Assignment solutions

First assignment 201001

What is the sum of the first 100 positive integers?

```
n = 100
result = n*(n+1)/2
Result
5050
```

Use the accessor $ to extract the state abbreviations and assign them to the object a. What is the class of this object?

```
a= murders$abb
class(a)
[1] "character"
```

Now use the square brackets to extract the state abbreviations and assign them to the object b. Use the identical function to determine if a and b are the same.

```
b = murders[names(murders) == 'abb']
class(b)
[1] "data.frame"
class(a)==class(b)
[1] FALSE
```

```
b= murders[,2]
class(b)
[1] "character"
class(a)==class(b)
[1] TRUE
```

First assignment 201001

The function table takes a vector and returns the frequency of each element. You can quickly see how many states are in each region by applying this function. Use this function in one line of code to create a table of states per region.

```
table(murders$region)
## ## Northeast South North Central West
## 9 17 12 13
```

Create two vectors of different dimensions and insert the second one in the first one between the 2nd and 3rd elements.

```
x = c(1,2,3,4)
y = c(5,6,7)
x = c(x[1:2],y,x[3:length(x)])
x
## [1] 1 2 5 6 7 3 4
```

First assignment 201001

Draw 100 numbers from a Uniform distribution on [0,1] and count how many values are larger than 0.5

```
sum(runif(100)>0.5)
```

Compute the per 100,000 murder rate for each state and store it in the object murder_rate. Then compute the average murder rate for the US using the function mean. What is the average?

```
murder_rate = murders$total/murders$population*100000
mean(murder_rate)
## [1] 2.779125
```

Write a script allowing to load a vector file and "remove" the missing values.

```
vector<-read_csv("./vector.csv)
vector
## 2,3NA,5,4)
 na.omit(vector)
vector=vector[!is.na(vector)]
vector
## 2,3,5,4
```

First assignment 201001

Create a histogram of the state populations.

```
hist(murders$population)
```

Generate boxplots of the state populations by region.

```
boxplot(population~region,data=murders)
```

Create a function that normalizes a vector:

```
norm_func= function(x){
return ((x-mean(x))/sd(x))
}
```

Use this function on the iris dataset so that each column is normalized

```
data("iris")
sapply(iris[1:4], function(x) norm_func(x))
```

```
iris1 = norm_func(iris[,1])
iris2 = norm_func(iris[,2])
iris3 = norm_func(iris[,3])
iris4 = norm_func(iris[,4])
Iris_norm = data.frame(iris1,iris2,iris3,iris4,iris[,5])
```

Second assignment 201003

Random vector

1. Generate a random normal vector of size 100
2. Compute its mean with for/repeat loop
3. Compute its variance withfor/repeat loop

```
vect = rnorm(100)
sum_vect = 0
for (i in vect){
sum_vect = sum_vect + i
}
mean_vect = sum_vect/length(vect)
mean_vect
sum_vect2 = 0
for (j in vect){
sum_vect2= sum_vect2+ (j-mean_vect)^2 }
var_vect=sum_vect2/(length(vect)-1)
var_vect
```

Second assignment 201003

missing values

1. Use the airquality dataset from base
2. Compute the percentage p_na of missing values in a column
3. If p_na > 0,5 → delete the column
4. If p_na <= 0,5 → replace the missing values by 0 or by the mean of the column, depending on a variable "type_na"

```
for (col in colnames(airquality)){
  s_na <- sum(is.na(airquality[[col]]))
  len <- length(airquality[[col]])
  p_na <- s_na / len
  p_na
```

```
airquality1 = airquality[,!(p_na > 0.05)]
```

```
replace_na = function(data, na) {
if (na == "0"){
for (i in 1:length(data)){
data[i][is.na(data[i])] = 0 }
} else if (na == "mean") {
for (i in 1:length(data)){
data[i][is.na(data[i])] = mean(data[,i],na.rm = TRUE)
}
}
return(data)
}
replace_na(data=airquality1, na = "0")
```

Second assignment 201003

mean and standard deviation over the columns

1. Compute the mean of all columns of iris dataset
2. Compute their standard deviation

```
data(iris)
Mean_iris <- apply(select(iris, -(Species)), 2, mean)
Std_iris <- apply(select(iris, -(Species)), 2, sd)
```

```
colMeans(iris[1:4])
sapply(iris[1:4], function(x) sd(x))
```

The graphical system

"Processing large dataset with R"

Introduction to ggplot2

We will be creating plots using the **ggplot2** package.

```
> library(dplyr)
> library(ggplot2)
```

There are also other packages for creating graphics such as **grid** and **lattice**. We chose to use **ggplot2** in this book because it breaks plots into components in a way that permits beginners to create relatively complex and aesthetically pleasing plots using syntax that is intuitive and comparatively easy to remember.

Advantages of ggplot2:

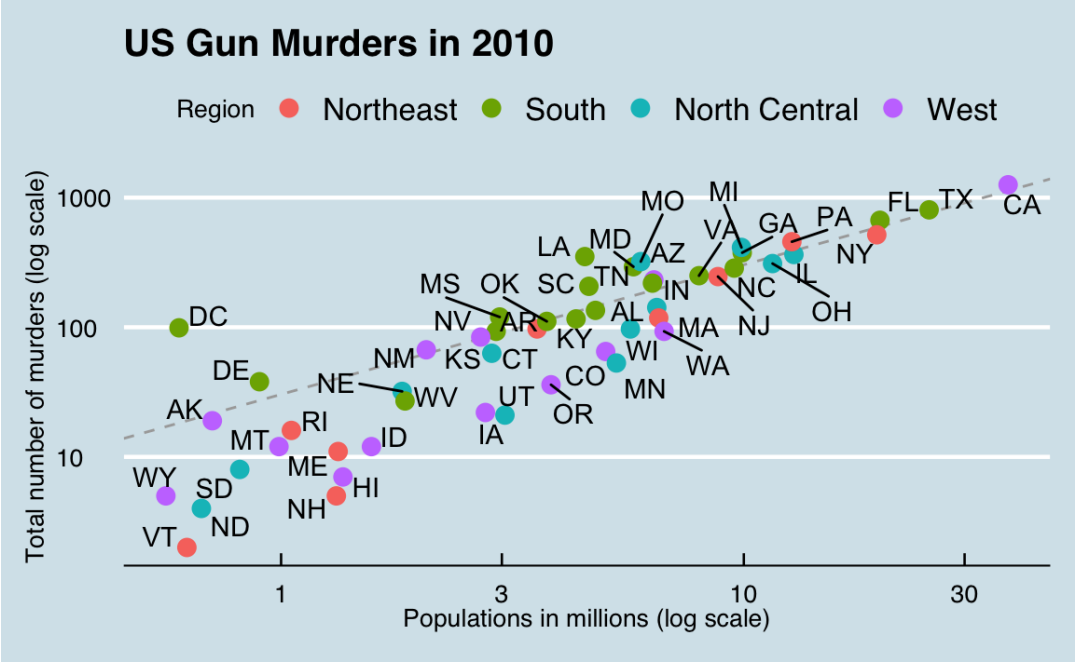
- ✓ Grammar of graphics
- ✓ Default behaviour
- ✓ ggplot2 sheet cheat

Disadvantages of ggplot2:

- ✗ One limitation is that **ggplot2** is designed to work exclusively with data tables in tidy format (where rows are observations and columns are variables).

The components of a graph

We will construct a graph that summarizes the US murders dataset that looks like this:



The main three components to note are:

- **Data**: The US murders data table is being summarized.
- **Geometry**: The plot above is a scatterplot. This is referred to as the **geometry** component.
- **Aesthetic mapping**: The plot uses several visual cues to represent the information provided by the dataset.

ggplot objects

```
> ggplot(data = murders)
```
or
```
> murders %>% ggplot()
```
or
```
> p <- ggplot(data = murders)
```


no geometry has been defined!

Geometries

In ggplot2 we create graphs by adding *layers*. Layers can define geometries, compute summary statistics, define what scales to use, or even change styles. To add layers, we use the the symbol +. In general, a line of code will look like this:

DATA %>% ggplot() + LAYER 1 + LAYER 2 + … + LAYER N

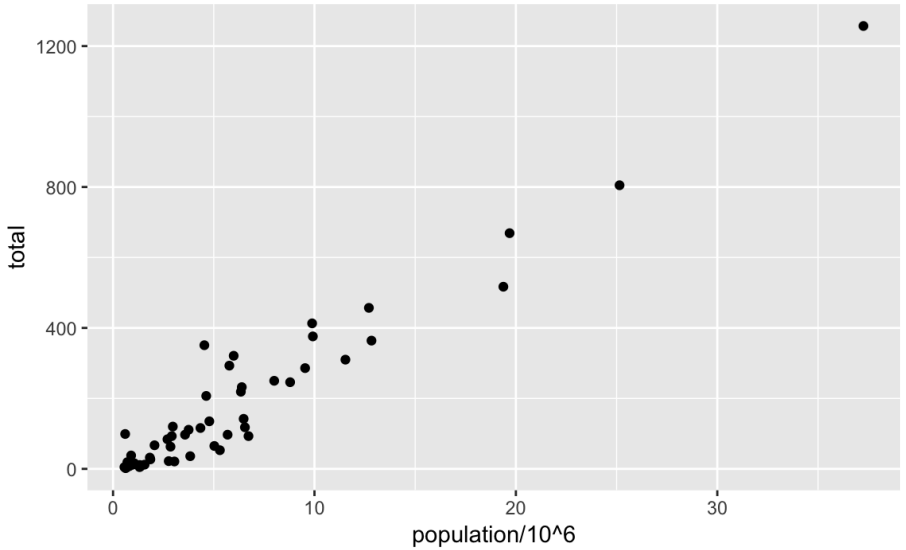
Geometry function names follow the pattern: geom_X where X is the name of the geometry. Some examples include geom_point, geom_bar and geom_histogram.

```
> Aesthetics
>
> geom_point understands the following aesthetics (required aesthetics are in bold):
> x
> y
> alpha
> colour
```

Aesthetic mappings

Aesthetic mappings describe how properties of the data connect with features of the graph, such as distance along an axis, size or color.

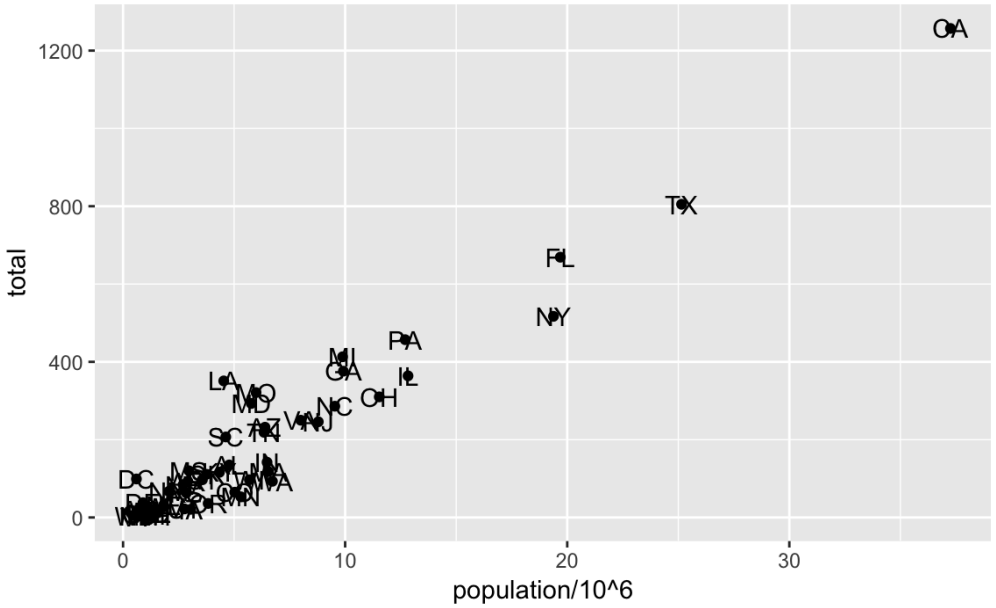
```
murders %>% ggplot() + geom_point(aes(x = population/10^6, y = total))

Or

p + geom_point(aes(population/10^6, total))
```



Layers

A second layer in the plot we wish to make involves adding a label to each point to identify the state. The geom_label and geom_text functions permit us to add text to the plot with and without a rectangle behind the text respectively.

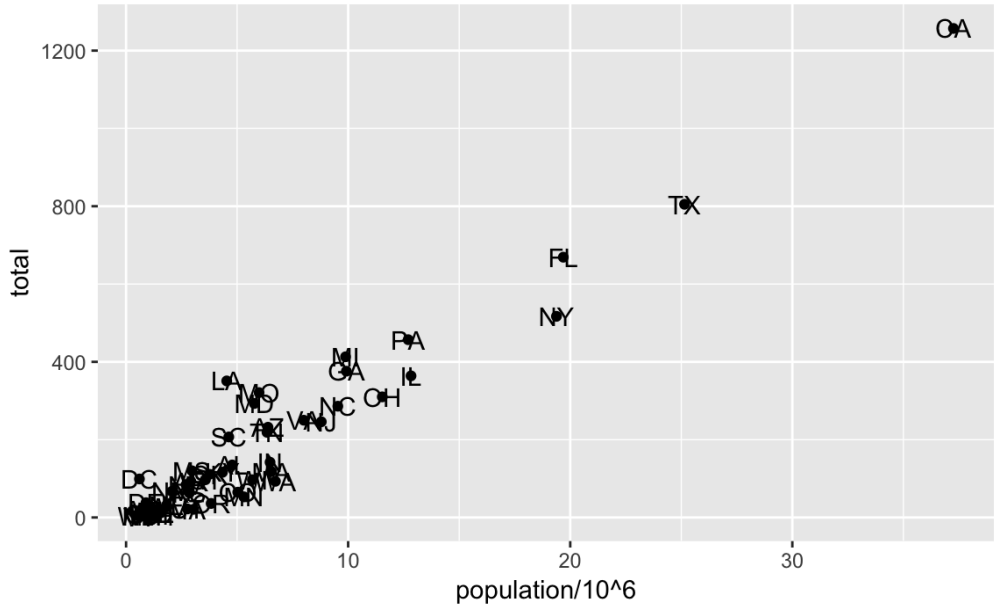
```
p + geom_point(aes(population/10^6, total)) + geom_text(aes(population/10^6, total, label = abb))
```

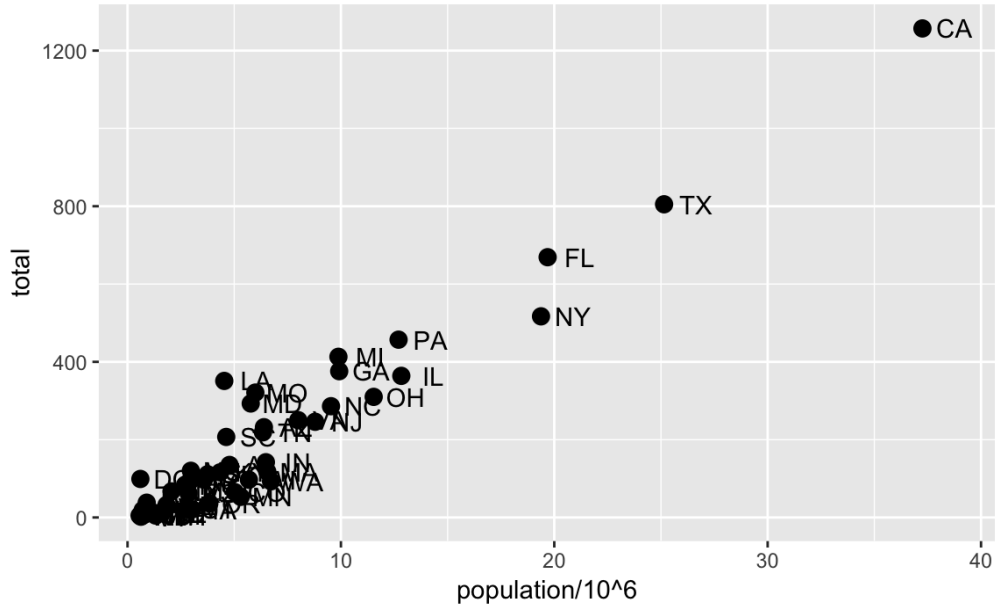


Layers

A second layer in the plot we wish to make involves adding a label to each point to identify the state. The geom_label and geom_text functions permit us to add text to the plot with and without a rectangle behind the text respectively.

```
p + geom_point(aes(population/10^6, total)) + geom_text(aes(population/10^6, total, label = abb))

p + geom_point(aes(population/10^6, total), size = 3) + geom_text(aes(population/10^6, total, label = abb), nudge_x = 1.(-5)
```





Global versus local aesthetic mappings

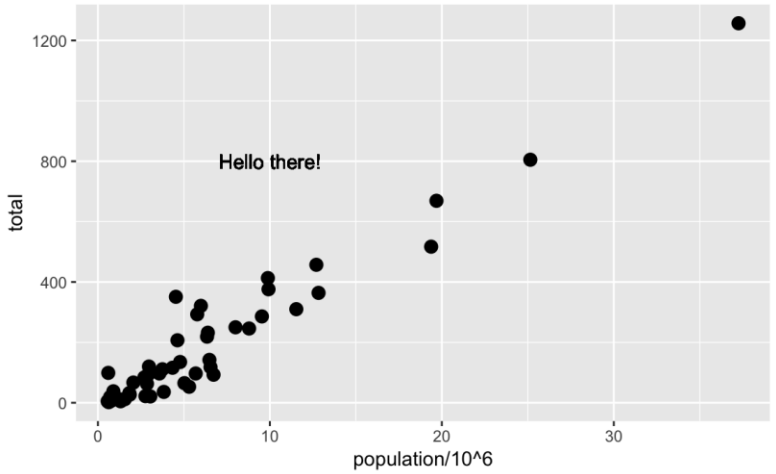
```
p + geom_point(aes(population/10^6, total), size = 3) + geom_text(aes(population/10^6, total, label = abb), nudge_x = 1.(-5)
```

Or

```
p <- murders %>% ggplot(aes(population/10^6, total, label = abb))

p + geom_point(size = 3) + geom_text(nudge_x = 1.5)
```

If necessary, we can override the global mapping by defining a new mapping within each layer. These *local* definitions override the *global*. Here is an example:

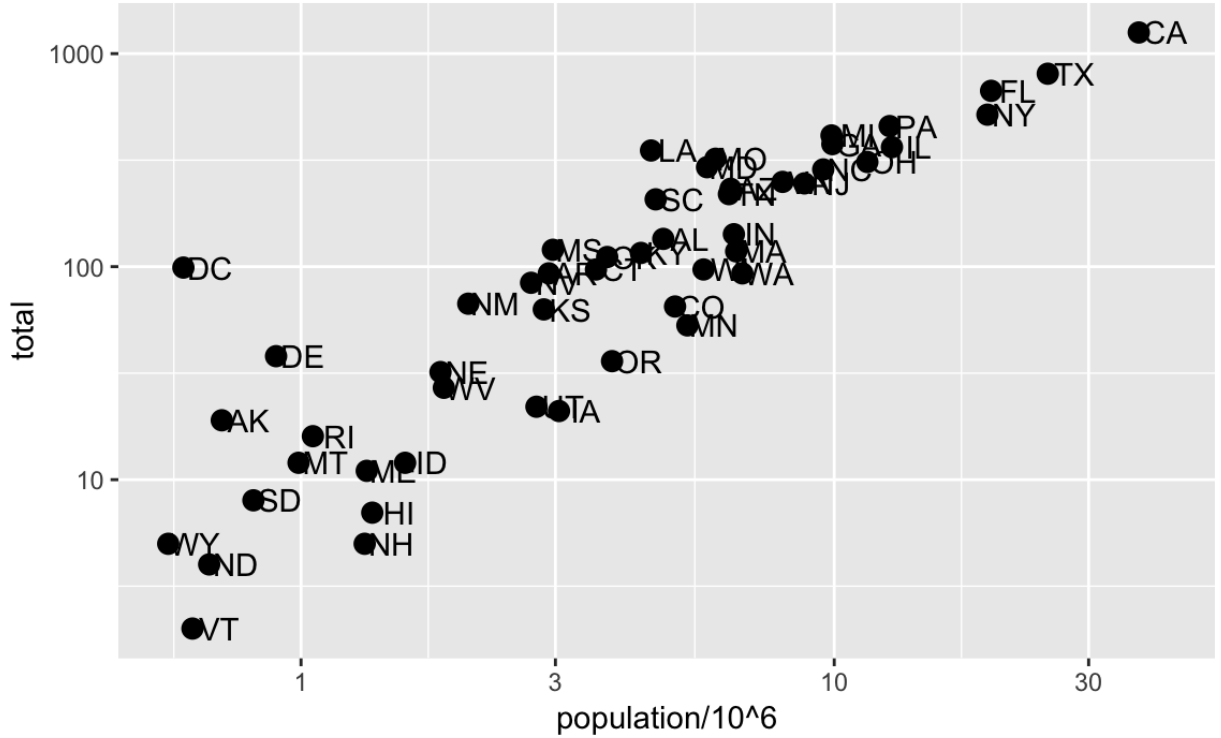
```
p + geom_point(size = 3) +
geom_text(aes(x = 10, y = 800, label =
"Hello there!"))
```



Scales

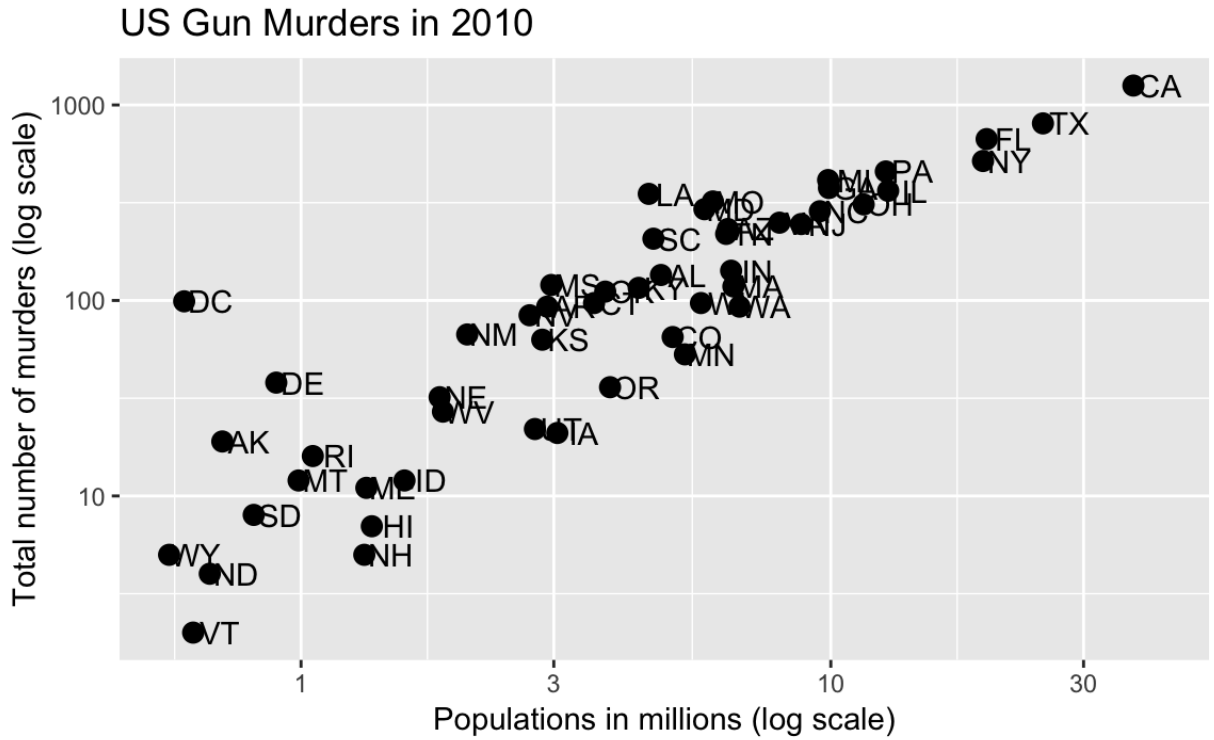
p + **geom_point**(size = 3) +
geom_text(nudge_x = 0.05) +
scale_x_continuous(trans = "log10") +
scale_y_continuous(trans = "log10")

p + **geom_point**(size = 3) +
geom_text(nudge_x = 0.05) +
scale_x_log10() + **scale_y_log10**()



Labels and titles

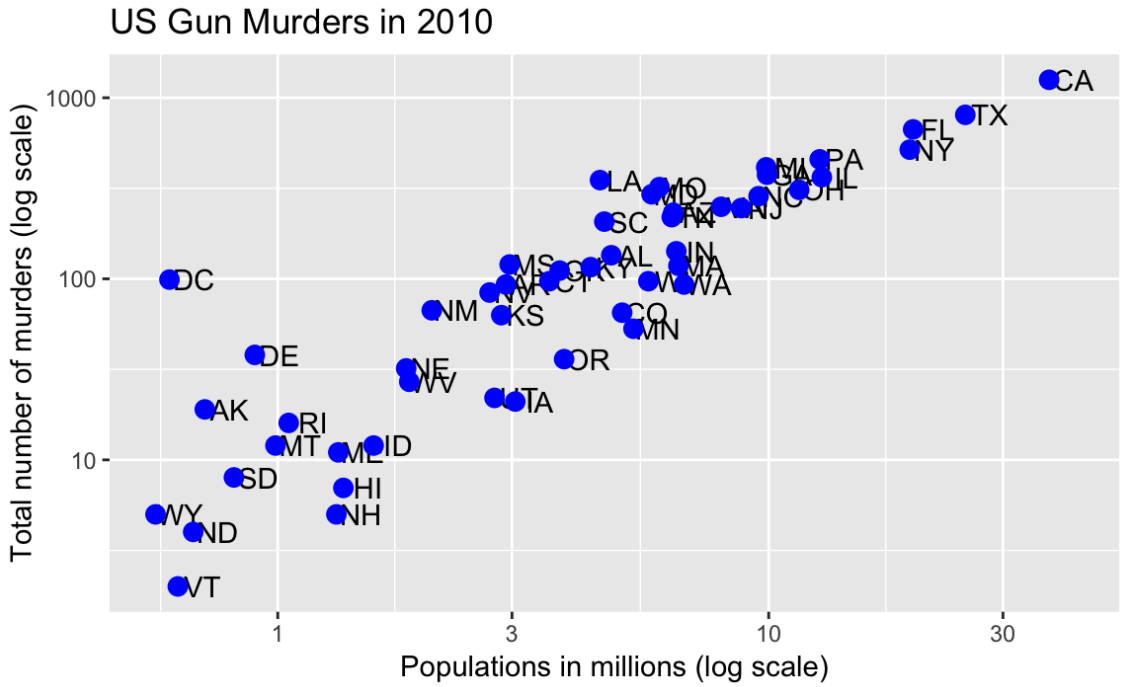
```
p + geom_point(size = 3) +
geom_text(nudge_x = 0.05) +
scale_x_log10() + scale_y_log10() +
xlab("Populations in millions (log scale)") +
ylab("Total number of murders (log scale)") +
ggtitle("US Gun Murders in 2010")
```



We are almost there! All we have left to do is add color, a legend and optional changes to the style.

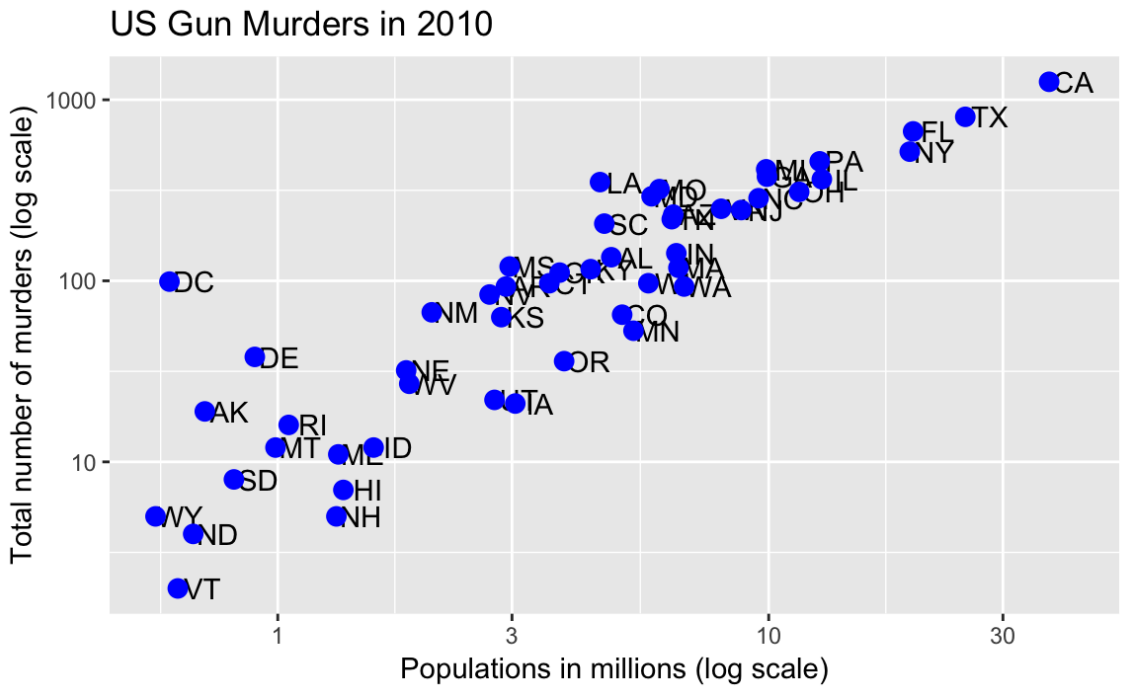
Categories as colors

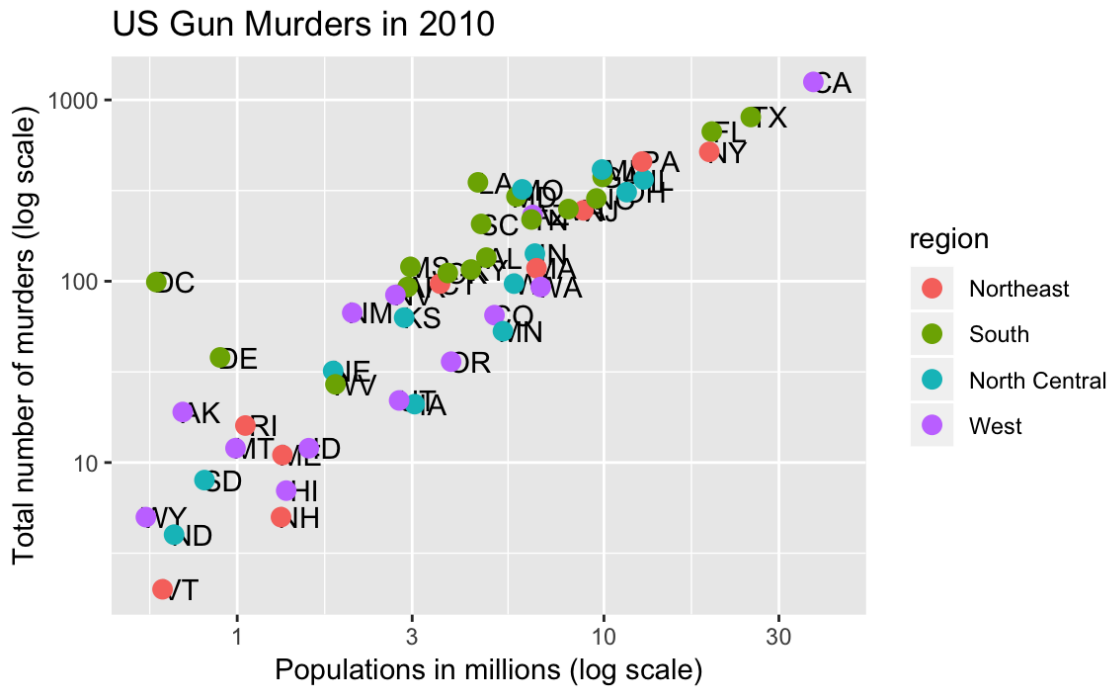
```
p <- murders %>% ggplot(aes(population/10^6, total, label = abb)) + geom_text(nudge_x = 0.05) + scale_x_log10() + scale_y_log10() + xlab("Populations in millions (log scale)") + ylab("Total number of murders (log scale)") + ggtitle("US Gun Murders in 2010")

p + geom_point(color="blue ", size = 3 )
```



Categories as colors

```
p <- murders %>% ggplot(aes(population/10^6, total, label = abb)) + geom_text(nudge_x = 0.05) + scale_x_log10() + scale_y_log10() + xlab("Populations in millions (log scale)") + ylab("Total number of murders (log scale)") + ggtitle("US Gun Murders in 2010")

p + geom_point(aes(col=region), size = 3 )
```





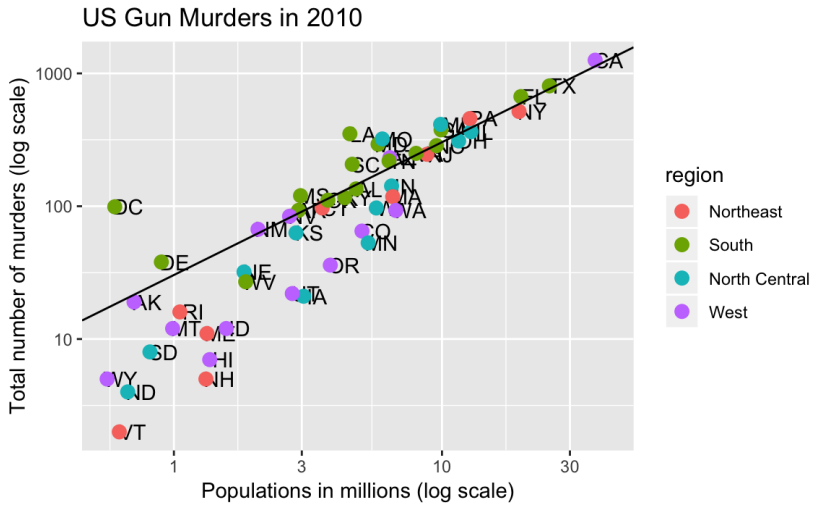
Annotation, shapes, and adjustments

Here we want to add a line that represents the average murder rate for the entire country.

```
r <- murders %>% summarize(rate = sum(total) / sum(population) * 10^6) %>% pull(rate)
```

To add a line we use the geom_abline function. **ggplot2** uses ab in the name to remind us we are supplying the intercept (a) and slope (b). The default line has slope 1 and intercept 0 so we only have to define the intercept:

```
p + geom_point(aes(col=region), size = 3) + geom_abline(intercept = log10(r))
```



Add-on packages

The power of **ggplot2** is augmented further due to the availability of add-on packages. The remaining changes needed to put the finishing touches on our plot require the **ggthemes** and **ggrepel** packages.

```
library(ggthemes)
p + theme_economist()
```

The add-on package **ggrepel** includes a geometry that adds labels while ensuring that they don't fall on top of each other. We simply change geom_text with geom_text_repel.

Putting it all together

Now that we are done testing, we can write one piece of code that produces our desired plot from scratch.

Putting it all together

```
library(ggthemes)
library(ggrepel)

r <- murders %>% summarize(rate = sum(total) / sum(population) * 10^6) %>%
pull(rate)

murders %>% ggplot(aes(population/10^6, total, label = abb)) +
geom_abline(intercept = log10(r), lty = 2, color = "darkgrey") +
geom_point(aes(col=region), size = 3) +
geom_text_repel() +
scale_x_log10() +
scale_y_log10() +
xlab("Populations in millions (log scale)") +
ylab("Total number of murders (log scale)") +
ggtitle("US Gun Murders in 2010") +
scale_color_discrete(name = "Region") +
theme_economist()
```

Quick plots with qplot

If we have values in two vectors, say:

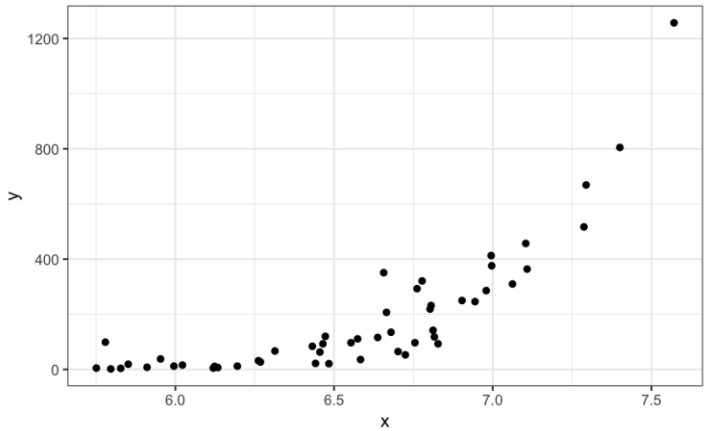
```
data(murders)
x <- log10(murders$population)
y <- murders$total
```

and we want to make a scatterplot with ggplot, we would have to type something like:

```
data.frame(x = x, y = y) %>% ggplot(aes(x, y)) + geom_point()
```

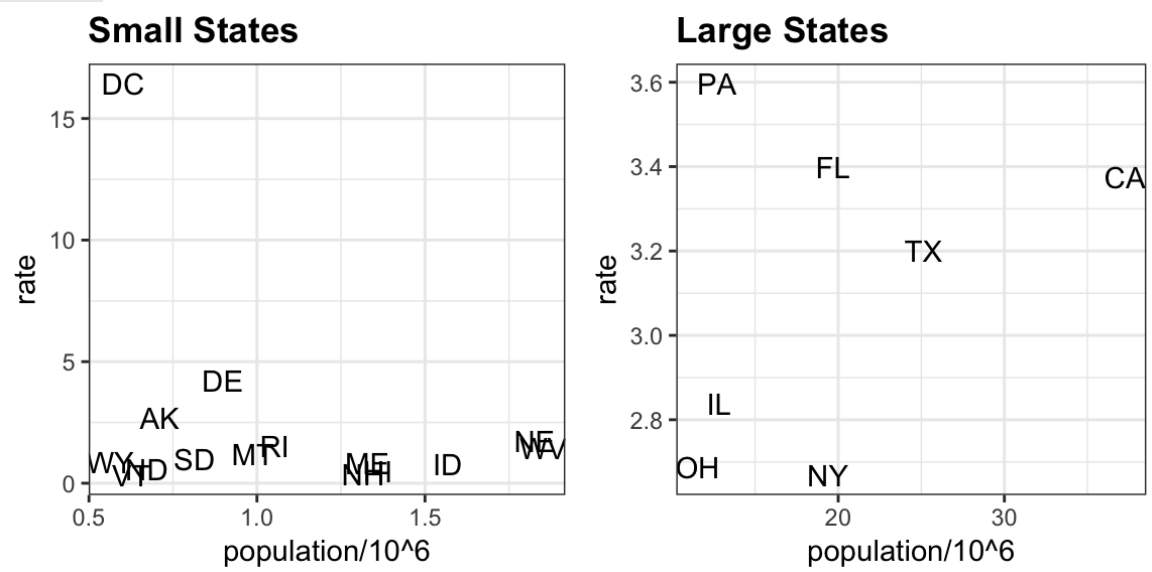
This seems like too much code for such a simple plot. The qplot function sacrifices the flexibility provided by the ggplot approach, but allows us to generate a plot quickly.

```
qplot(x, y)
```



Grids of plots

```
library(gridExtra)
#> Attaching package: 'gridExtra'
#> The following object is masked from 'package:dplyr':
 #> combine

p1 <- murders %>% mutate(rate = total/population*10^5) %>%
filter(population < 2*10^6) %>%
ggplot(aes(population/10^6, rate, label = abb))
+ geom_text()
+ ggtitle("Small States")

p2 <- murders %>% mutate(rate = total/population*10^5) %>%
filter(population > 10*10^6) %>%
ggplot(aes(population/10^6, rate, label = abb)) +
geom_text() +
ggtitle("Large States")

grid.arrange(p1, p2, ncol = 2)
```



Exercise

1. Create a grid of plots with (including title, axis labels, colors….):

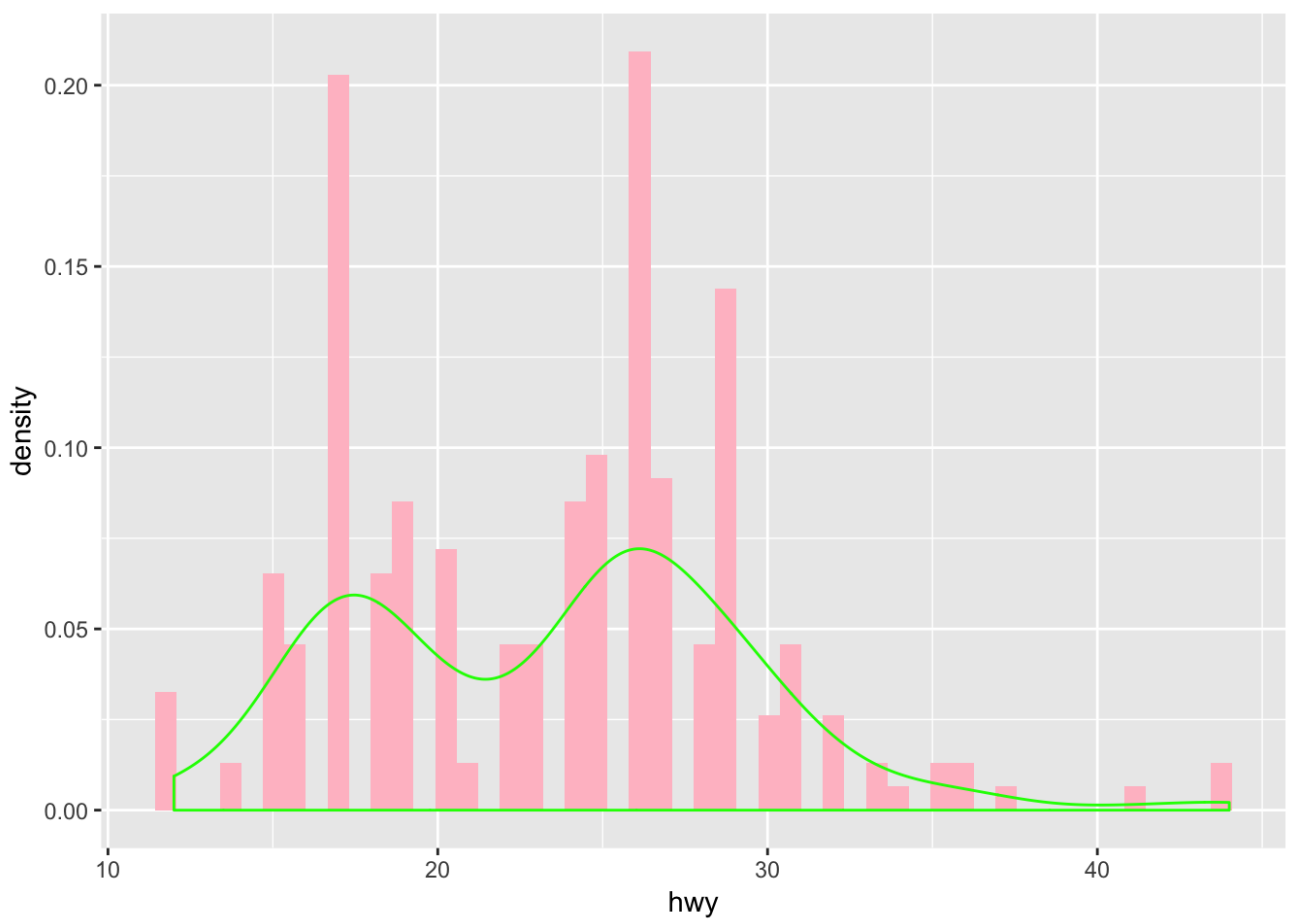
A. state and abb.

B. total_murders and population_size.

2. Repeat the previous exercise but now change both axes to be in the log scale.

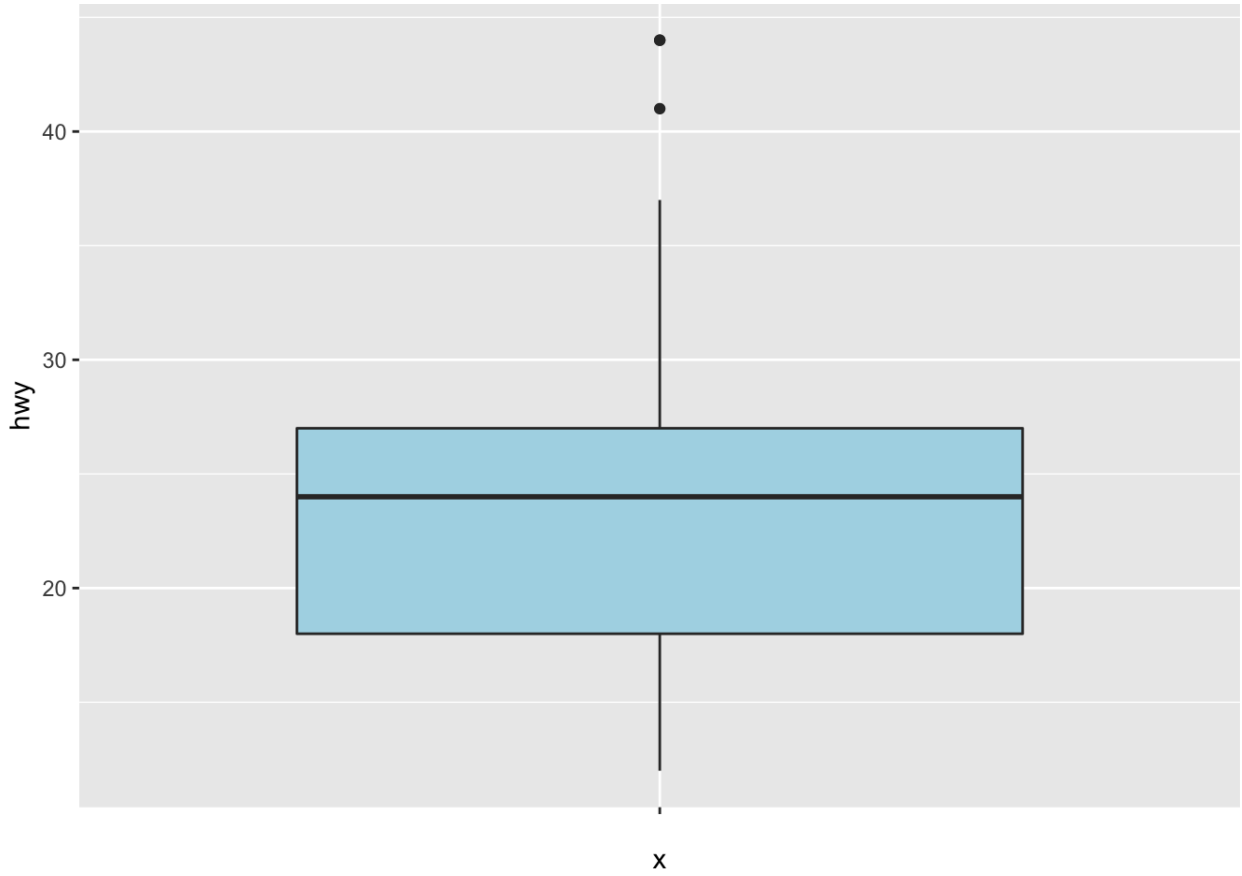
Histograms

ggplot(data = mpg) + **geom_histogram**(**aes**(x = hwy, y = ..density..), bins=50, fill = 'pink') + **geom_density**(**aes**(x = hwy),col = 'green')



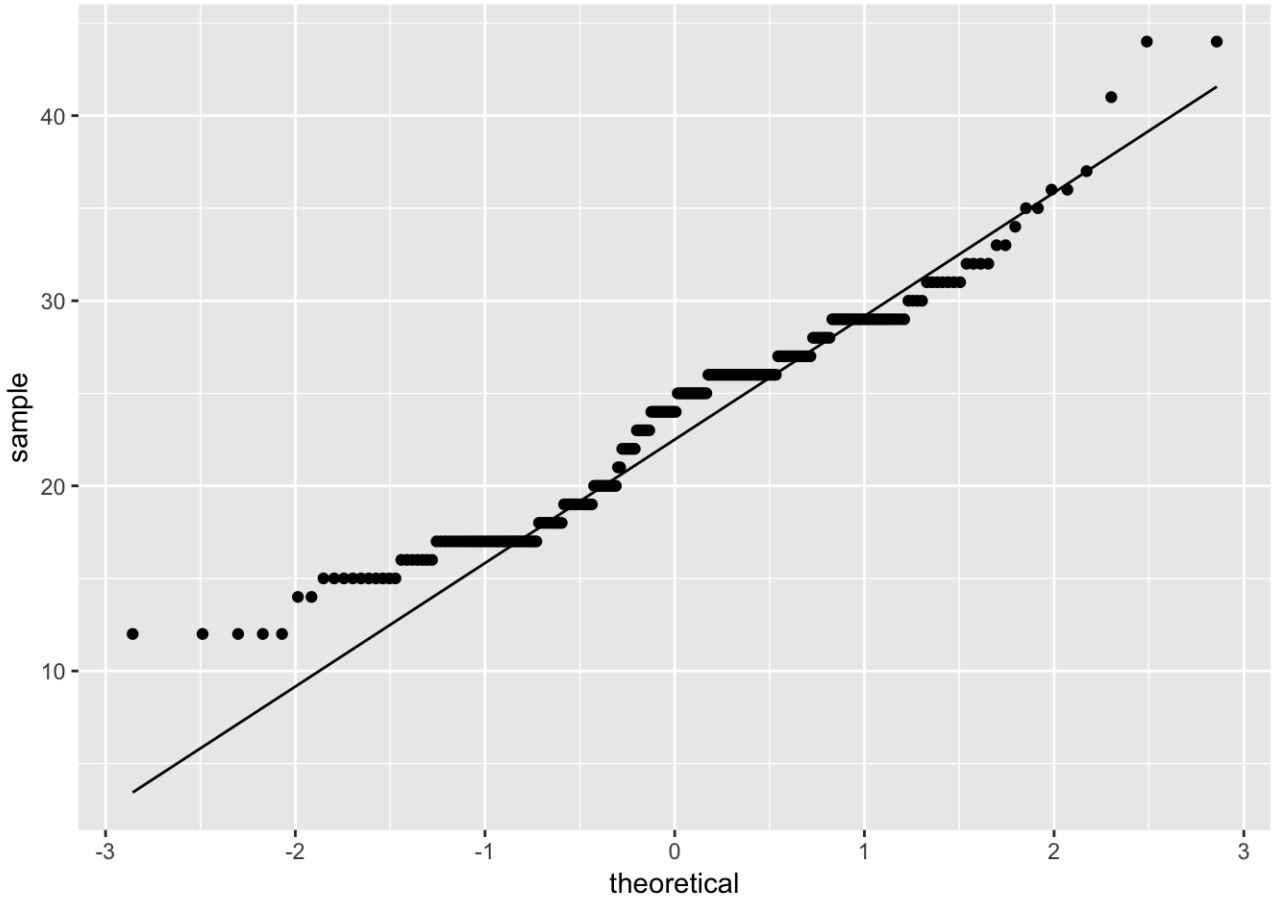
Boxplots

```
ggplot(data = mpg) + geom_boxplot(aes(x = '',y = hwy), fill = 'lightblue')
```



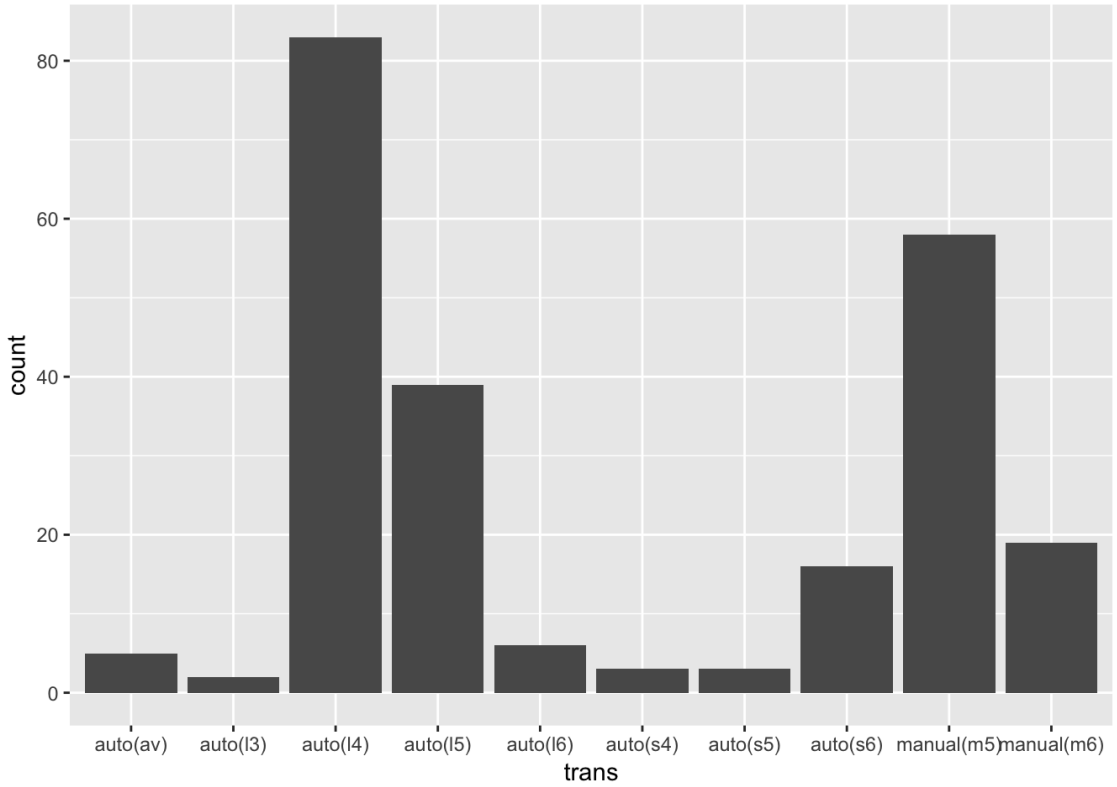
Compare distributions

```
ggplot(data = mpg) + geom_qq(aes(sample = hwy)) + geom_qq_line(aes(sample = hwy))
```

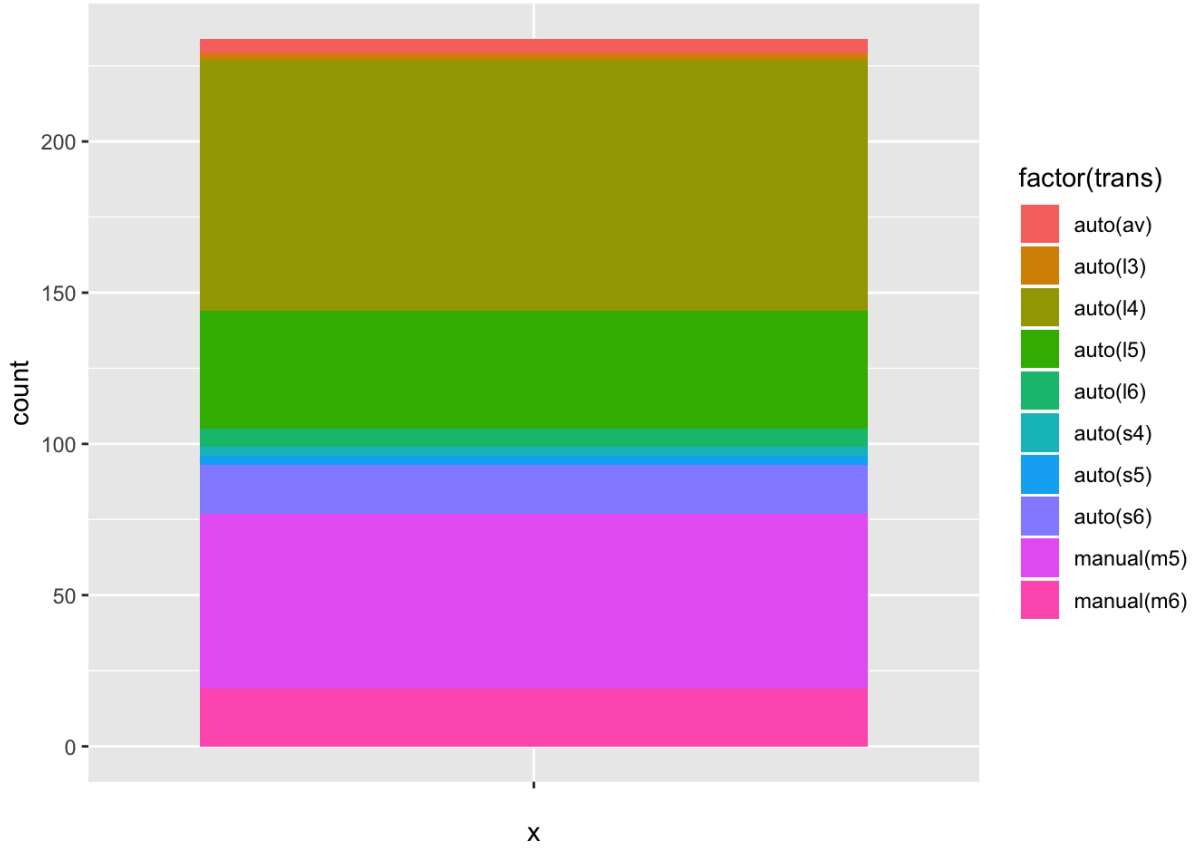


Barplots

ggplot(data = mpg) + **geom_bar**(**aes**(x = trans))

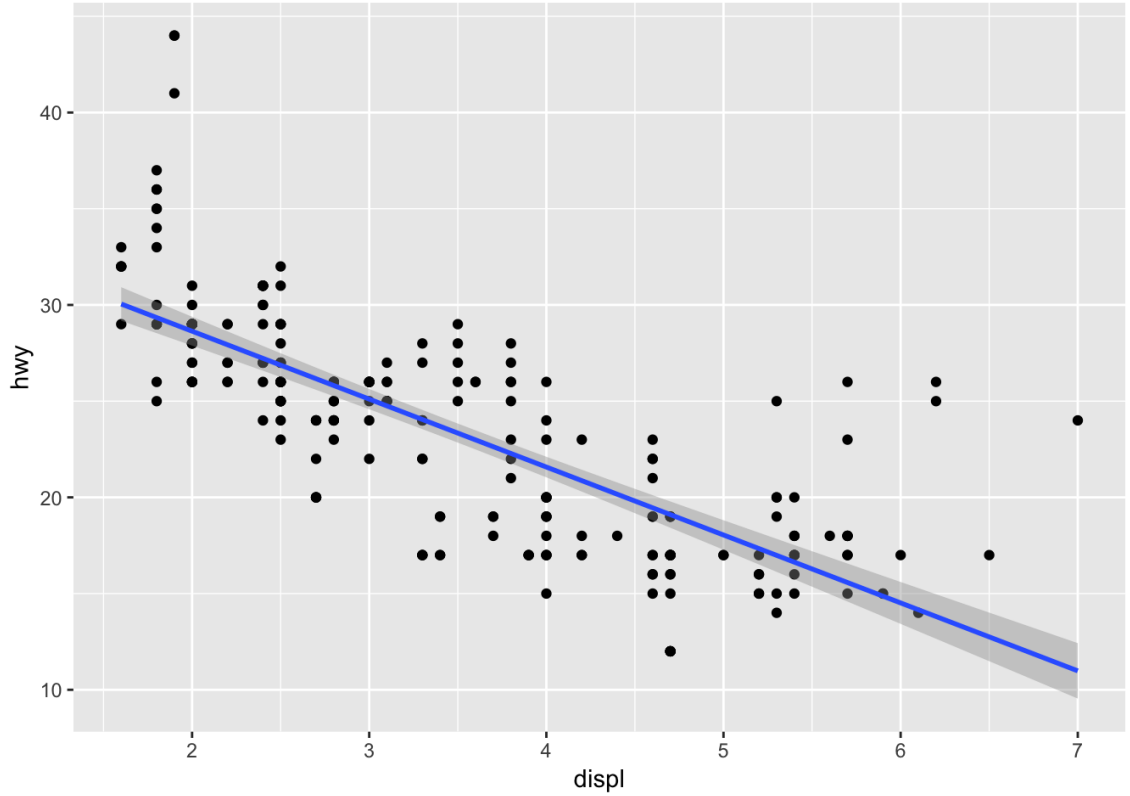


ggplot(data = mpg) + **geom_bar**(**aes**(x = "", fill = **factor**(trans)))



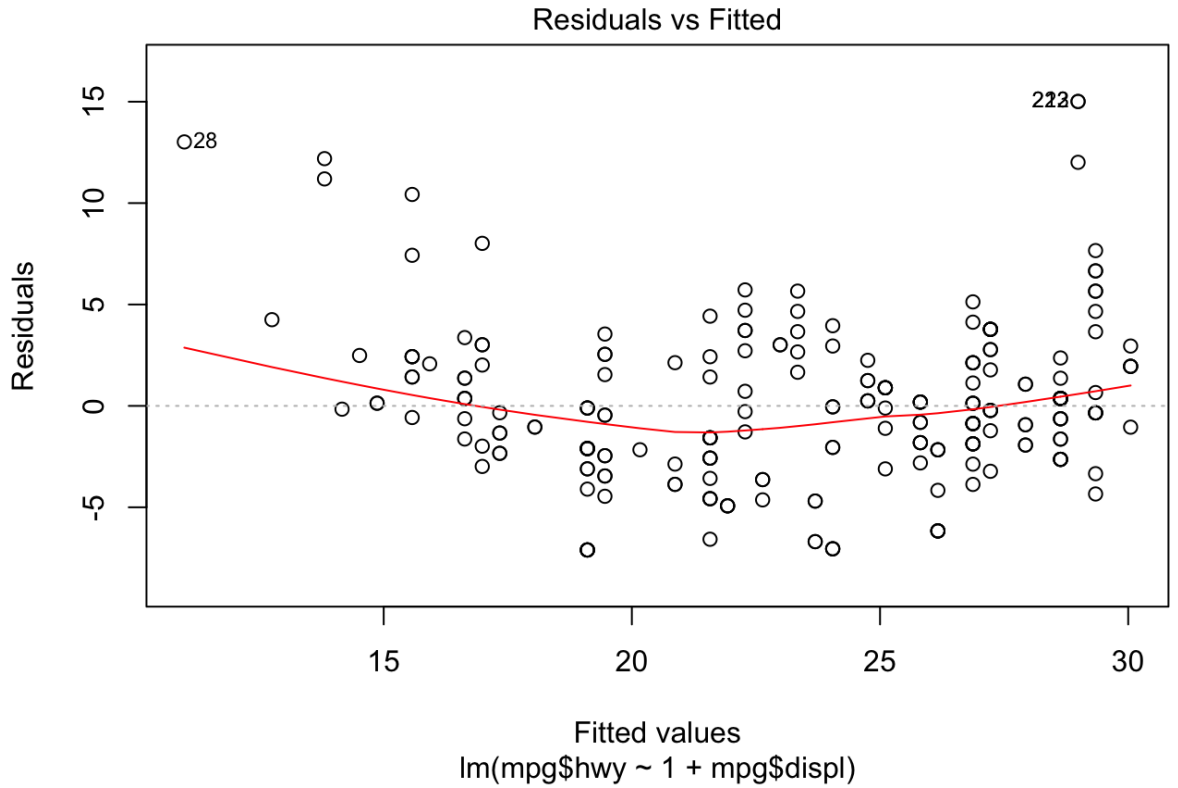
Linear model

gplot(data = mpg) + **geom_point**(mapping = **aes**(x = displ, y = hwy)) + **geom_smooth**(mapping = **aes**(x = displ, y = hwy),method = 'lm')



Linear model

```
out = lm(mpg$hwy ~ 1 + mpg$displ)
plot(out)
```



Exercise

Use the starwars data set in the dplyr package to:

- list the different human characters,
- list the different worlds,
- compute the average weight and height of the different character types,
- display on a plot the number of characters of each type in a deacresing order,

```
ggplot(data = mpg) + geom_bar(aes(x = trans))
```

```
Species$count = table(starwars$species)
```

- visualize the relationship between the height and weight of the different characters.

Exercise

Compare two simulated datasets with a plot and a hypothesis test.
Use a functions that:
 visualises the two distributions with a histogram,
 uses a t-test to compares means and summarises the results with a string