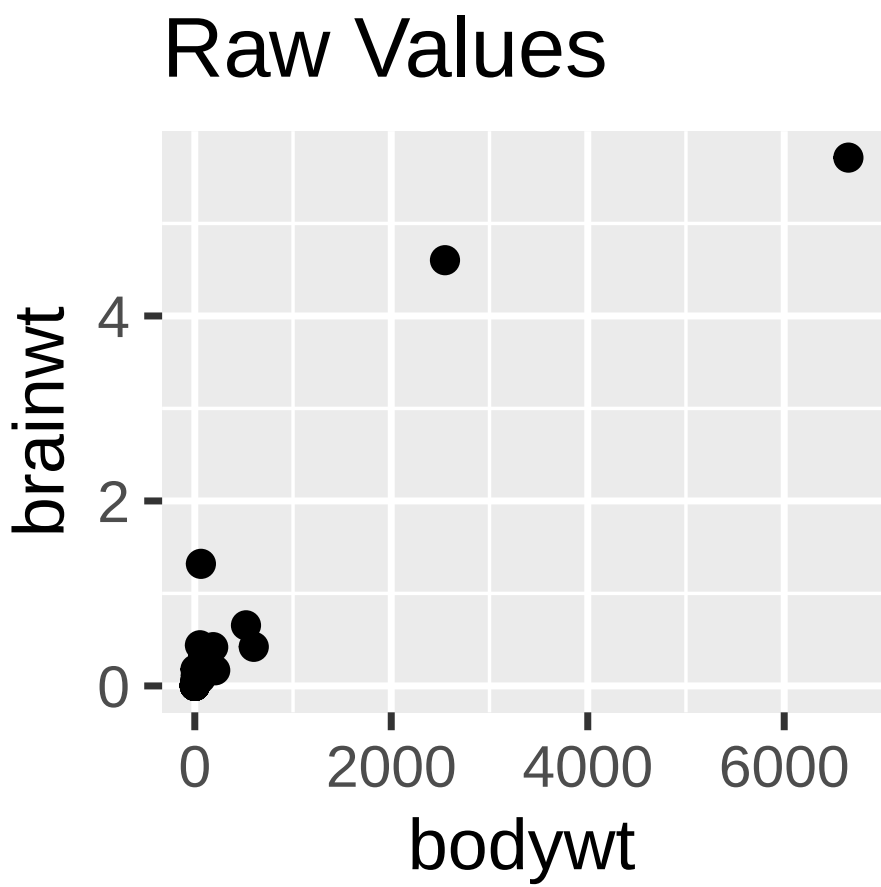
This can be useful since log scales can be somewhat unintuitive.

Let's see this in action with positively skewed data - the brain and body weight of 51 mammals from the msleep dataset.

Coordinates vs. scales

Using the msleep dataset, plot the raw values of brainwt against bodywt values as a scatter plot.

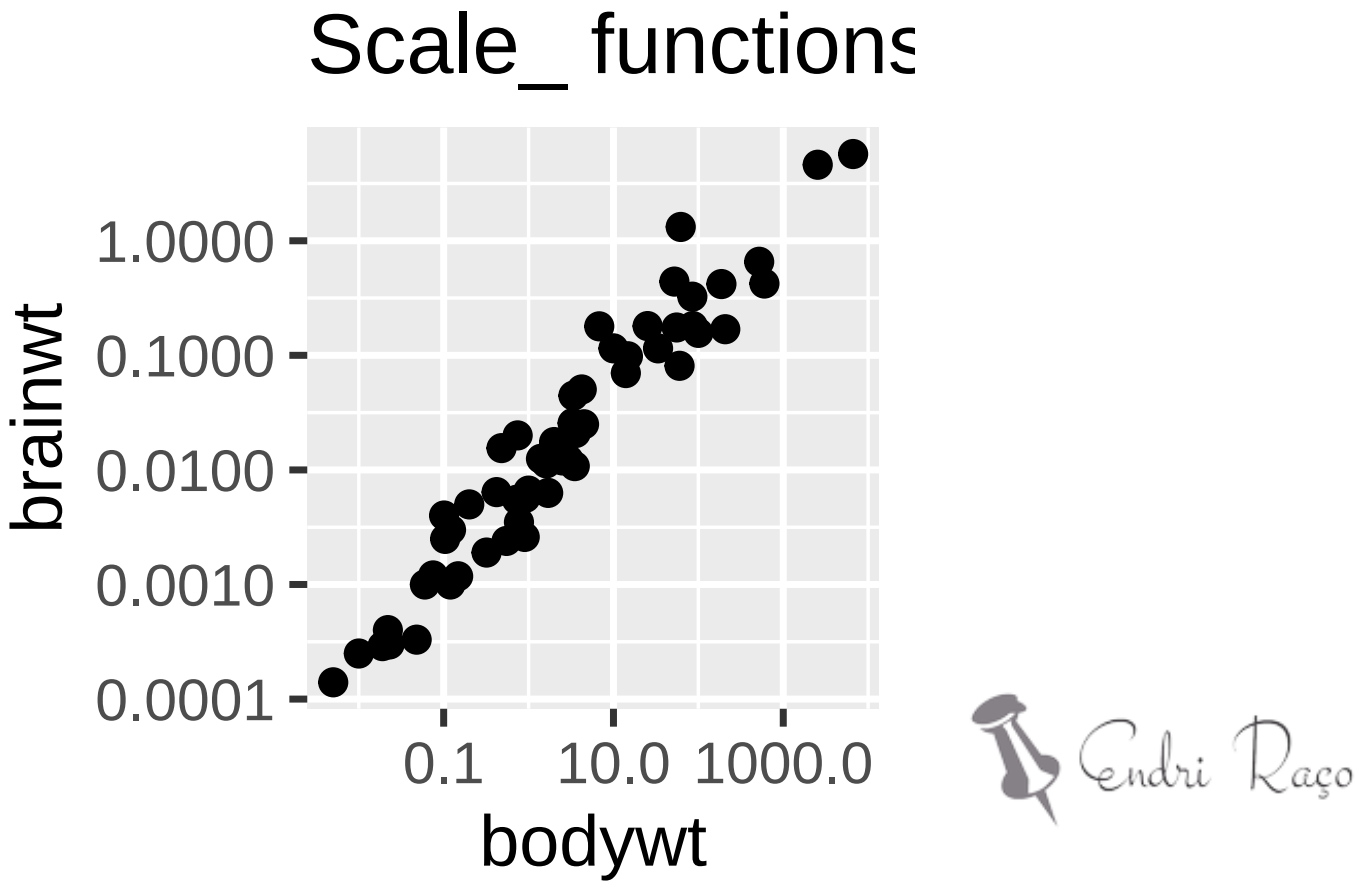
```
# Produce a scatter plot of brainwt vs. bodywt
ggplot(msleep, aes(bodywt, brainwt)) + geom_point() + ggtitle("Raw Values")
```



Coordinates vs. scales

Add the *scale_x_log10()* and *scale_y_log10()* layers with default values to transform the data before plotting.

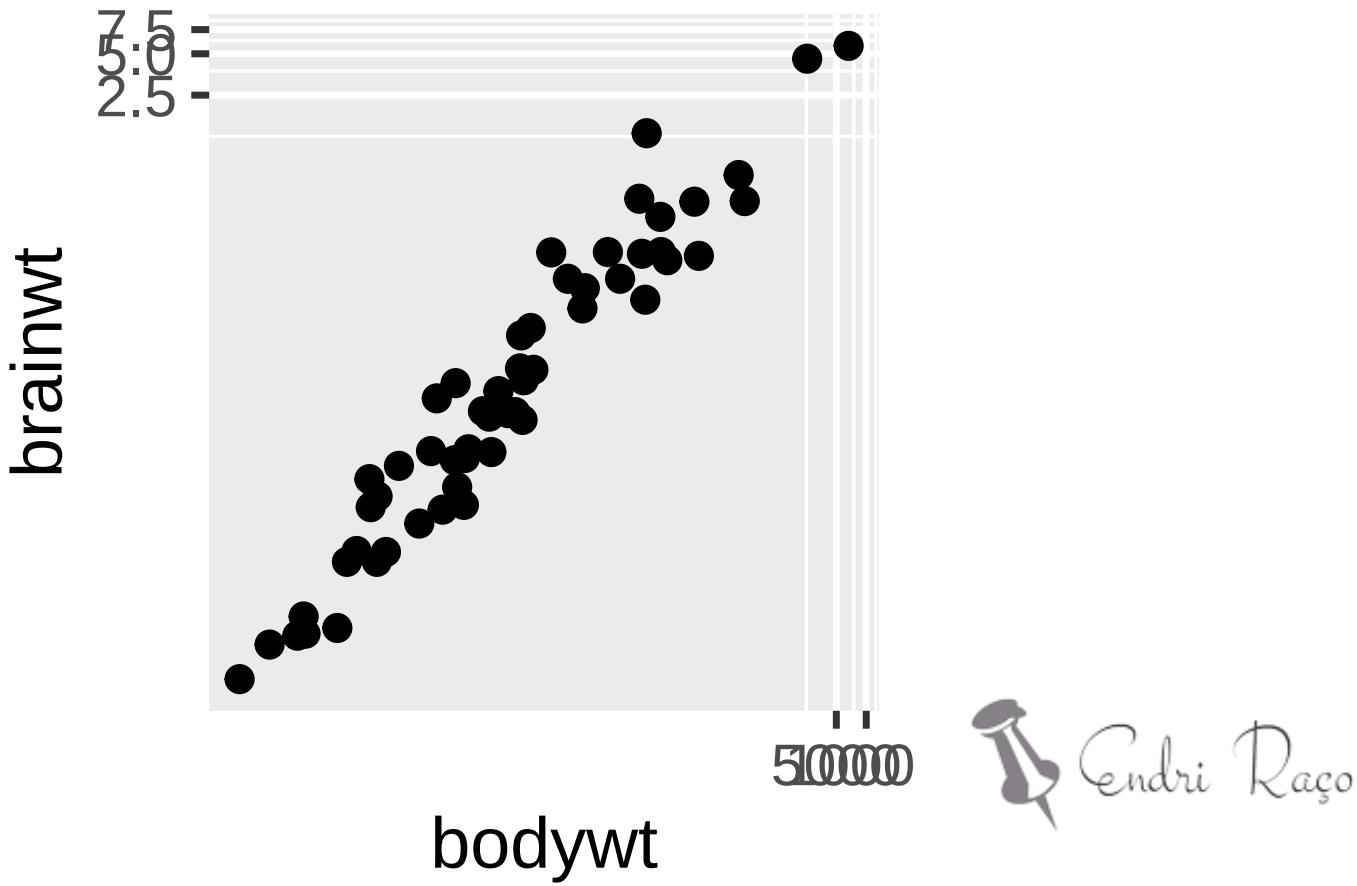
```
# Add scale_*_*() functions
ggplot(msleep, aes(bodywt, brainwt)) + geom_point() + scale_x_log10() +
    scale_y_log10() + ggtitle("Scale_ functions")
```



Coordinates vs. scales

Use coord_trans() to apply a "log10" transformation to both the x and y scales

```
# Perform a log10 coordinate system transformation
ggplot(msleep, aes(bodywt, brainwt)) + geom_point() + coord_trans(x = "log10",
    y = "log10")
```



Adding stats to transformed scales

In the last exercise, we saw the usefulness of the coord_trans() function, but be careful!

Remember that statistics are calculated on the untransformed data.

Adding stats to transformed scales

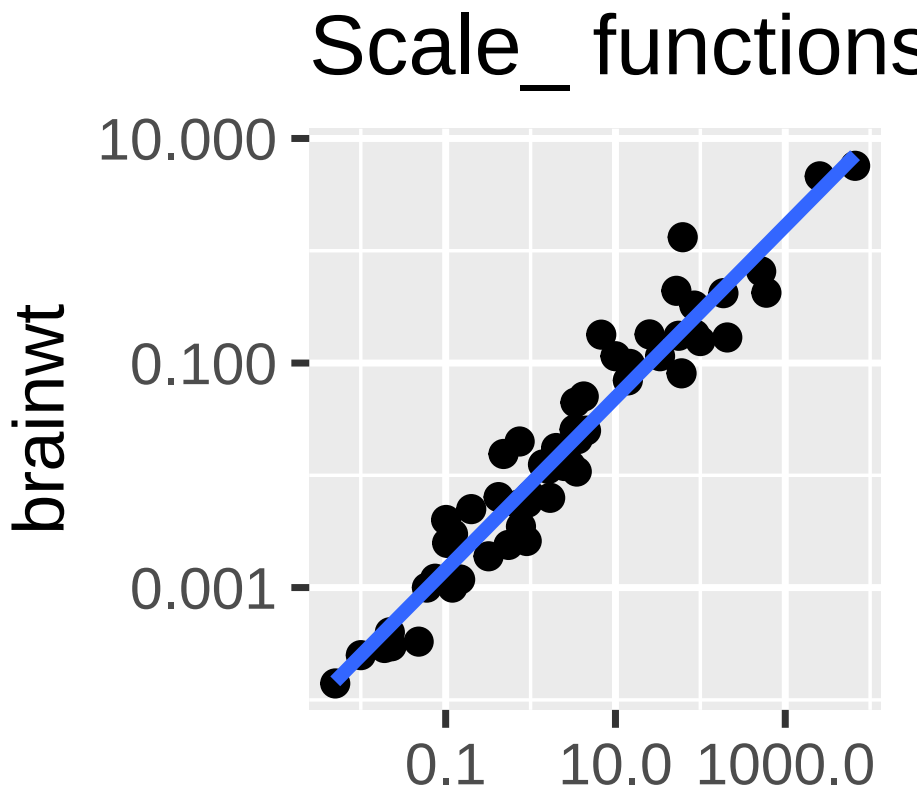
A linear model may end up looking not-so-linear after an axis transformation.

Let's revisit the two plots from the previous exercise and compare their linear models.

Adding stats to transformed scales

Add log10 transformed scales to the x and y axes.

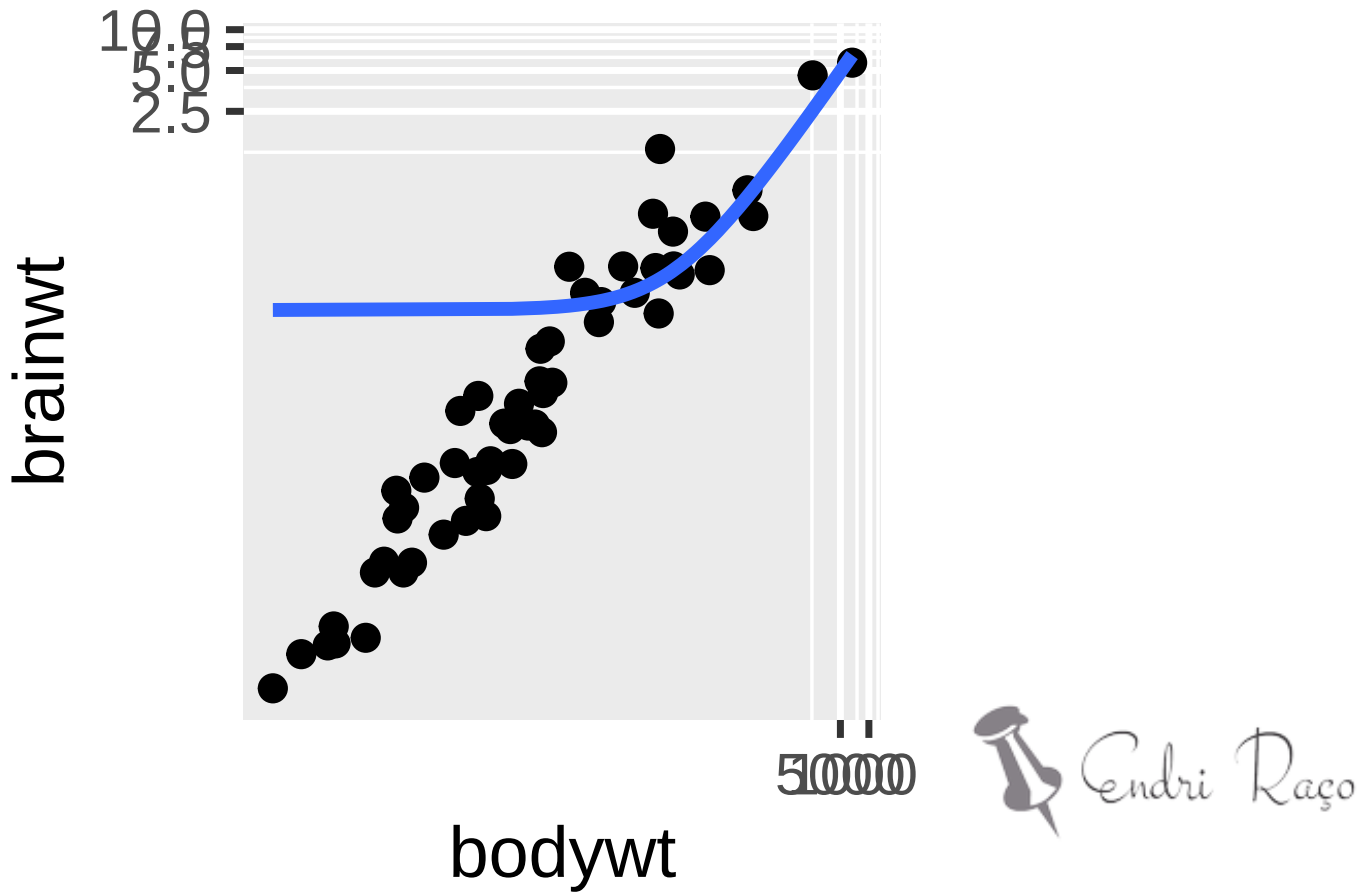
```
# Plot with a scale_*_*() function:
ggplot(msleep, aes(bodywt, brainwt)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  scale_x_log10() + # Add a log10 x scale
  scale_y_log10() + # Add a log10 y scale
  ggtitle("Scale_ functions")
```



Adding stats to transformed scales

Plot with transformed coordinates

```
# Plot with transformed coordinates
ggplot(msleep, aes(bodywt, brainwt)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) + # Add a log10 coordinate transformation for x and y axes
  coord_trans(x = "log10", y = "log10")
```



Double and flipped axes

- Useful double axes Double x and y-axes are a contentious topic in data visualization.
- Here, I want to review a great use case where double axes actually do add value to a plot.

Double and flipped axes

Our goal plot is displayed in the viewer.

```
library(lubridate)
airquality <- airquality %>%
    mutate(Date = make_date(1974, Month, Day))
```

Double and flipped axes

The two axes are the raw temperature values on a Fahrenheit scale and the transformed values on a Celsius scale.

You can imagine a similar scenario for Log-transformed and original values, miles and kilometers, or pounds and kilograms.

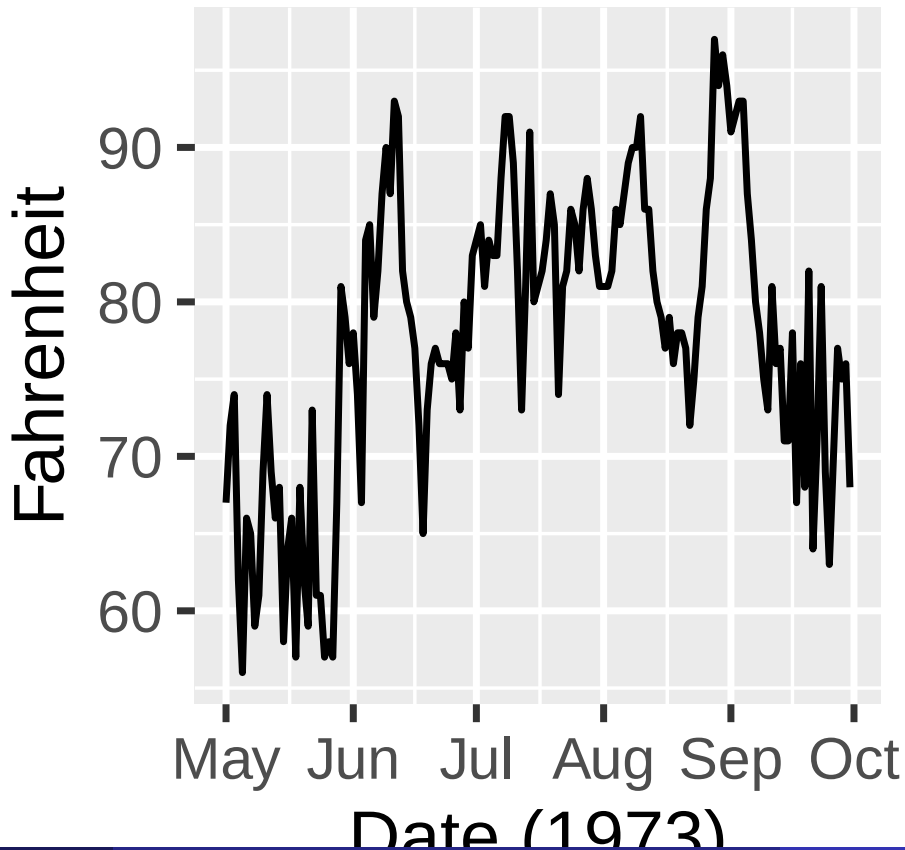
Double and flipped axes

A scale that is unintuitive for many people can be made easier by adding a transformation as a double axis.

Double and flipped axes

Begin with a standard line plot, of Temp described by Date in the airquality dataset.

```
# Using airquality, plot Temp vs. Date
ggplot(airquality, aes(x = Date, y = Temp)) +
  geom_line() + # Add a line layer
  labs(x = "Date (1973)", y = "Fahrenheit")
```



Double and flipped axes

Convert y_breaks from Fahrenheit to Celsius (subtract 32, then multiply by 5, then divide by 9).

```
# Define breaks (Fahrenheit)
y_breaks <- c(59, 68, 77, 86, 95, 104)

# Convert y_breaks from Fahrenheit to Celsius
y_labels <- (y_breaks - 32) * 5/9
```

Double and flipped axes

Define the secondary y-axis using sec_axis(). Use the identity transformation. Set the breaks and labels to the defined objects y_breaks and y_labels, respectively.

```
# Create a secondary x-axis
secondary_y_axis <- sec_axis(
  # Use identity transformation
  trans = identity,
  name = "Celsius",
  # Define breaks and labels as above
  breaks = y_breaks,
  labels = y_labels
)

# Examine the object
secondary_y_axis
```

```
<ggproto object: Class AxisSecondary, gg>
    axis: NULL
    break_info: function
    breaks: 59 68 77 86 95 104
    create_scale: function
    detail: 1000
```

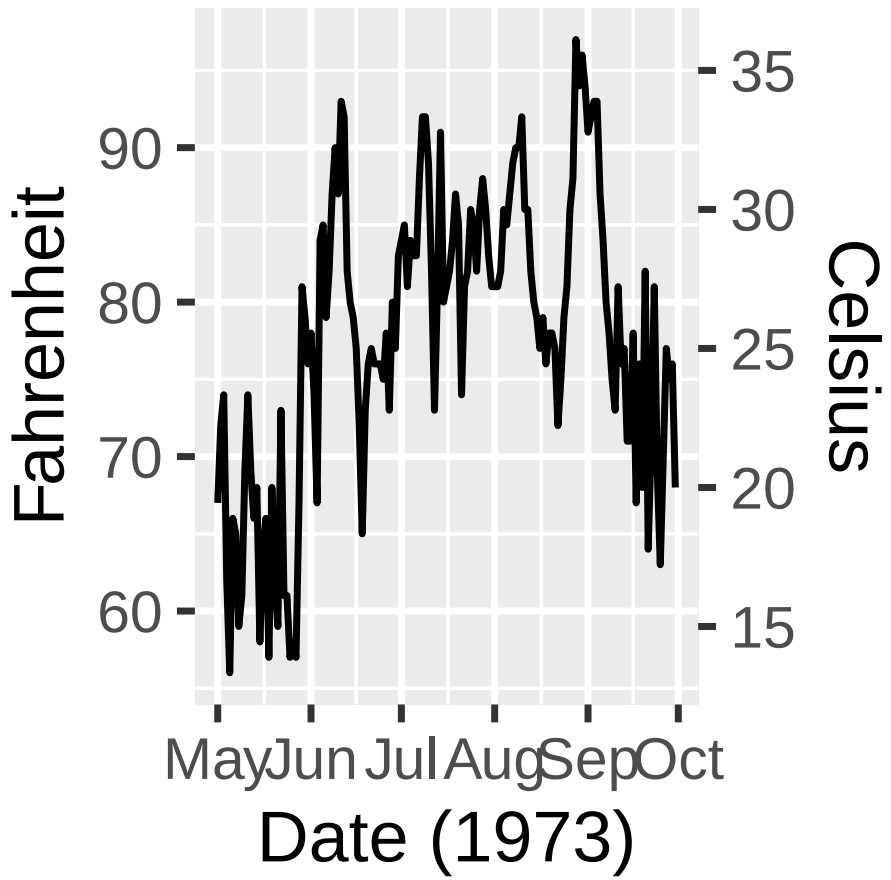
Double and flipped axes

Add your secondary y-axis to the sec.axis argument of *scale_y_continuous*().

```
# From previous step
y_breaks <- c(59, 68, 77, 86, 95, 104)
y_labels <- (y_breaks - 32) * 5/9
secondary_y_axis <- sec_axis(trans = identity, name = "Celsius",
    breaks = y_breaks, labels = y_labels)
```

Update the plot

```
# Update the plot
ggplot(airquality, aes(x = Date, y = Temp)) +
  geom_line() +
  scale_y_continuous(sec.axis = secondary_y_axis) + # Add the secondary y-axis
  labs(x = "Date (1973)", y = "Fahrenheit")
```



Flipping axes I

Flipping axes means to reverse the variables mapped onto the x and y aesthetics.

We can just change the mappings in $aes()$, but we can also use the $coord\_flip()$ layer function.

There are two reasons to use this function:

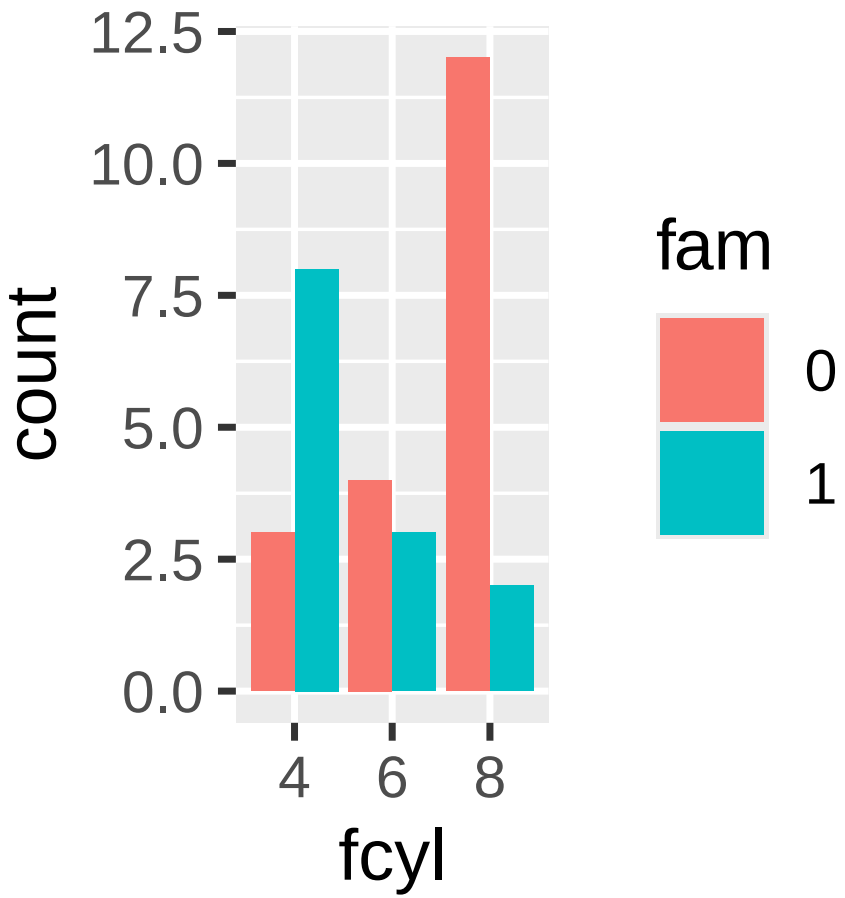
Flipping axes I

We want a vertical geom to be horizontal, or We've completed a long series of plotting functions and want to flip it without having to rewrite all our commands.

Flipping axes I

Create a side-by-side ("dodged") bar chart of fcyl, filled according to fam.

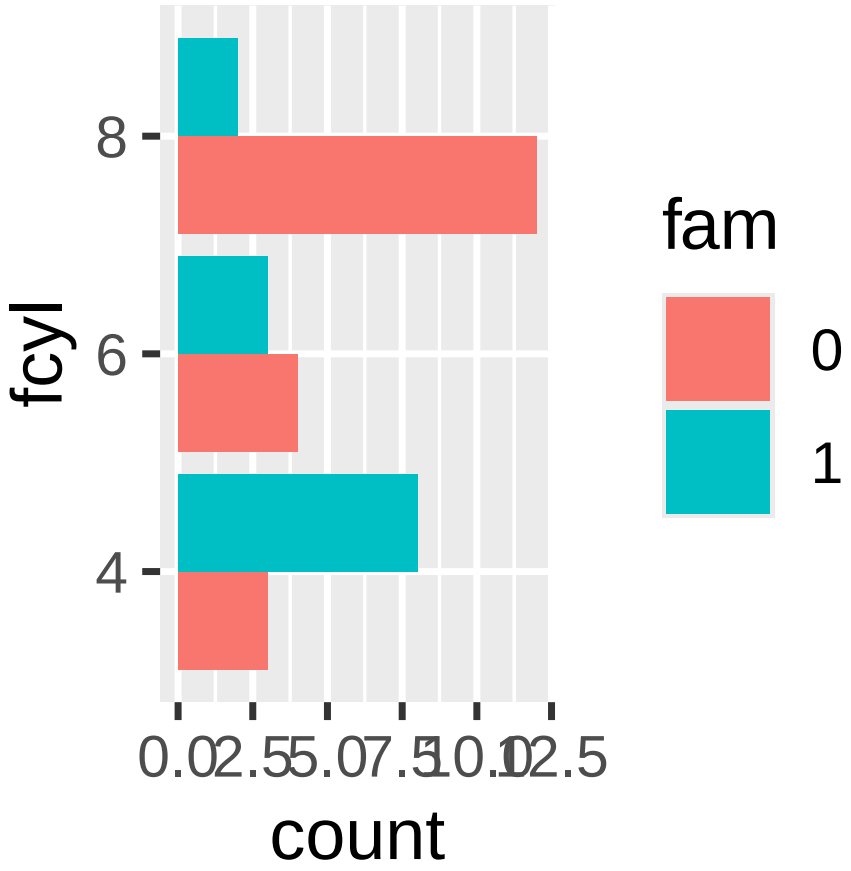
```
# Plot fcyl bars, filled by fam
ggplot(mtcars, aes(fcyl, fill = fam)) + # Place bars side by side
  geom_bar(position = "dodge")
```



Flipping axes I

To get horizontal bars, add a *coord_flip()* function.

```
ggplot(mtcars, aes(fcyl, fill = fam)) +
  geom_bar(position = "dodge") + # Flip the x and y coordinates
  coord_flip()
```

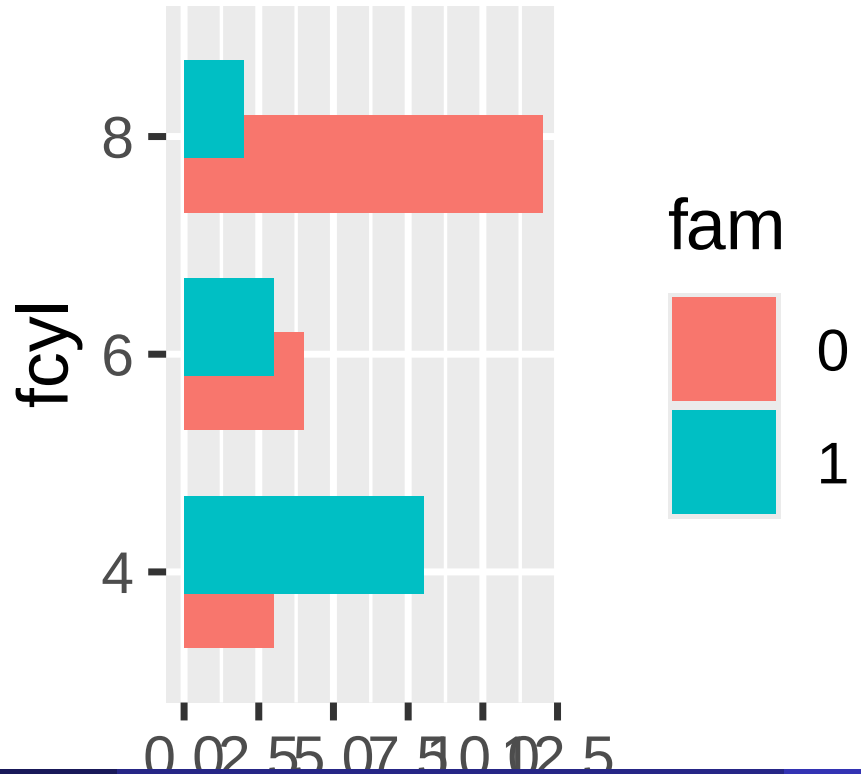


Flipping axes I

Partially overlapping bars are popular with “infoviz” in magazines.

Update the position argument to use *position_dodge*() with a width of 0.5.

```
ggplot(mtcars, aes(fcyl, fill = fam)) +  # Set a dodge width of 0.5 for partially overlapping bars
  geom_bar(position = position_dodge(0.5)) +
  coord_flip()
```



Flipping axes II

In this exercise, we'll continue to use the $coord\_flip()$ layer function to reverse the variables mapped onto the x and y aesthetics.

Flipping axes II

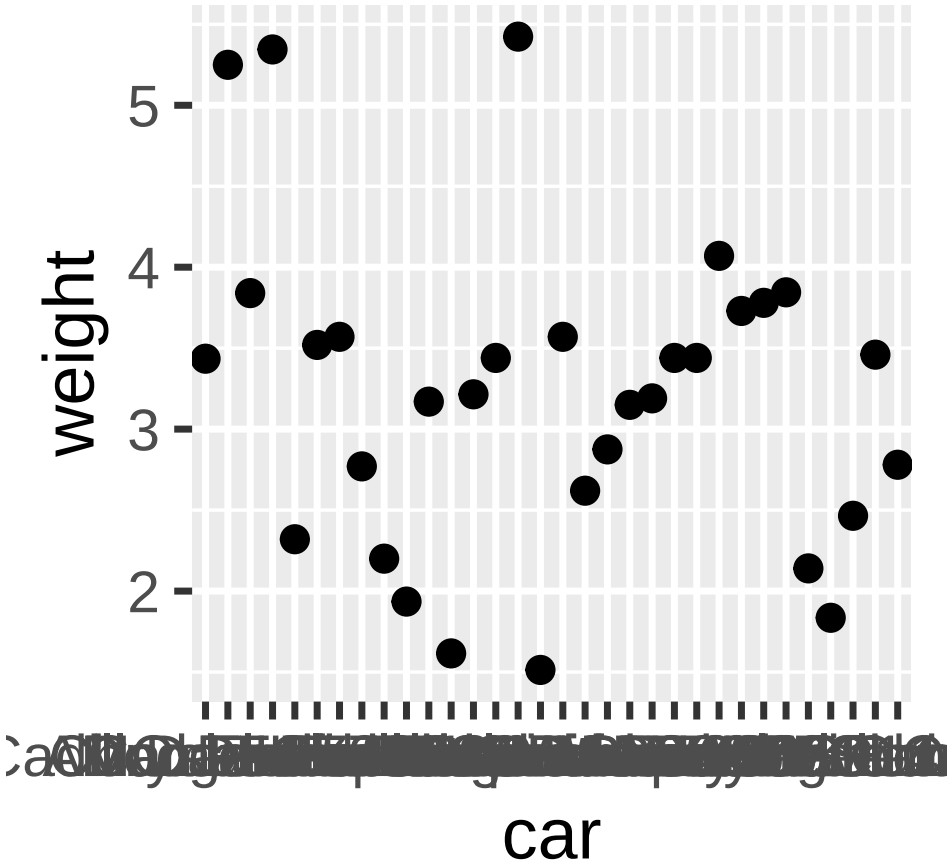
Within the **mtcars** dataset, **car** is the name of the car and **wt** is its weight.

```
# Add car names as a column
mtcars <- mtcars %>%
    mutate(car = rownames(mtcars), fam = as.factor(am), fcyl = as.factor(cyl),
        fvs = as.factor(vs))
```

Flipping axes II

Create a scatter plot of wt versus car using the mtcars dataset.

```
# Plot of wt vs. car
ggplot(mtcars, aes(car, wt)) + geom_point() + labs(x = "car",
    y = "weight")
```



Flipping axes II

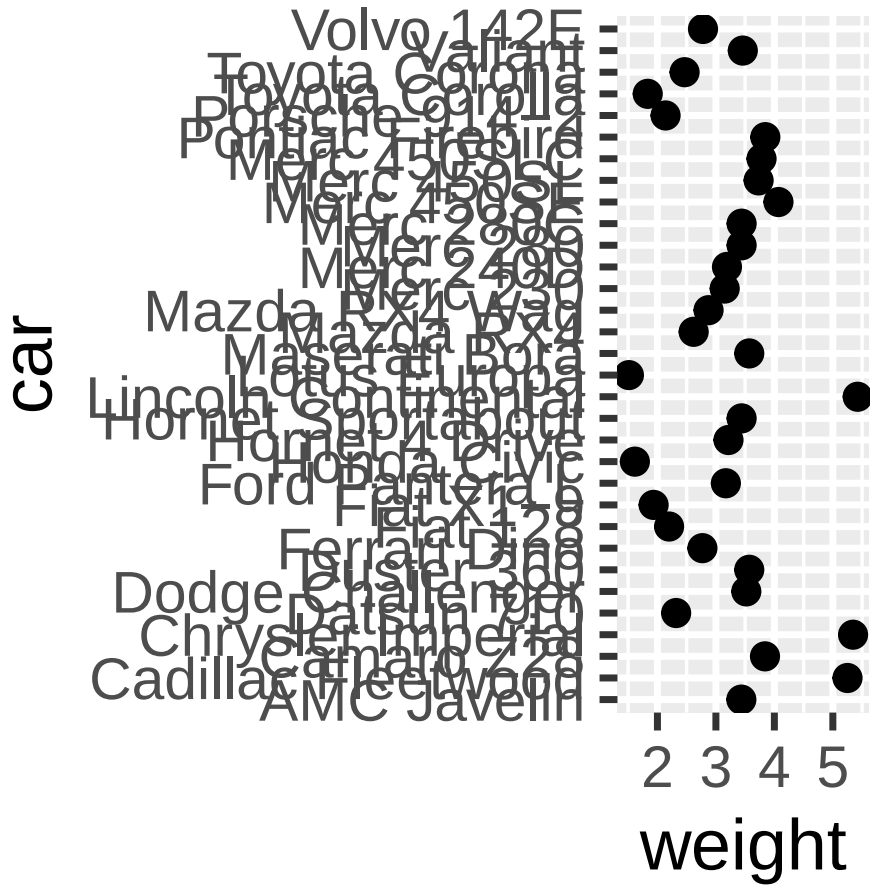
We'll flip the axes in the next step.

It would be easier to read if car was mapped to the y axis.

Flipping axes II

Flip the coordinates. Notice that the labels also get flipped!

```
# Flip the axes to set car to the y axis
ggplot(mtcars, aes(car, wt)) + geom_point() + labels(x = "car",
    y = "weight") + coord_flip()
```



Pie charts

The *coord_polar*() function converts a planar x-y Cartesian plot to polar coordinates.

This can be useful if you are producing pie charts.

Polar coordinates

We can imagine two forms for pie charts - the typical filled circle, or a colored ring.

Polar coordinates

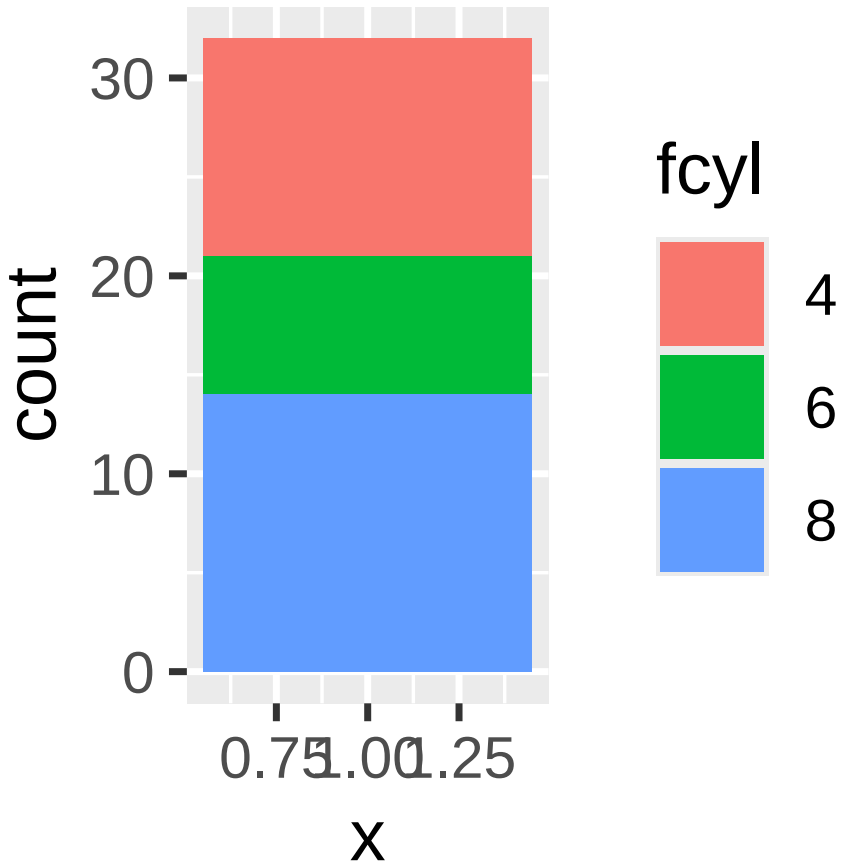
Typical pie charts omit all of the non-data ink, which we saw in the themes previously.

Pie charts are not really better than stacked bar charts, but we'll come back to this point in the next chapter.

Polar coordinates

A bar plot using mtcars of the number of cylinders (as a factor), fcyl, is shown below.

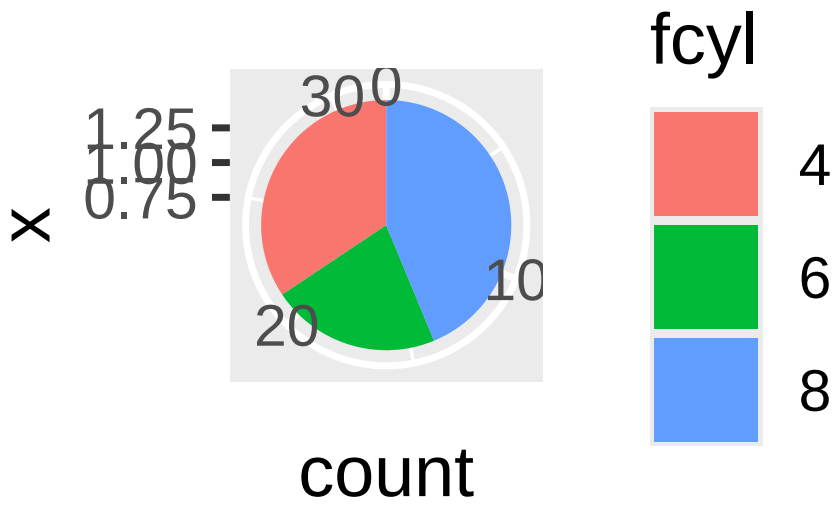
```
# Run the code, view the plot, then update it
ggplot(mtcars, aes(x = 1, fill = fcyl)) + geom_bar()
```



Polar coordinates

Add a polar coordinate system, mapping the angle to the y variable by setting theta to “y”.

```
# Run the code, view the plot, then update it
ggplot(mtcars, aes(x = 1, fill = fcyl)) + geom_bar() + coord_polar(theta = "y")  # Add a polar coordinate syste
```

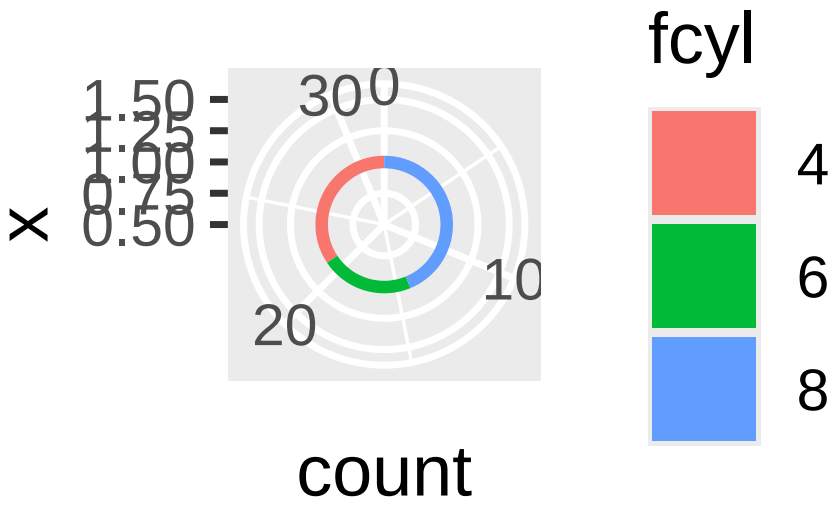


Polar coordinates

Reduce the width of the bars to 0.1.

Make it a ring plot by adding a continuous x scale with limits from 0.5 to 1.5.

```
ggplot(mtcars, aes(x = 1, fill = fcyl)) + geom_bar(width = 0.1) +
    coord_polar(theta = "y") + scale_x_continuous(limits = c(0.5,
    1.5))  # Add a continuous x scale from 0.5 to 1.5
```



Wind rose plots

- Polar coordinate plots are well-suited to scales like compass direction or time of day.
- A popular example is the “wind rose”.

Wind rose plots

The **mydata** dataset is taken from the openair package and contains hourly measurements for windspeed (ws) and direction (wd) from London in 2003.

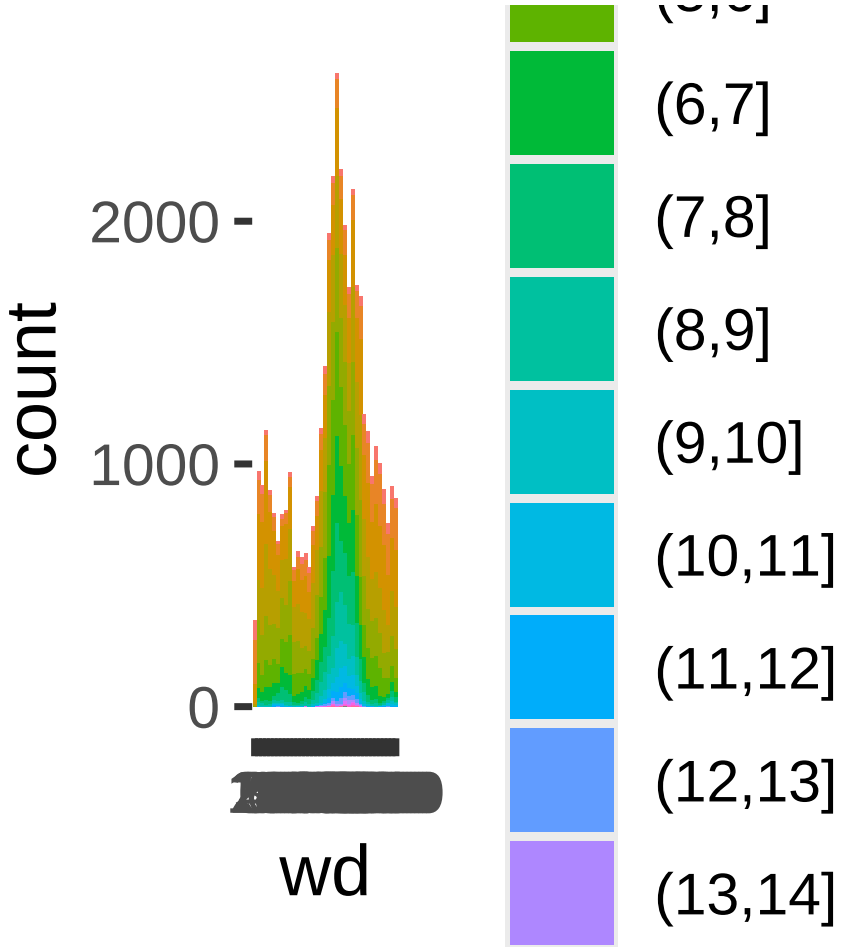
```
library(openair)
# Load wind data
data(mydata)

# Remove NA values
mydata <- na.omit(mydata)

# Bin wind speed into categories for better visualization
mydata <- mydata %>%
    mutate(ws_bin = cut(ws, breaks = seq(0, max(ws, na.rm = TRUE),
        by = 1), include.lowest = TRUE))
# Ensure wind direction (wd) is categorical
mydata$wd <- factor(mydata$wd)
head(mydata)
```

```
# A tibble: 6 x 11
  date                  ws wd      nox   no2    o3  pm10   so
  <dttm>             <dbl> <fct> <int> <int> <int> <int> <dbl
1 1998-05-01 07:00:00   3.6 350      81    37    13    24   2.9
2 1998-05-01 08:00:00   3.6 350     107    43    12    23   3.1
```

Wind rose plots

Make a classic bar plot mapping **wd** onto the **x** aesthetic and **ws** onto fill.

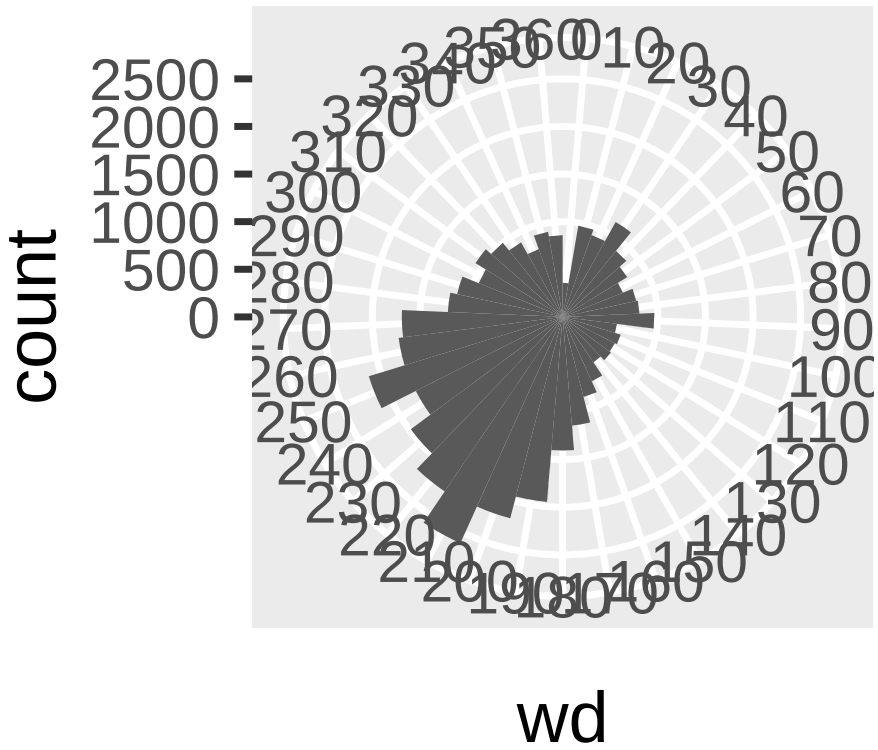
```
# Create a polar bar plot
ggplot(mydata, aes(x = wd, fill = ws_bin)) + geom_bar(width = 1)
```



Wind rose plots

Convert the Cartesian coordinate space into a polar coordinate space with *coord_polar()*.

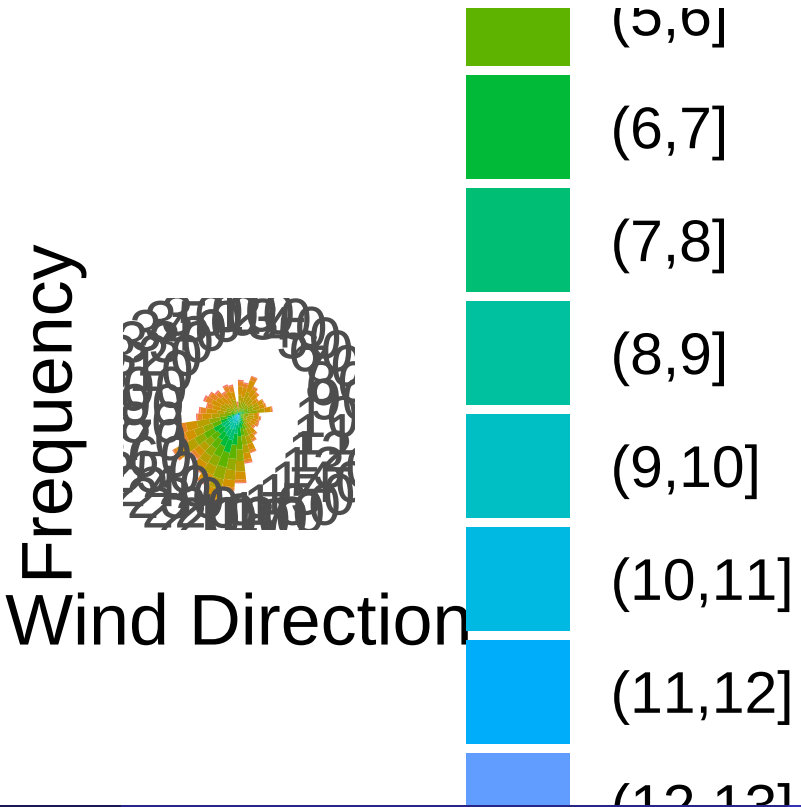
```
# Convert to polar coordinates:
ggplot(mydata, aes(x = wd, fill = ws)) +
  geom_bar(width = 1) +  # Use bars with no spacing
  coord_polar()
```



Wind rose plots

Set the start argument to $-\pi/16$ to position North at the top of the plot.

```
# Create a polar bar plot
ggplot(mydata, aes(x = wd, fill = ws_bin)) +
  geom_bar(width = 1) +  # Use bars with no spacing
  coord_polar(start = -pi/16) +  # Convert to polar coordinates, with North at top
  labs(x = "Wind Direction", y = "Frequency", fill = "Wind Speed") +
  theme_minimal() +
  theme(axis.text.y = element_blank(),  # Remove y-axis text for cleaner look
        panel.grid = element_blank())   # Remove grid for minimal appearance
```



Section 3

Facets

Facets

Facets let you split plots into multiple panes, each displaying subsets of the dataset.

Here you'll learn how to wrap facets and arrange them in a grid, as well as providing custom labeling.

Facet layer basics

Faceting splits the data up into groups, according to a categorical variable, then plots each group in its own panel.

For splitting the data by one or two categorical variables, `facet_grid()` is best.

Facet layer basics

Given categorical variables **A** and **B**, the code pattern is:

```
plot + facet_grid(rows = vars(A), cols = vars(B))
```

```
NULL
```

This draws a panel for each pairwise combination of the values of A and B.

Facet layer basics

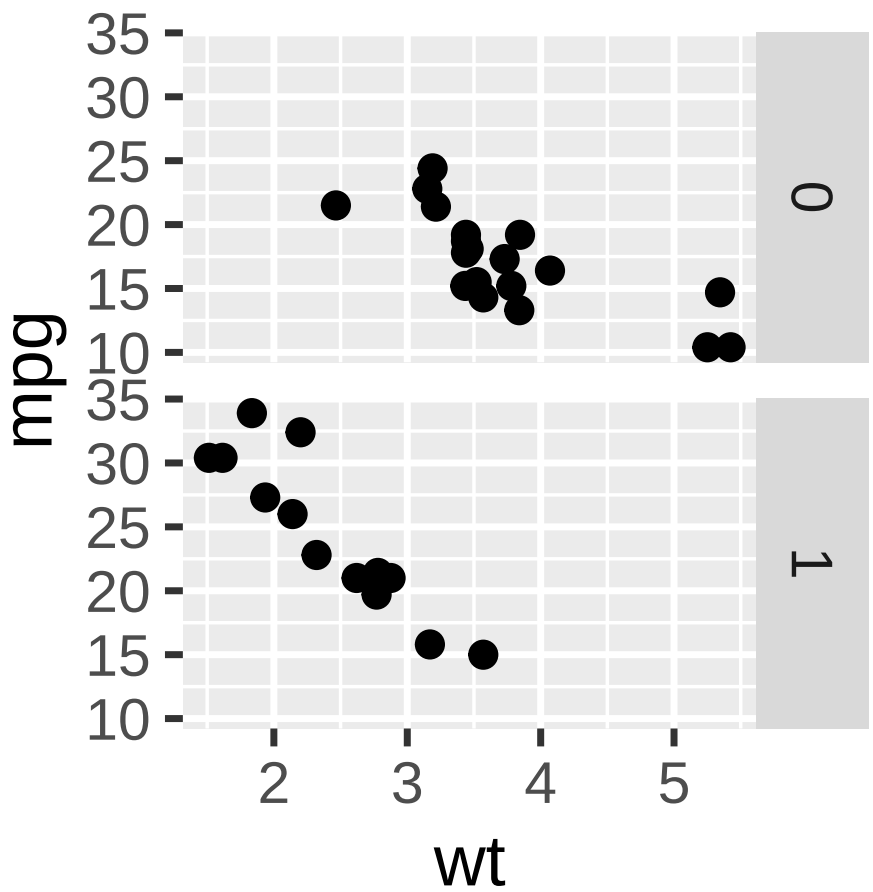
Here, we'll use the mtcars dataset to practice.

Although cyl and am are not encoded as factor variables in the dataset, ggplot2 will coerce variables to factors when used in facets.

Facet layer basics

Facet the plot in a grid, with each am value in its own row.

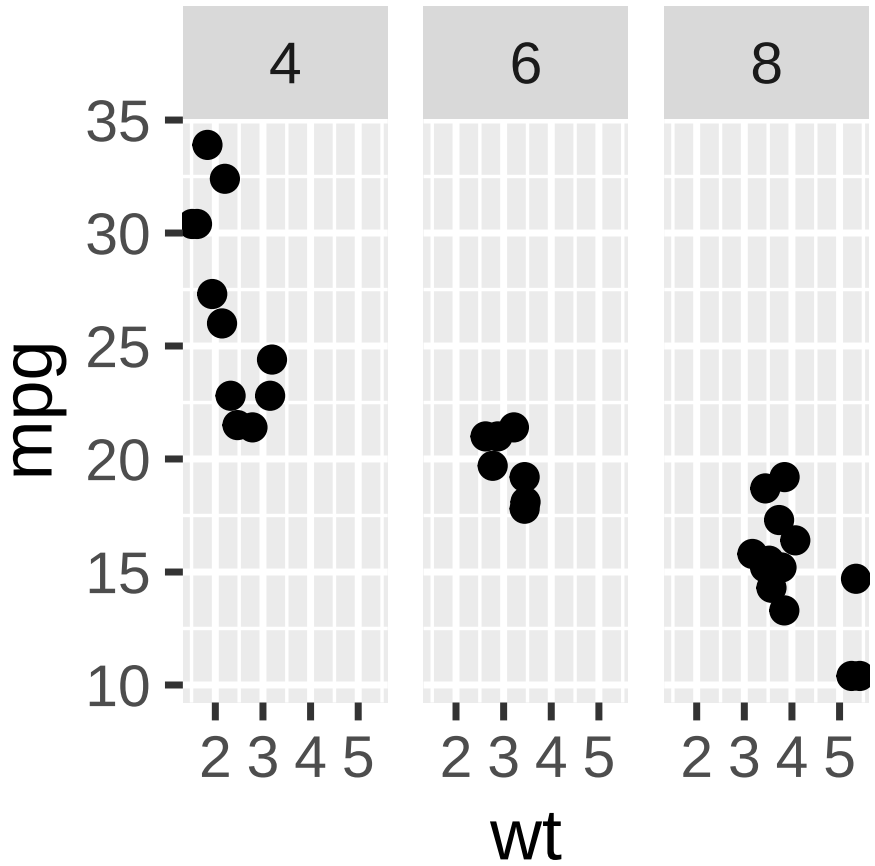
```
# Facet rows by am
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(rows = vars(am))
```



Facet layer basics

Facet the plot in a grid, with each cyl value in its own column.

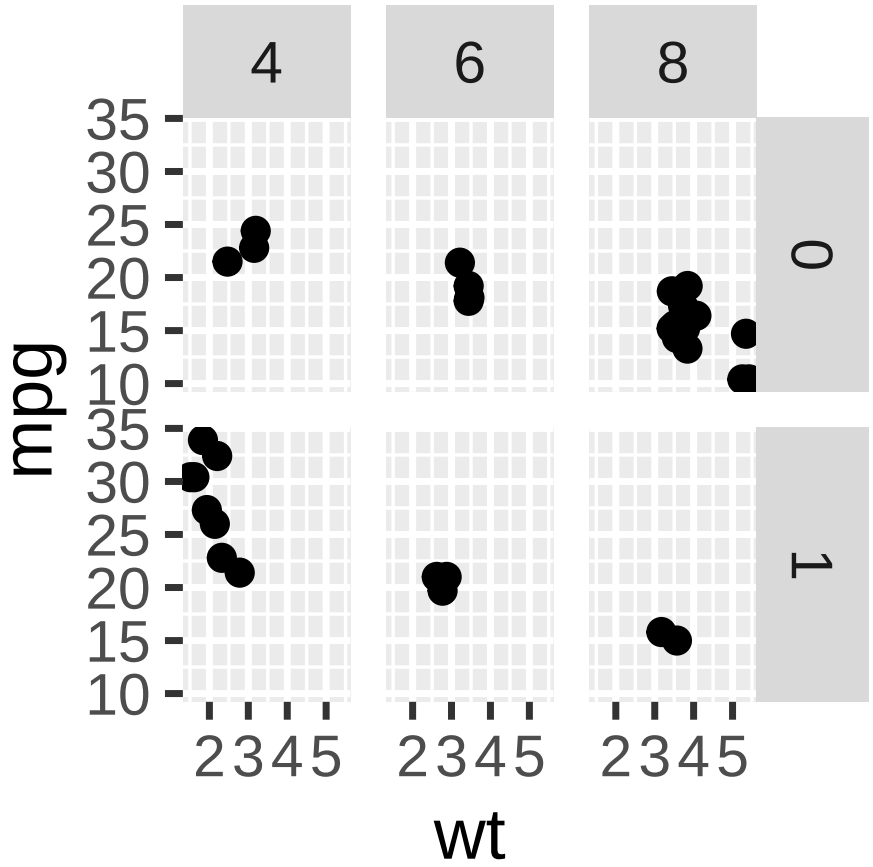
```
# Facet columns by cyl
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(cols = vars(cyl))
```



Facet layer basics

Facet the plot in a grid, with each am value in its own row and each cyl value in its own column.

```
# Facet rows by am and columns by cyl
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(rows = vars(am),
    cols = vars(cyl))
```



Many Variables

In addition to aesthetics, facets are another way of encoding factor (i.e., categorical) variables.

They can be used to reduce the complexity of plots with many variables.

Many Variables

Our goal is to create a plot containing 7 variables.

Many Variables

Two variables are mapped onto the color aesthetic, using hue and lightness.

Many Variables

To achieve this, we combined fcyl and fam into a single interaction variable, $fcyl\_fam$.

This allows us to take advantage of Color Brewer's Paired color palette.

Mapping Multiple Variables

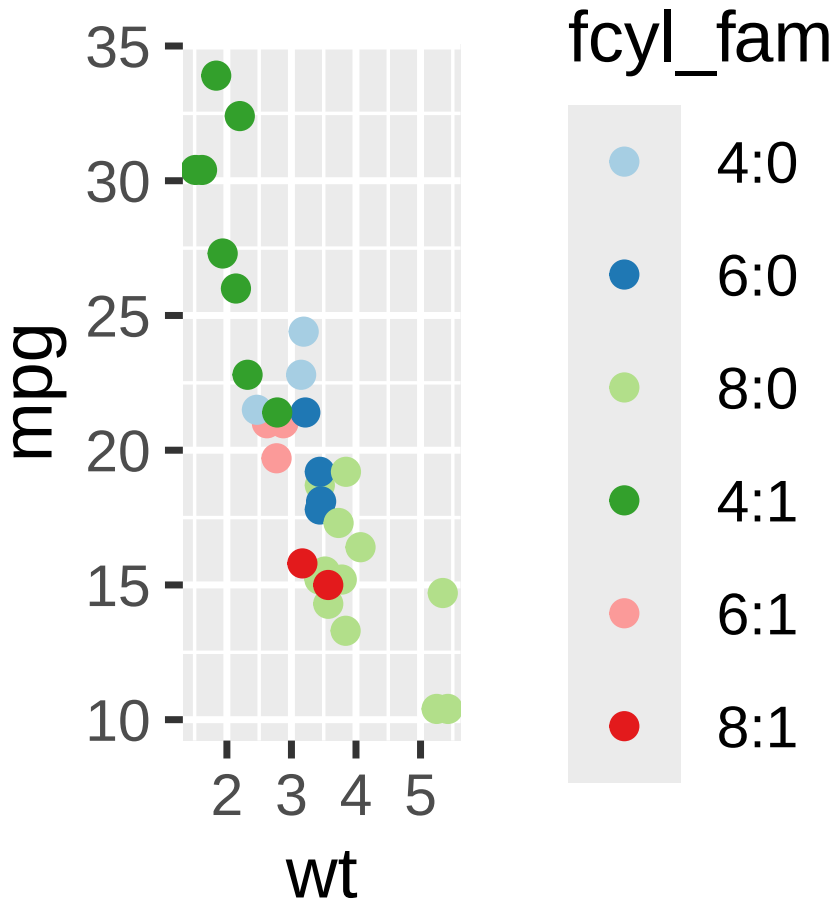
Map $fcyl\_fam$ onto the a color aesthetic.

```
library(dplyr)
# Create interaction variable
mtcars <- mtcars %>%
    mutate(fcyl_fam = interaction(cyl, am, sep = ":"))
```

Mapping Multiple Variables

Add a *scale_color_brewer()* layer and set "Paired" as the palette.

```
# Color the points by fcyl_fam
ggplot(mtcars, aes(x = wt, y = mpg, color = fcyl_fam)) + geom_point() +
    scale_color_brewer(palette = "Paired")
```

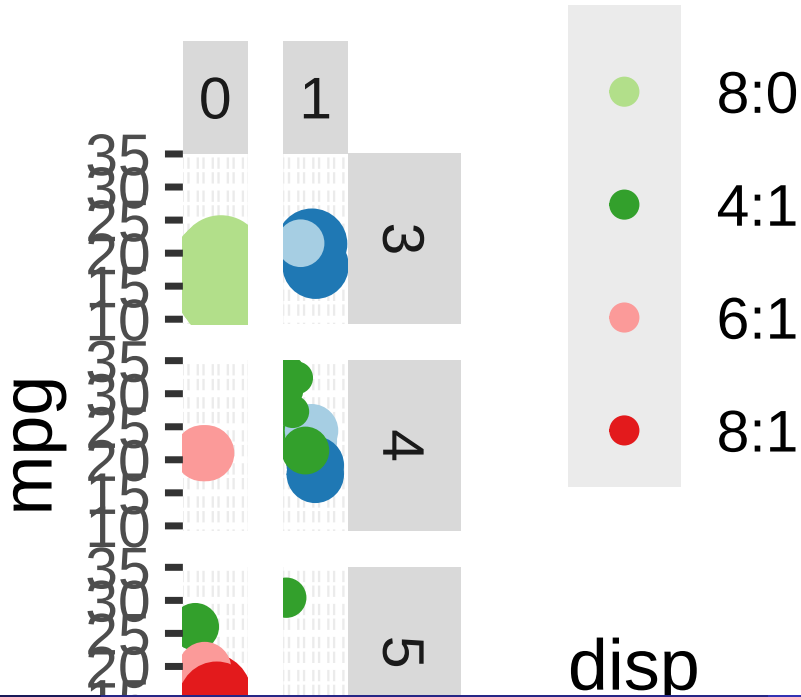


Mapping Multiple Variables

Map **disp**, the displacement volume from each cylinder, onto the **size** aesthetic.

Add a *facet_grid()* layer, faceting the plot according to gear on rows and vs on columns.

```
# Map disp (engine displacement) to size
ggplot(mtcars, aes(x = wt, y = mpg, color = fcyl_fam, size = disp)) +
    geom_point() + scale_color_brewer(palette = "Paired") + facet_grid(rows = vars(gear),
    cols = vars(vs))
```



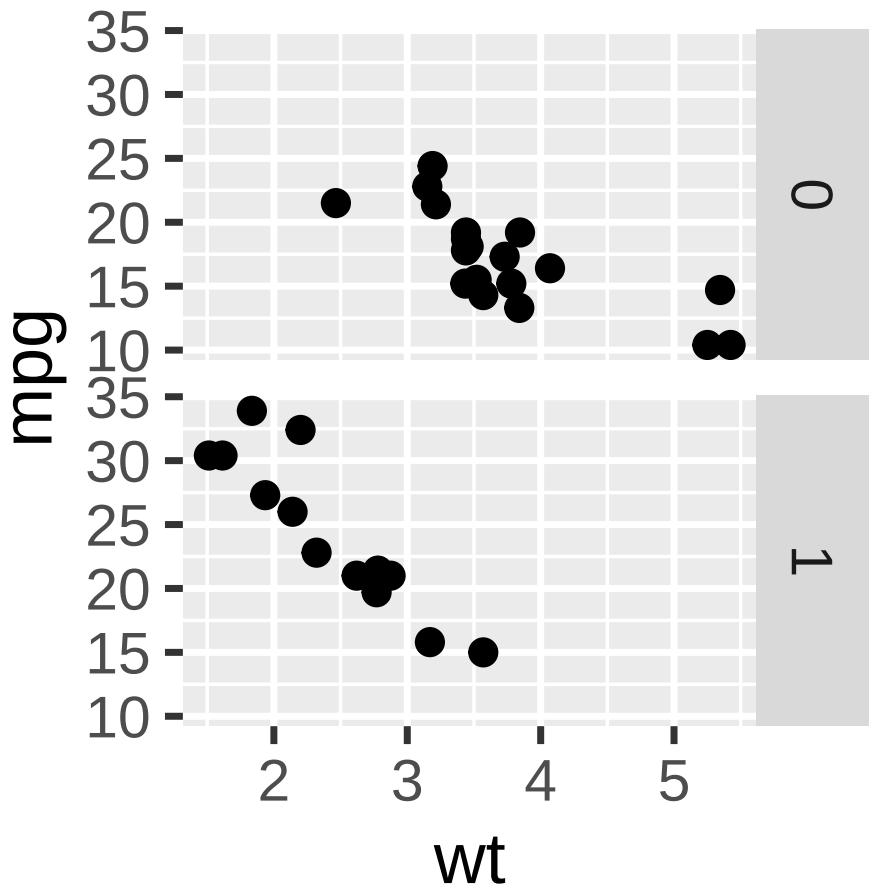
Formula Notation

Instead of *vars*(), we can use formula notation to specify facets.

Modern notation	Formula notation
`facet_grid(rows = vars(A))`	`facet_grid(A ~ .)`
`facet_grid(cols = vars(B))`	`facet_grid(. ~ B)`
`facet_grid(rows = vars(A), cols = vars(B))`	`facet_grid(A ~ B)`

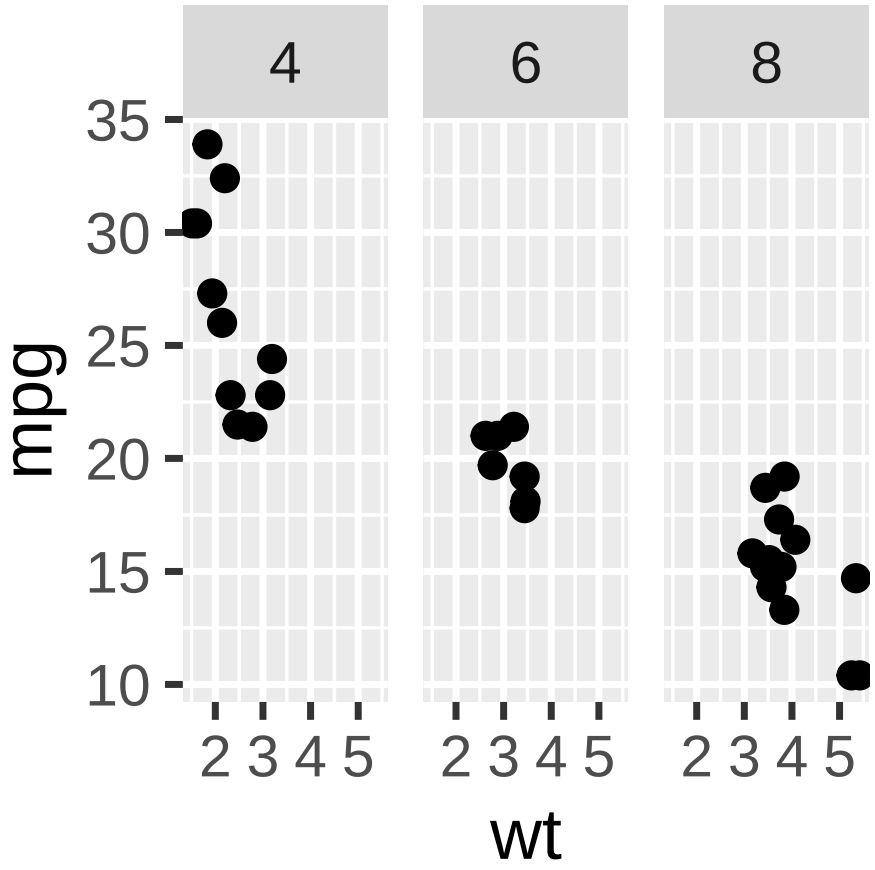
Using Formula Notation

```
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(am ~
    .)
```



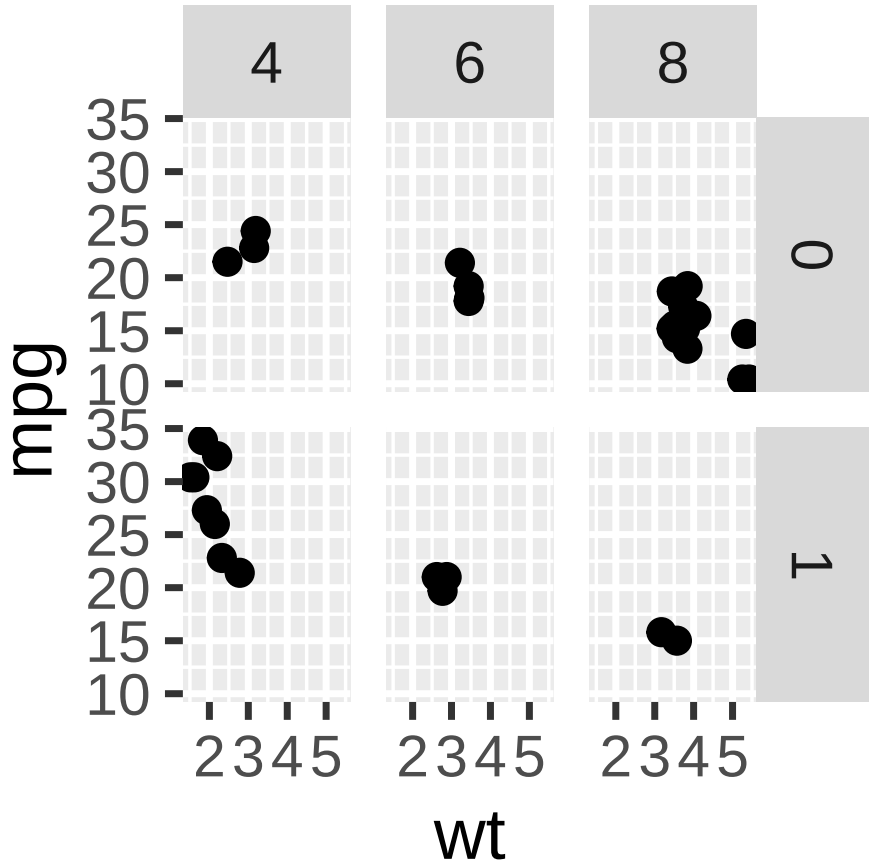
Using Formula Notation

```
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(. ~
    cyl)
```



Using Formula Notation

```
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(am ~
    cyl)
```



Facet labels and order

If your factor levels are not clear, your facet labels may be confusing.

You can assign proper labels in your original data before plotting (see next exercise), or you can use the labeller argument in the facet layer.

Facet labels and order

The default value is

label_value: Default, displays only the value

Facet labels and order

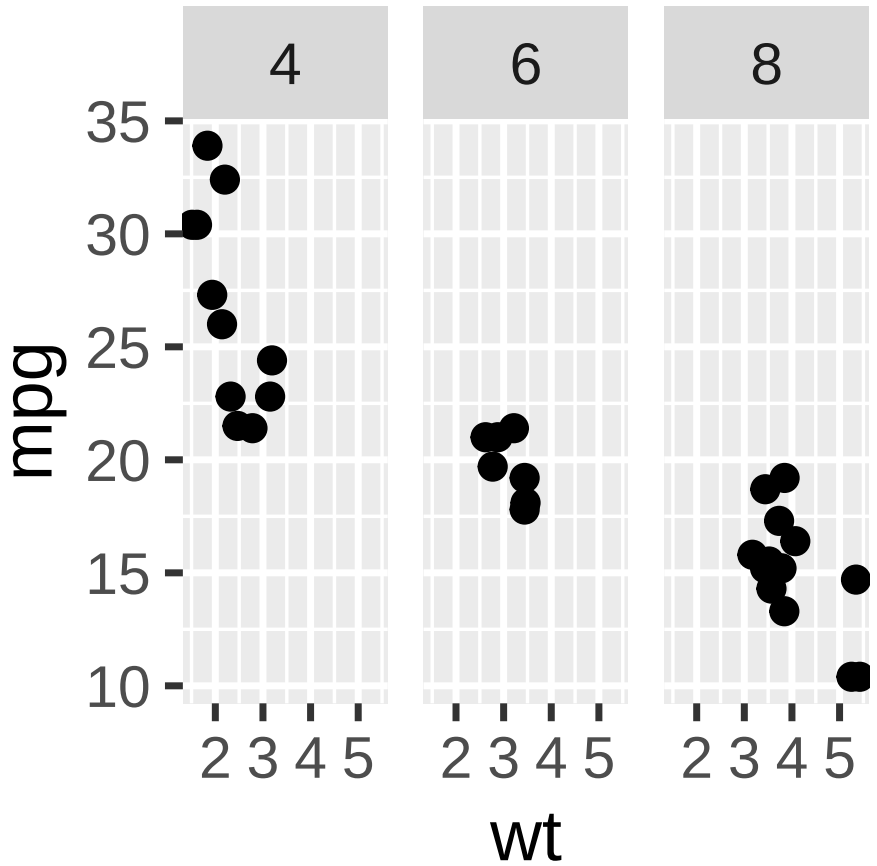
Common alternatives are:

- label_both: Displays both the value and the variable name
- label_context: Displays only the values or both the values and variables depending on whether multiple factors are faceted

Facet labels and order

Add a *facet_grid*() layer and facet cols according to the cyl using vars(). There is no labeling.

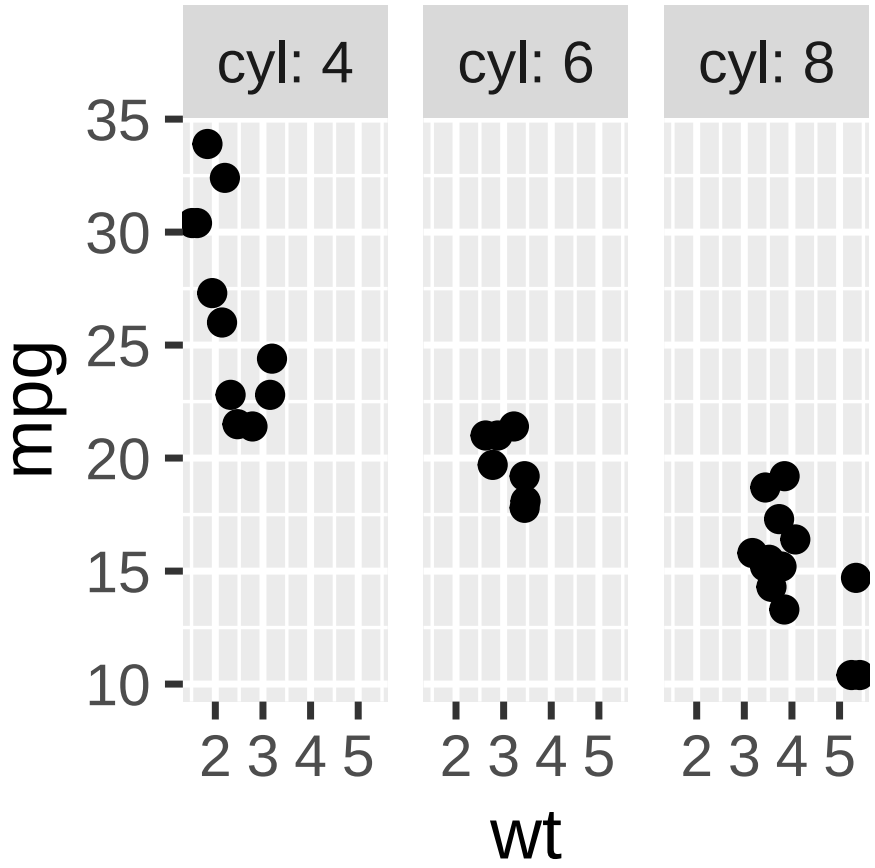
```
# Plot wt by mpg
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(cols = vars(cyl))  # The default is label_value
```



Facet labels and order

Apply *label_both* to the labeller argument and check the output.

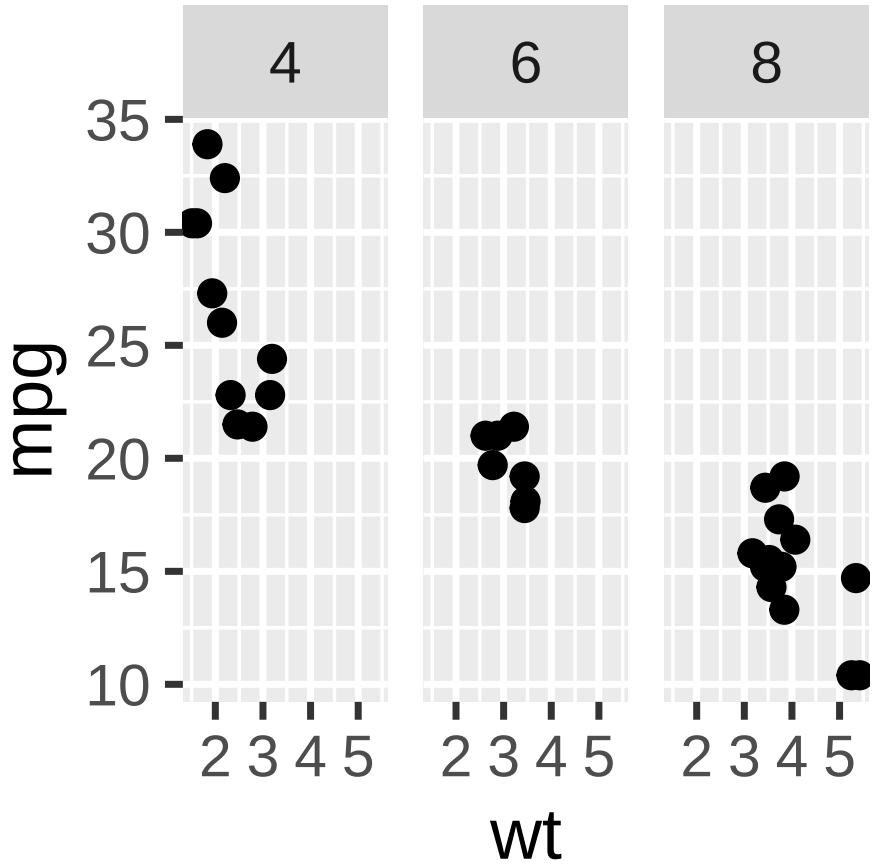
```
# Plot wt by mpg
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(cols = vars(cyl),
    labeller = label_both)  # Displaying both the values and the variables
```



Facet labels and order

Apply *label_context* to the labeller argument and check the output.

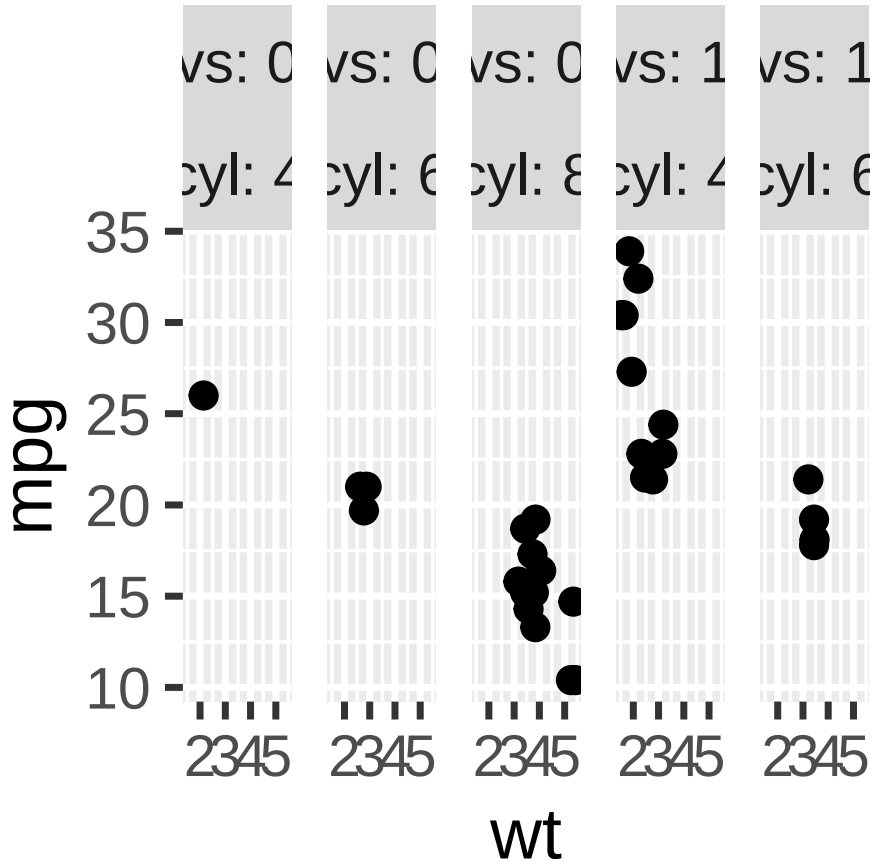
```
# Plot wt by mpg
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(cols = vars(cyl),
    labeller = label_context)  # Label context
```



Facet labels and order

In addition to *label_context*, let's facet by one more variable: vs.

```
# Plot wt by mpg
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(cols = vars(vs,
    cyl), labeller = label_context)  # Two variables
```



Setting order

If you want to change the order of your facets, it's best to properly define your factor variables before plotting.

Let's see this in action with the mtcars transmission variable am. In this case, $0 = \text{[}automatic\text{]}$ and $1 = \text{[}manual\text{]}$.

Setting order

Here, we'll make am a factor variable and relabel the numbers to proper names.

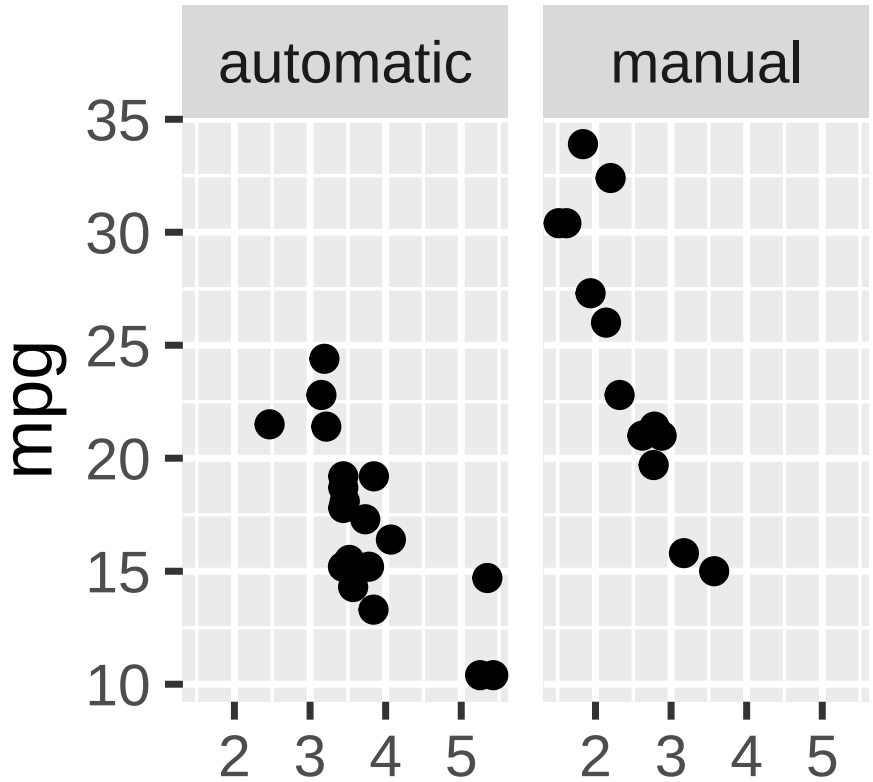
The default order is alphabetical.

To rearrange them we'll call $fct\_rev()$ from the forcats package to reverse the order.

Setting order

Explicitly label the 0 and 1 values of the am column as “automatic” and “manual”, respectively.

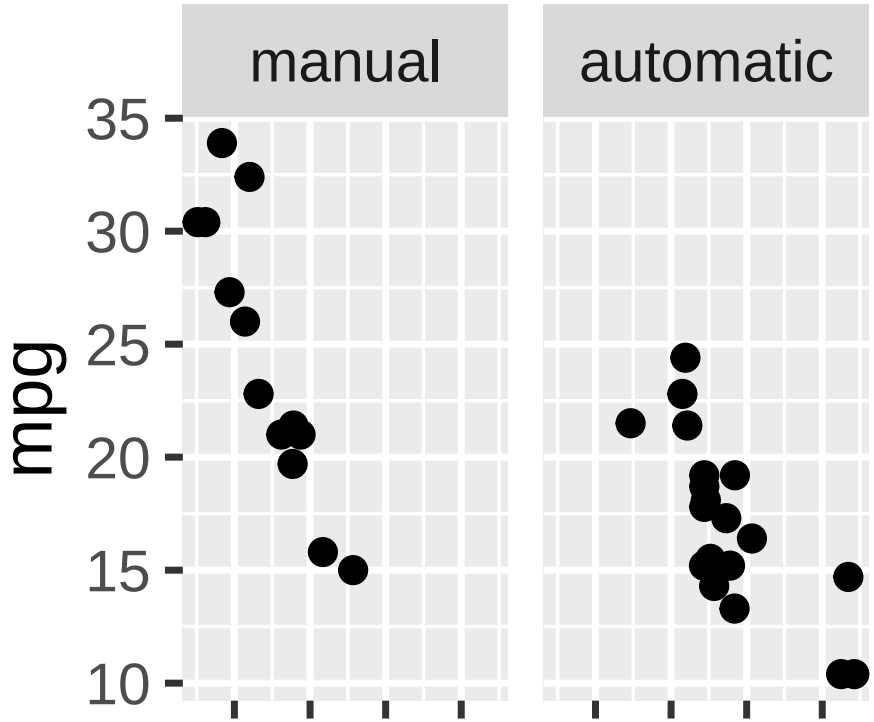
```
# Make factor, set proper labels explictly
mtcars$fam <- factor(mtcars$am, labels = c(`0` = "automatic",
    `1` = "manual"))
# Default order is alphabetical
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(cols = vars(fam))
```



Setting order

Define a specific order using separate levels and labels arguments. Recall that 1 is “manual” and 0 is “automatic”.

```
# Make factor, set proper labels explictly, and manually
# set the label order
mtcars$fam <- factor(mtcars$am, levels = c(1, 0), labels = c("manual",
    "automatic"))

# View again
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(cols = vars(fam))
```



Variable plotting spaces I: continuous variables

By default every facet of a plot has the same axes.

If the data ranges vary wildly between facets, it can be clearer if each facet has its own scale.

Variable plotting spaces I: continuous variables

This is achieved with the scales argument to facet_grid().

Variable plotting spaces I: continuous variables

- "fixed" (default): axes are shared between facets.
- free: each facet has its own axes.
- $free\_x$: each facet has its own x-axis, but the y-axis is shared.
- $free\_y$: each facet has its own y-axis, but the x-axis is shared.

Variable plotting spaces I: continuous variables

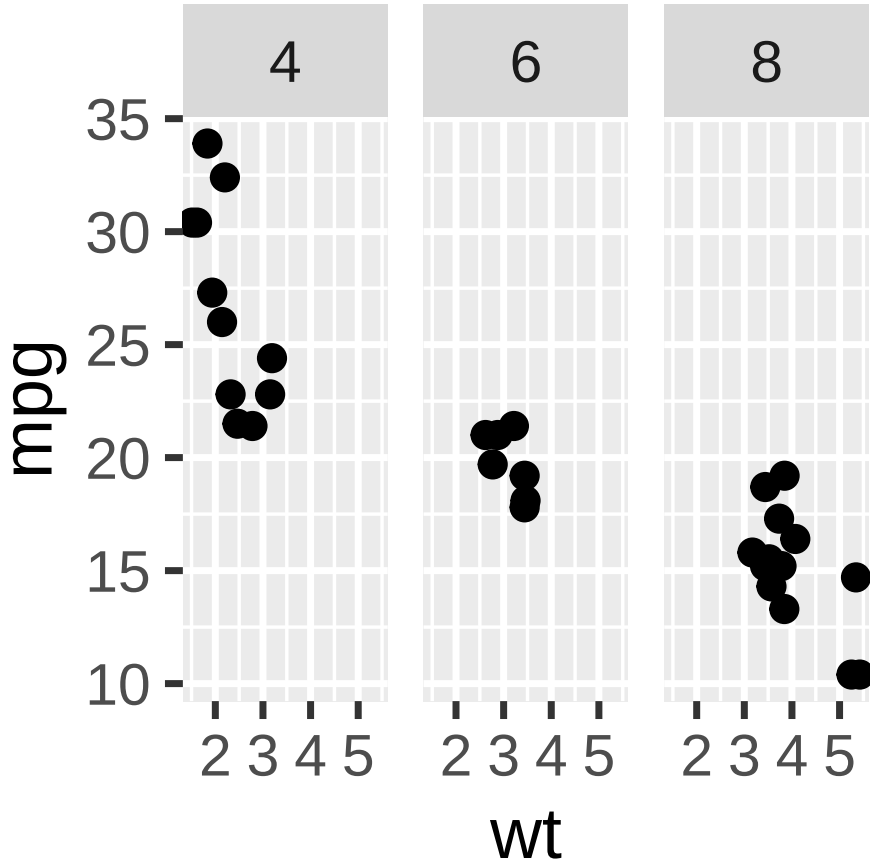
When faceting by columns, $free\_y$ has no effect, but we can adjust the x-axis.

In contrast, when faceting by rows, $free\_x$ has no effect, but we can adjust the y-axis.

Variable plotting spaces I: continuous variables

Update the plot to facet columns by cyl.

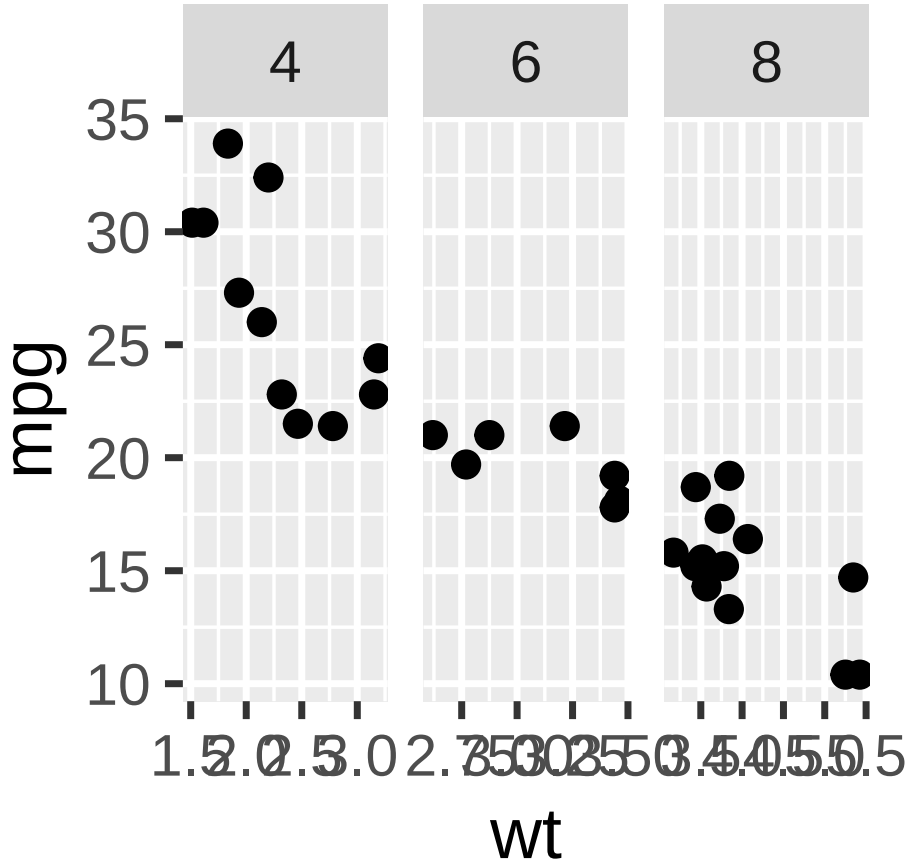
```
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(cols = vars(cyl))  # Facet columns by cyl
```



Variable plotting spaces I: continuous variables

Update the faceting to free the x-axis scales.

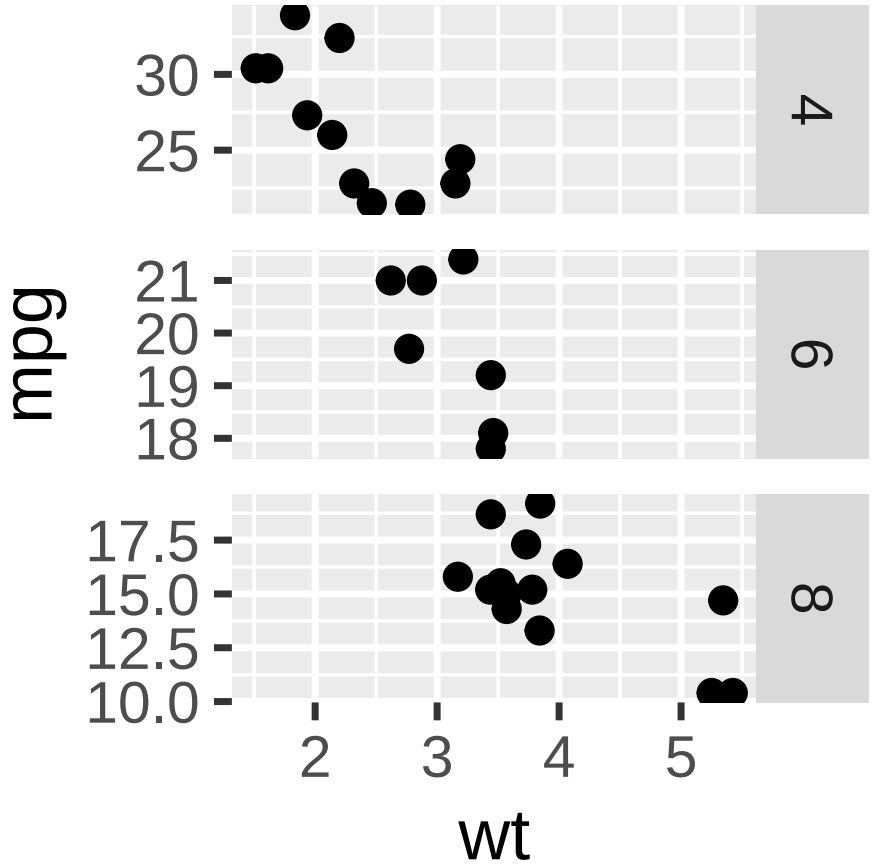
```
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(cols = vars(cyl),
    scales = "free_x")  # Update the faceting to free the x-axis scales
```



Variable plotting spaces I: continuous variables

Facet rows by cyl (rather than columns).

```
ggplot(mtcars, aes(wt, mpg)) + geom_point() + facet_grid(rows = vars(cyl),
    scales = "free_y")  # Update the faceting to free the y-axis scales
```



Variable plotting spaces II: categorical variables

When you have a categorical variable with many levels which are not all present in each sub-group of another variable, it's usually desirable to drop the unused levels.

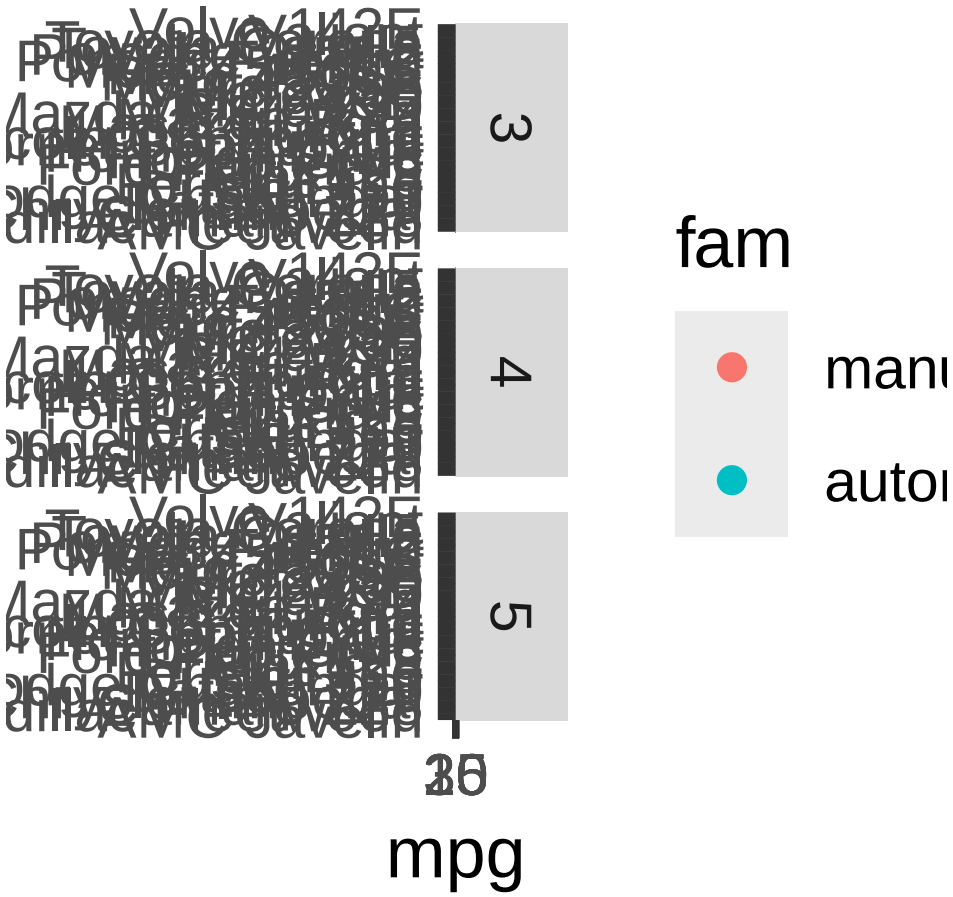
Variable plotting spaces II: categorical variables

- By default, each facet of a plot is the same size.
- This behavior can be changed with the spaces argument, which works in the same way as scales: $free\_x$ allows different sized facets on the x-axis, $free\_y$, allows different sized facets on the y-axis, "free" allows different sizes in both directions.

Variable plotting spaces II: categorical variables

- Facet the plot by rows according to gear using *vars*().

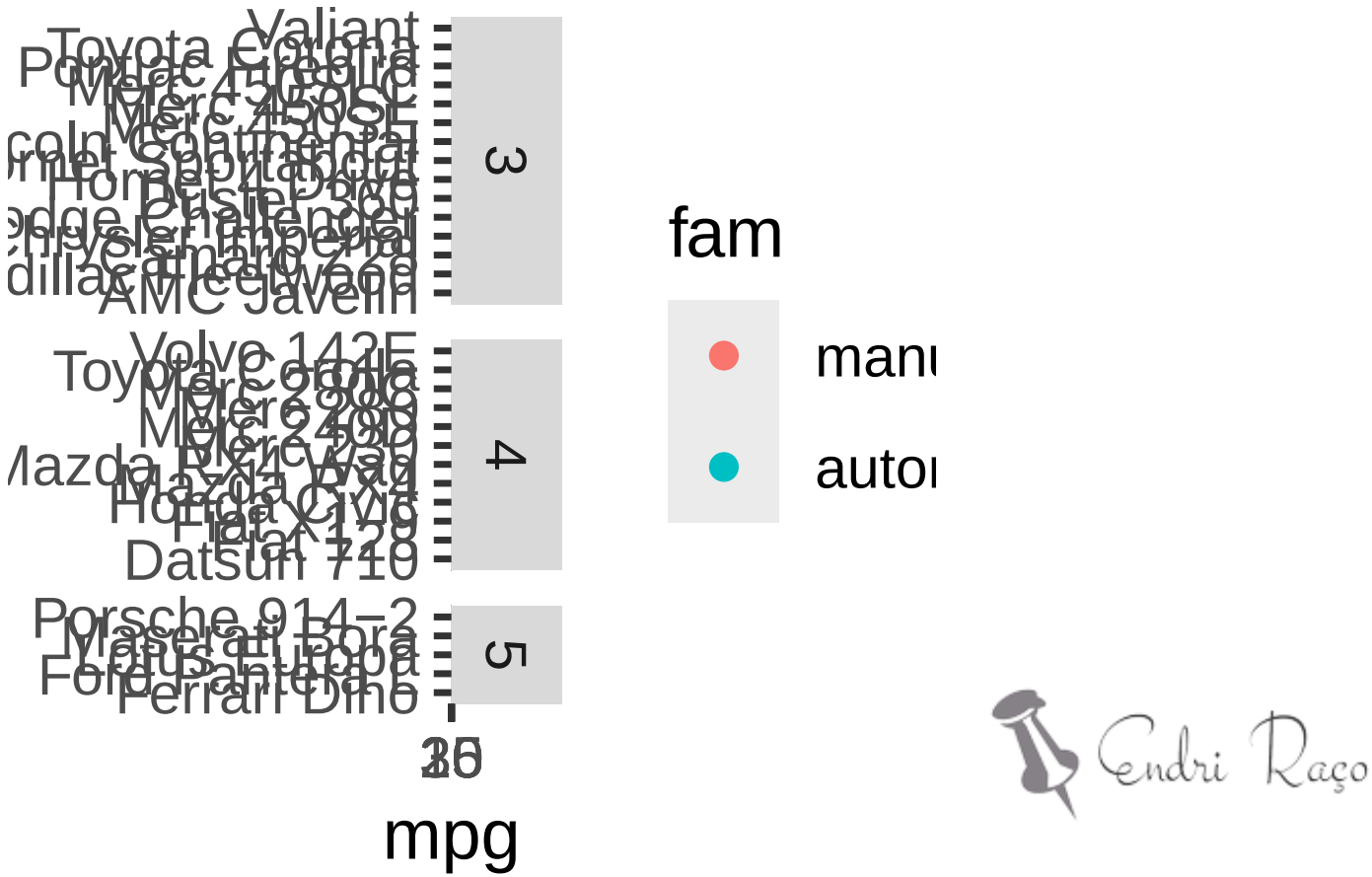
```
ggplot(mtcars, aes(x = mpg, y = car, color = fam)) + geom_point() +
    facet_grid(rows = vars(gear))  # Facet rows by gear
```



Variable plotting spaces II: categorical variables

To remove blank lines, set the scales and space arguments in *facet_grid()* to *free_y*.

```
ggplot(mtcars, aes(x = mpg, y = car, color = fam)) + geom_point() +
    # Free the y scales and space
facet_grid(rows = vars(gear), scales = "free_y", space = "free_y")
```



Wrapping for many levels

- $facet\_grid()$ is fantastic for categorical variables with a small number of levels.
- Although it is possible to facet variables with many levels, the resulting plot will be very wide or very tall, which can make it difficult to view.

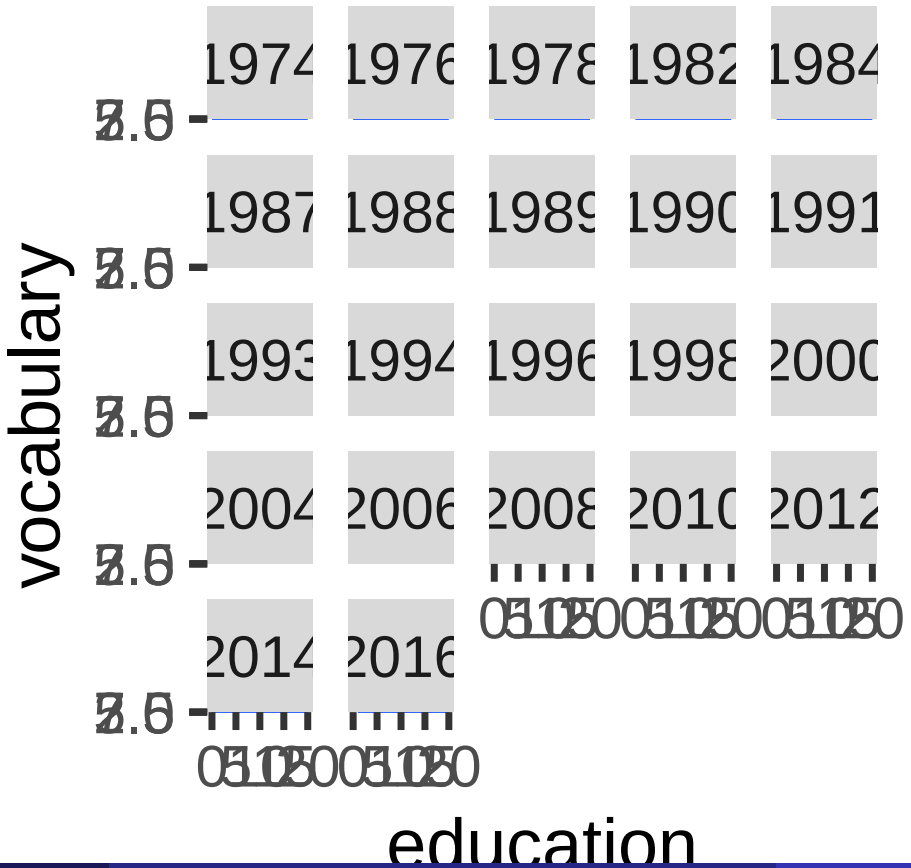
Wrapping for many levels

- The solution is to use facet_wrap() which separates levels along one axis but wraps all the subsets across a given number of rows or columns.
- For this plot, we'll use the Vocab dataset that we've already seen. The base layer is provided.

Wrapping for many levels

Since we have many years, it doesn't make sense to use *facet_grid()*, so let's try *facet_wrap()* instead.

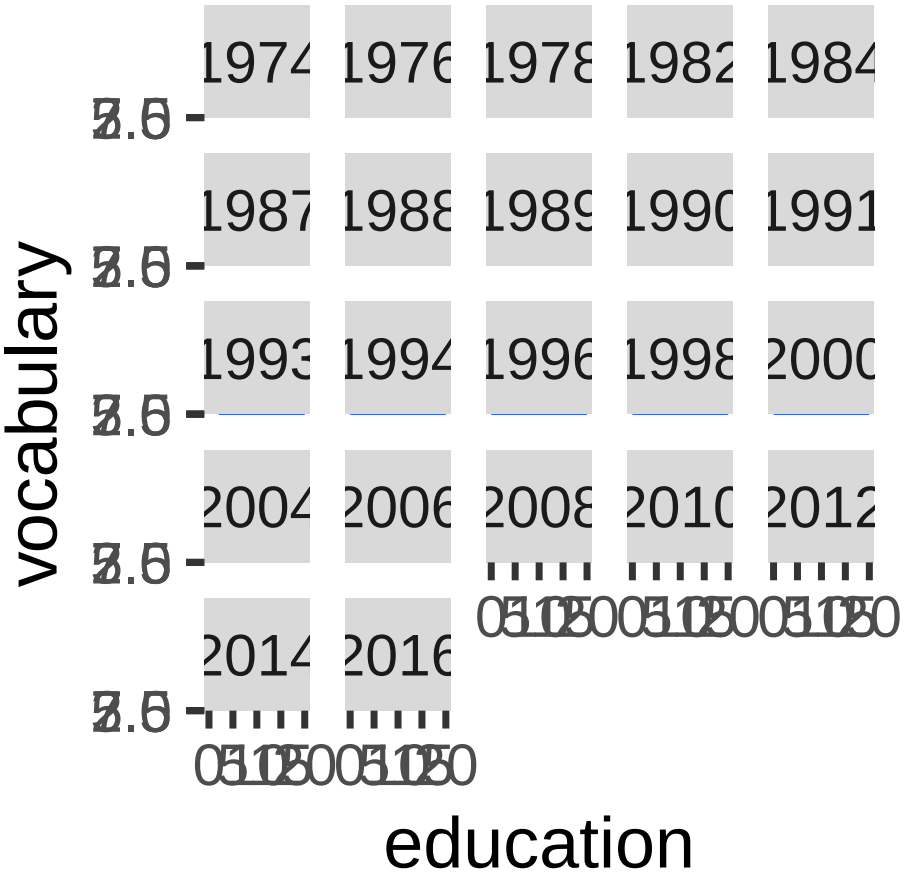
```
ggplot(Vocab, aes(x = education, y = vocabulary)) + stat_smoot
    se = FALSE) + facet_wrap(vars(year))  # Create facets, wr
```



Wrapping for many levels

Add a *facet_wrap()* layer and specify:

```
ggplot(Vocab, aes(x = education, y = vocabulary)) + stat_smooth(method = "lm",
    se = FALSE) + facet_wrap(~year)  # Create facets, wrapping by year, using a formula
```



Wrapping for many levels

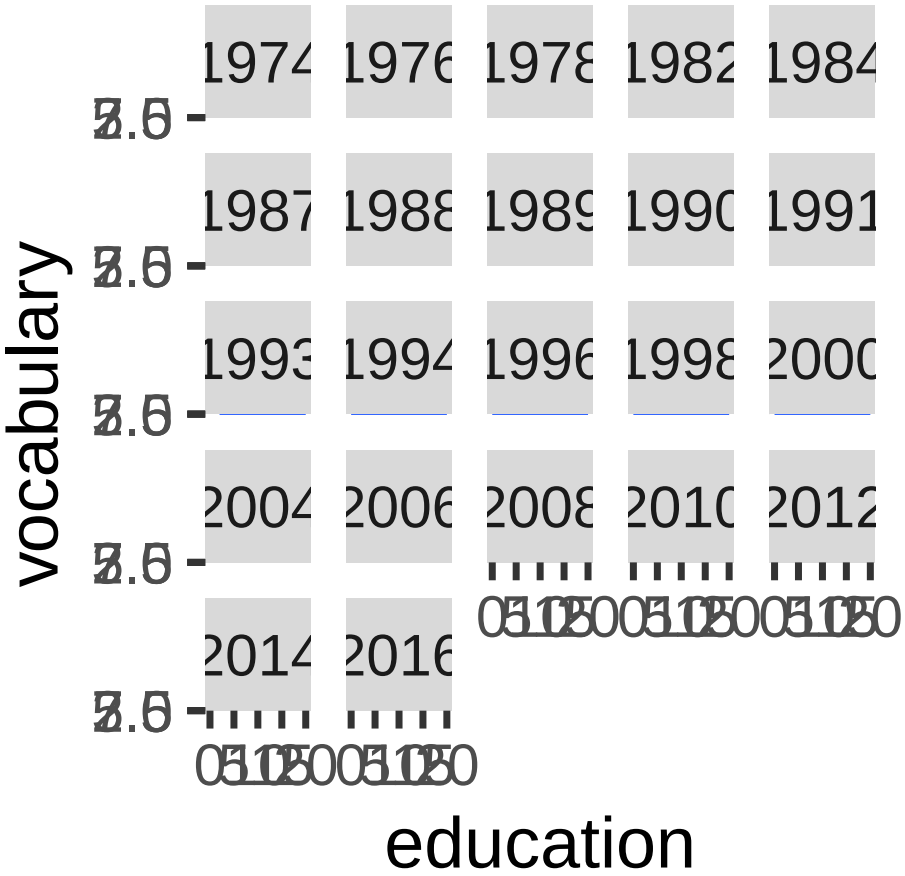
The year variable with an argument using the $vars()$ function,

Add a $facet\_wrap()$ layer and specify the year variable with a formula notation ($\sim$).

Wrapping for many levels

Add a $facet\_wrap()$ layer and specify:

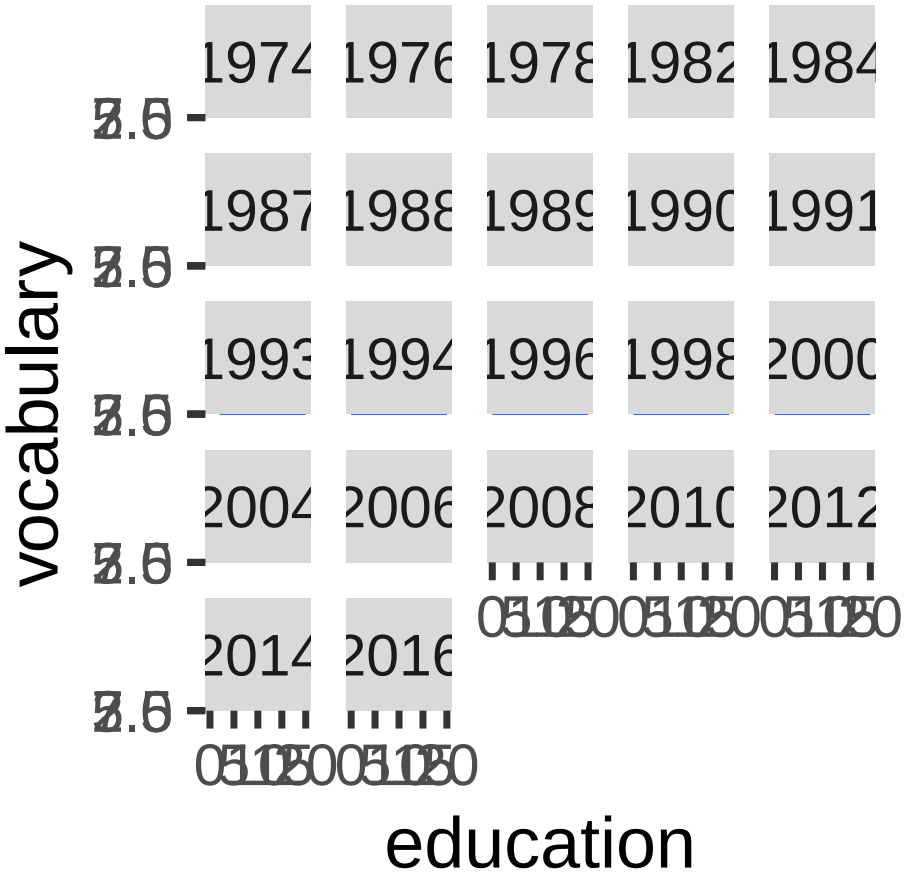
```
ggplot(Vocab, aes(x = education, y = vocabulary)) + stat_smooth(method = "lm",
    se = FALSE) + facet_wrap(vars(year))  # Create facets, wrapping by year, using vars()
```



Wrapping for many levels

Add a *facet_wrap()* layer and specify:

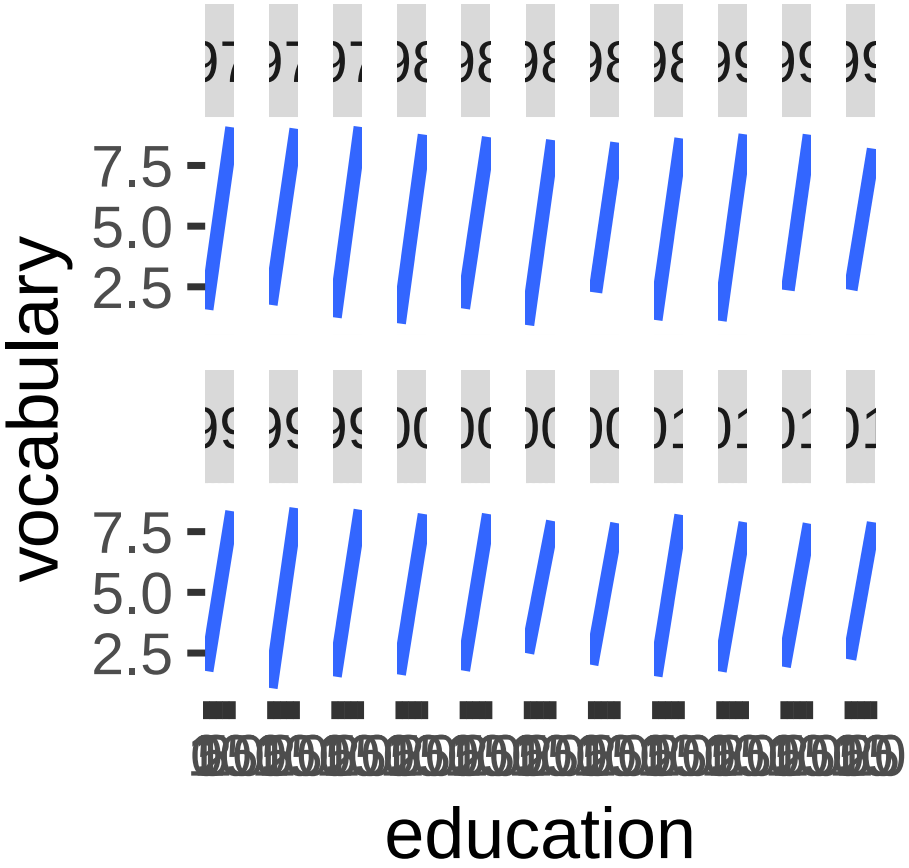
```
ggplot(Vocab, aes(x = education, y = vocabulary)) + stat_smooth(method = "lm",
    se = FALSE) + facet_wrap(~year)  # Create facets, wrapping by year, using a formula
```



Wrapping for many levels

Formula notation as before, and ncol set to 11.

```
ggplot(Vocab, aes(x = education, y = vocabulary)) + stat_smooth(method = "lm",
    se = FALSE) + facet_wrap(~year, ncol = 11)  # Update the facet layout, using 11 columns
```



Margin plots

Facets are great for seeing subsets in a variable, but sometimes you want to see both those subsets and all values in a variable.

Here, the margins argument to $facet\_grid()$ is your friend.

Margin plots

FALSE (default): no margins.

TRUE: add margins to every variable being faceted by.

Margin plots

c("variable1", "variable2"): only add margins to the variables listed.

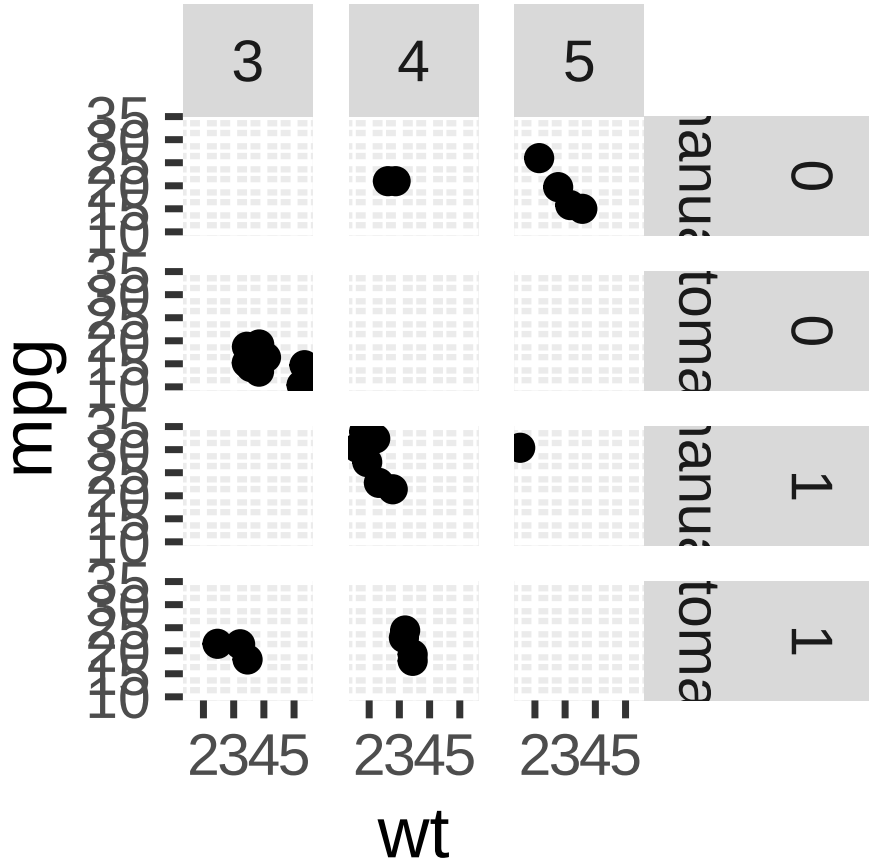
Margin plots

To make it easier to follow the facets, we've created two factor variables with proper labels — fam for the transmission type, and fvs for the engine type, respectively.

Margin plots

Zoom the graphics window to better view your plots.

```
ggplot(mtcars, aes(x = wt, y = mpg)) + geom_point() + facet_grid(rows = vars(fvs,
    fam), cols = vars(gear))  # Facet rows by fvs and fam, and cols by gear
```



Section 4

Best Practices

Best Practices

- Now that you have the technical skills to make great visualizations, it's important that you make them as meaningful as possible.
- In this part, you'll review three plot types that are commonly discouraged in the data viz community: heat maps, pie charts, and dynamite plots.
- You'll learn the pitfalls with these plots and how to avoid making these mistakes yourself.

Bar plots: dynamite plots

- We saw many reasons why "dynamite plots" (bar plots with error bars) are not well suited for their intended purpose of depicting distributions.
- If you really want error bars on bar plots, you can of course get them, but you'll need to set the positions manually.
- A point geom will typically serve you much better.

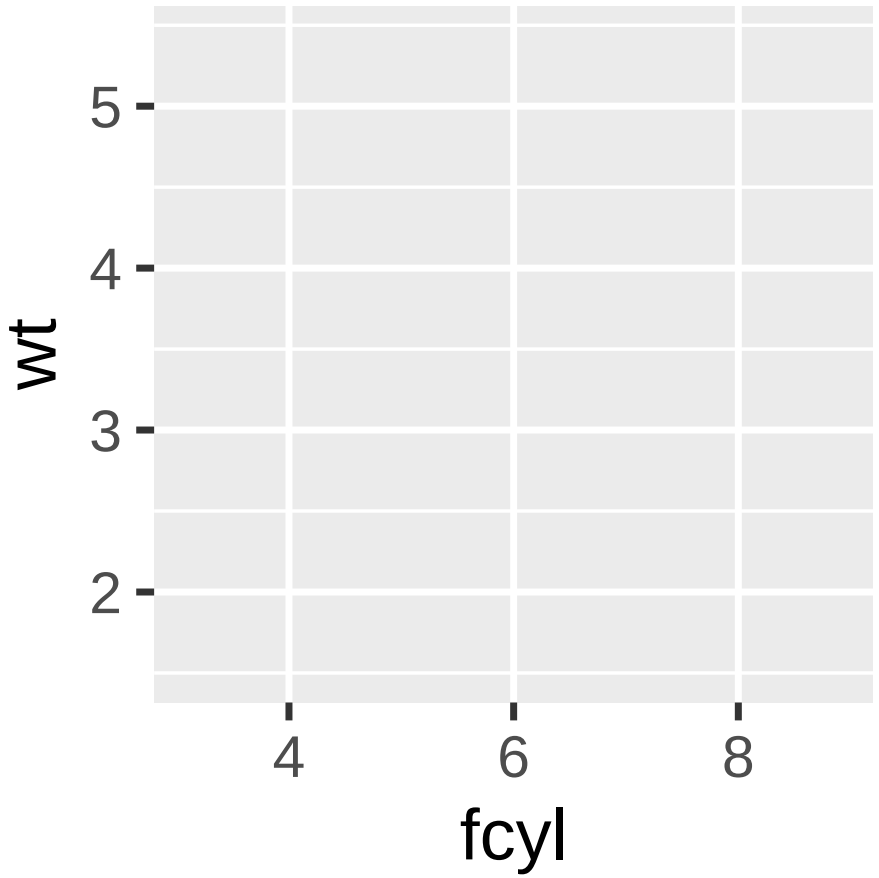
Bar plots: dynamite plots

Nonetheless, you should know how to handle these kinds of plots, so let's give it a try.

Bar plots: dynamite plots

Using mtcars,, plot wt versus fcyl.

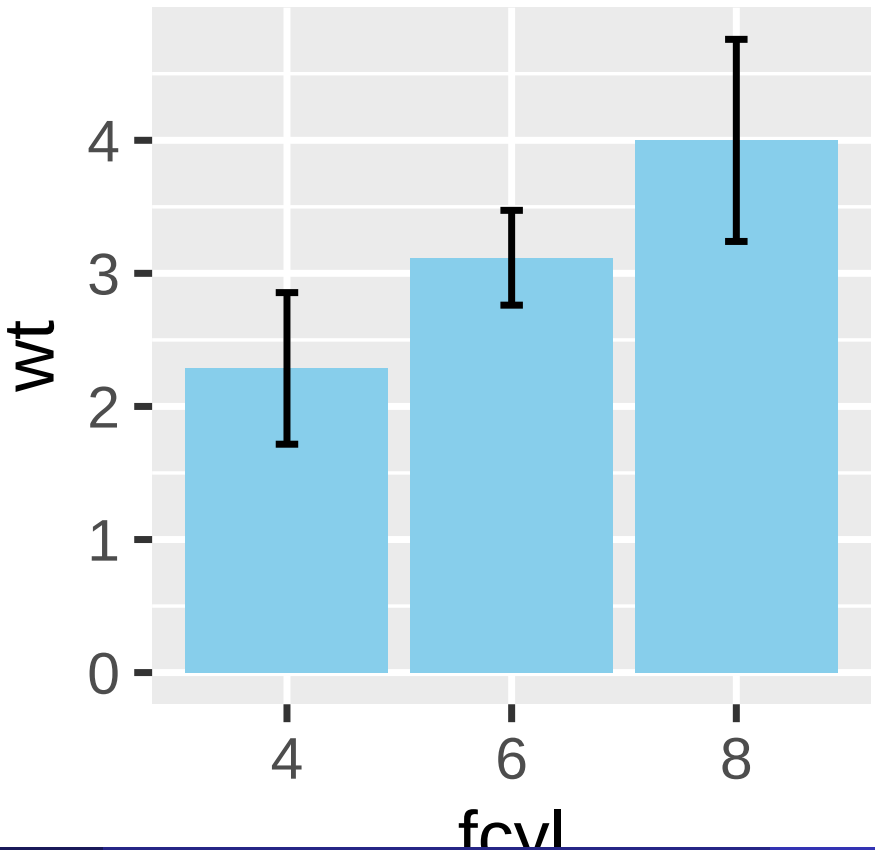
```
# Plot wt vs. fcyl
ggplot(mtcars, aes(x = fcyl, y = wt))
```



Bar plots: dynamite plots

Add a bar summary stat, aggregating the wts by their mean, filling the bars in a skyblue color.

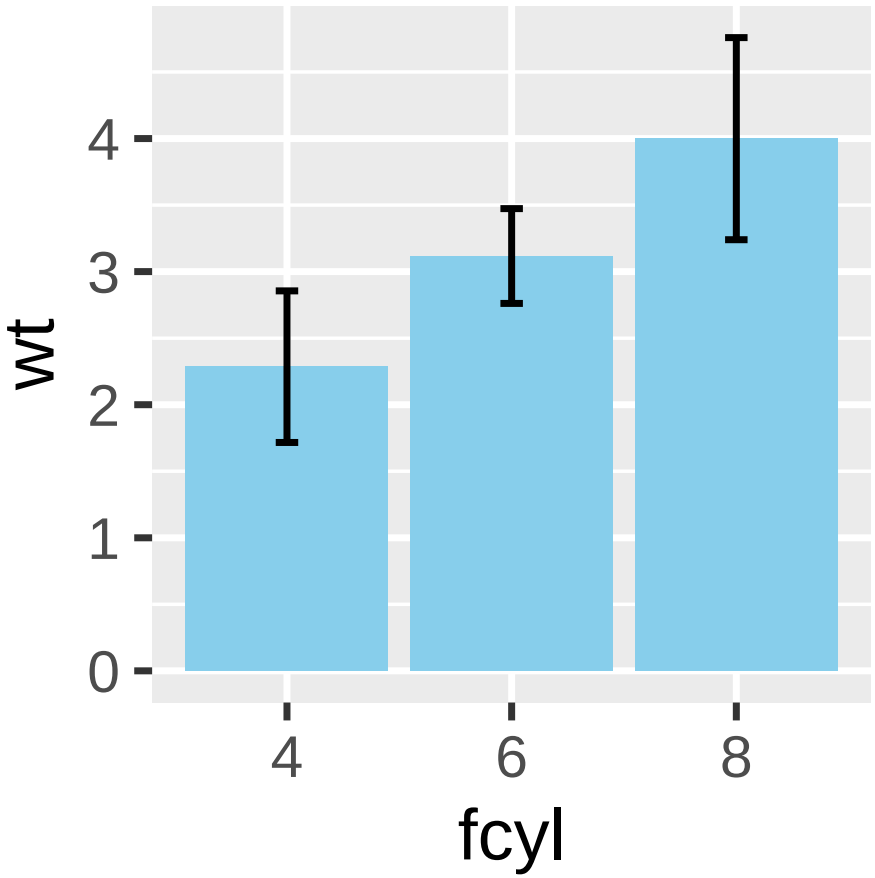
```
# Plot wt vs. fcyl
ggplot(mtcars, aes(x = fcyl, y = wt)) + stat_summary(fun = mean,
    geom = "bar", fill = "skyblue") + stat_summary(fun.data = mean_sdl,
    fun.args = list(mult = 1), geom = "errorbar", width = 0.1)
```



Bar plots: dynamite plots

Add an errorbar summary stat, aggregating the wts by mean_sdl.

```
# Plot wt vs. fcyl
ggplot(mtcars, aes(x = fcyl, y = wt)) + stat_summary(fun = mean,
    geom = "bar", fill = "skyblue") + stat_summary(fun.data = mean_sdl,
    fun.args = list(mult = 1), geom = "errorbar", width = 0.1)
```



Bar plots: position dodging

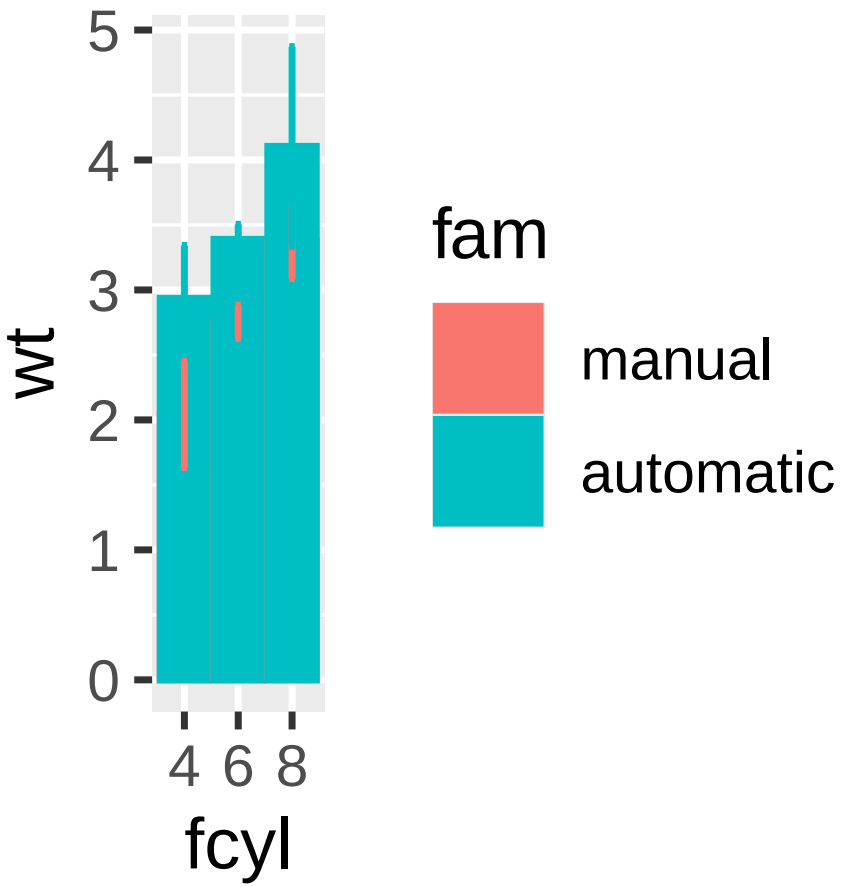
In the previous exercise we used the mtcars dataset to draw a dynamite plot about the weight of the cars per cylinder type.

In this exercise we will add a distinction between transmission type, fam, for the dynamite plots and explore position dodging (where bars are side-by-side).

Bar plots: position dodging

Add two more aesthetics so the bars are colored and filled by fam.

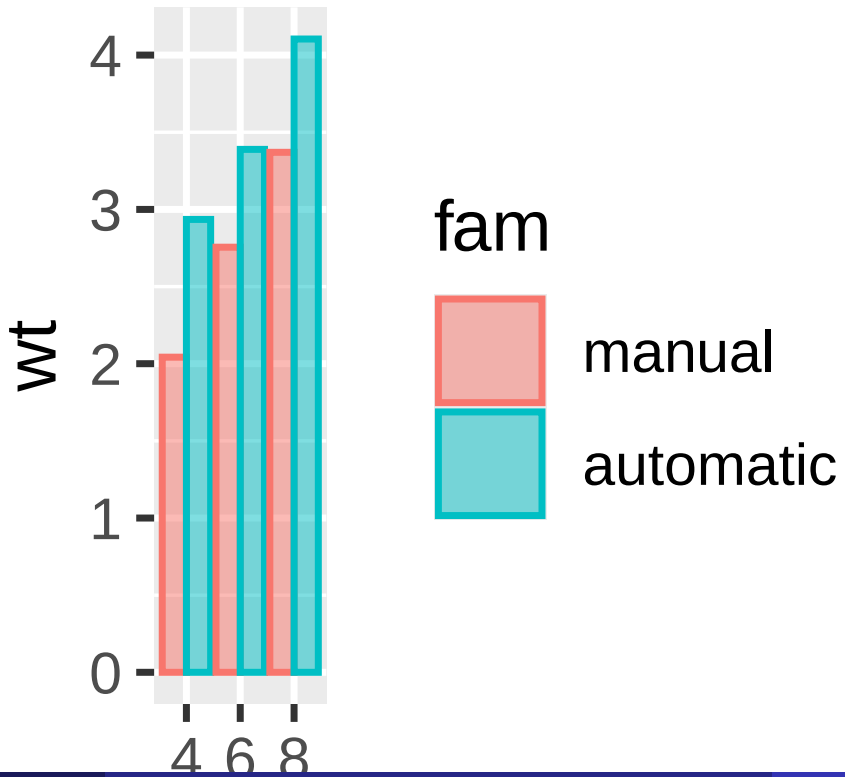
```
# Update the aesthetics to color and fill by fam
ggplot(mtcars, aes(x = fcyl, y = wt, color = fam, fill = fam)) +
    stat_summary(fun = mean, geom = "bar") + stat_summary(fun.data = mean_sdl,
    fun.args = list(mult = 1), geom = "errorbar", width = 0.1)
```



Bar plots: position dodging

The stacked bars are tricky to interpret. Make them transparent and side-by-side. Make the bar summary statistic transparent by setting alpha to 0.5.

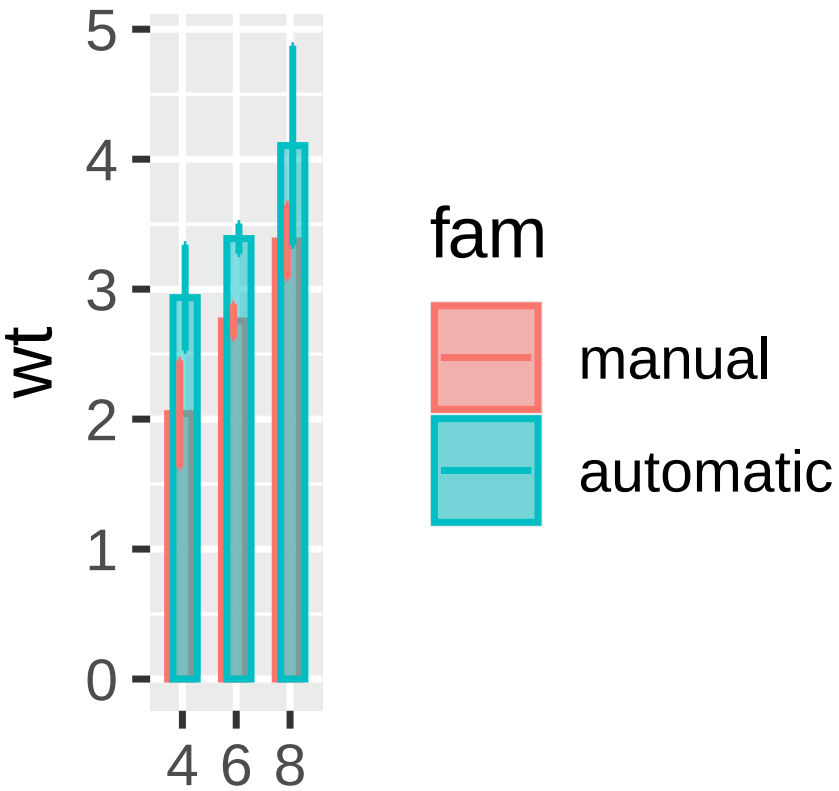
```
# For each summary stat, set the position to dodge
ggplot(mtcars, aes(x = fcyl, y = wt, color = fam, fill = fam)) +
    stat_summary(fun = mean, geom = "bar", position = "dodge",
        alpha = 0.5)
```



Bar plots: position dodging

For each of the summary statistics, set the bars' position to "dodge". The error bars are incorrectly positioned. Use a position object.

```
# For each summary stat, update the position to posn_d
ggplot(mtcars, aes(x = fcyl, y = wt, color = fam, fill = fam)) +
    stat_summary(fun = mean, geom = "bar", position = posn_d,
        alpha = 0.5) + stat_summary(fun.data = mean_sdl, fun.args = list(mult = 1),
    geom = "errorbar", position = posn_d, width = 0.1)
```



Bar plots: Using aggregated data

If it is appropriate to use bar plots, then it nice to give an impression of the number of values in each group.

Bar plots: Using aggregated data

- *stat_summary*() doesn't keep track of the count.
- *stat_sum*() does (that's the whole point), but it's difficult to access.
- It's more straightforward to calculate exactly what we want to plot ourselves.

Bar plots: Using aggregated data

Here, we've created a summary data frame called $mtcars\_by\_cyl$ which contains the average ($mean\_wt$), standard deviations (sd_wt) and count (n_wt) of car weights, for each cylinder group, cyl.

Bar plots: Using aggregated data

It also contains the proportion (prop) of each cylinder represented in the entire dataset.

Use the console to familiarize yourself with the *mtcars_by_cyl* data frame.

Bar plots: Using aggregated data

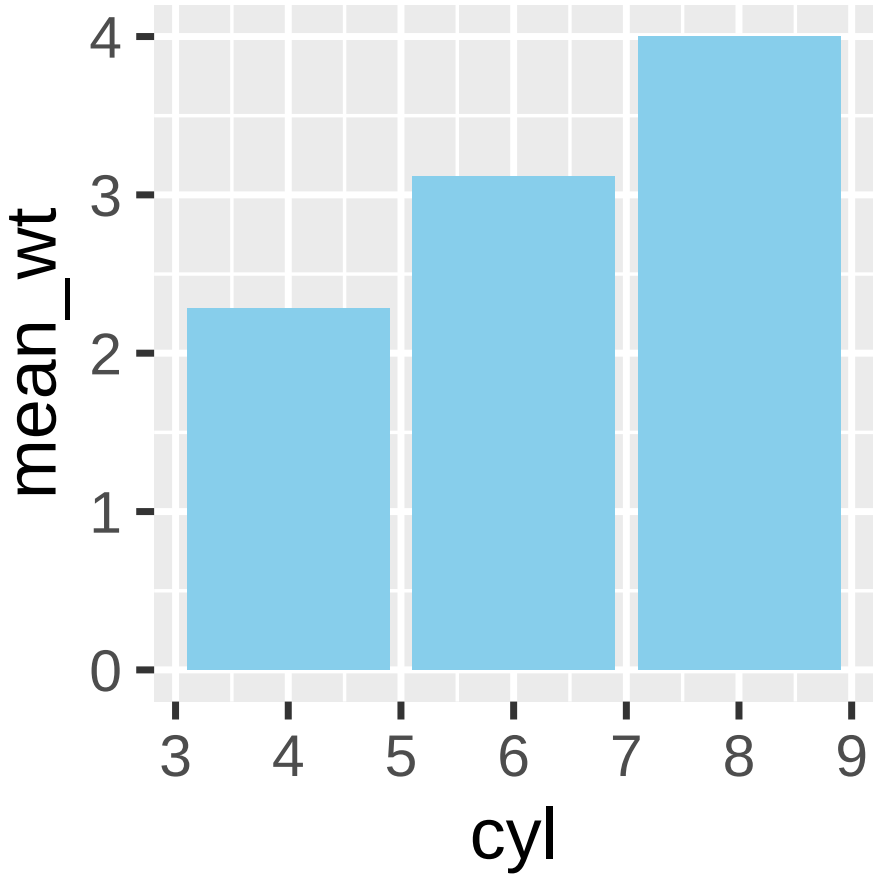
Draw a bar plot with *geom_bar()*.

```
mtcars_by_cyl <- mtcars %>%
    group_by(cyl) %>%
    summarize(mean_wt = mean(wt), sd_wt = sd(wt), n_wt = n()) %>%
    mutate(prop = n_wt/sum(n_wt))
```

Bar plots: Using aggregated data

Using *mtcars_by_cyl*, plot *mean_wt* versus cyl.

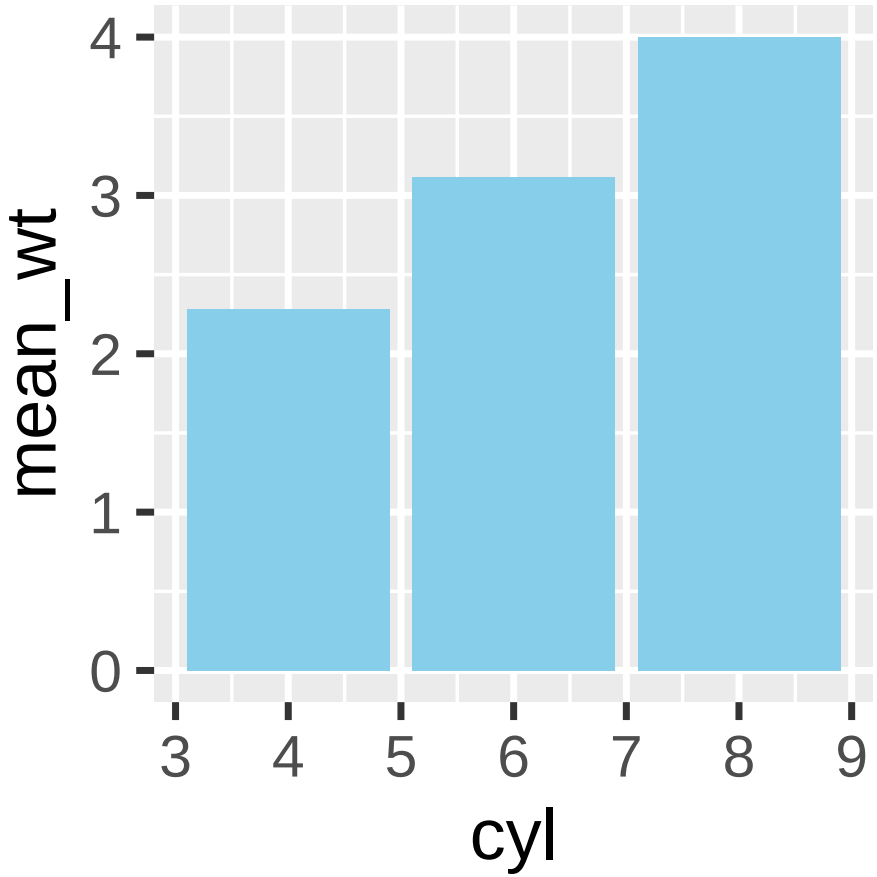
```
# Using mtcars_cyl, plot mean_wt vs. cyl
ggplot(mtcars_by_cyl, aes(x = cyl, y = mean_wt)) + geom_bar(stat = "identity",
    fill = "skyblue")  # Add a bar layer with identity stat, filled skyblue
```



Bar plots: Using aggregated data

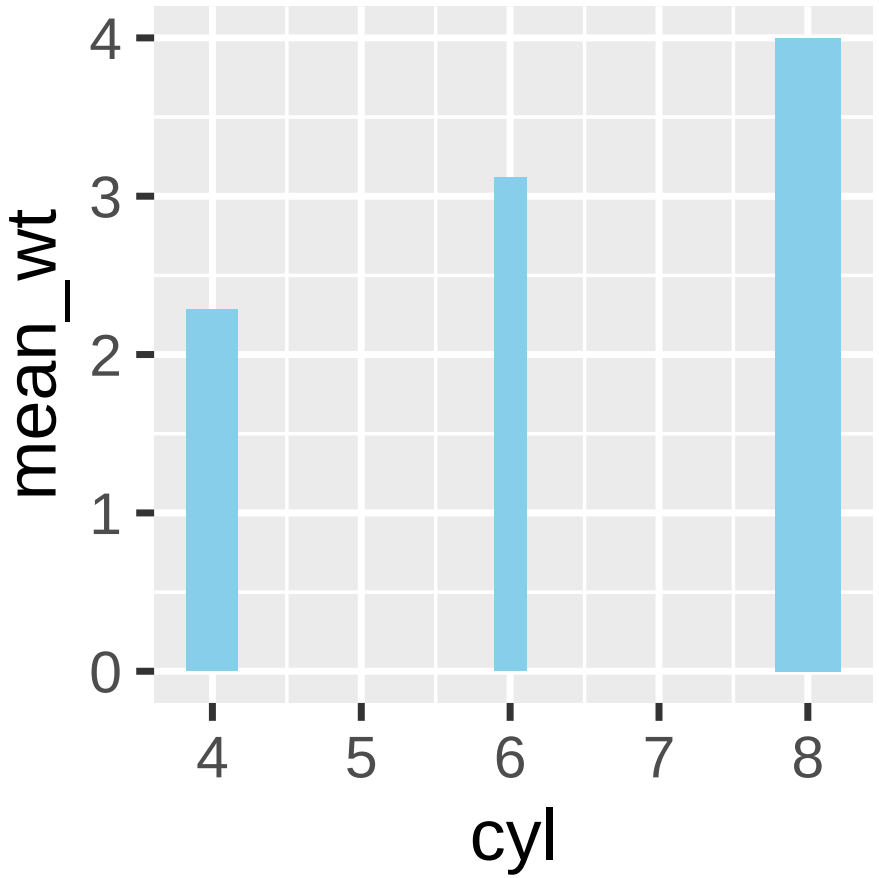
Add a bar layer, with stat set to "identity" an fill-color "skyblue". Draw the same plot with *geom_col()*

```
ggplot(mtcars_by_cyl, aes(x = cyl, y = mean_wt)) + geom_col(fill = "skyblue")  # Swap geom_bar() for geom_col()
```



Bar plots: Using aggregated data

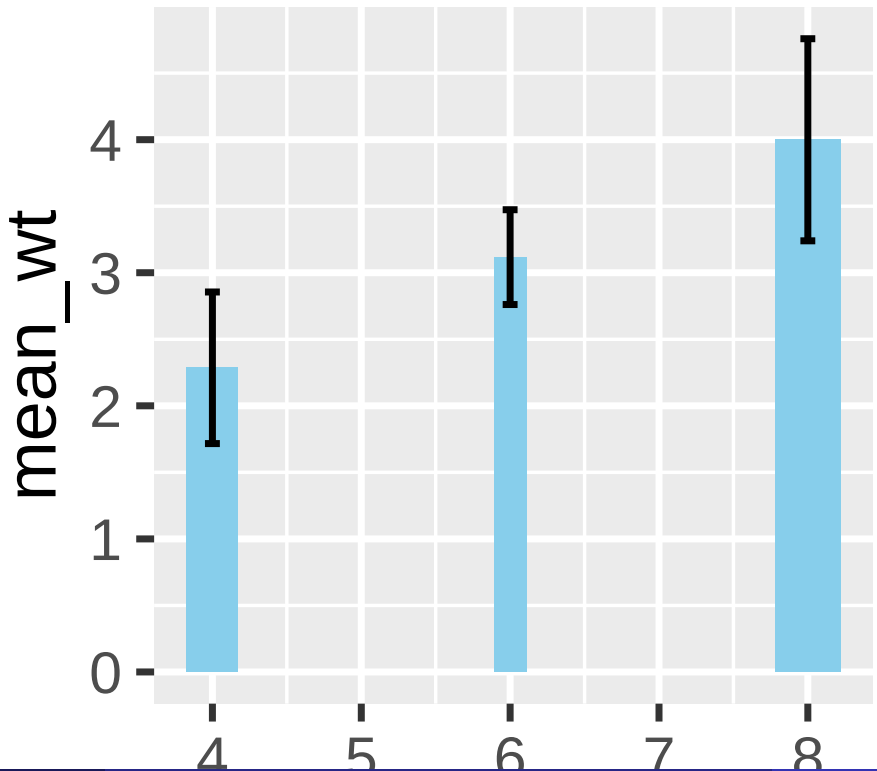
```
ggplot(mtcars_by_cyl, aes(x = cyl, y = mean_wt)) + geom_col(aes(width = prop),
    fill = "skyblue")  # Set the width aesthetic to prop
```



Bar plots: Using aggregated data

Replace *geom_bar()* with *geom_col()*.

```
ggplot(mtcars_by_cyl, aes(x = cyl, y = mean_wt)) +
  geom_col(aes(width = prop), fill = "skyblue") +
  # Add an errorbar layer
  geom_errorbar(
    aes(ymin = mean_wt - sd_wt, ymax = mean_wt + sd_wt),
    # with width 0.1
    width = 0.1
  )
```



Heatmaps use case scenario

- Since heat maps encode color on a continuous scale, they are difficult to accurately decode, a topic we discussed in the first lecture.
- Hence, heat maps are most useful if you have a small number of boxes and/or a clear pattern that allows you to overcome decoding difficulties.

Heatmaps use case scenario

- To produce them, map two categorical variables onto the x and y aesthetics, along with a continuous variable onto fill.
- The *geom_tile*() layer adds the boxes.

Heatmaps use case scenario

- We'll produce the heat map we saw in the video (in the viewer) with the built-in barley dataset.
- The barley dataset is in the lattice package and has already been loaded for you. Use *str*() to explore the structure.

Heatmaps use case scenario

- Using barley, plot variety versus year, filled by yield.
- Add a *geom_tile*() layer.

Heatmaps use case scenario

- Add a $facet\_wrap()$ function with facets as vars(site) and $ncol = 1$.
- Strip names will be above the panels, not to the side (as with $facet\_grid()$).

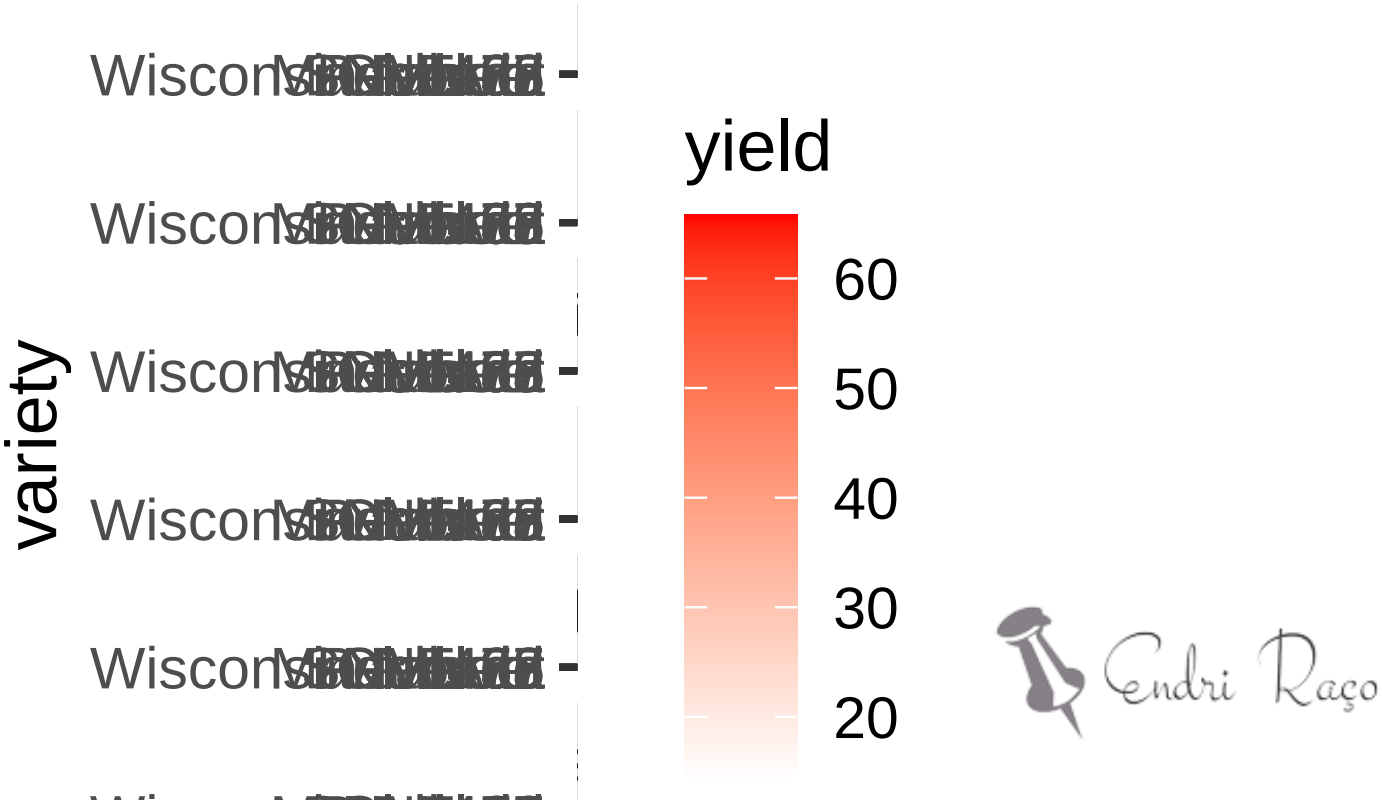
Heatmaps use case scenario

- Give the heat maps a 2-color palette using $scale\_fill\_gradient()$.
- Set low and high to “white” and “red”, respectively.

Heatmaps use case scenario

- A color palette of 9 reds, made with *brewer.pal()*, is provided as *red_brewer_palette*.

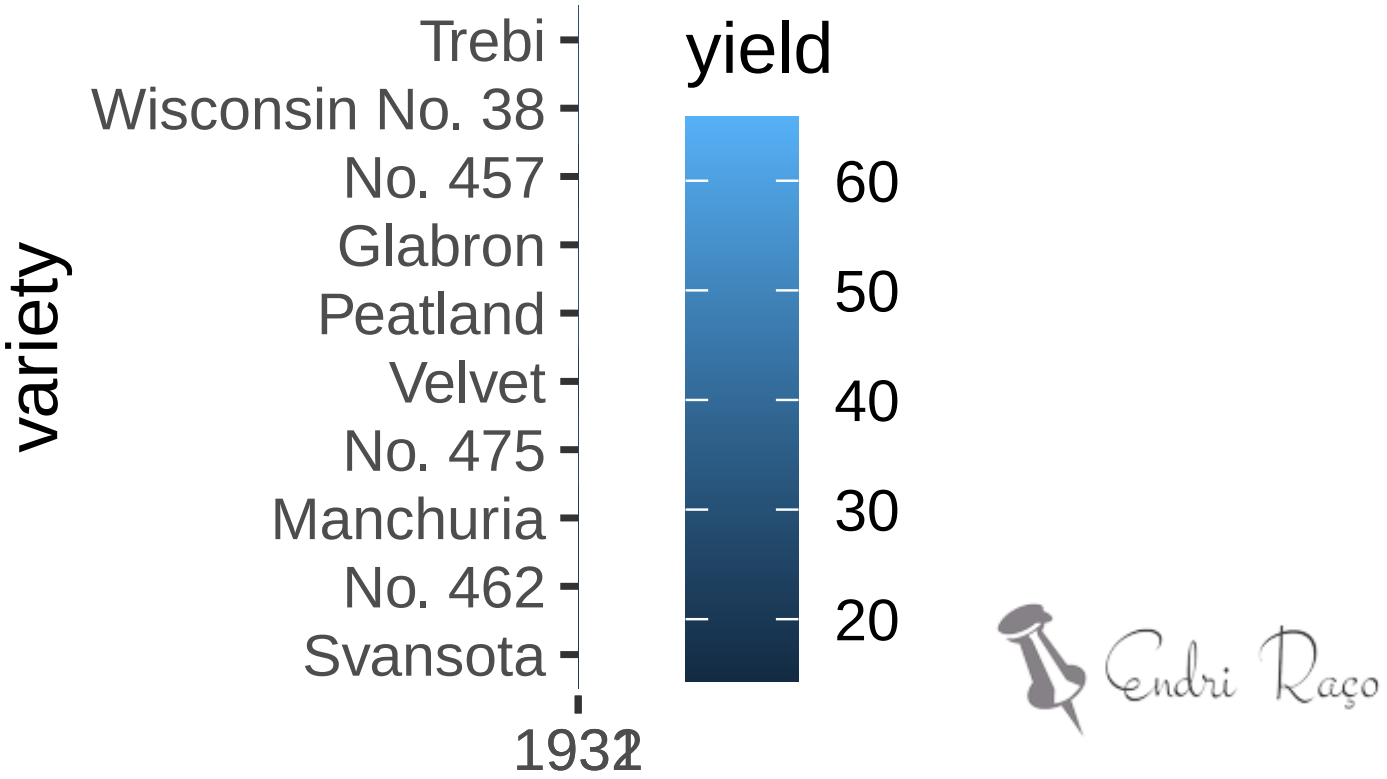
```
library(lattice)  # Contains the 'barley' dataset
# Load the dataset explicitly
data("barley", package = "lattice")
ggplot(barley, aes(x = year, y = variety, fill = yield)) + geom_tile() +
    facet_wrap(facets = vars(site), ncol = 1) + scale_fill_gradient(low = "white",
    high = "red")
```



Heatmaps use case scenario

- Update the fill scale to use an $n - color$ gradient with $scale\_fill\_gradientn()$ (note the n).

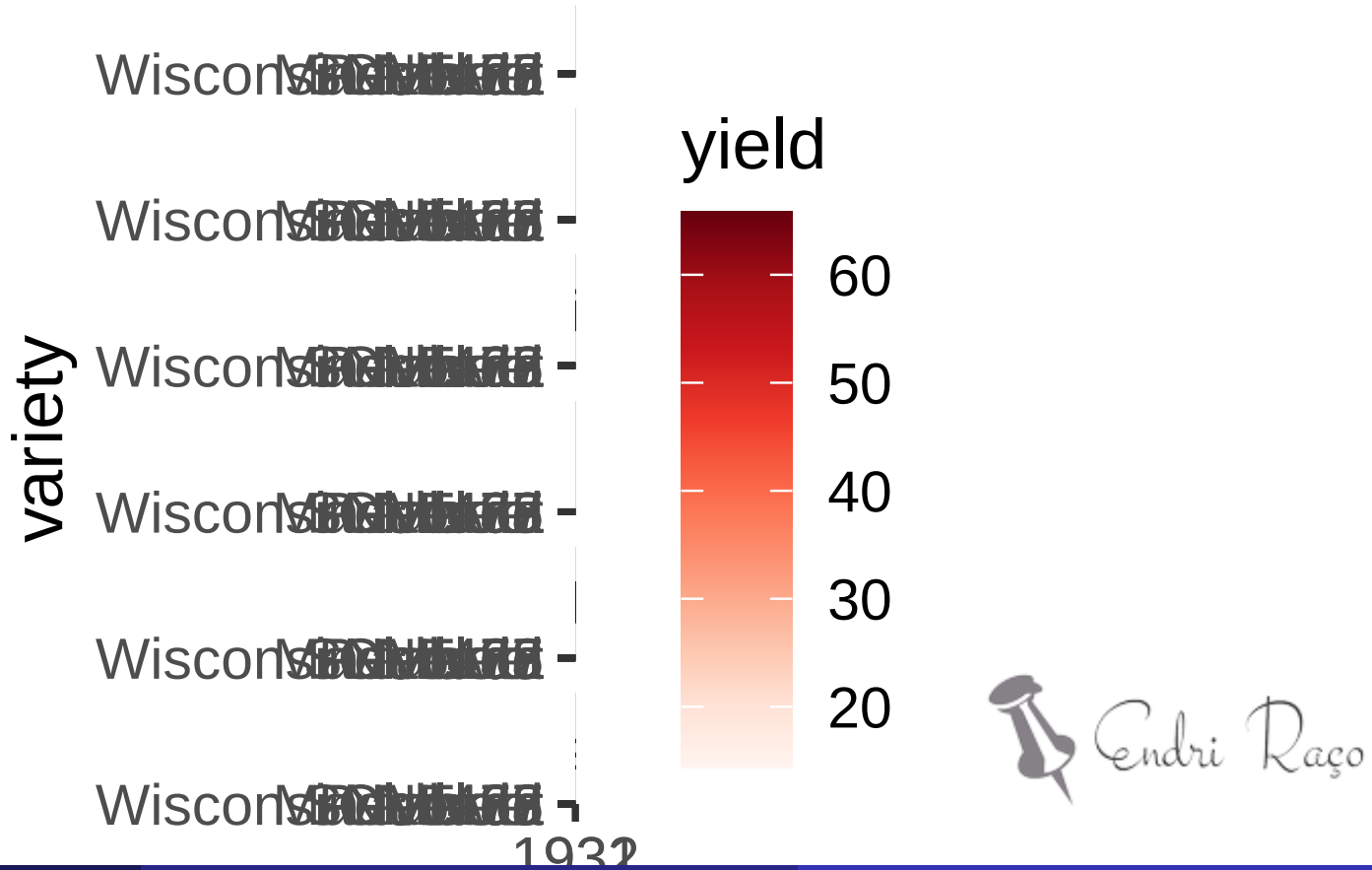
```
library(lattice)
library(RColorBrewer)

# Using barley, plot variety vs. year, filled by yield
ggplot(barley, aes(x = year, y = variety, fill = yield)) + geom_tile()  # Add a tile geom
```



Heatmaps use case scenario

- Set the scale colors to the red brewer palette.

```
# A palette of 9 reds
red_brewer_palette <- brewer.pal(9, "Reds")

# Update the plot
ggplot(barley, aes(x = year, y = variety, fill = yield)) + geom_tile() +
    facet_wrap(facets = vars(site), ncol = 1) + scale_fill_gradientn(colors = red_brewer_palette)  # Update sca
```



Useful heat maps

- Heat maps are often a poor data viz solution because they typically don't convey useful information.
- We saw a nice alternative in the last exercise.

Useful heat maps

- But sometimes they are really good.
- Which of the following scenarios is not one of those times?

Useful heat maps

- When data has been sorted, e.g. according to a clustering algorithm, and we can see clear trends.
- When there are few groups with large differences.

Useful heat maps

- When we have a large data set and we want to impress our colleagues with how complex our work is!
- When using explanatory plots to communicate a clear message to a non-scientific audience.

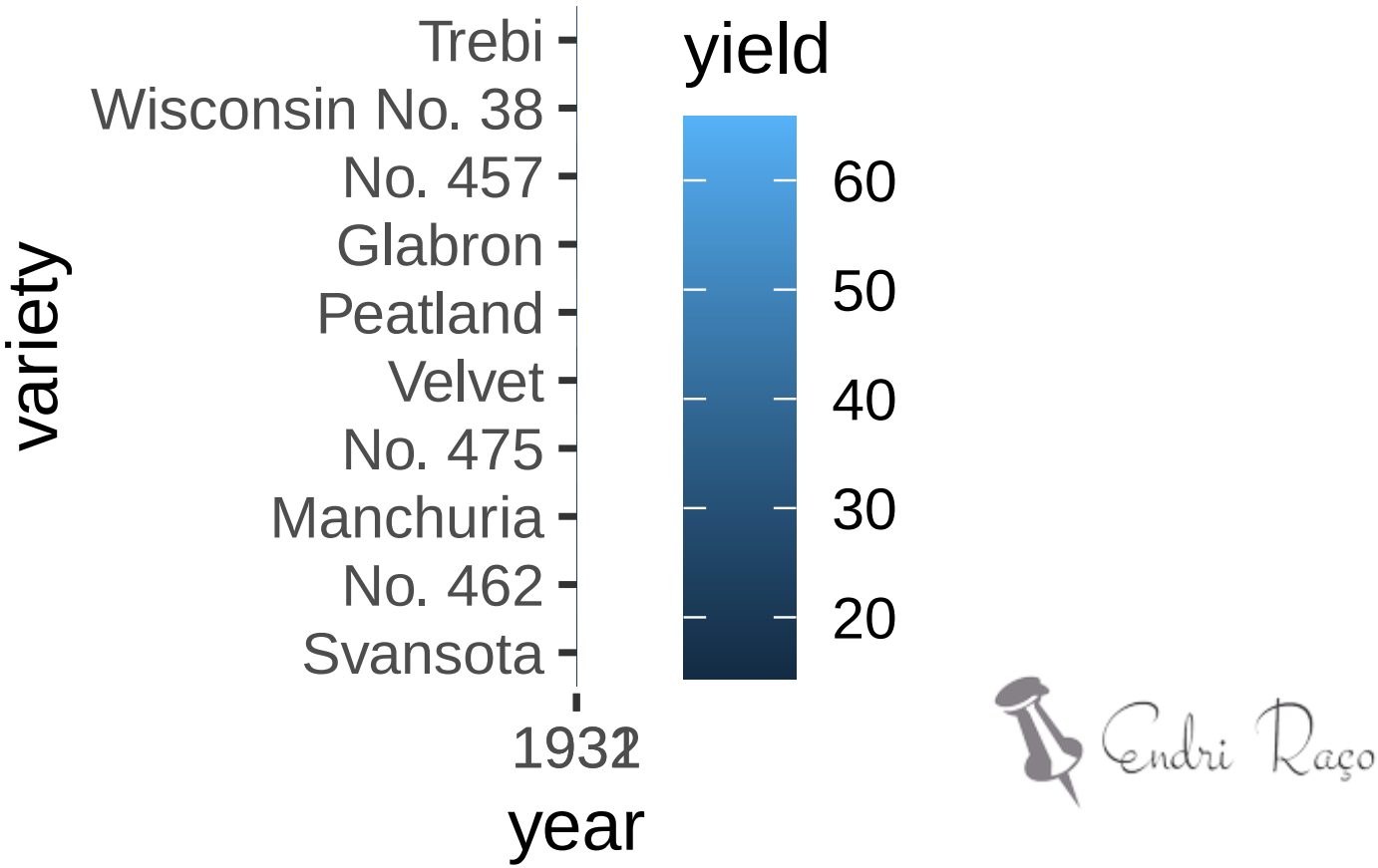
Heat map alternatives

- There are several alternatives to heat maps.
- The best choice really depends on the data and the story you want to tell with this data.
- If there is a time component, the most obvious choice is a line plot.

Useful heat maps

- Using barley, plot yield versus year, colored and grouped by variety.

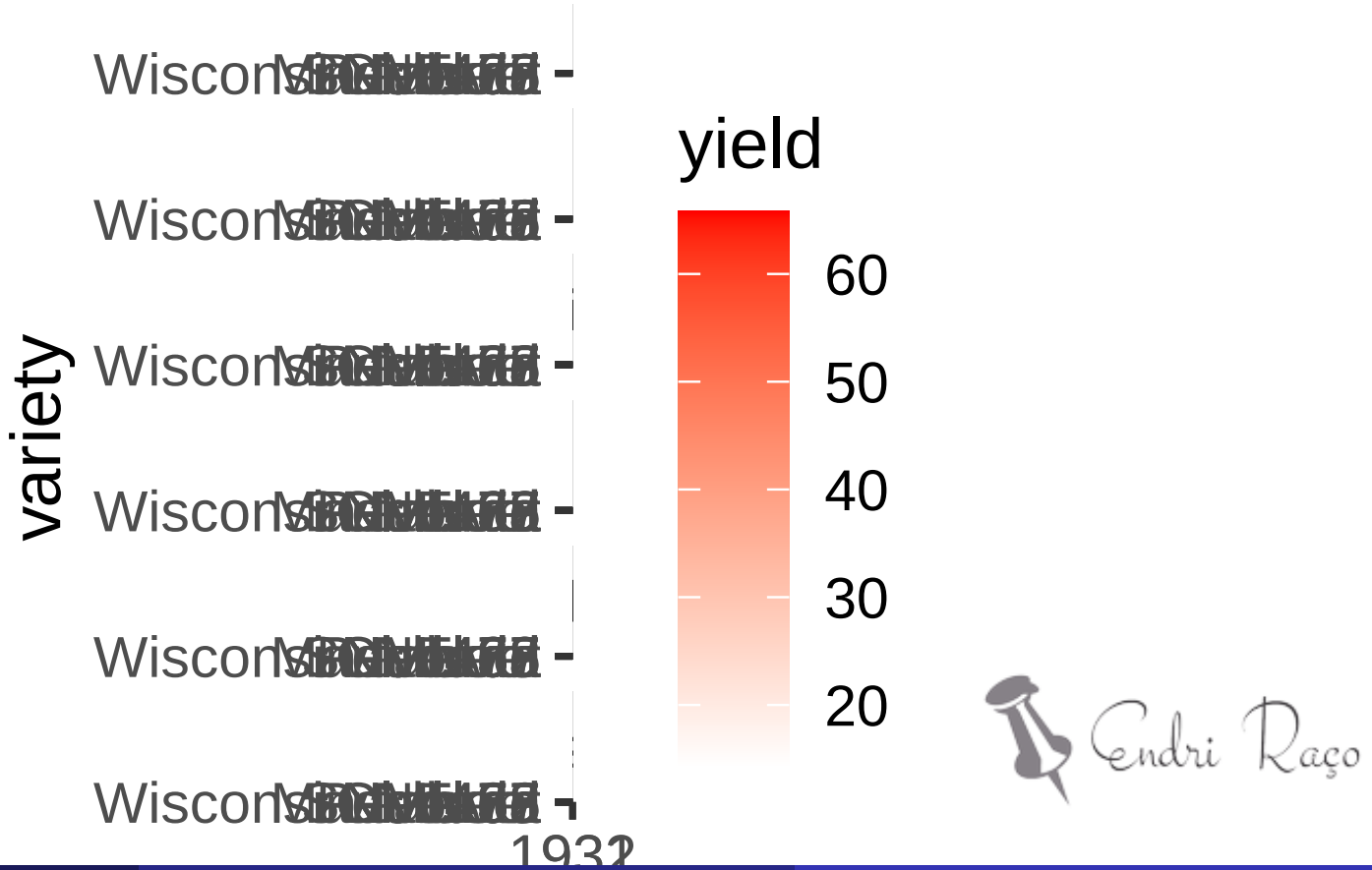
```
library(lattice)
library(RColorBrewer)

# Using barley, plot variety vs. year, filled by yield
ggplot(barley, aes(x = year, y = variety, fill = yield)) + geom_tile()  # Add a tile geom
```



Useful heat maps

Add a line layer. Facet, wrapping by site, with 1 row. Display only means and ribbons for spread.

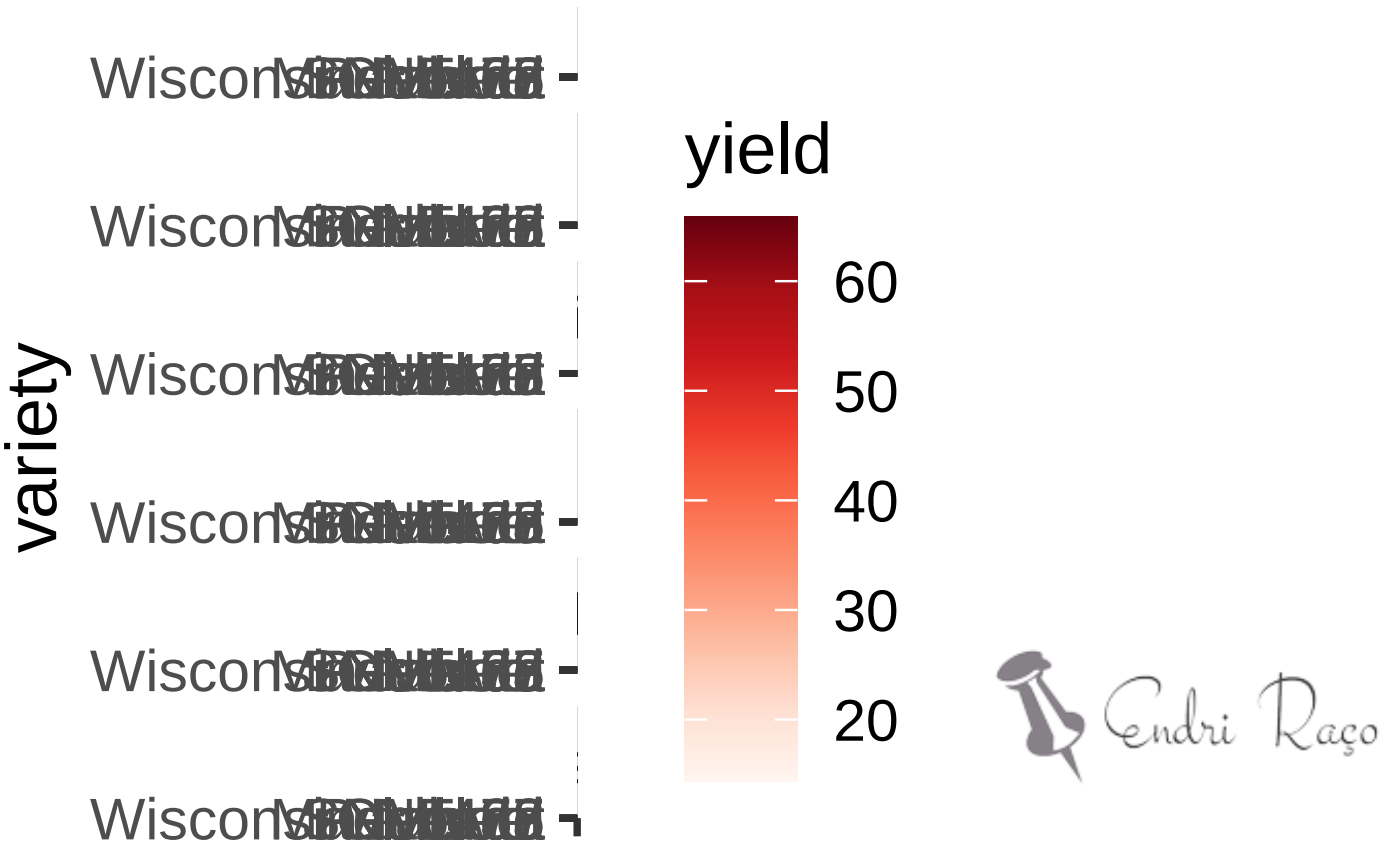
```
# Previously defined
ggplot(barley, aes(x = year, y = variety, fill = yield)) + geom_tile() +
    facet_wrap(facets = vars(site), ncol = 1) + scale_fill_gradient(low = "white",
    high = "red")
```



Useful heat maps

Map site onto color, group and fill. Add a $stat\_summary()$ layer. set $fun = mean$, and $geom = "line"$.

```
# A palette of 9 reds
red_brewer_palette <- brewer.pal(9, "Reds")
# Update the plot
ggplot(barley, aes(x = year, y = variety, fill = yield)) + geom_tile() +
    facet_wrap(facets = vars(site), ncol = 1) + scale_fill_gradientn(colors = red_brewer_palette)
```



Suppression of the origin

Suppression of the origin refers to not showing 0 on a continuous scale. When is it inappropriate to suppress the origin?

When good data makes bad plots

- When the scale has a natural zero, like height or distance.
- When the scale doesn't have a natural zero, like temperature (in C or F).
- When there is a large amount of whitespace between the origin and the actual data.
- When it does not obscure the shape of the data.

Color blindness

Red-Green color blindness is surprisingly prevalent, which means that part of your audience will not be able to ready your plot if you are relying on color aesthetics.

Color blindness

Why would it be appropriate to use red and green in a plot?

- When red and green are the actual colors in the sample (e.g. fluorescence in biological assays).
- When red means stop/bad and green means go/good.
- Because red and green are complimentary colors and look great together.
- When red and green have different intensities (e.g. light red and dark green).

Typical problems

- When you first encounter a data visualization, either from yourself or a colleague, you always want to critically ask if it's obscuring the data in any way.
- Let's take a look at the steps we could take to produce and improve the plot in the view.

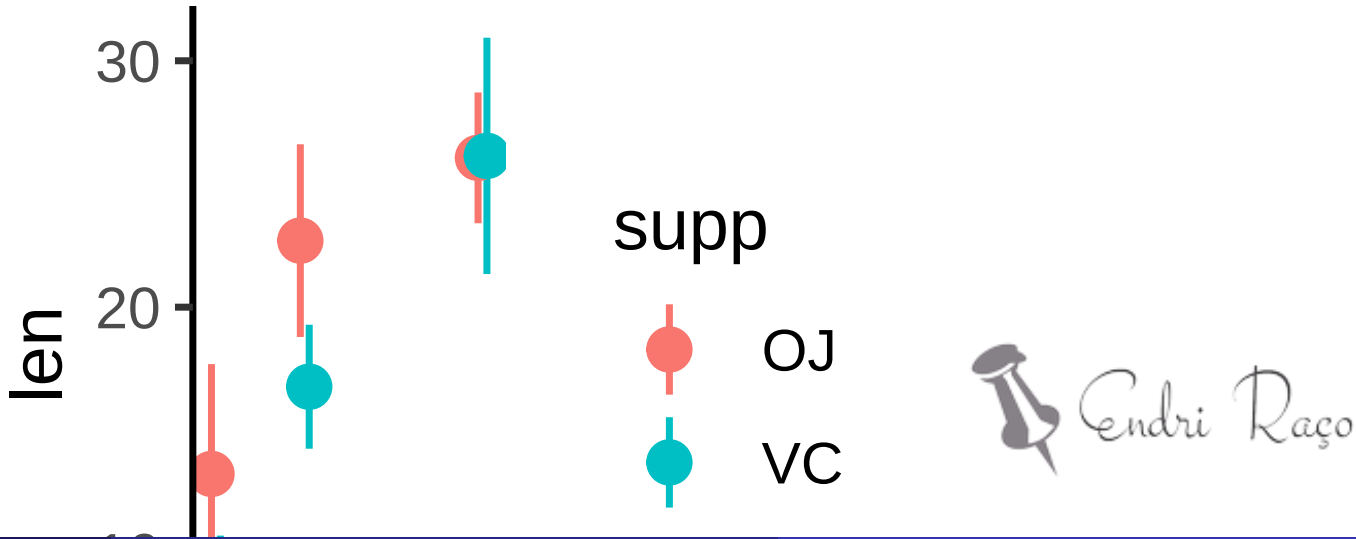
Typical problems

- The data comes from an experiment where the effect of two different types of vitamin C sources, orange juice or ascorbic acid, were tested on the growth of the odontoblasts (cells responsible for tooth growth) in 60 guinea pigs.
- The data is stored in the TG data frame, which contains three variables: dose, len, and supp.

Typical problems

- The first plot contains purposely illegible labels. It's a common problem that can occur when resizing plots. There is also too much non-data ink.

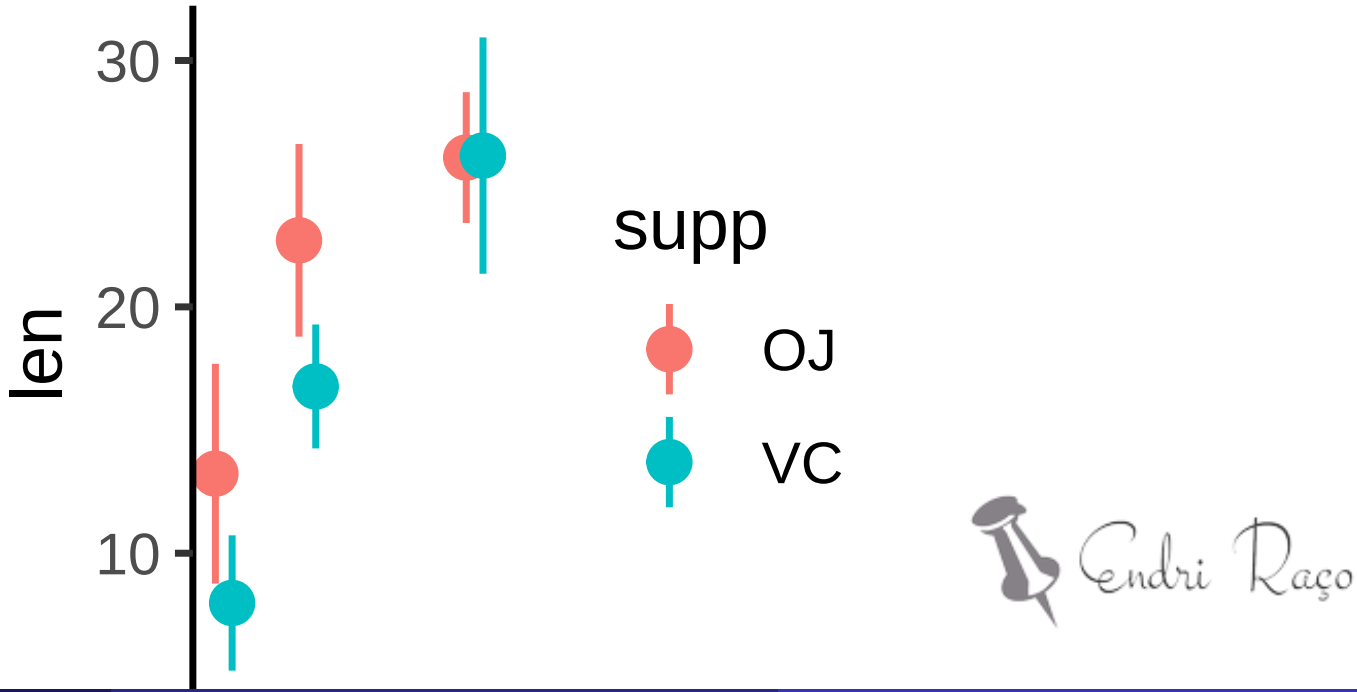
```
library(datasets)
TG <- ToothGrowth

# Initial plot
growth_by_dose <- ggplot(TG, aes(dose, len, color = supp)) +
    stat_summary(fun.data = mean_sdl, fun.args = list(mult = 1),
        position = position_dodge(0.1)) + theme_classic()

# View plot
growth_by_dose
```



Typical problems

Change *theme_gray*(3) to *theme_classic*().

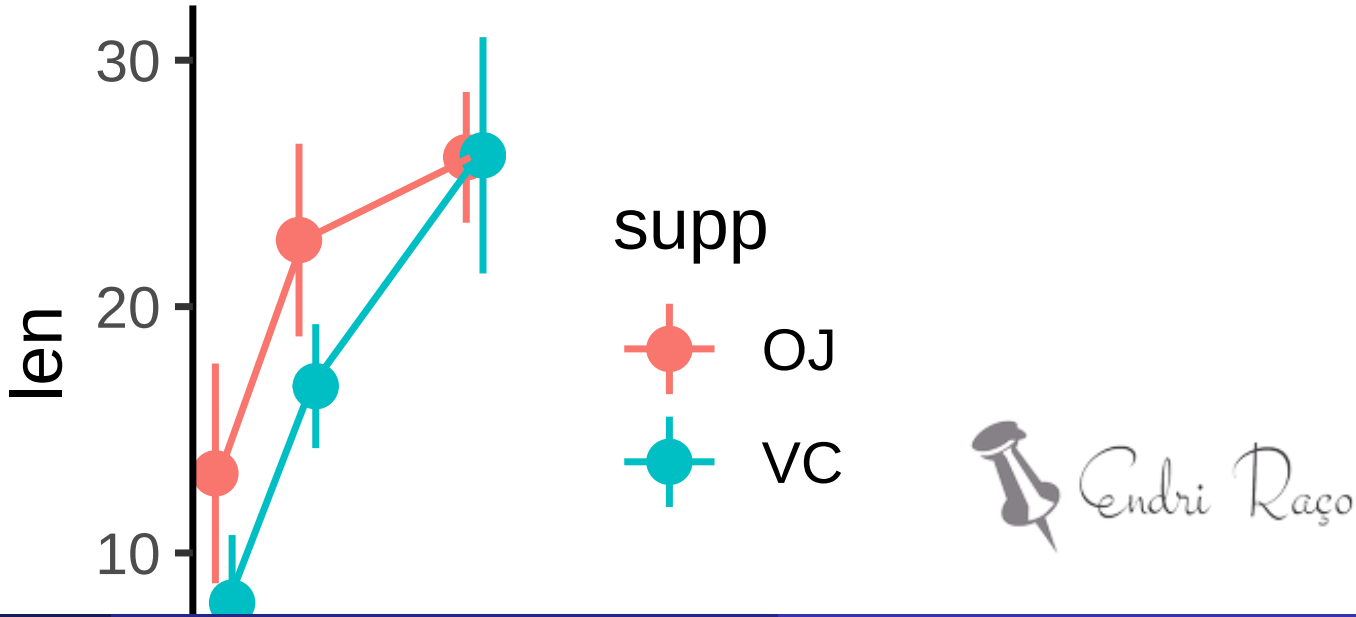
```
# Change type
TG$dose <- as.numeric(as.character(TG$dose))

# Plot
growth_by_dose <- ggplot(TG, aes(dose, len, color = supp)) +
    stat_summary(fun.data = mean_sdl, fun.args = list(mult = 1),
        position = position_dodge(0.2)) + theme_classic()

# View plot
growth_by_dose
```



Typical problems

Our previous plot still has a major problem, dose is stored as a factor variable. That's why the spacing is off between the levels.

```
# Change type
TG$dose <- as.numeric(as.character(TG$dose))
# Plot
growth_by_dose <- ggplot(TG, aes(dose, len, color = supp)) +
    stat_summary(fun.data = mean_sdl, fun.args = list(mult = 1),
        position = position_dodge(0.2)) + stat_summary(fun = mean,
    geom = "line", position = position_dodge(0.1)) + theme_classic()

# View plot
growth_by_dose
```



Typical problems

- Use $as.character()$ wrapped in $as.numeric()$ to convert the factor variable to real (continuous) numbers.
- Use the appropriate geometry for the data:

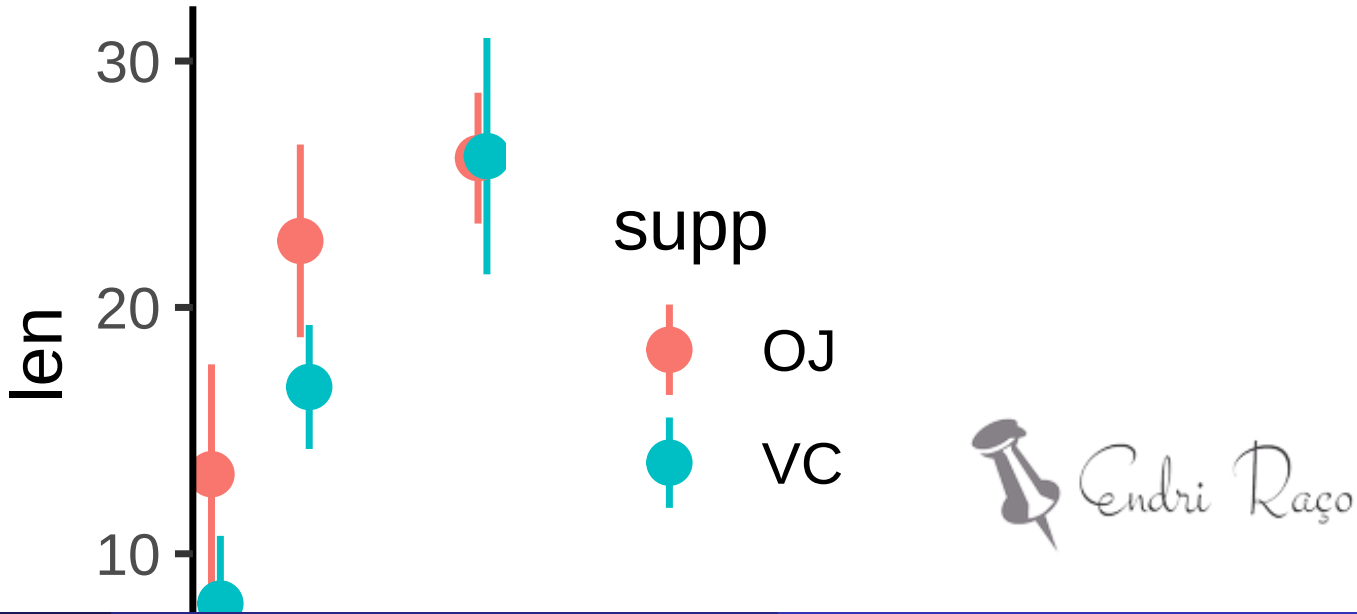
Typical problems

- In the new *stat_summary*() function, set fun to to calculate the mean and the geom to a "line" to connect the points at their mean values.
- Make sure the labels are informative:

Typical problems

Add the units "(mg/day)" and "(mean, standard deviation)" to the x and y labels, respectively.

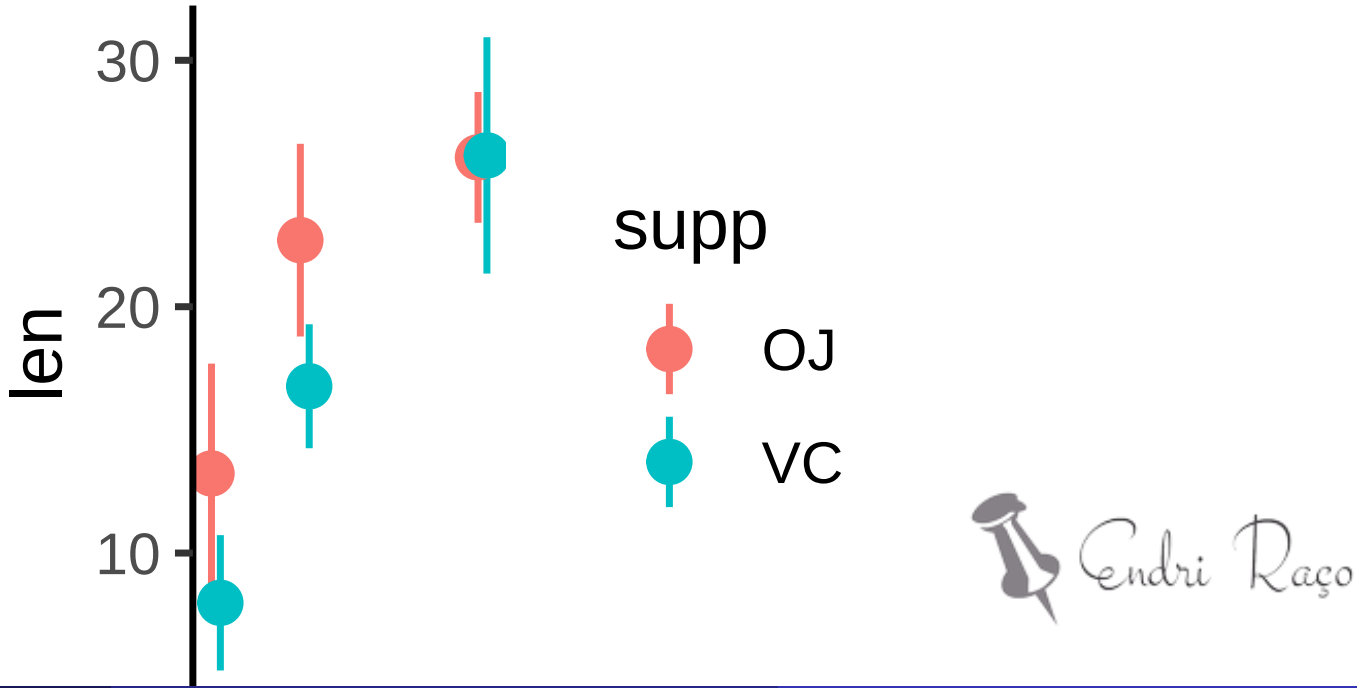
```
library(datasets)
TG <- ToothGrowth

# Initial plot
growth_by_dose <- ggplot(TG, aes(dose, len, color = supp)) +
    stat_summary(fun.data = mean_sdl, fun.args = list(mult = 1),
        position = position_dodge(0.1)) + theme_classic()

# View plot
growth_by_dose
```



Typical problems

Use the "Set1" palette.

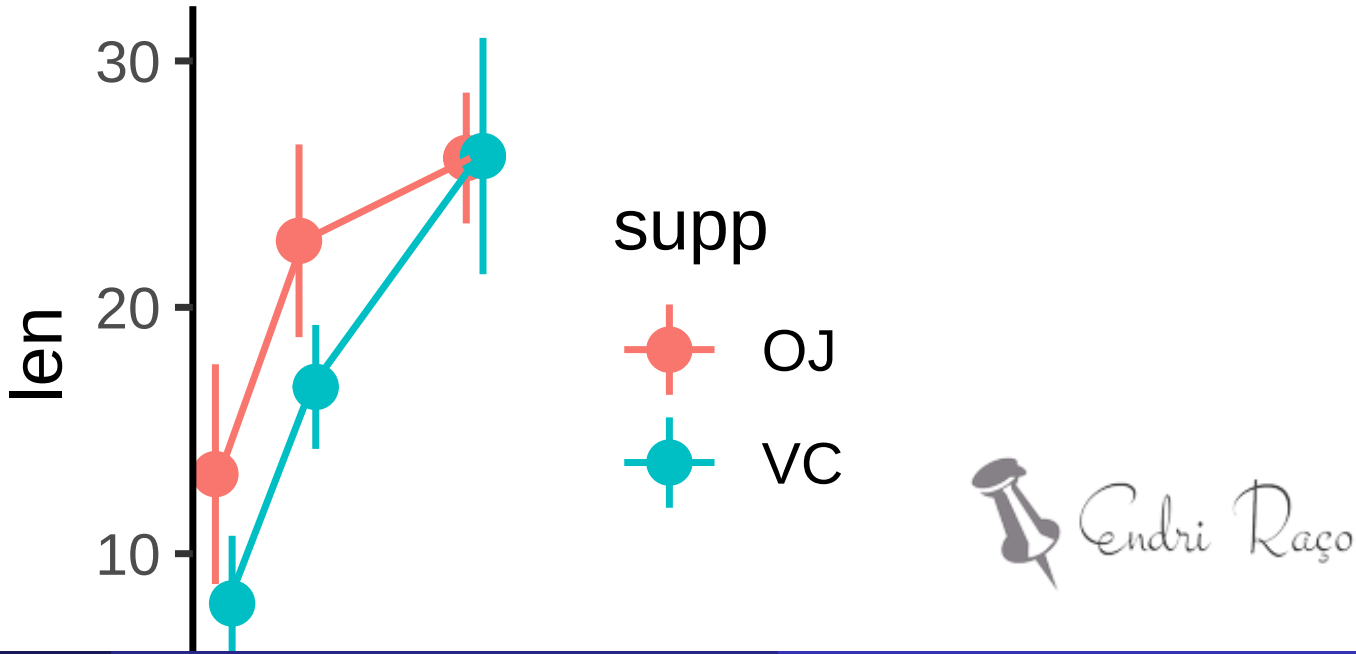
```
library(datasets)
TG <- ToothGrowth

# Initial plot
growth_by_dose <- ggplot(TG, aes(dose, len, color = supp)) +
    stat_summary(fun.data = mean_sdl, fun.args = list(mult = 1),
        position = position_dodge(0.1)) + theme_classic()

# View plot
growth_by_dose
```



Typical problems

Set the legend labels to “Orange juice” and “Ascorbic acid”.

```
# Change type
TG$dose <- as.numeric(as.character(TG$dose))

# Plot
growth_by_dose <- ggplot(TG, aes(dose, len, color = supp)) +
    stat_summary(fun.data = mean_sdl, fun.args = list(mult = 1),
        position = position_dodge(0.2)) + stat_summary(fun = mean,
    geom = "line", position = position_dodge(0.1)) + theme_classic()

# View plot
growth_by_dose
```



Typical problems

```
# Change type
TG$dose <- as.numeric(as.character(TG$dose))

# Plot
growth_by_dose <- ggplot(TG, aes(dose, len, color = supp)) +
    stat_summary(fun.data = mean_sdl, fun.args = list(mult = 1),
        position = position_dodge(0.2)) + stat_summary(fun = mean,
    geom = "line", position = position_dodge(0.1)) + theme_classic() +
    # Adjust labels and colors:
labs(x = "Dose (mg/day)", y = "Odontoblasts length (mean, standard deviation)",
    color = "Supplement") + scale_color_brewer(palette = "Set1",
    labels = c("Orange juice", "Ascorbic acid")) + scale_y_continuous(limits = c(0,
    35), breaks = seq(0, 35, 5), expand = c(0, 0))

# View plot
growth_by_dose
```