

Day 2

# Iteration

In programming it's important to **reduce duplication**. A rule of thumb is to *never copy and paste the same code more than twice*.

Iteration helps you to *do the same thing to multiple inputs* (e.g. repeating the same operation on different columns, or on different datasets... ).

There are a few ways to iterate in R:

- loops (for loops and while loops - we only focus on the for loop)
- The tidyverse map() functions (even more condense than for loops, but require more knowledge about R than you will get here...)

# Iteration

We have this simple data frame and want to compute the median of each column. We can copy and paste the median() function like this:

```
> df
# A tibble: 10 x 4
      a      b      c      d
  <dbl> <dbl> <dbl> <dbl>
1  1.31  -0.0818 -0.316 -1.06
2 -0.0405 -0.886 -1.30  0.185
3  0.455  -1.50  0.799 -0.283
4  0.0979 -0.552  0.891  1.09
5  0.305   0.160 -0.699  1.18
6 -1.48    0.418 -0.946 -0.580
7 -0.242   1.12  -0.286  1.47
8  0.900   0.136 -0.215 -1.44
9  0.201  -0.697 -0.154  0.0178
10 -1.57    0.919  0.631  0.691
```

```
median(df$a)
#> [1] -0.2457625
median(df$b)
#> [1] -0.2873072
median(df$c)
#> [1] -0.05669771
median(df$d)
#> [1] 0.1442633
```

Remember the  
“accessor”?

# for loop

We have this simple data frame and want to compute the median of each column.  
We can use a **for loop**:

```
output <- vector("double", ncol(df)) # 1. output
for (i in seq_along(df)) {           # 2. sequence
  output[i] <- median(df[[i]])        # 3. body
}
output
#> [1] -0.24576245 -0.28730721 -0.05669771  0.14426335
```

# For loop

Let's look at a simpler example...

```
for(i in 1:5){  
  print(i)  
}  
  
#> [1] 1  
#> [1] 2  
#> [1] 3  
#> [1] 4  
#> [1] 5
```

# for loop

Every for loop has three components:

The **output**

The **sequence**

The **body**

```
output <- vector("double", ncol(df)) # 1. output
for (i in seq_along(df)) {           # 2. sequence
  output[i] <- median(df[[i]])        # 3. body
}
output
#> [1] -0.24576245 -0.28730721 -0.05669771  0.14426335
```

# for loop

Before we start the loop we need to allocate sufficient space for the output (if not it can be very slow).

A general way of creating an empty vector of given length is the `vector()` function. It has two arguments: the type of the vector (“logical”, “integer”, “double”, “character”, etc) and the length of the vector.

```
output <- vector("double", ncol(df)) # 1. output
```

# The vector data type

In R a vector is a kind of list of elements (list is actually something else in R, but never mind...). Vectors are created with the function `c()`.

```
> x <- c(1, 2, 3)
> x
[1] 1 2 3
> x[2]
[1] 2
```



# The vector data type

In R a vector is a kind of list of elements (list is actually something else in R, but never mind...). Vectors are created with the function `c()`.

Vectors can be numeric, character, logic, and more.

```
> murders$state
[1] "Alabama"      "Alaska"      "Arizona"
[4] "Arkansas"     "California"  "Colorado"
[7] "Connecticut"  "Delaware"    "District of Columbia"
[10] "Florida"      "Georgia"     "Hawaii"
[13] "Idaho"        "Illinois"    "Indiana"
[16] "Iowa"         "Kansas"      "Kentucky"

> class(murders$state)
[1] "character"

> murders$total
[1] 135 19 232 93 1257 65 97 38 99 669 376 7 12 364 142 21
[17] 63 116 351 11 293 118 413 53 120 321 12 32 84 5 246 67
[33] 517 286 4 310 111 36 457 16 207 8 219 805 22 2 250 93
[49] 27 97 5

> class(murders$total)
[1] "numeric"
```

# Subsetting

Notice the numbers in brackets in the output. These give hint about how to retrieve certain elements of a vector. This is called subsetting, or indexing (this works on many other data types in R as well).

```
> murders$state[1]
[1] "Alabama"
> murders$state[3:6]
[1] "Arizona"      "Arkansas"      "California" "Colorado"
> murders$state[c(6, 3, 5, 4)]
[1] "Colorado"      "Arizona"      "California" "Arkansas"
> murders$state[c(-6, -3, -5, -4)]
[1] "Alabama"      "Alaska"      "Connecticut"
[4] "Delaware"      "District of Columbia" "Florida"
...
```

# for loop

Before we start the loop we need to allocate sufficient space for the output (if not it can be very slow).

A general way of creating an empty vector of given length is the `vector()` function. It has two arguments: the type of the vector (“logical”, “integer”, “double”, “character”, etc) and the length of the vector.

```
output <- vector("double", ncol(df)) # 1. output
```

The **result of the loop** (output) is a **vector** of type “double” (decimal numbers) and the same length as the number of columns in the data frame.

# The sequence

The sequence determines **what to loop over**. (`seq_along()` is a function that generates a sequence of numbers from 1 to the length of the dataframe - similar to `seq()`).

“i” can be whatever. E.g. “file” in `for (file in seq_along(list_of_files))`.

```
for (i in seq_along(df))           # 2. sequence
```

The loop will iterate for the same number of times as there are columns in the data frame (i.e. 4 columns). “i” will be updated for every iteration (i.e. first iteration i = 1, second iteration i = 2, third i = 3 and fourth i = 4).

# The body

The body is the code that does the work. It's run repeatedly, each time with a different value for "i".

```
output[i] <- median(df[[i]])      # 3. body
```

`df[[i]]` extracts column "i" as a vector of numbers. The function `median()` calculates the median of these numbers. The median is then entered into position "i" in the "output" vector. (the double brackets are needed to extract only the values in the column, and not the entire column with header).

The first iteration of the loop will be:

```
output[1] <- median(df[[1]])
```

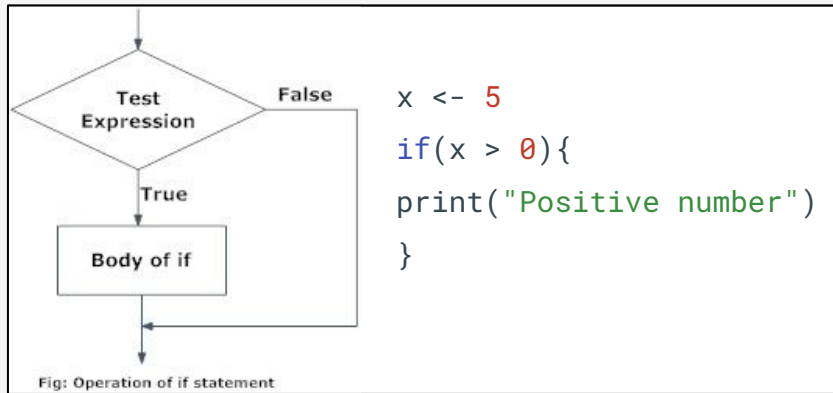
Do Exercise 5

if statements

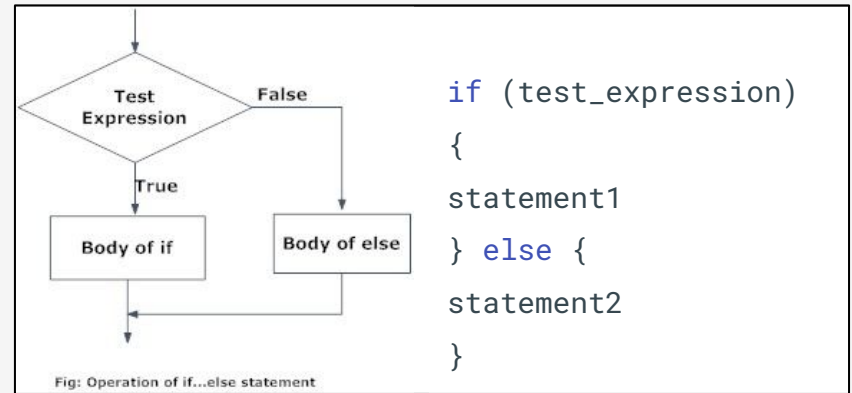
# if statements (conditional expressions)

Conditional expressions are one of the basic features of programming. They are used for what is called *flow control*. The most common conditional expression is the if statement (or the if-else statement)

## Syntax of the if-statement



## Syntax of the if-else statement





# if-else statement

Here is a very simple example that tells us which states, if any, have a murder rate lower than 0.5 per 100,000. The else statement protects us from the case in which no state satisfies the condition.

```
ind <- which.min(murders$rate)

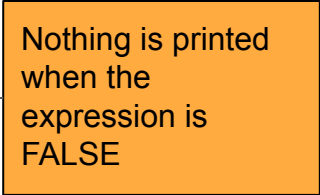
if(murders$rate[ind] < 0.5){
  print(murders$state[ind])
} else{
  print("No state has murder rate that low")
}

#> [1] "Vermont"
```

```
if(murder_rate[ind] < 0.25){
  print(murders$state[ind])
}
>

if(murder_rate[ind] < 0.25){
  print(murders$state[ind])
} else{
  print("No state has a murder rate that low.")
}

#> [1] "No state has a murder rate that low."
```



Do Exercise 6

# Running R from the command line

# R scripts

The first thing we'll do is to log on to Saga and enter your home directory.

From there type:

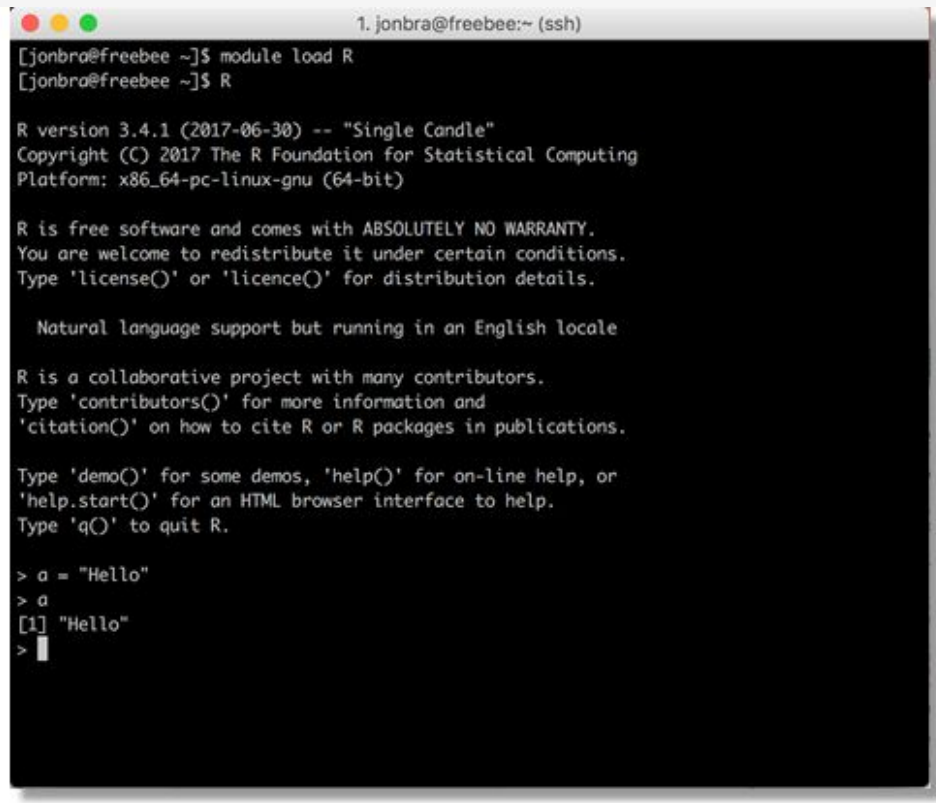
*module load R/4.1.0-foss-2021a*

Then start R by typing “R” and “Enter”.

You should see something similar to the image.

If you see the prompt (“>”) then type:  
*install.packages(“tidyverse”).*

This could take a while...

A screenshot of a terminal window with a dark background and light-colored text. The window title bar shows three colored circles (red, yellow, green) on the left and the text '1. jonbra@freebee:~ (ssh)' on the right. The terminal content shows the user typing 'module load R' and 'R', followed by the R version 3.4.1 startup message. The user then types a command to install the tidyverse package, and the terminal shows the R prompt '>' and the output of the command.

```
1. jonbra@freebee:~ (ssh)
[jonbra@freebee ~]$ module load R
[jonbra@freebee ~]$ R

R version 3.4.1 (2017-06-30) -- "Single Candle"
Copyright (C) 2017 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> a = "Hello"
> a
[1] "Hello"
> 
```

# R scripts

If tidyverse is still installing, open a new Terminal window and log on to Saga again. Otherwise use the same window as before.

Then clone the BIOS-IN5410 GitHub repo to your home directory by first typing `cd` and Enter, and then:

*git clone [https://github.com/jonbra/BIOS-IN5410\\_H2021.git](https://github.com/jonbra/BIOS-IN5410_H2021.git)*

(NB: use the https link).

```
jonbra@login-5:~  
$ git clone https://github.com/jonbra/BIOS-IN5410_H2021.git  
Cloning into 'BIOS-IN5410_H2021'...  
remote: Enumerating objects: 277, done.  
remote: Counting objects: 100% (277/277), done.  
remote: Compressing objects: 100% (255/255), done.  
remote: Total 277 (delta 140), reused 20 (delta 5), pack-reused 0  
Receiving objects: 100% (277/277), 5.74 MiB | 0 bytes/s, done.  
Resolving deltas: 100% (140/140), done.  
Checking out files: 100% (20/20), done.
```

# Exercise 7

Log on to Saga and do Exercise 7.

You can try it yourself, but I will go through each Part separately and explain what is going on.

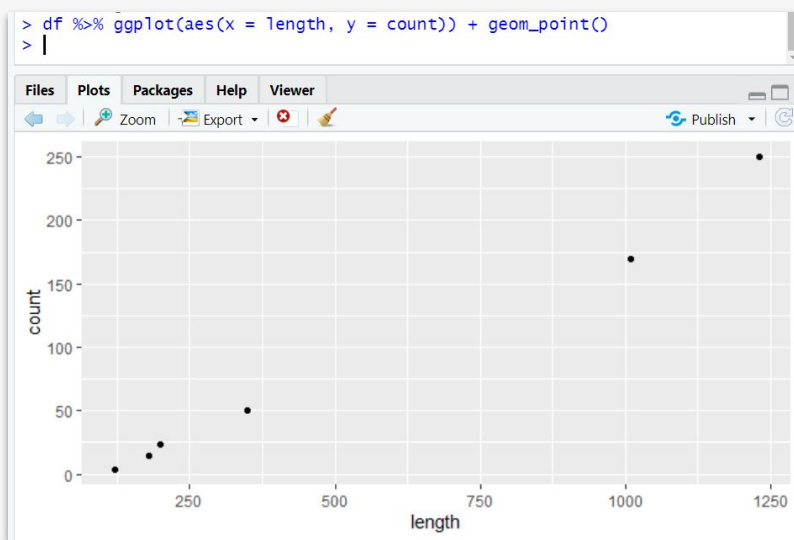
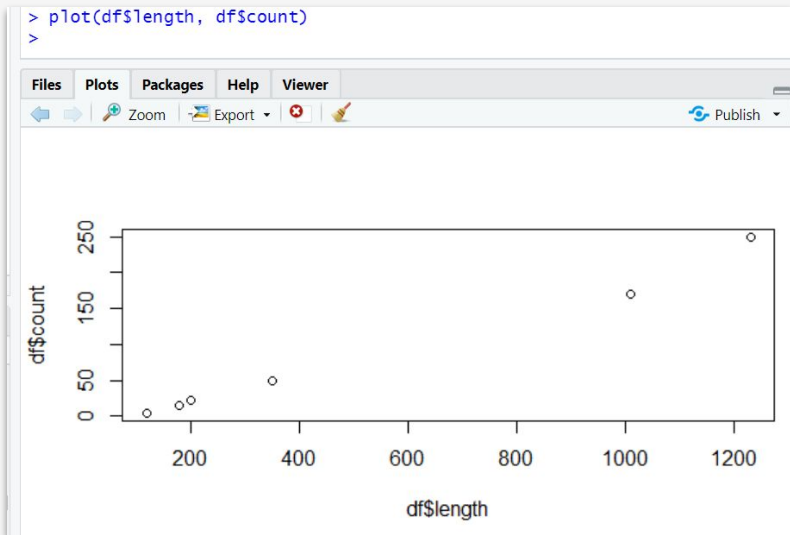
# Plotting with ggplot2

# Plotting with ggplot2

On Friday you made some simple plots with base R plotting functions.

You can make great plots with base R, don't worry. But there's a very popular package for plotting in R, ggplot2, that is very useful to know about.

ggplot2 is automatically activated when you load Tidyverse, and it's particularly suited to operate on tidy data.

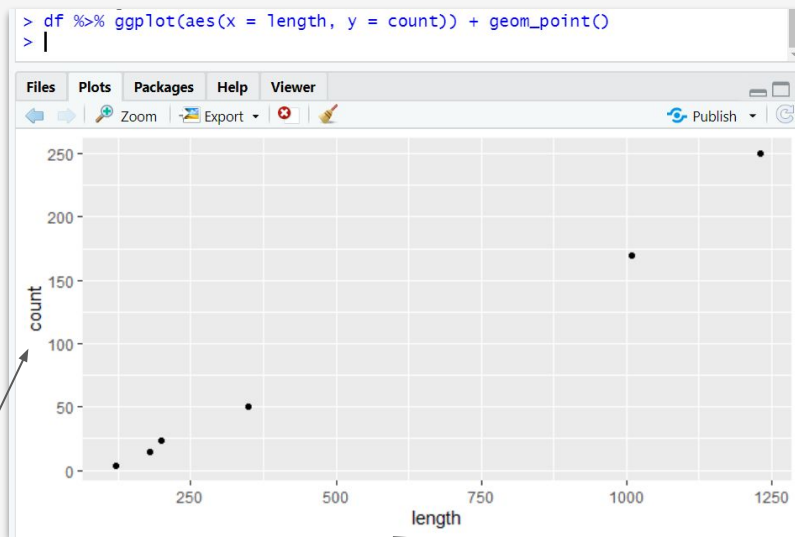




# Plotting with ggplot2

```
> df
# A tibble: 6 x 3
  Gene count length
<chr> <dbl> <dbl>
1 A      4    120
2 B     50   350
3 C     23   200
4 D    250  1230
5 E     15   180
6 F    170  1010
```

```
> df %>%
  ggplot(aes(x = length, y = count)) +
  geom_point()
```



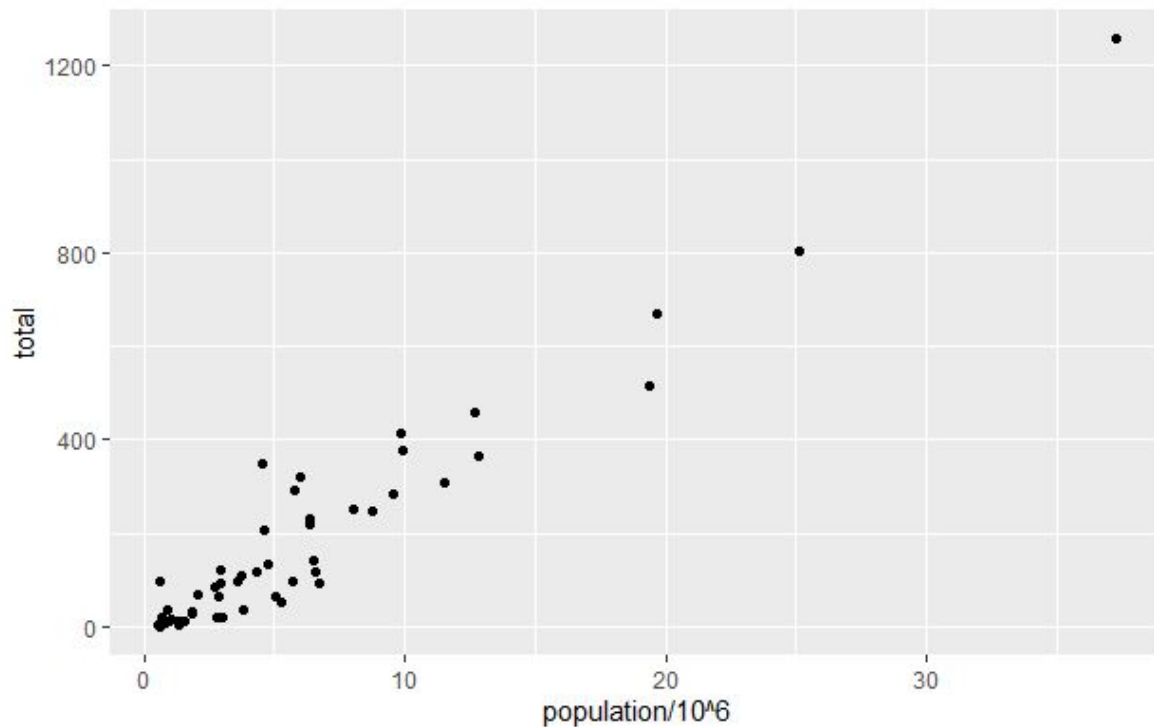
Plots are initiated with the function **ggplot()**. Then the different subfunctions are tied together in layers using the “+” symbol (like a “pipe”).

**Aesthetics** (aes) is a mapping of the variables in the data the different properties of the plot (the geom), like x and y axes, color, etc.

# Plotting with ggplot2

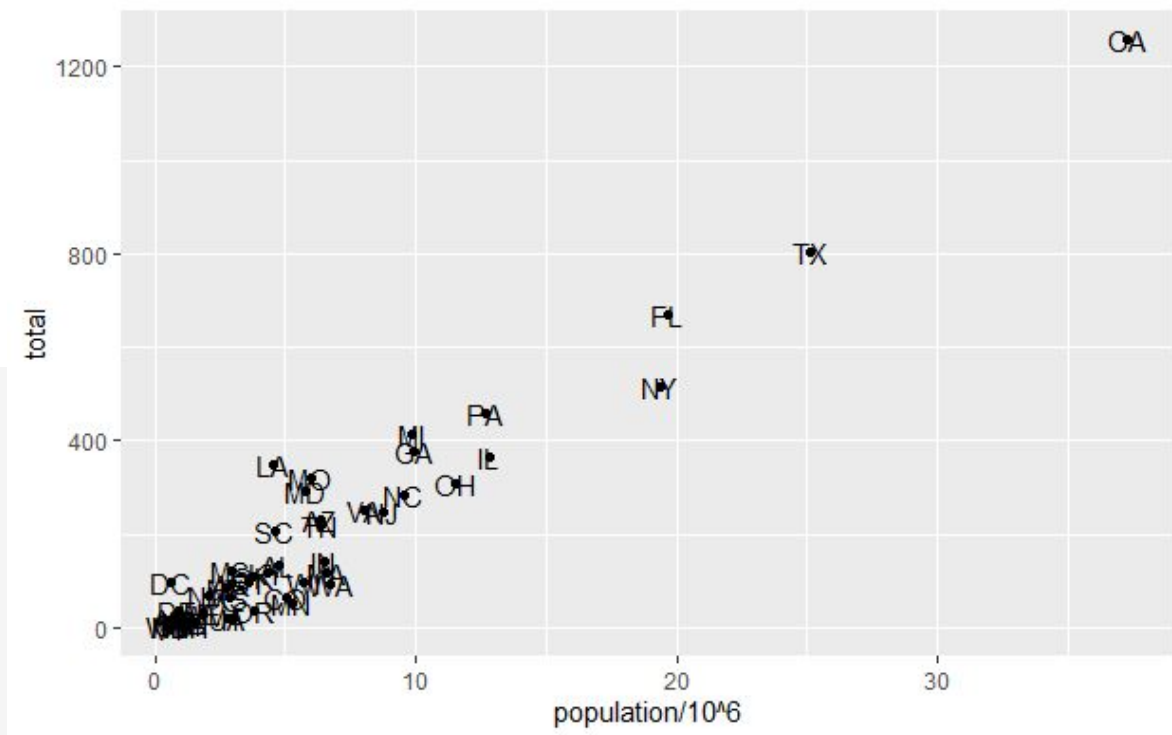
A quick demonstration of how ggplot2 plots are built up by adding layers

```
murders %>% ggplot() +  
  geom_point(aes(x =  
    population/10^6, y = total))
```



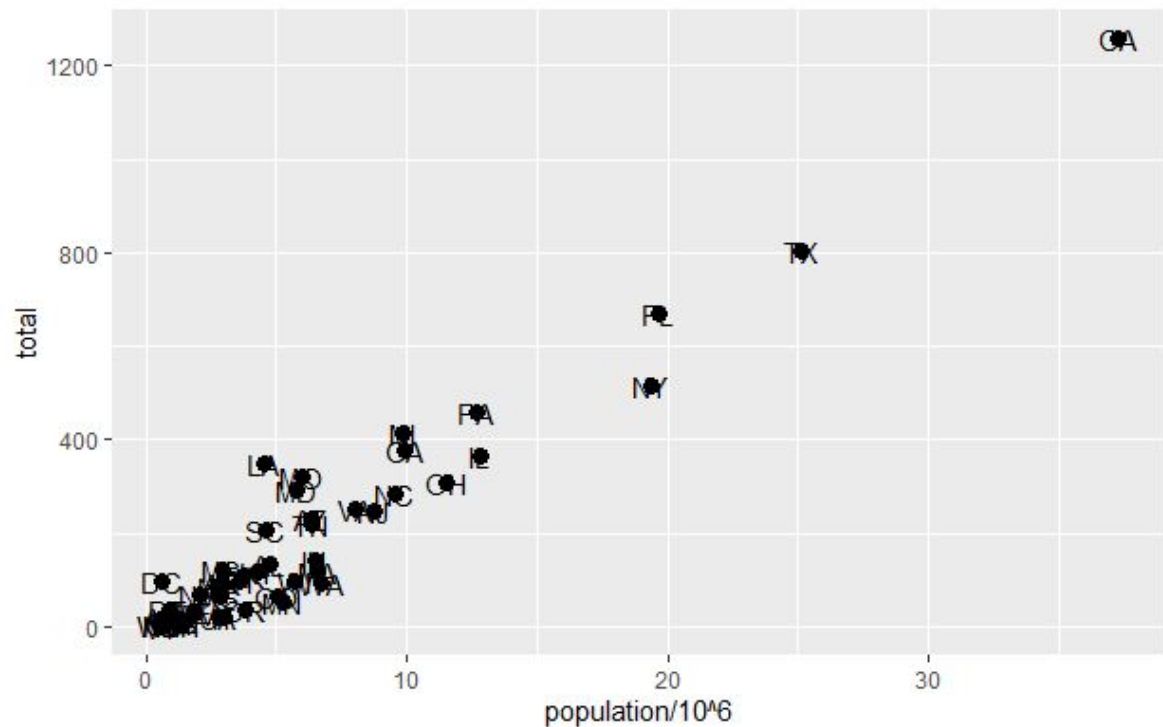
# Plotting with ggplot2

```
murders %>% ggplot() +  
  geom_point(aes(x =  
population/10^6, y = total)) +  
  geom_text(aes(population/10^6,  
total, label = abb))
```



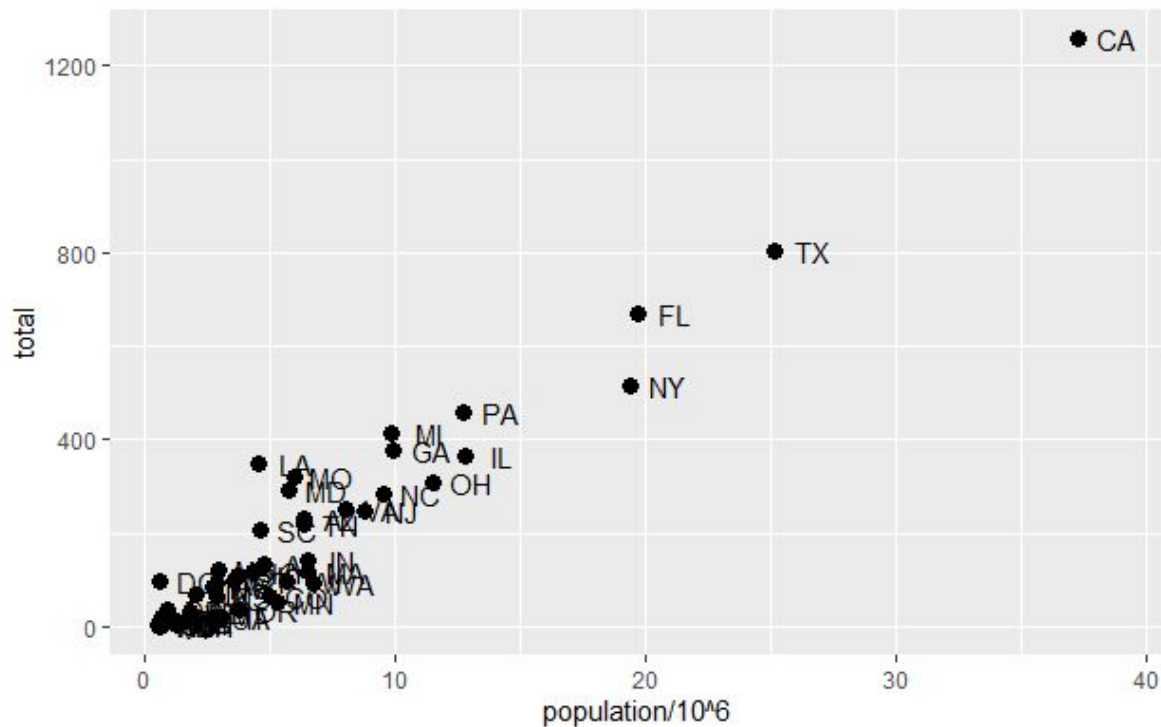
# Plotting with ggplot2

```
murders %>% ggplot() +  
  geom_point(aes(x =  
population/106, y = total), size  
= 3) +  
  geom_text(aes(population/106,  
total, label = abb))
```



# Plotting with ggplot2

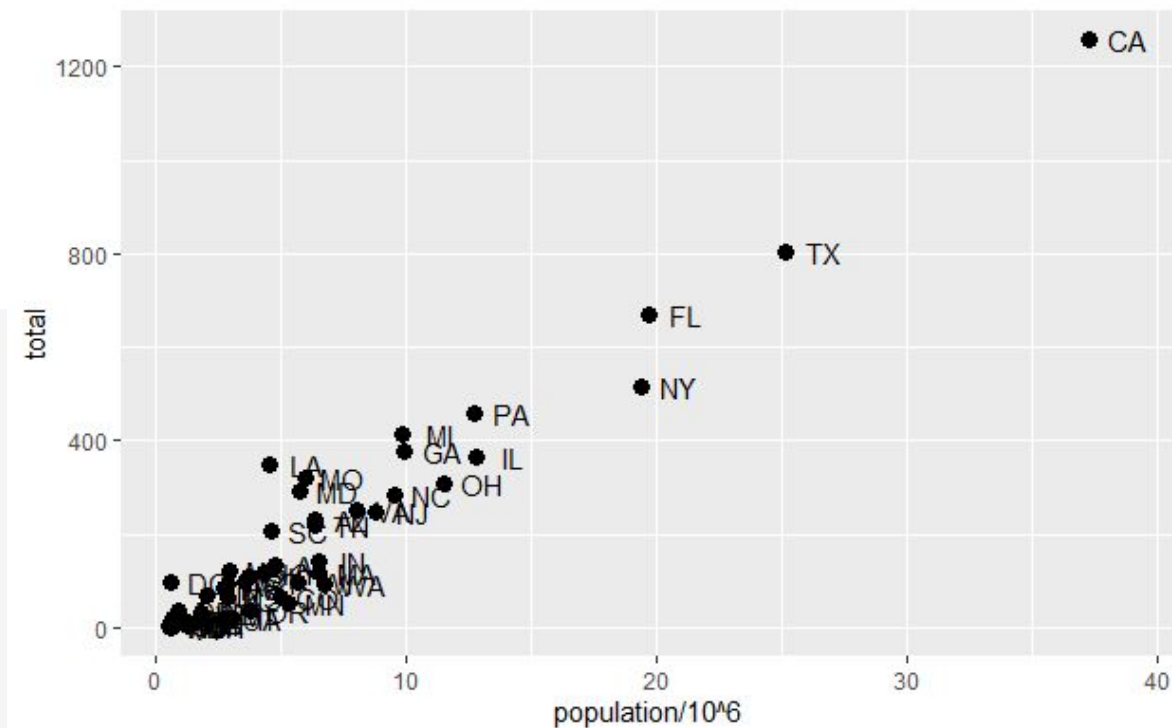
```
murders %>% ggplot() +  
  geom_point(aes(x =  
population/10^6, y = total), size  
= 3) +  
  geom_text(aes(population/10^  
6, total, label = abb), nudge_x =  
1.5)
```



# Plotting with ggplot2

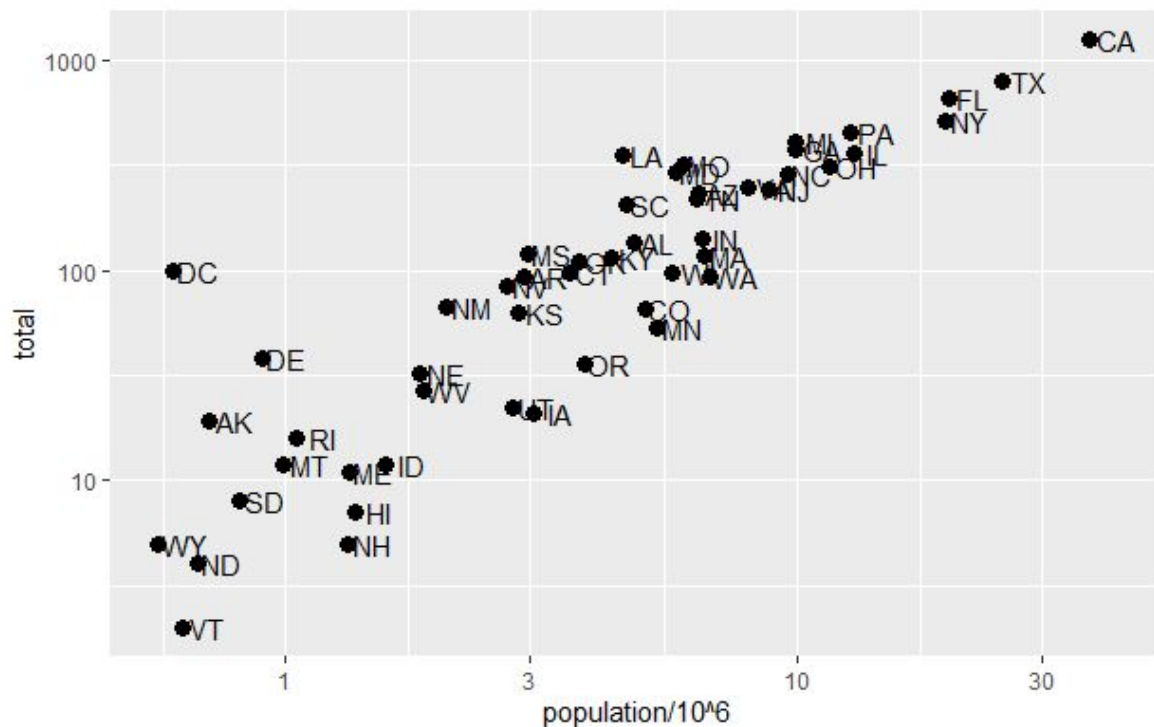
Global aesthetics. Apply to all layers

```
murders %>%  
  ggplot(aes(population/10^6,  
total, label = abb)) +  
  geom_point(size = 3) +  
  geom_text(nudge_x = 1.5)
```



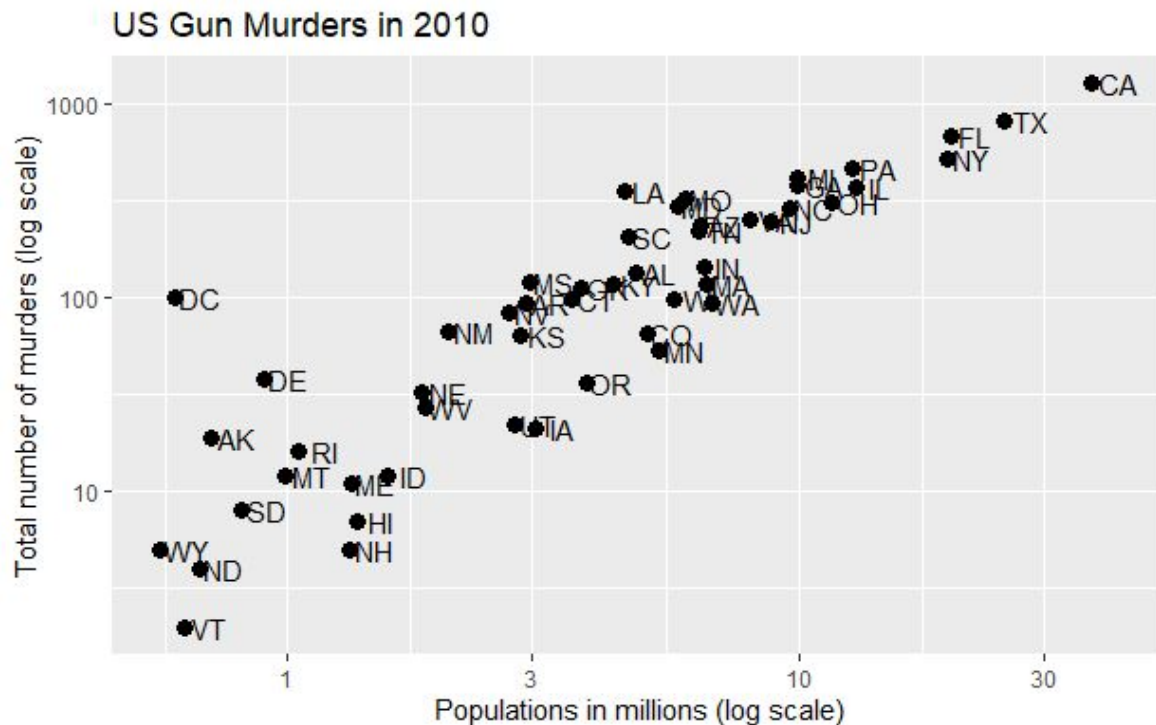
# Plotting with ggplot2

```
murders %>%  
  ggplot(aes(population/10^6,  
total, label = abb)) +  
  geom_point(size = 3) +  
  geom_text(nudge_x = 0.05) +  
  scale_x_continuous(trans =  
"log10") +  
  scale_y_continuous(trans =  
"log10")
```



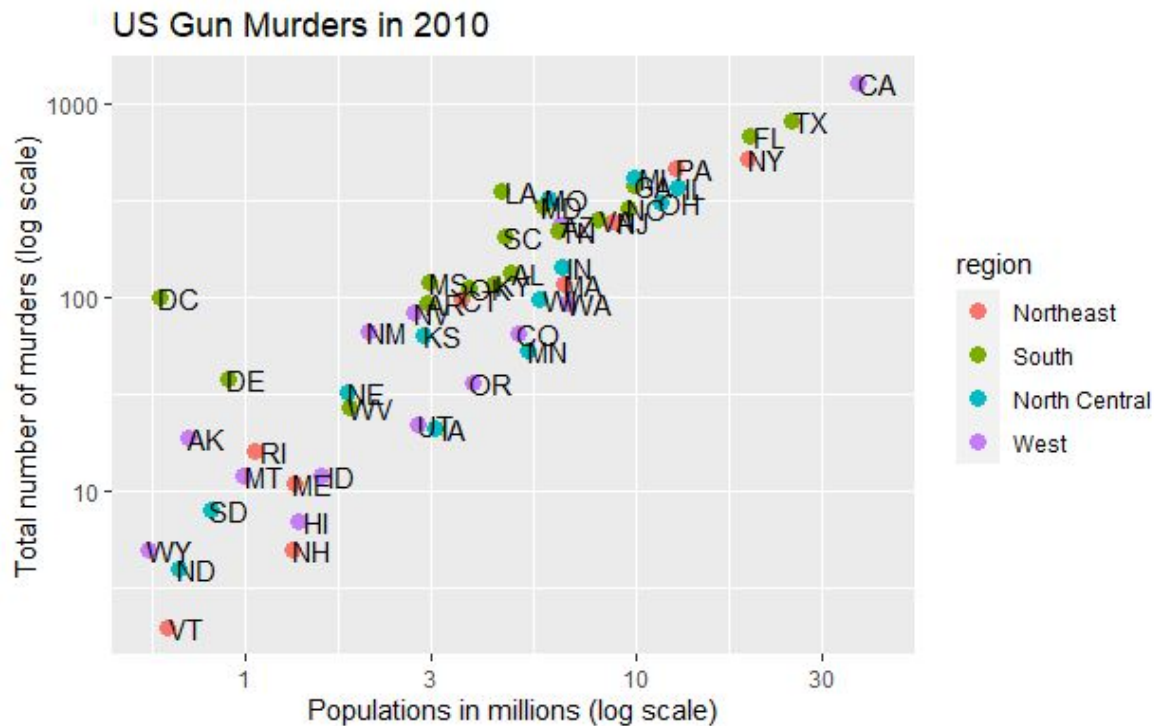
# Plotting with ggplot2

```
murders %>%  
  ggplot(aes(population/10^6,  
total, label = abb)) +  
  geom_point(size = 3) +  
  geom_text(nudge_x = 0.05) +  
  scale_x_continuous(trans =  
"log10") +  
  scale_y_continuous(trans =  
"log10") +  
  xlab("Populations in millions  
(log scale)") +  
  ylab("Total number of murders  
(log scale)") +  
  ggtitle("US Gun Murders in  
2010")
```

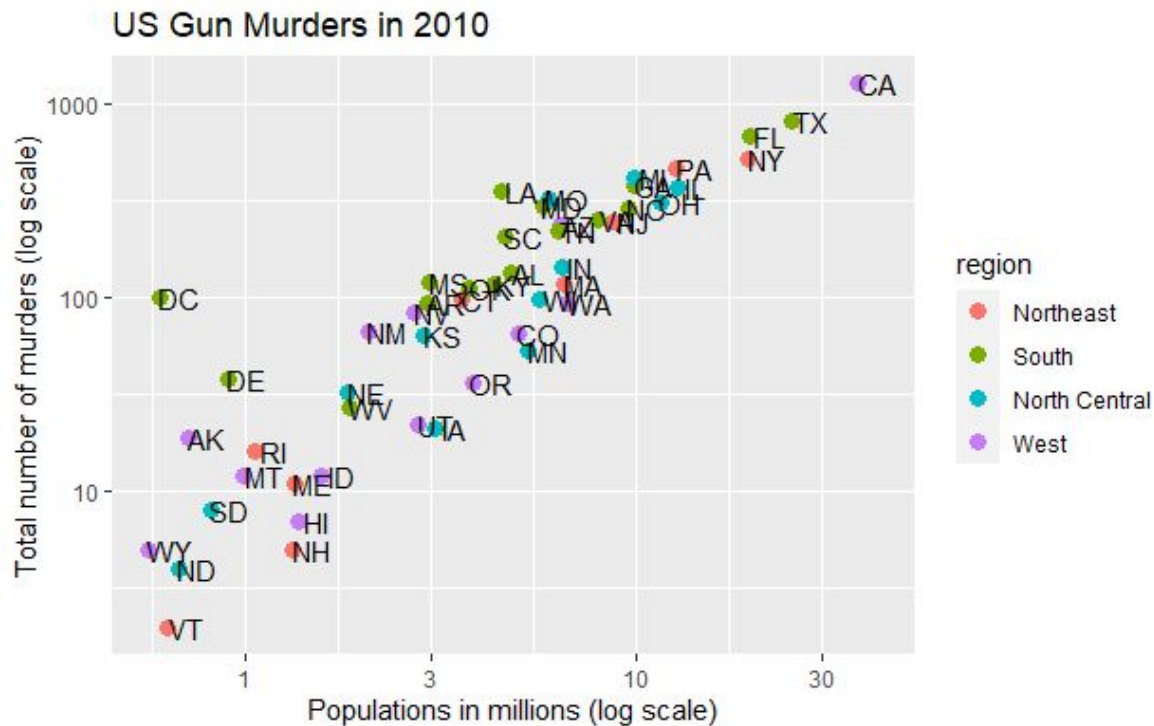




```
murders %>%
  ggplot(aes(population/10^6, total,
    label = abb)) +
  geom_point(aes(col = region), size
    = 3) +
  geom_text(nudge_x = 0.05) +
  scale_x_continuous(trans =
    "log10") +
  scale_y_continuous(trans =
    "log10") +
  xlab("Populations in millions (log
    scale)") +
  ylab("Total number of murders (log
    scale)") +
  ggtitle("US Gun Murders in 2010")
```



```
murders %>%
  ggplot(aes(population/10^6, total,
    label = abb)) +
  geom_point(aes(col = region), size
    = 3) +
  geom_text(nudge_x = 0.05) +
  scale_x_continuous(trans =
    "log10") +
  scale_y_continuous(trans =
    "log10") +
  xlab("Populations in millions (log
    scale)") +
  ylab("Total number of murders (log
    scale)") +
  ggtitle("US Gun Murders in 2010")
```



Do Exercise 8