Class5: Data Viz with ggplot

Hanhee

Graphs and plots in R

R has tones of different graphics systems. These include **"base R"** (e.g. the `plot()` function) and add on packages like **ggplot2**

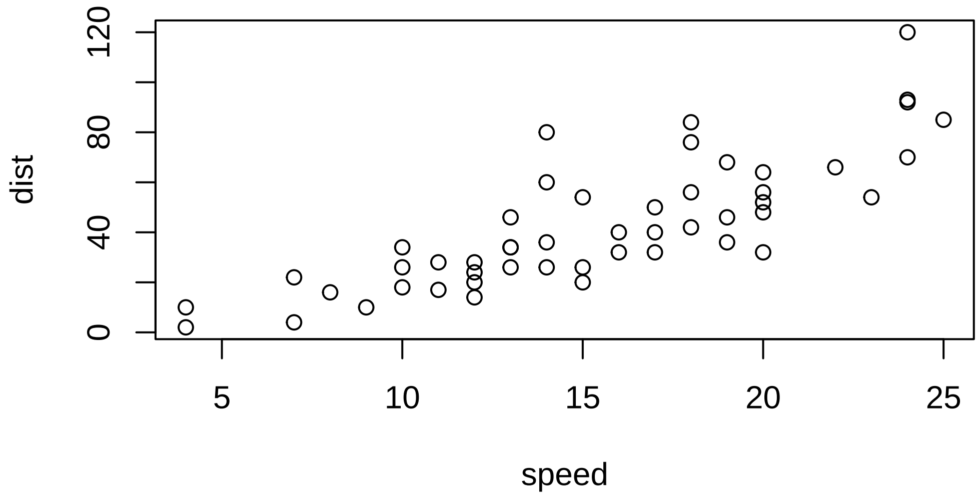
Let's start with plotting a simple dataset in "base R" and then ggplot2 to see how they differ.

```
head(cars)
```

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

To plot this in base R, I just use `plot()`

```
plot(cars)
```

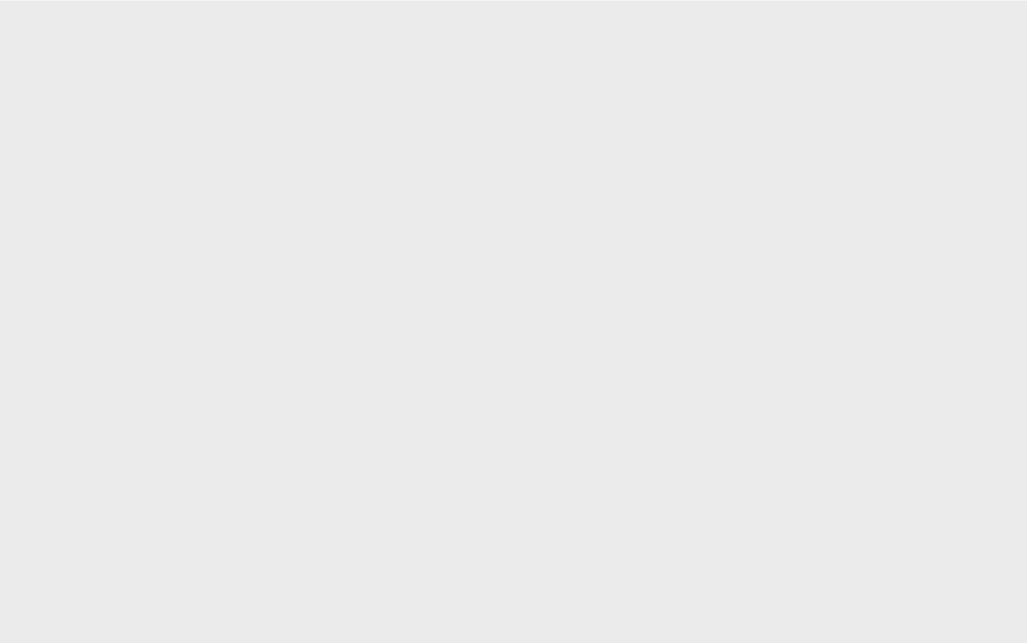


First to use ggplot2 I need install the package. For this I use the `install.packages()` function.

> I don't want to run `install.packages()` in my quarto documents as this would re-install the package every time I render the document. So install it at the Console section.

The main function in the ggplot2 package is `ggplot()`. Before i can use this function I need to load the package with a `library()` call.

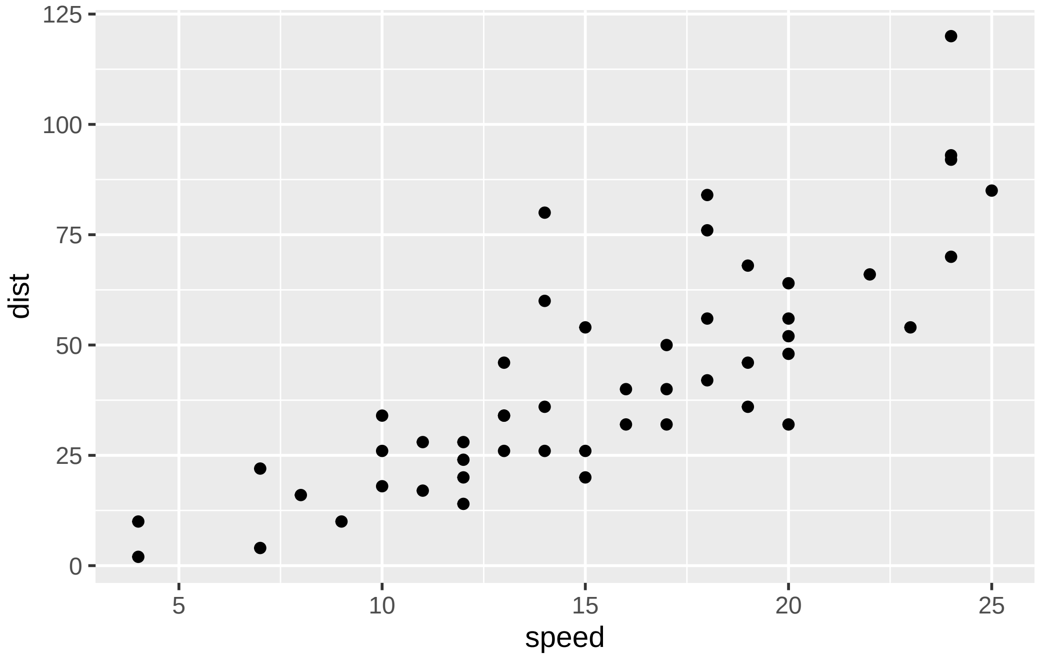
```r
library(ggplot2)
ggplot(cars)
```



There are at least 3 things that every ggplot needs:

- the **data** (the data I want to plot)
- the **aes**thetics 9how the data maps to my plot)
- the **geoms** or geometries (the type of plot)

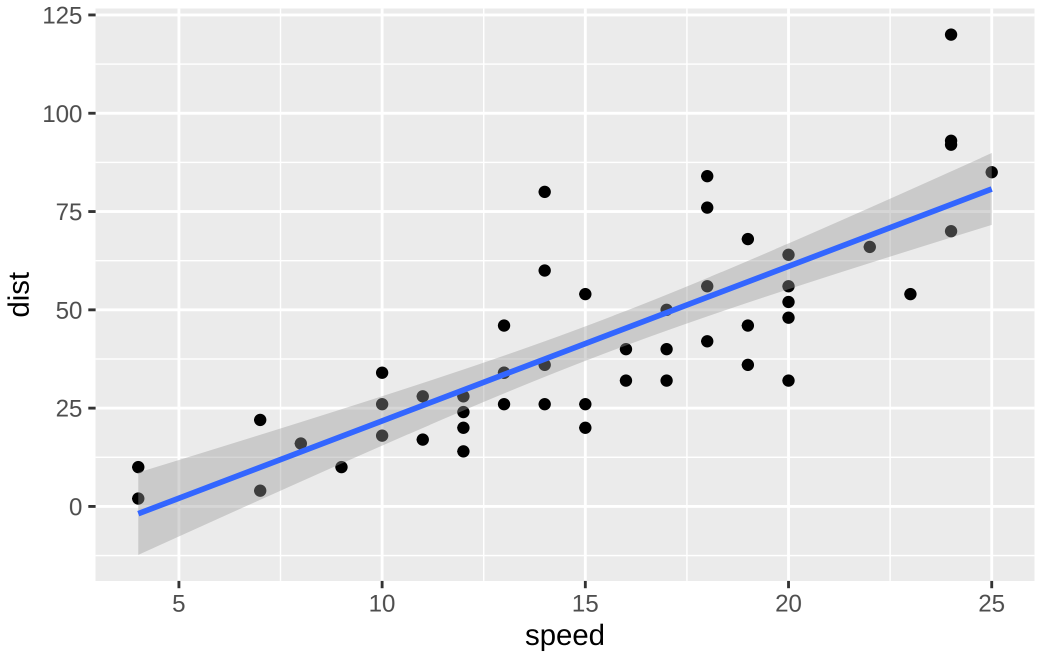
```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point()
```



```
p1 <- ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth(method = "lm")
```

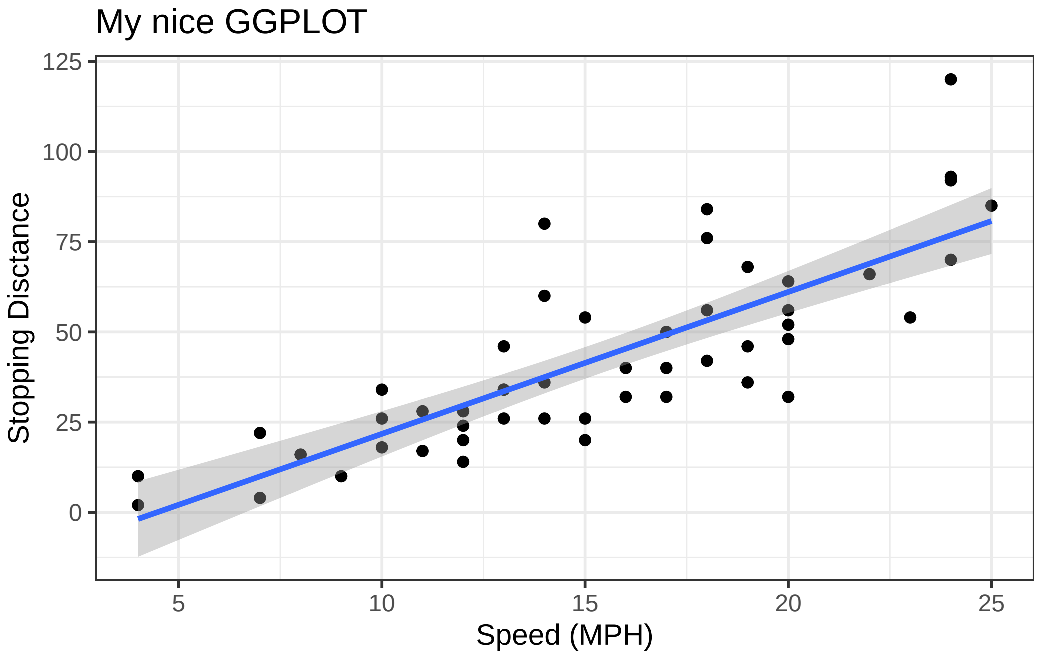
```
p1
```

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



```
p1 + labs(title="My nice GGPLOT",
          x="Speed (MPH)",
          y="Stopping Disctance") +
  theme_bw()
```

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



A RNASeq plot with more aes() values

```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. Use the nrow() function to find out how many genes are in this dataset. What is your answer?

```r
nrow(genes)
```

```
[1] 5196
```

> Q. Use the colnames() function and the ncol() function on the genes data frame to find out what the column names are (we will need these later) and how many columns there are. How many columns did you find?

```
ncol(genes)
```

```
[1] 4
```

> Q. Use the table() function on the State column of this data.frame to find out how many 'up' regulated genes there are. What is your answer?

```
sum(genes$State =="up")
```

```
[1] 127
```

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

```

      down unchanging         up 
        72       4997        127 
```

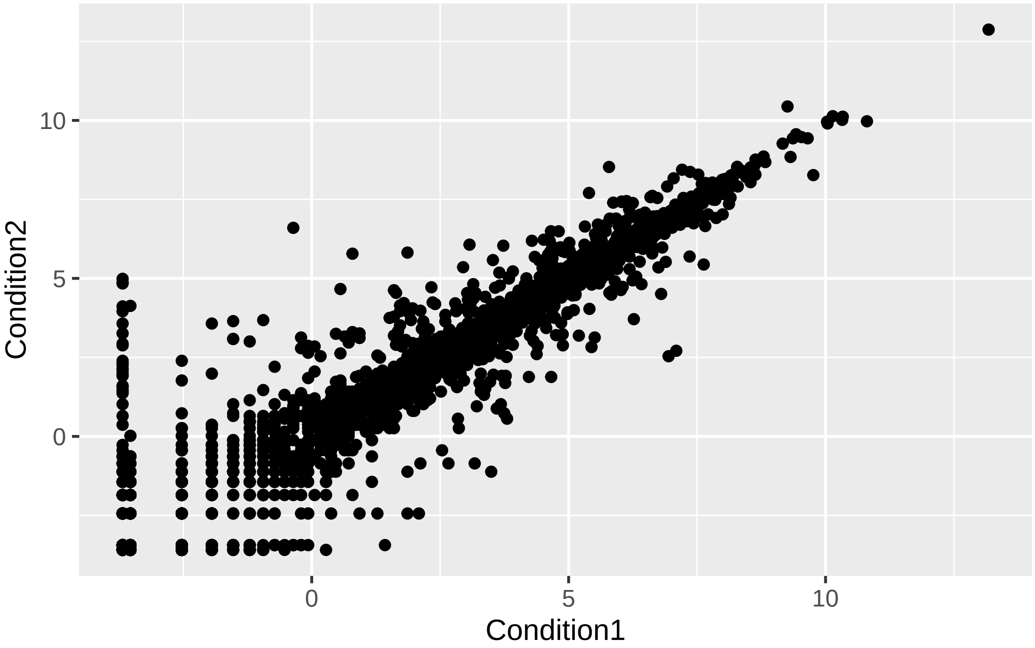
> Q. Using your values above and 2 significant figures. What fraction of total genes is up-regulated in this dataset?

```
table(genes$State) / nrow(genes) * 100
```

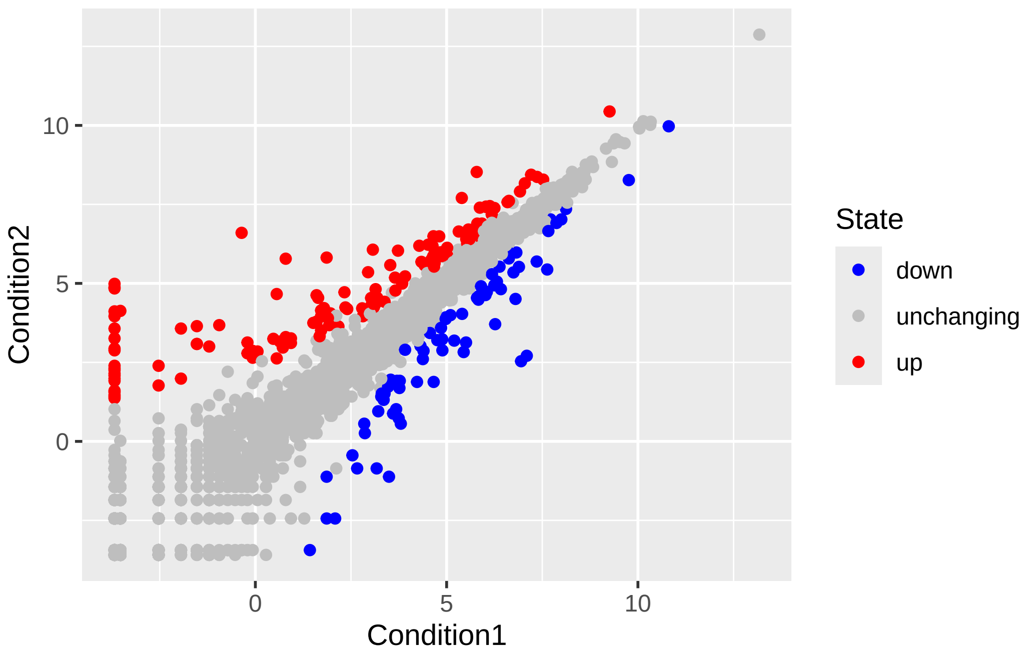
```

      down unchanging         up 
  1.385681  96.170131   2.444188 
```

> Q. Complete the code below to produce the following plot

```
ggplot(genes) + 
    aes(x=Condition1, y=Condition2) +
    geom_point()
```

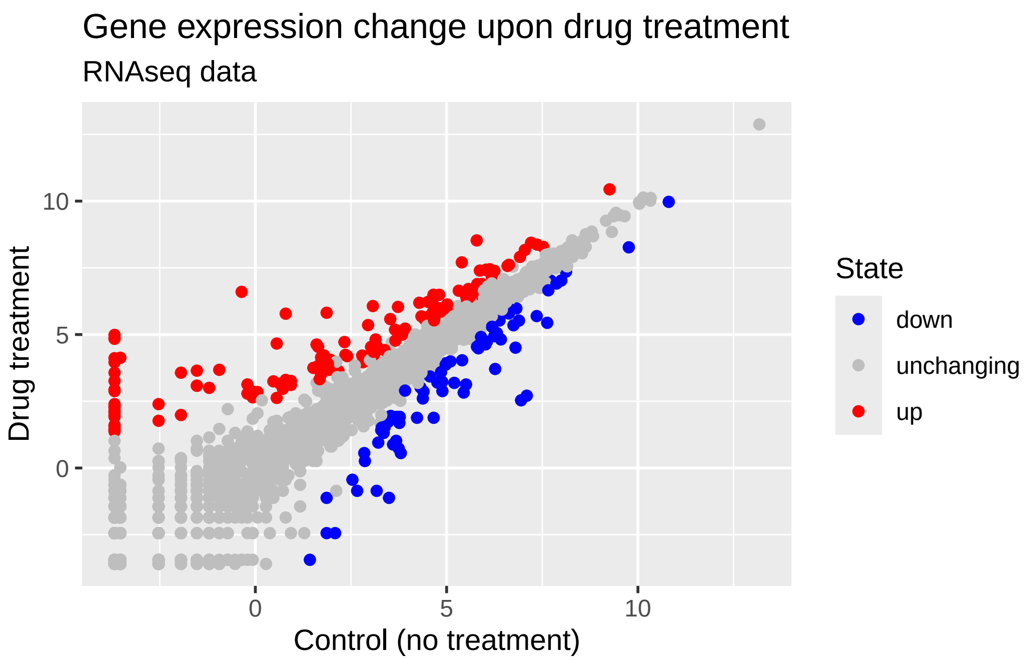


```
ggplot(genes) +
    aes(x=Condition1, y=Condition2, col=State) +
    geom_point() +
    scale_color_manual(values = c("blue", "grey", "red"))
```



```
p2 <- ggplot(genes) +
    aes(x=Condition1, y=Condition2, col=State) +
    geom_point() +
    scale_color_manual(values = c("blue", "grey", "red"))
```

```
p2 + labs(title="Gene expression change upon drug treatment",
         subtitle = "RNAseq data",
         x= "Control (no treatment)",
         y= "Drug treatment")
```



Gapminder dataset plots

We can get exposure to setting more `aes()` parameters with datasets that include more columns of useful data. For example the **gapminder** dataset on GPD and life expendency for different countries over time.

```
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.

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

How many entries (i.e. rows)

```
nrow(gapminder)
```

```
[1] 1704
```

Have a wee peak ar the first 6 rows

```
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
```

How many unique countries are there in the dataset?

```
length(unique(gapminder$country))
```

```
[1] 142
```

What years does the dataset cover?

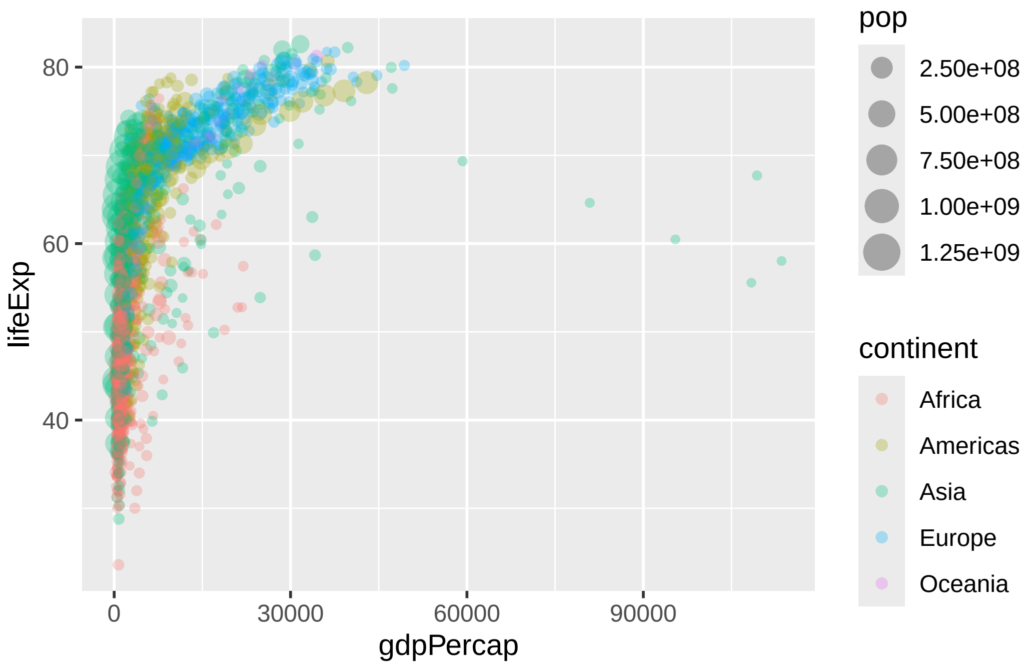
```
table(gapminder$year)
```

```

1952 1957 1962 1967 1972 1977 1982 1987 1992 1997 2002 2007 
 142  142  142  142  142  142  142  142  142  142  142  142 
```

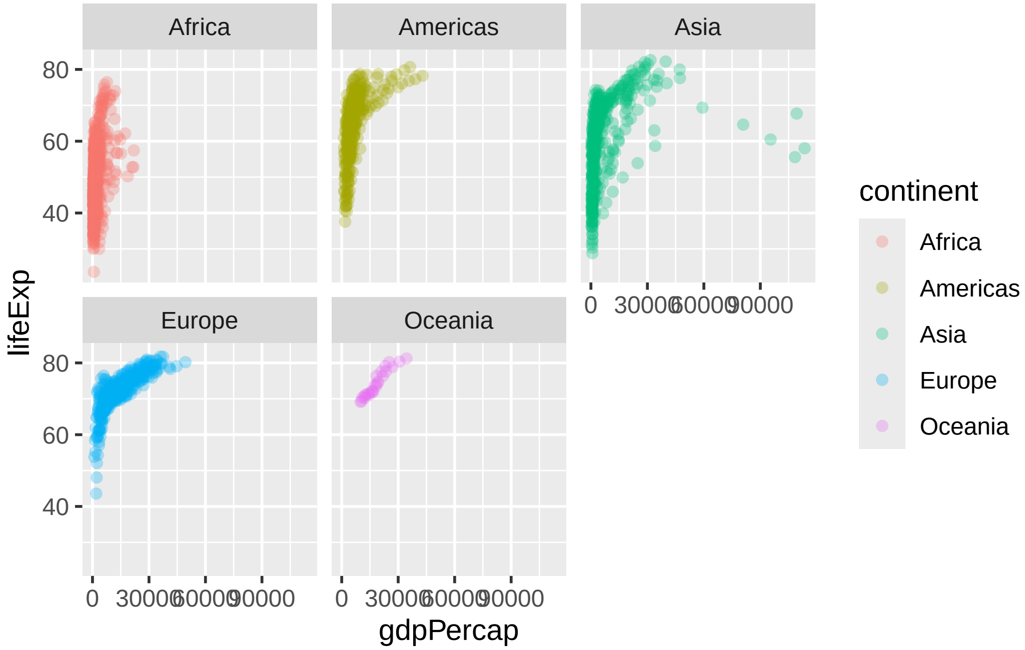
Key function that will be useful in our R ourney include:

- nrow()
- ncol()
- length()
- unique()
- table()

```
ggplot(gapminder) +
  aes(x=gdpPercap, y=lifeExp, col=continent, size=pop) +
  geom_point(alpha=0.3)
```



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



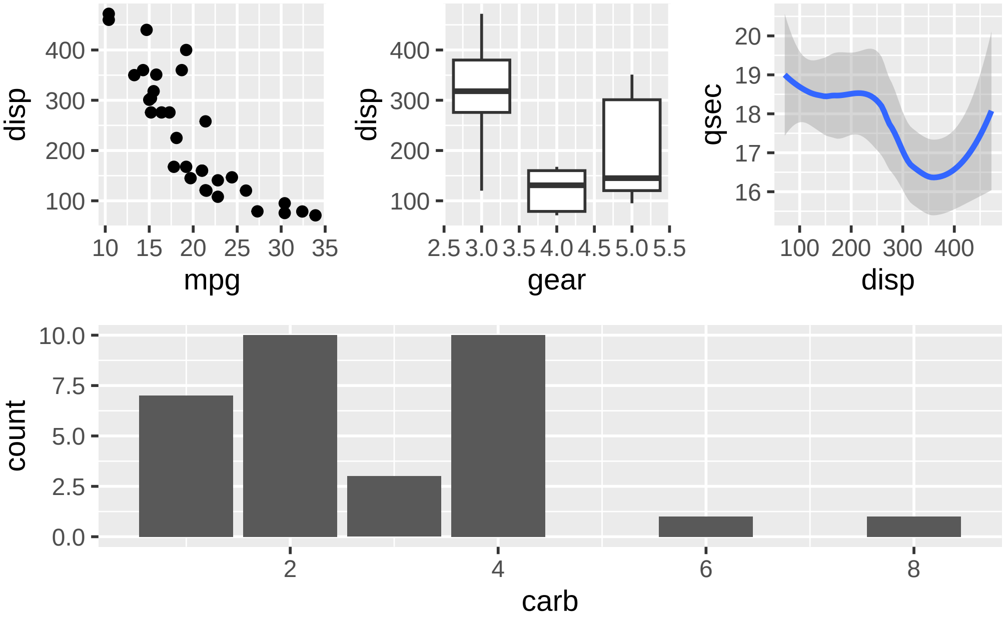
Combining plots

```
library(patchwork)
```

```
Warning: package 'patchwork' was built under R version 4.3.3
```

```
# Setup some example plots
p1 <- ggplot(mtcars) + geom_point(aes(mpg, disp))
p2 <- ggplot(mtcars) + geom_boxplot(aes(gear, disp, group = gear))
p3 <- ggplot(mtcars) + geom_smooth(aes(disp, qsec))
p4 <- ggplot(mtcars) + geom_bar(aes(carb))

# Use patchwork to combine them here:
(p1 | p2 | p3) /
      p4
```

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


disp
400
300
200
100
10
15
20
25
30
35
mpg
disp
400
300
200
100
2.5
3.0
3.5
4.0
4.5
5.0
5.5
gear
qsec
20
19
18
17
16
100
200
300
400
disp
count
10.0
7.5
5.0
2.5
0.0
2
4
6
8
carb