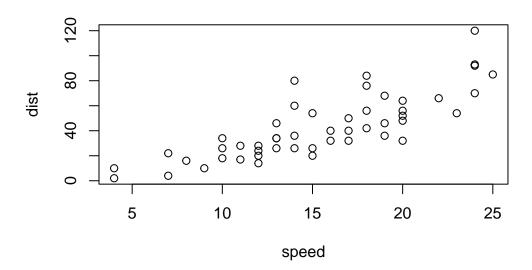
# Class05

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# Plotting in R

R has lot's of ways to make plots and figures. This includes so-called **base** graphics and packages like **ggplot** 

plot(cars)



This is a base R plaot of the in-built 'cars' dataset that has only two column

head(cars)

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

Q. How would we plot this wee dataset with ggplot2

All ggplot figures have at least 3 layers

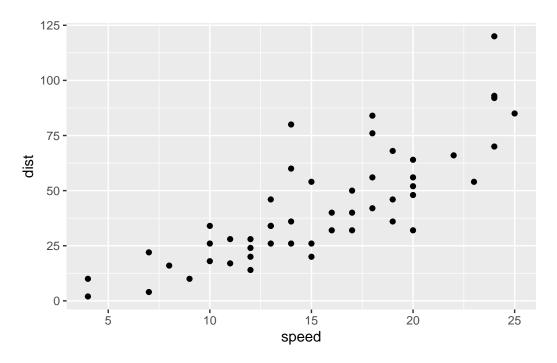
data aesthetics (how the data map to the plot) **geoms** (how we draw the plot, lines, points, etc.)

Before I use any new package I need to download and install it with the 'install.packages()' command.

I never use install.packages() within my quarto document otherwise I will install the package over and over again - which is silly!

Once a package is installed i can load it up with the library() function.

```
#install.packages("ggplots")
library(ggplot2)
ggplot(cars)+
  aes(x=speed,y=dist)+
  geom_point()
```



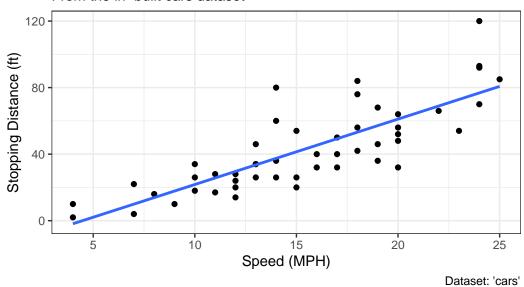
**Key point**: For simple fplots (like the one above) ggplot is more verbose (we need to do more typing) bus as plots get more complicated ggplot starts to be more clear and simple than base R plot()

#shortcut(option command i)

<sup>`</sup>geom\_smooth()` using formula = 'y ~ x'

## Stopping distance of old cars

From the in-built cars dataset



Q. Which plot types are typically NOT used to compare distributions of numeric variables?

Network graphs

Q. Which statement about data visualization with ggplot2 is incorrect? ggplot2 is the only way to create plots in R

### **Scatterplot**

Results of a differential expression analysis where a new anti-viral drug is being tested

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

```
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?

#### 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?

#### colnames(genes)

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

#### 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?

#### table(genes\$State)

${\tt down}$	${\tt unchanging}$	up
72	4997	127

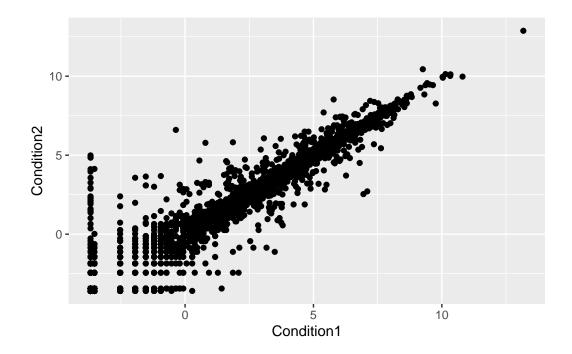
Q. Using your values above and 2 significant figures. What fraction of total genes is up-regulated in this dataset?

```
round( table(genes$State)/nrow(genes) * 100, 2 )
```

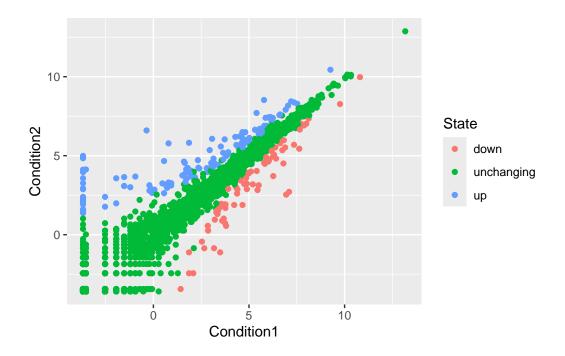
```
down unchanging up
1.39 96.17 2.44
```

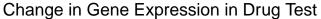
A first plot:

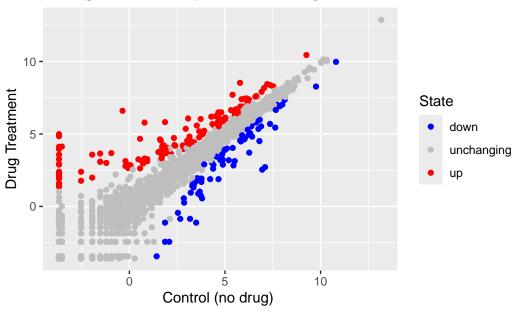
```
ggplot(genes) +
  aes(x=Condition1, y=Condition2) +
  geom_point()
```



```
p<-ggplot(genes)+
  aes(x=Condition1, y=Condition2, col=State)+
  geom_point()
p</pre>
```







# **Going Further**

The gapminder dataset contains economic and demographic data about various countries since 1952. The data itself is available as either a tab-delimited file online, or via the gapmider package.

```
# File location online
url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts
gapminder <- read.delim(url)
library(dplyr)</pre>
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

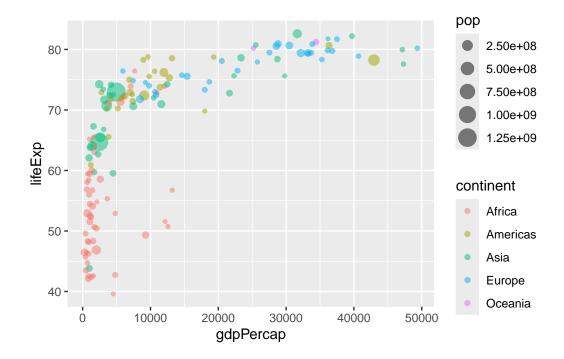
The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
gapminder_2007 <- gapminder %>% filter(year==2007)
```

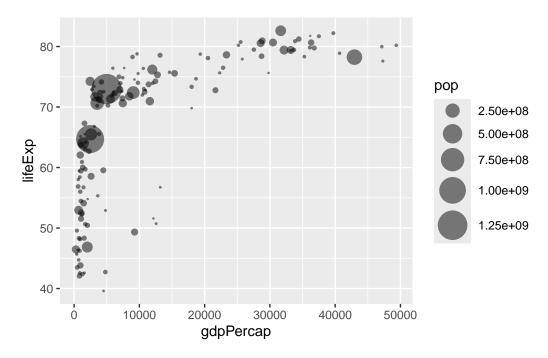
Let's consider the gapminder\_2007 dataset which contains the variables GDP per capita gdp-Percap and life expectancy lifeExp for 142 countries in the year 2007

```
ggplot(gapminder_2007) +
aes(x=gdpPercap,
    y=lifeExp,
    color=continent,
    size=pop) +
geom_point(alpha=0.5) #alpha=changes point transparancy
```

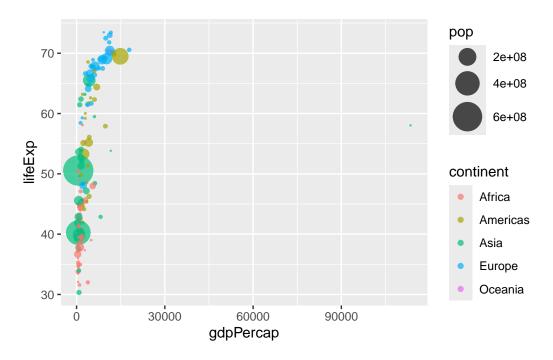


#### Adjust Point Size

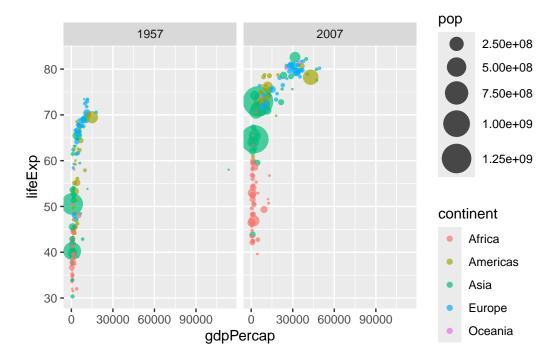
```
geom_point(alpha=0.5)+
scale_size_area(max_size = 10) #reflect the population differences by the point size
p2007
```



#### Plot for 1957



#### 1957 and 2007



Q. Extract data fro the US in 1992

country continent year lifeExp pop gdpPercap
1 United States Americas 1992 76.09 256894189 32003.93

Q. What is the population of Ireland in 2007

```
filter(gapminder, country=="Ireland", year==2007)
```

country continent year lifeExp pop gdpPercap 1 Ireland Europe 2007 78.885 4109086 40676

- Q. What countries in data set had pop smaller than Ireland in 2007?
- 1. First limit/subset the data set to the year 2007
- 2. Then find the pop value for Ireland
- 3. Then extract all rows with pop less than Ireland's

```
Ireland2007<- filter(gapminder,year==2007,country=="Ireland") #Step 1</pre>
Ireland2007$pop #Step 2
```

#### [1] 4109086

```
nrow(filter(gapminder,year==2007,pop<Ireland2007$pop)) #Step 3</pre>
```

[1] 31

##Box Charts

Below you can find an example showing the number of people (in millions) in the five biggest countries by population in 2007

```
gapminder_top5 <- gapminder %>%
  filter(year==2007) %>%
  arrange(desc(pop)) %>%
  top_n(5, pop)

gapminder_top5
```

```
        country
        continent
        year
        lifeExp
        pop
        gdpPercap

        1
        China
        Asia
        2007
        72.961
        1318683096
        4959.115

        2
        India
        Asia
        2007
        64.698
        1110396331
        2452.210

        3
        United States
        Americas
        2007
        78.242
        301139947
        42951.653

        4
        Indonesia
        Asia
        2007
        70.650
        223547000
        3540.652

        5
        Brazil
        Americas
        2007
        72.390
        190010647
        9065.801
```

The echo: false option disables the printing of code (only output is displayed).