Class 5: Data Viz with ggplot

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Background

There are many graphics systems available in R. These include "base" R and tones of add on packages like **ggplot2**.

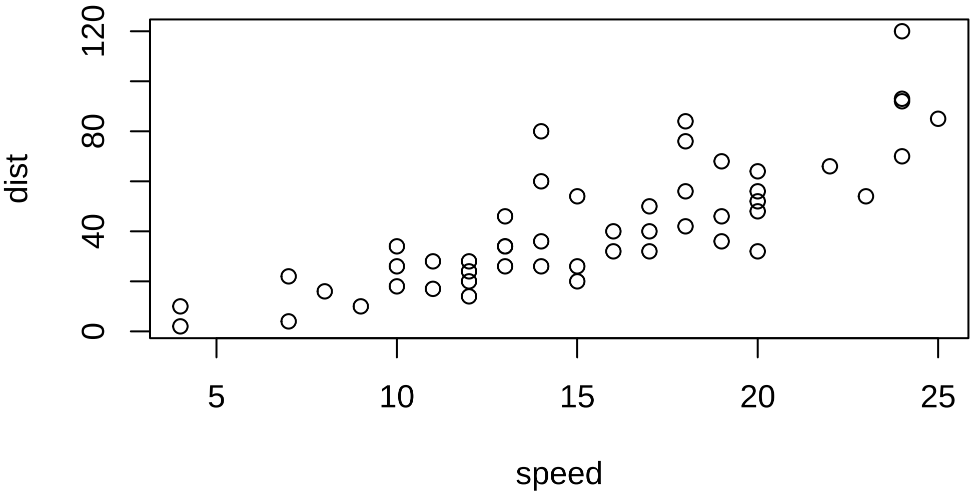
Let's compare "base" and **ggplot2** briefly. We can use some example data that is built-in with R called `cars`:

```r
head(cars)
```

```
  speed dist
1     4    2
2     4   10
3     7    4
4     7   22
5     8   16
6     9   10
```

In base R I can just call `plot()`

```r
plot(cars)
```



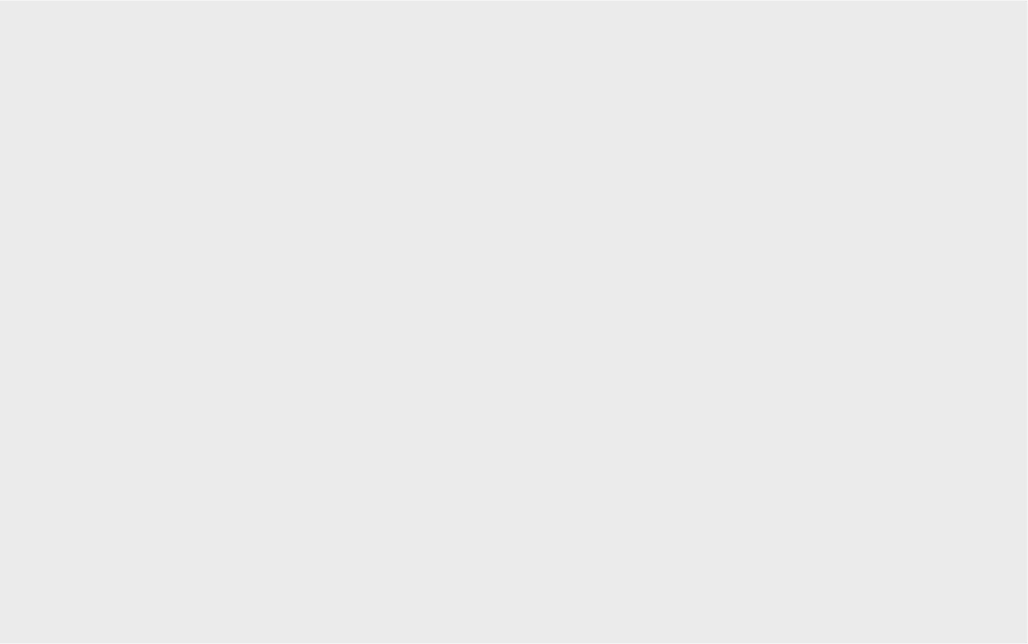
How can we do this with **ggplot2**

First we need to install the package. We do this `install.packages("ggplot2")`. I only need to do this once and then it will be available on my computer from then on.

> Key point: I only install packages in the R console not within quarto docs or R scripts.

Before I use any add-on package I must load it up with a call to `library()`

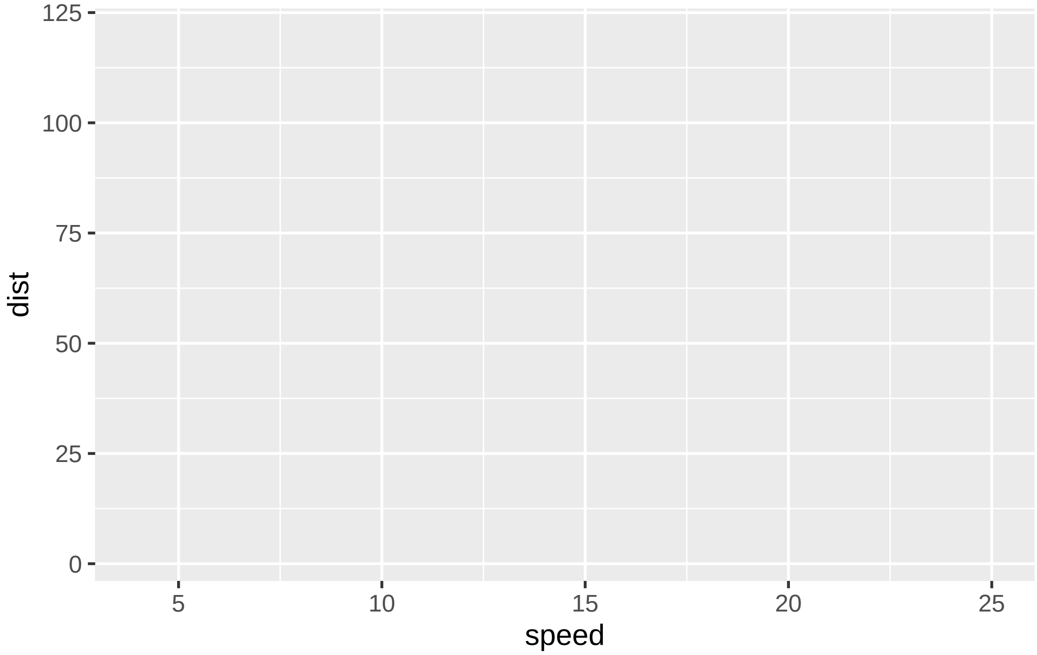
```r
library(ggplot2)
ggplot(cars)
```



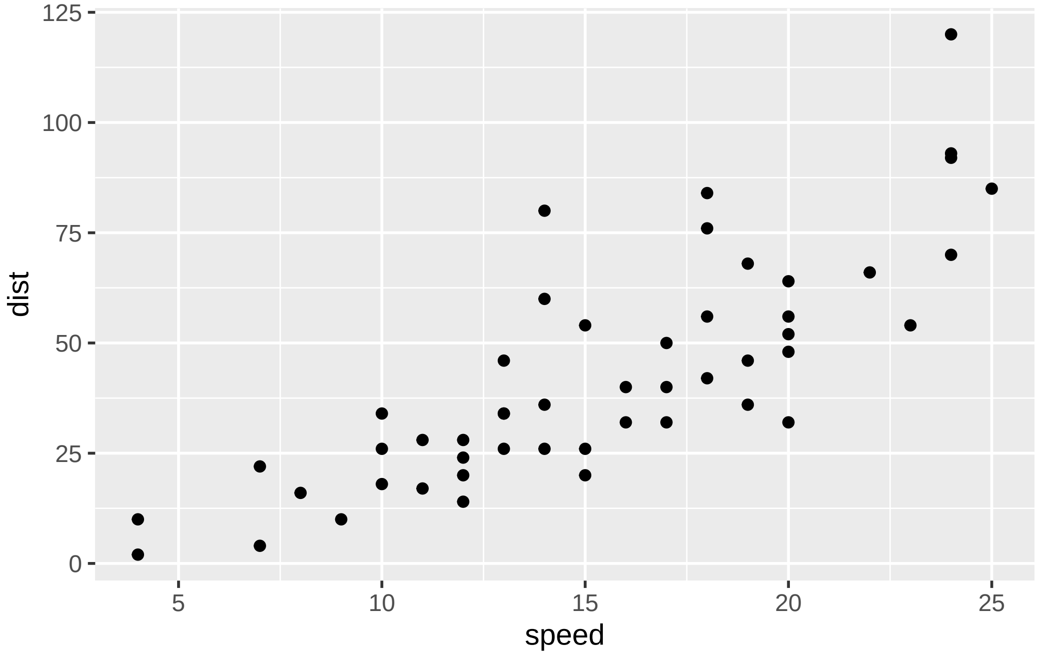
Every ggplot has at least 3 things:

- the **data** (in our case `cars`)
- the **aes**thetics (how the data map to the plot)
- the **geom**s that determine how the plot is drawn (lines, points, columns, etc.)

```r
ggplot(cars) +
  aes(x=speed, y=dist)
```



```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()
```



For “simple” plots ggplot is much more verbose than base R but the defaults are nicer and for complicated plots it becomes much more efficient and structured.

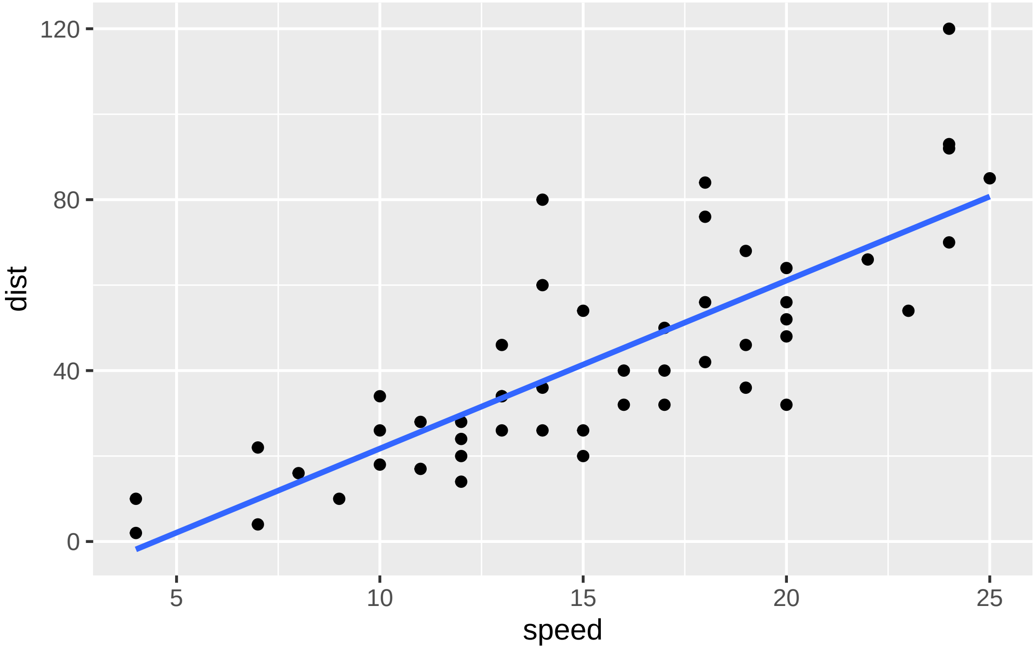
> Q. Add a line to show the relationship of speed to stopping distance (i.e. add another “layer”)

```
p <- ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(se=FALSE, method="lm")
```

I can always save any ggplot object (i.e. plot) and then use it later for adding more layers.

```
p
```

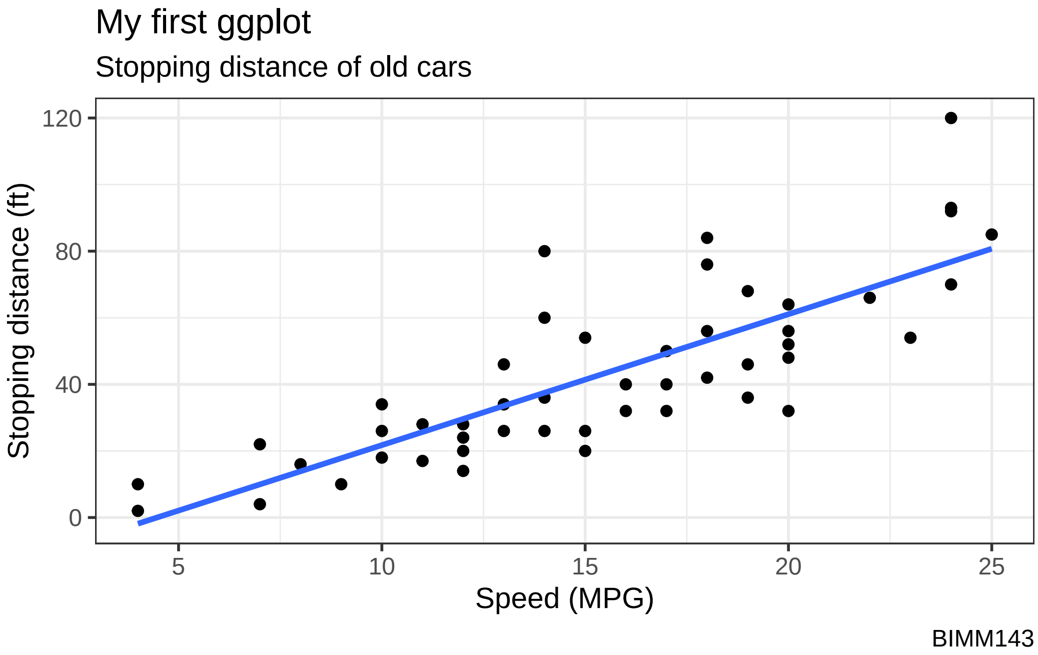
```
`geom_smooth()` using formula = 'y ~ x'
```



> Q. Add a title and subtitle to the plot

```
p + labs(title="My first ggplot",
         subtitle="Stopping distance of old cars",
         caption="BIMM143",
         x="Speed (MPG)",
         y="Stopping distance (ft)") +
  theme_bw()
```

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



Gene expression plot

Read input data into R

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

```
        Gene Condition1 Condition2      State
1      A4GNT -3.6808610 -3.4401355 unchanging
```

```
2       AAAS  4.5479580  4.3864126 unchanging
3      AASDH  3.7190695  3.4787276 unchanging
4       AATF  5.0784720  5.0151916 unchanging
5       AATK  0.4711421  0.5598642 unchanging
6 AB015752.4 -3.6808610 -3.5921390 unchanging
```

> Q. How many genes are in ths wee dataset?

```
nrow(genes)
```

```
[1] 5196
```

> Q. How many columns are there?

```
ncol(genes)
```

```
[1] 4
```

> Q. What are the column names?

```
colnames(genes)
```

```
[1] "Gene"       "Condition1" "Condition2" "State"
```

> Q. How many "up" and "down" regulated genes are there?

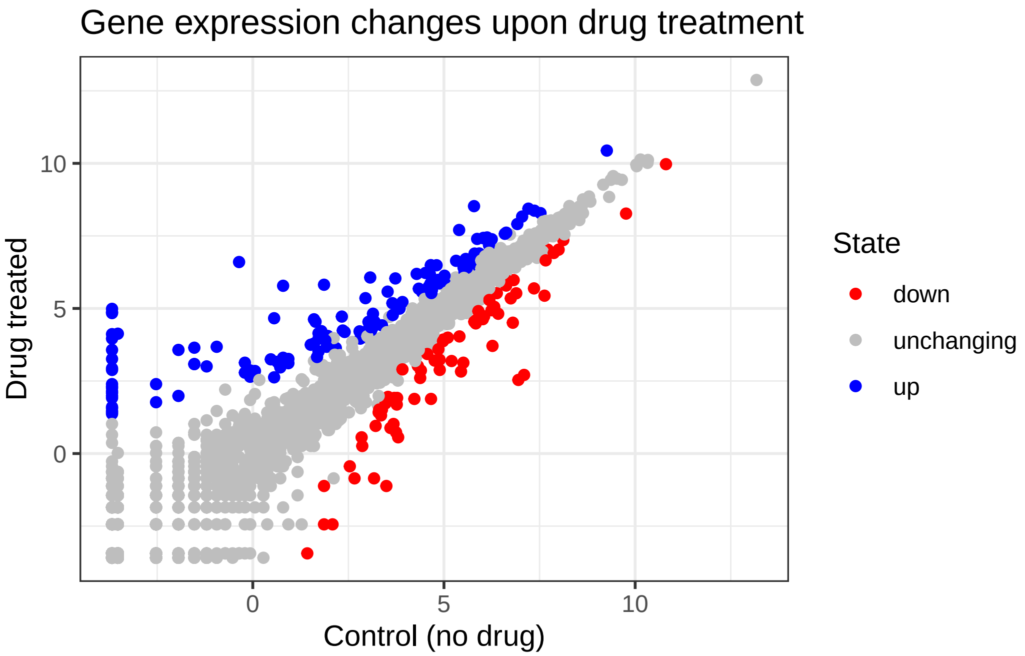
```
table(genes$State)
```

```

      down unchanging         up 
        72       4997        127 
```

Custom color plot

> Q. Make a first plot of this data

```r
ggplot(genes) +
  aes(x=Condition1, y=Condition2, col=State) +
  scale_color_manual( values=c("red", "grey", "blue")) +
  geom_point() +
  labs(title="Gene expression changes upon drug treatment",
       x="Control (no drug)",
       y="Drug treated") +
  theme_bw()
```



Using different geoms

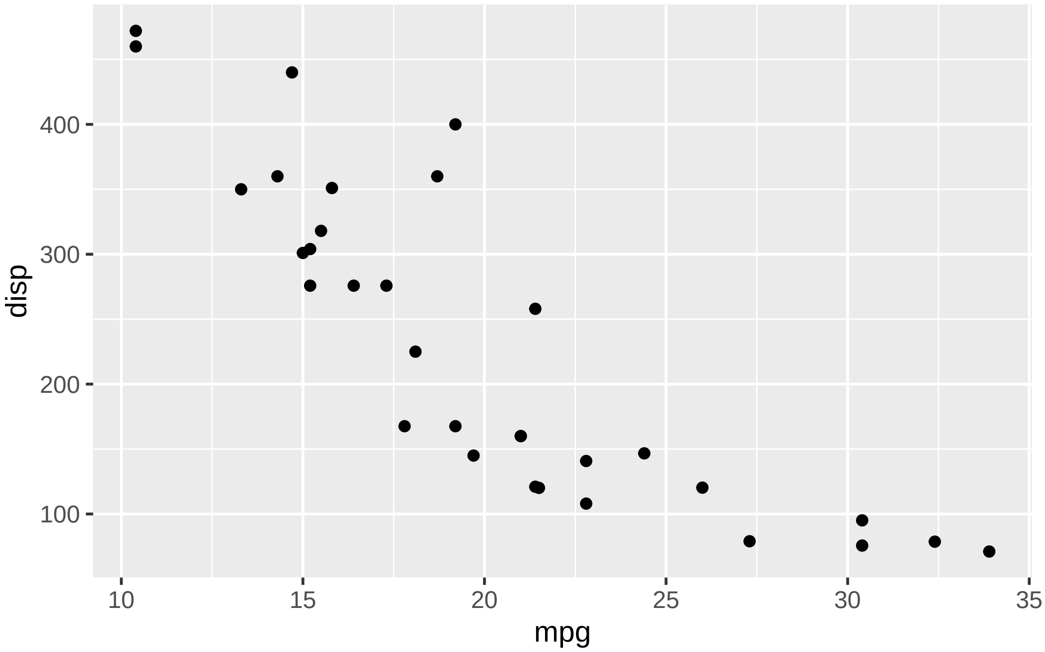
Let's plot some aspects of the in-built `mtcars` dataset.

```r
head(mtcars)
```

```
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

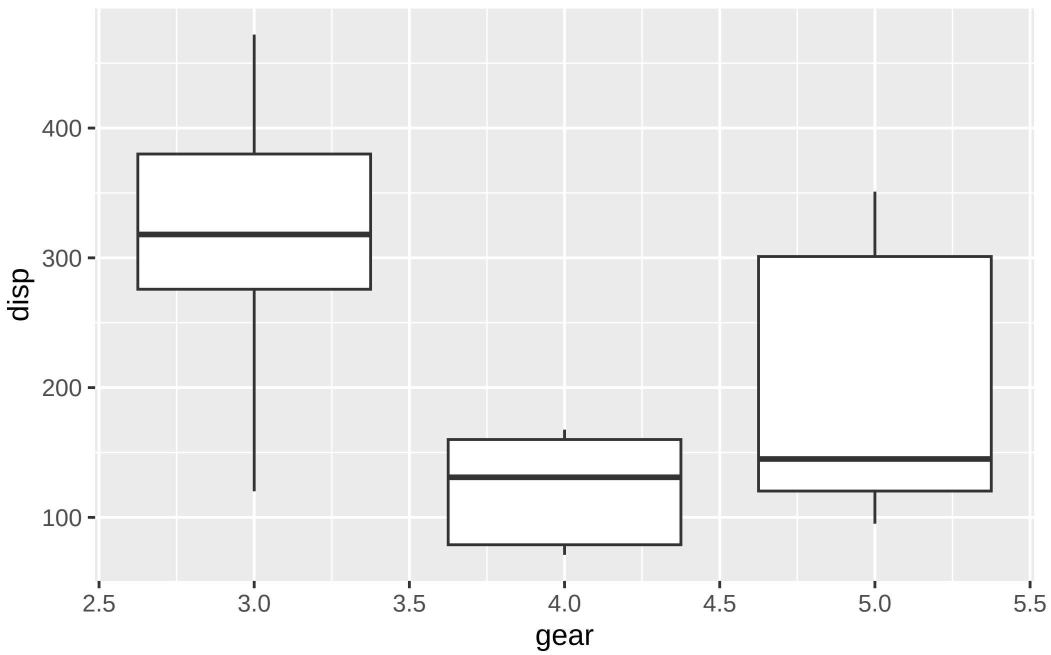
Q. Scatter plot of `mpg` vs `disp`

```
p1 <- ggplot(mtcars) +
  aes(x=mpg, y=disp) +
  geom_point()

p1
```



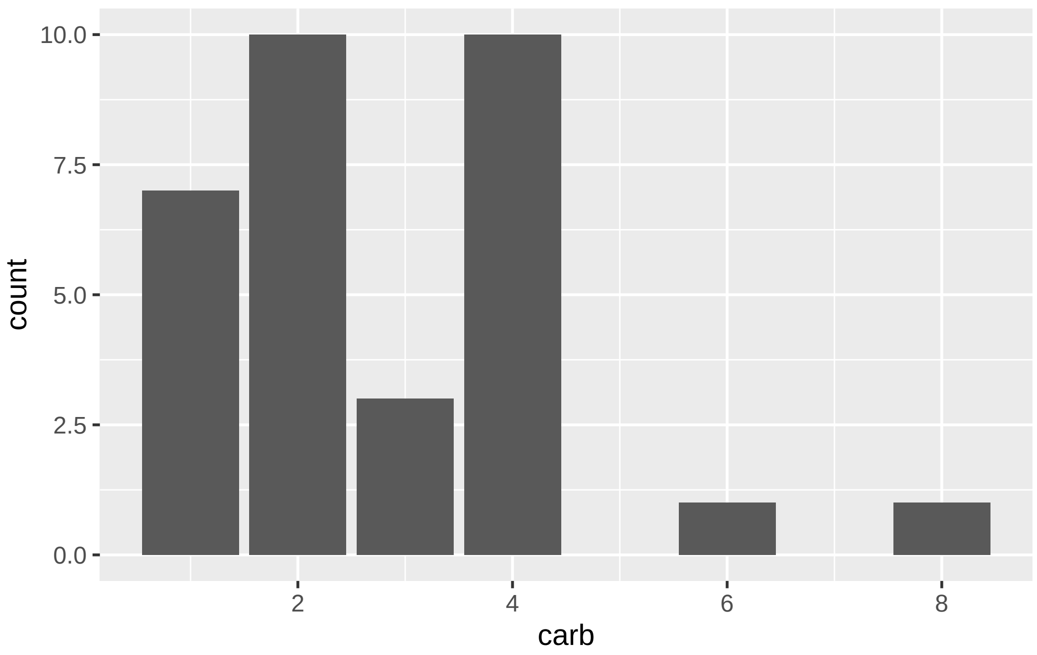
Q. boxplot of `gear` vs `disp`

```
p2 <- ggplot(mtcars) +
  aes(x=gear, y=disp, group=gear) +
  geom_boxplot()

p2
```



Q. barplot of `carb`

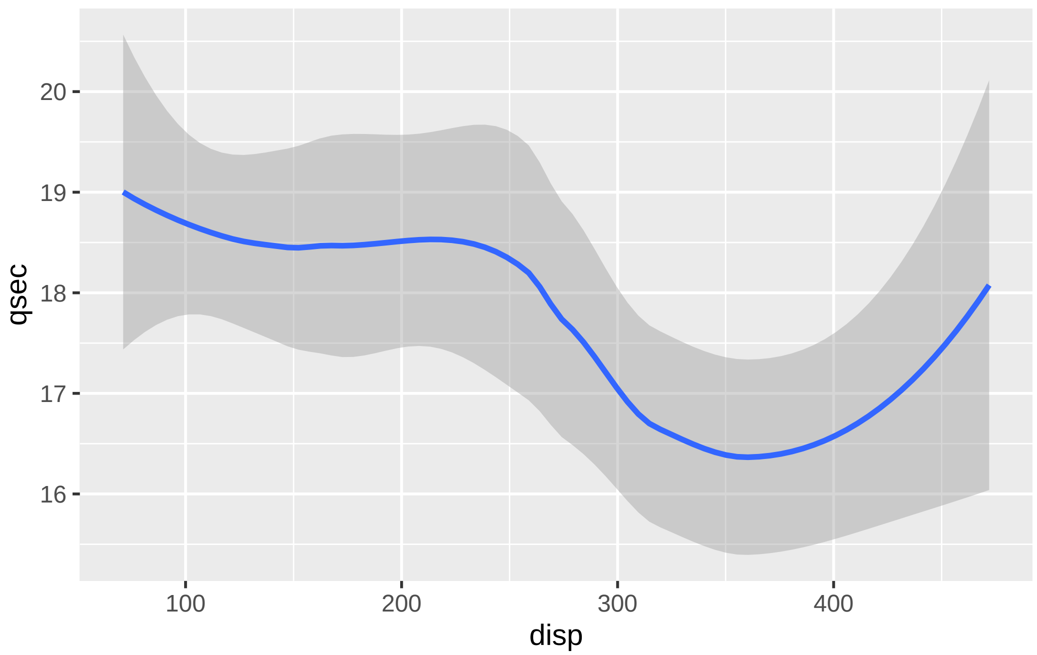
```
p3 <- ggplot(mtcars) +
  aes(carb) +
  geom_bar()

p3
```



Q. Smooth of `disp` vs `qsec`

```
p4 <- ggplot(mtcars) +
  aes(disp, qsec) +
  geom_smooth()

p4
```

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

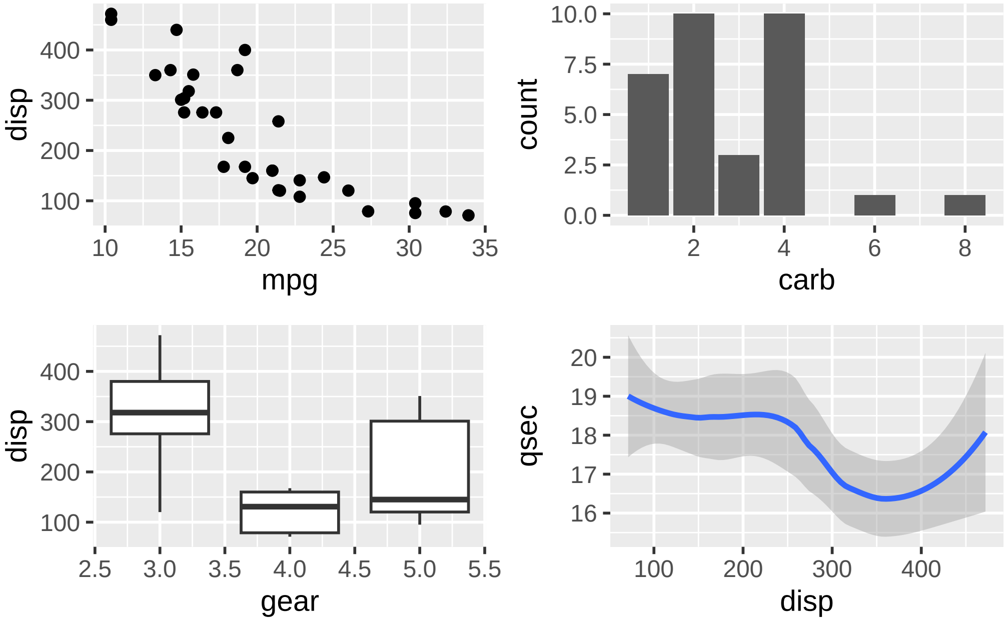


I want to combine all these plots into one figure with multiple pannels.

We can use the **patchwork** package to do this.

```
library(patchwork)

(p1 / p2 | p3 / p4)
```

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



```r
ggsave(filename="myplot.png", width=5, height=3)
```

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

Faceting

```r
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts

gapminder <- read.delim(url)
```

And a wee peak

```r
head(gapminder)
```

```
      country continent year lifeExp      pop gdpPercap
1 Afghanistan      Asia 1952  28.801  8425333  779.4453
2 Afghanistan      Asia 1957  30.332  9240934  820.8530
3 Afghanistan      Asia 1962  31.997 10267083  853.1007
```

```
4 Afghanistan      Asia 1967  34.020 11537966  836.1971
5 Afghanistan      Asia 1972  36.088 13079460  739.9811
6 Afghanistan      Asia 1977  38.438 14880372  786.1134
```

< Q. How many countries are in this dataset?

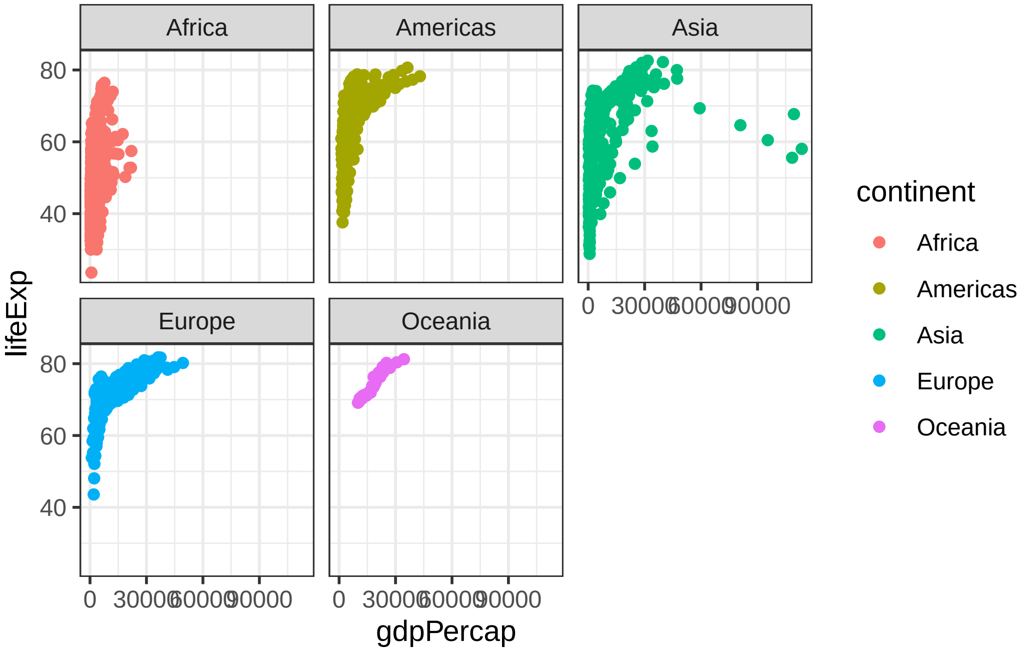
```
length(table(gapminder$country))
```

```
[1] 142
```

Q. Plot gdpPercap vs lifeExp color by continent

```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, col=continent) +
  geom_point(aplha=0.3) +
  facet_wrap(~continent) +
  theme_bw()
```

```
Warning in geom_point(aplha = 0.3): Ignoring unknown parameters: `aplha`
```


Africa
Americas
Asia
Europe
Oceania
lifeExp
gdpPercap
continent
● Africa
● Americas
● Asia
● Europe
● Oceania