Data Science Visualization

The textbook for the Data Science course series is freely available online.

Learning Objectives

- Data visualization principles to better communicate data-driven findings
- How to use ggplot2 to create custom plots
- The weaknesses of several widely used plots and why you should avoid them

Course Overview

Section 1: Introduction to Data Visualization and Distributions

You will get started with data visualization and distributions in R.

Section 2: Introduction to ggplot2

You will learn how to use ggplot2 to create plots.

Section 3: Summarizing with dplyr

You will learn how to summarize data using dplyr.

Section 4: Gapminder

You will see examples of ggplot2 and dplyr in action with the Gapminder dataset.

Section 5: Data Visualization Principles

You will learn general principles to guide you in developing effective data visualizations.

Section 1 Overview

Section 1 introduces you to Data Visualization and Distributions.

After completing Section 1, you will:

- understand the importance of data visualization for communicating data-driven findings.
- be able to use distributions to summarize data.
- be able to use the average and the standard deviation to understand the normal distribution.
- be able to assess how well a normal distribution fits the data using a quantile-quantile plot.
- be able to interpret data from a boxplot.

Introduction to Data Visualization

The textbook for this section is available here

Key points

- Plots of data easily communicate information that is difficult to extract from tables of raw values.
- Data visualization is a key component of exploratory data analysis (EDA), in which the properties of data are explored through visualization and summarization techniques.
- Data visualization can help discover biases, systematic errors, mistakes and other unexpected problems in data before those data are incorporated into potentially flawed analysis.
- This course covers the basics of data visualization and EDA in R using the **ggplot2** package and motivating examples from world health, economics and infectious disease.

Code

```
if(!require(dslabs)) install.packages("dslabs")
```

```
## Loading required package: dslabs
```

```
library(dslabs)
data(murders)
head(murders)
```

```
##        state abb region population total
## 1    Alabama  AL  South    4779736   135
## 2     Alaska  AK   West     710231    19
## 3    Arizona  AZ   West    6392017   232
## 4   Arkansas  AR  South    2915918    93
## 5 California  CA   West   37253956  1257
## 6   Colorado  CO   West    5029196    65
```

Introduction to Distributions

The textbook for this section is available here

Key points

- The most basic statistical summary of a list of objects is its distribution.
- We will learn ways to visualize and analyze distributions in the upcoming videos.
- In some cases, data can be summarized by a two-number summary: the average and standard deviation. We will learn to use data visualization to determine when that is appropriate.

Data Types

The textbook for this section is available here

Key points

- Categorical data are variables that are defined by a small number of groups.
  - Ordinal categorical data have an inherent order to the categories (mild/medium/hot, for example).

  - Non-ordinal categorical data have no order to the categories.
- Numerical data take a variety of numeric values.
  - Continuous variables can take any value.
  - Discrete variables are limited to sets of specific values.

Assessment - Data Types

1. The type of data we are working with will often influence the data visualization technique we use.

We will be working with two types of variables: categorical and numeric. Each can be divided into two other groups: categorical can be ordinal or not, whereas numerical variables can be discrete or continuous.

We will review data types using some of the examples provided in the `dslabs` package. For example, the `heights` dataset.

```
library(dslabs)
data(heights)
```

```
data(heights)
names(heights)
```

```
## [1] "sex"    "height"
```

2. We saw that `sex` is the first variable. We know what values are represented by this variable and can confirm this by looking at the first few entires:

```
head(heights)
```

```
##      sex height
## 1   Male     75
## 2   Male     70
## 3   Male     68
## 4   Male     74
## 5   Male     61
## 6 Female     65
```

What data type is the `sex` variable?

☐ A. Continuous
☒ B. Categorical
☐ C. Ordinal
☐ D. None of the above

3. Keep in mind that discrete numeric data can be considered ordinal.

Although this is technically true, we usually reserve the term ordinal data for variables belonging to a small number of different groups, with each group having many members.

The `height` variable could be ordinal if, for example, we report a small number of values such as short, medium, and tall. Let's explore how many unique values are used by the heights variable. For this we can use the `unique` function:

```r
x <- c(3, 3, 3, 3, 4, 4, 2)
unique(x)
```

```r
x <- heights$height
length(unique(x))
```

```
## [1] 139
```

4. One of the useful outputs of data visualization is that we can learn about the distribution of variables.

For categorical data we can construct this distribution by simply computing the frequency of each unique value. This can be done with the function `table`. Here is an example:

```r
x <- c(3, 3, 3, 3, 4, 4, 2)
table(x)
```

```r
x <- heights$height
tab <- table(x)
```

5. To see why treating the reported heights as an ordinal value is not useful in practice we note how many values are reported only once.

In the previous exercise we computed the variable tab which reports the number of times each unique value appears. For values reported only once tab will be 1. Use logicals and the function sum to count the number of times this happens.

```r
tab <- table(heights$height)
sum(tab==1)
```

```
## [1] 63
```

6. Since there are a finite number of reported heights and technically the height can be considered ordinal, which of the following is true:

☒ A. It is more effective to consider heights to be numerical given the number of unique values we observe and the fact that if we keep collecting data even more will be observed.
☐ B. It is actually preferable to consider heights ordinal since on a computer there are only a finite number of possibilities.
☐ C. This is actually a categorical variable: tall, medium or short.
☐ D. This is a numerical variable because numbers are used to represent it.

Describe Heights to ET

The textbook for this section is available:

- Case Study describing student heights
- Distribution Function
- CDF Intro
- Histograms

Key points

- A distribution is a function or description that shows the possible values of a variable and how often those values occur.
- For categorical variables, the distribution describes the proportions of each category.
- A *frequency table* is the simplest way to show a categorical distribution. Use `prop.table` to convert a table of counts to a frequency table. *Barplots* display the distribution of categorical variables and are a way to visualize the information in frequency tables.
- For continuous numerical data, reporting the frequency of each unique entry is not an effective summary as many or most values are unique. Instead, a distribution function is required.
- The *cumulative distribution function (CDF)* is a function that reports the proportion of data below a value a for all values of a: $F(a) = Pr(x \leq a)$.
- The proportion of observations between any two values a and b can be computed from the CDF as $F(b) - F(a)$.
- A *histogram* divides data into non-overlapping bins of the same size and plots the counts of number of values that fall in that interval.

Code

```
# load the dataset
library(dslabs)
data(heights)
```

```
# make a table of category proportions
prop.table(table(heights$sex))
```

```
##
##    Female      Male
## 0.2266667 0.7733333
```

Smooth Density Plots

The textbook for this section is available here

Key points

- *Smooth density plots* can be thought of as histograms where the bin width is extremely or infinitely small. The smoothing function makes estimates of the true continuous trend of the data given the available sample of data points.
- The degree of smoothness can be controlled by an argument in the plotting function. (We will learn functions for plotting later.)
- While the histogram is an assumption-free summary, the smooth density plot is shaped by assumptions and choices you make as a data analyst.
- The y-axis is scaled so that the area under the density curve sums to 1. This means that interpreting values on the y-axis is not straightforward. To determine the proportion of data in between two values, compute the area under the smooth density curve in the region between those values.
- An advantage of smooth densities over histograms is that densities are easier to compare visually.

A further note on histograms: note that the choice of binwidth has a determinative effect on shape. There is no "true" choice for binwidth, and you can sometimes gain insights into the data by experimenting with binwidths.

Assessment - Distributions

1. You may have noticed that numerical data is often summarized with the average value.

For example, the quality of a high school is sometimes summarized with one number: the average score on a standardized test. Occasionally, a second number is reported: the standard deviation. So, for example, you might read a report stating that scores were 680 plus or minus 50 (the standard deviation). The report has summarized an entire vector of scores with with just two numbers. Is this appropriate? Is there any important piece of information that we are missing by only looking at this summary rather than the entire list? We are going to learn when these 2 numbers are enough and when we need more elaborate summaries and plots to describe the data.

Our first data visualization building block is learning to summarize lists of factors or numeric vectors. The most basic statistical summary of a list of objects or numbers is its distribution. Once a vector has been summarized as distribution, there are several data visualization techniques to effectively relay this information. In later assessments we will practice to write code for data visualization. Here we start with some multiple choice questions to test your understanding of distributions and related basic plots.

In the murders dataset, the region is a categorical variable and on the right you can see its distribution. To the closest 5%, what proportion of the states are in the North Central region?

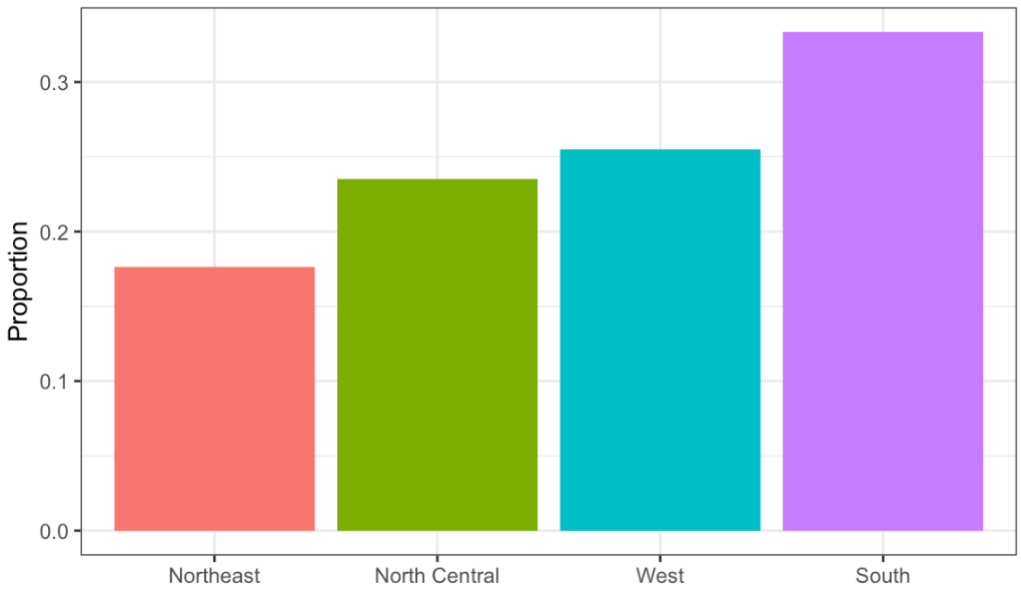


Figure 1: Region vs. Proportion

☐ A. 75%
☐ B. 50%
☒ C. 20%
☐ D. 5%

2. In the murders dataset, the region is a categorical variable and to the right is its distribution.

Which of the following is true:

☐ A. The graph above is a histogram.

☒ B. The graph above shows only four numbers with a bar plot.
☐ C. Categories are not numbers, so it does not make sense to graph the distribution.
☐ D. The colors, not the height of the bars, describe the distribution.

3. The plot shows the eCDF for male heights.

Based on the plot, what percentage of males are shorter than 75 inches?

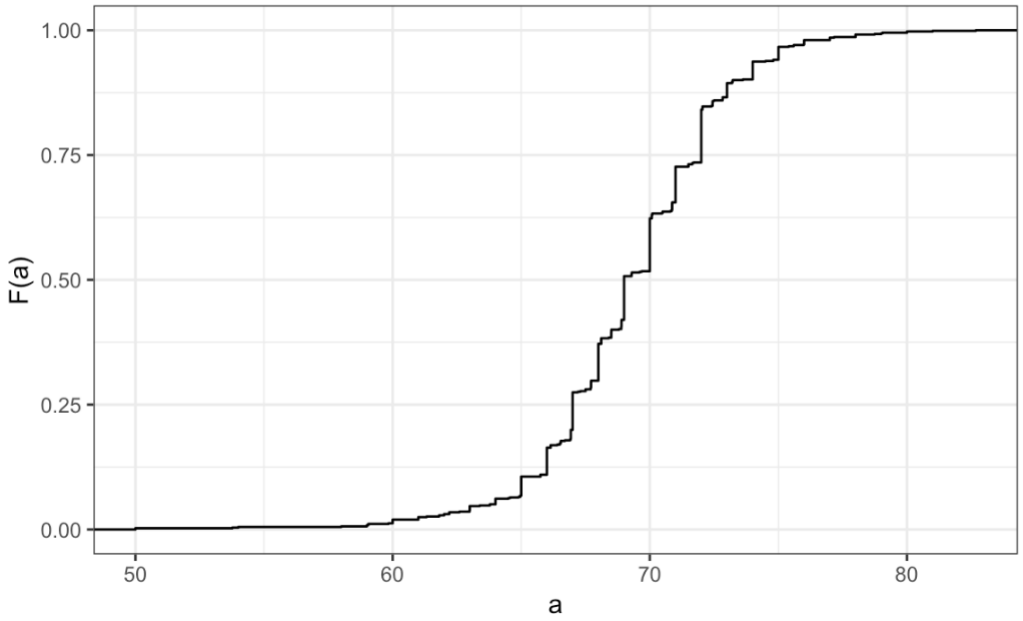


Figure 2: eCDF for male heights

☐ A. 100%
☒ B. 95%
☐ C. 80%
☐ D. 72 inches

4. To the closest inch, what height `m` has the property that 1/2 of the male students are taller than `m` and 1/2 are shorter?

☐ A. 61 inches
☐ B. 64 inches
☒ C. 69 inches
☐ D. 74 inches

5. Here is an eCDF of the murder rates across states.

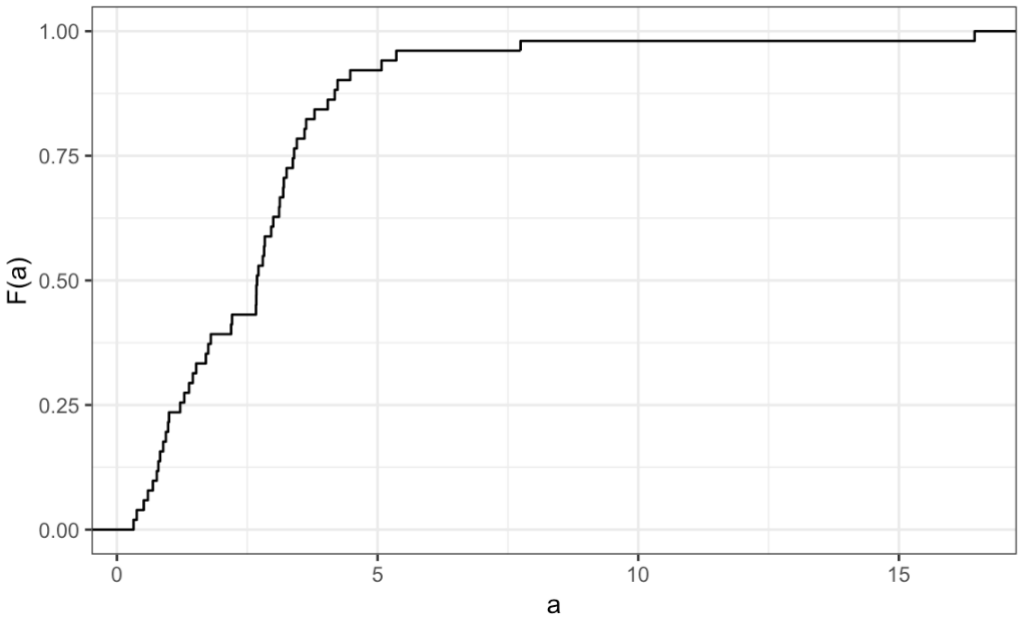


Figure 3: eCDF of the murder rates across states

Knowing that there are 51 states (counting DC) and based on this plot, how many states have murder rates larger than 10 per 100,000 people?

☒ A. 1
☐ B. 5
☐ C. 10
☐ D. 50

6. Based on the eCDF above, which of the following statements are true.

☐ A. About half the states have murder rates above 7 per 100,000 and the other half below.
☐ B. Most states have murder rates below 2 per 100,000.
☐ C. All the states have murder rates above 2 per 100,000.
☒ D. With the exception of 4 states, the murder rates are below 5 per 100,000.

7. Here is a histogram of male heights in our `heights` dataset.

Based on this plot, how many males are between 62.5 and 65.5?

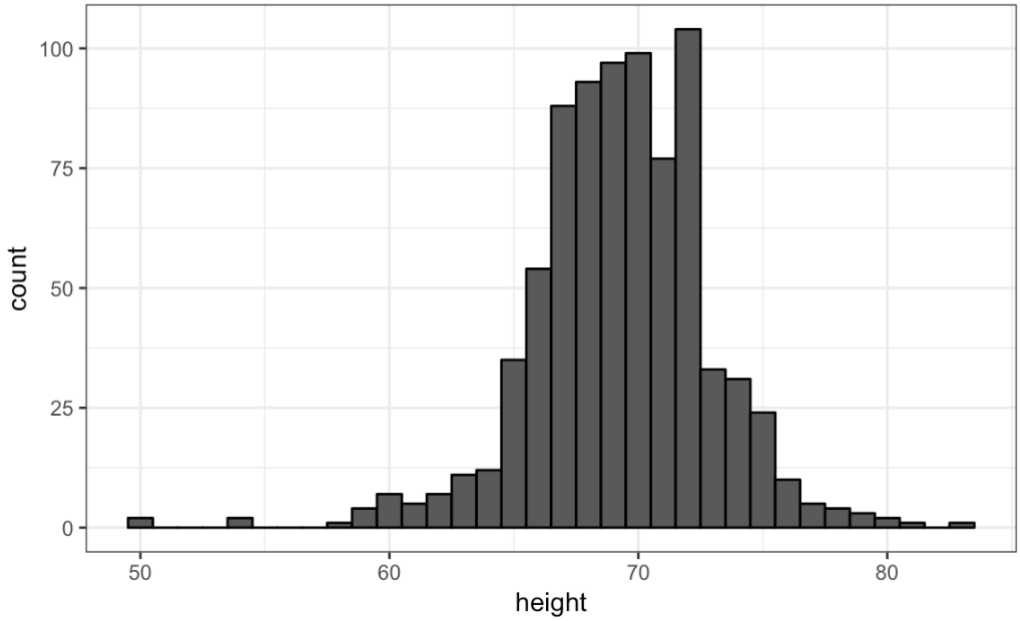


Figure 4: Histogram of male heights

☐ A. 11
☐ B. 29
☒ C. 58
☐ D. 99

8. About what percentage are shorter than 60 inches?

☒ A. 1%
☐ B. 10%
☐ C. 25%
☐ D. 50%

9. Based on this density plot, about what proportion of US states have populations larger than 10 million?

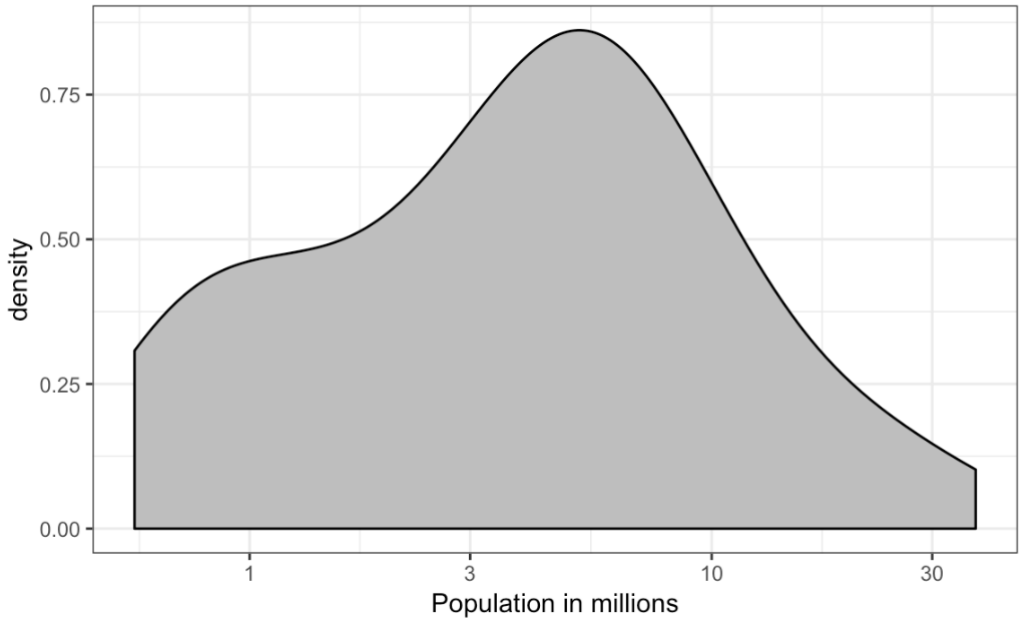


Figure 5: Density plot population

☐ A. 0.02
☒ B. 0.15
☐ C. 0.50
☐ D. 0.55

10. Below are three density plots. Is it possible that they are from the same dataset?

Which of the following statements is true?

☐ A. It is impossible that they are from the same dataset.
☐ B. They are from the same dataset, but the plots are different due to code errors.
☐ C. They are the same dataset, but the first and second plot undersmooth and the third oversmooths.
☒ D. They are the same dataset, but the first is not in the log scale, the second undersmooths and the third oversmooths.

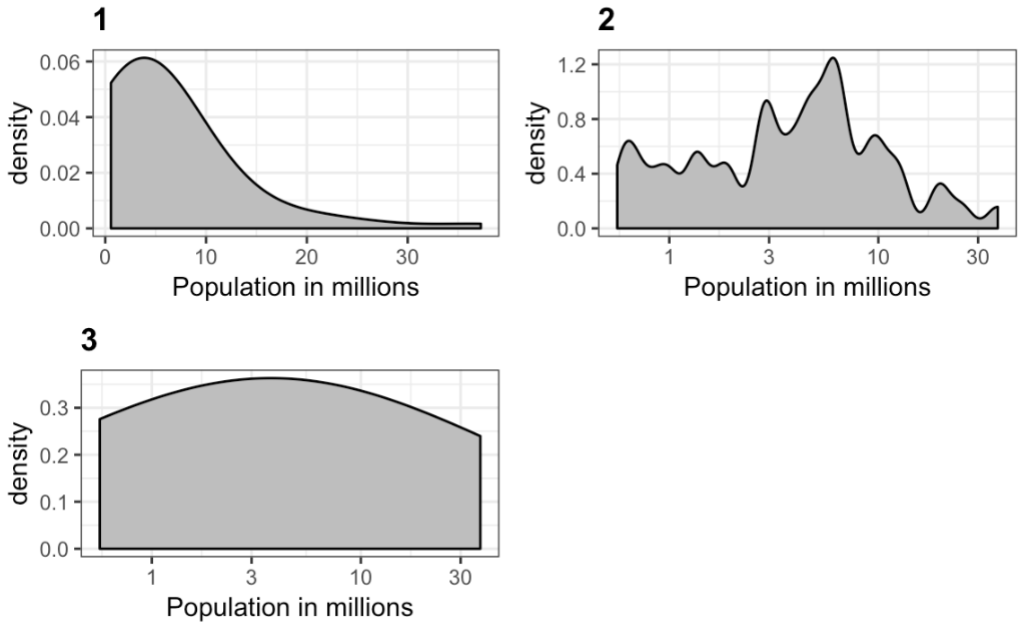


Figure 6: Three density plots

Normal Distribution

The textbook for this section is available here

Key points

- The normal distribution:
  - Is centered around one value, the *mean*
  - Is symmetric around the mean
  - Is defined completely by its mean (μ) and standard deviation (σ)
  - Always has the same proportion of observations within a given distance of the mean (for example, 95% within 2 σ)
- The standard deviation is the average distance between a value and the mean value.
- Calculate the mean using the `mean` function.
- Calculate the standard deviation using the `sd` function or manually.
- Standard units describe how many standard deviations a value is away from the mean. The z-score, or number of standard deviations an observation x is away from the mean (μ):
  $Z = \frac{x-\mu}{\sigma}$
- Compute standard units with the `scale` function.
- **Important:** to calculate the proportion of values that meet a certain condition, use the `mean` function on a logical vector. Because TRUE is converted to 1 and FALSE is converted to 0, taking the mean of this vector yields the proportion of TRUE.

Equation for the normal distribution

The normal distribution is mathematically defined by the following formula for any mean μ and standard deviation σ:

$Pr(a < x < b) = \int_a^b \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{1}{2}(\frac{x-\mu}{\sigma})^2} dx$

Code

```
if(!require(tidyverse)) install.packages("tidyverse")
```

```
## Loading required package: tidyverse
```

```
## -- Attaching packages ---------------------------------------------------------------------------
```

```
## v ggplot2 3.3.2     v purrr   0.3.4
## v tibble  3.0.3     v dplyr   1.0.0
## v tidyr   1.1.0     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.5.0
```

```
## -- Conflicts ------------------------------------------------------------------------------------
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
# define x as vector of male heights
library(tidyverse)
index <- heights$sex=="Male"
x <- heights$height[index]

# calculate the mean and standard deviation manually
average <- sum(x)/length(x)
SD <- sqrt(sum((x - average)^2)/length(x))

# built-in mean and sd functions - note that the audio and printed values disagree
average <- mean(x)
SD <- sd(x)
c(average = average, SD = SD)
```

```
##   average        SD
## 69.314755  3.611024
```

```
# calculate standard units
z <- scale(x)

# calculate proportion of values within 2 SD of mean
mean(abs(z) < 2)
```

```
## [1] 0.9495074
```

Note about the sd function: The built-in R function `sd` calculates the standard deviation, but it divides by `length(x)-1` instead of `length(x)`. When the length of the list is large, this difference is negligible and you can use the built-in `sd` function. Otherwise, you should compute σ by hand. For this course series, assume that you should use the `sd` function unless you are told not to do so.

Assessment - Normal Distribution

1. Histograms and density plots provide excellent summaries of a distribution.

But can we summarize even further? We often see the average and standard deviation used as summary statistics: a two number summary! To understand what these summaries are and why they are so widely used, we need to understand the normal distribution.

The normal distribution, also known as the bell curve and as the Gaussian distribution, is one of the most famous mathematical concepts in history. A reason for this is that approximately normal distributions occur in many situations. Examples include gambling winnings, heights, weights, blood pressure, standardized test scores, and experimental measurement errors. Often data visualization is needed to confirm that our data follows a normal distribution.

Here we focus on how the normal distribution helps us summarize data and can be useful in practice.

One way the normal distribution is useful is that it can be used to approximate the distribution of a list of numbers without having access to the entire list. We will demonstrate this with the heights dataset.

Load the height data set and create a vector `x` with just the male heights:

```
library(dslabs)
data(heights)
x <- heights$height[heights$sex == "Male"]
```

What proportion of the data is between 69 and 72 inches (taller than 69 but shorter or equal to 72)? A proportion is between 0 and 1.

```
x <- heights$height[heights$sex == "Male"]
mean(x > 69 & x <= 72)
```

```
## [1] 0.3337438
```

2. Suppose all you know about the height data from the previous exercise is the average and the standard deviation and that its distribution is approximated by the normal distribution.

We can compute the average and standard deviation like this:

```
library(dslabs)
data(heights)
x <- heights$height[heights$sex=="Male"]
avg <- mean(x)
stdev <- sd(x)
```

Suppose you only have `avg` and `stdev` below, but no access to `x`, can you approximate the proportion of the data that is between 69 and 72 inches?

Given a normal distribution with a mean `mu` and standard deviation `sigma`, you can calculate the proportion of observations less than or equal to a certain `value` with `pnorm(value, mu, sigma)`. Notice that this is the CDF for the normal distribution. We will learn much more about `pnorm` later in the course series, but you can also learn more now with `?pnorm`.

```
x <- heights$height[heights$sex=="Male"]
avg <- mean(x)
stdev <- sd(x)
pnorm(72, avg, stdev) - pnorm(69, avg, stdev)
```

```
## [1] 0.3061779
```

3. Notice that the approximation calculated in the second question is very close to the exact calculation in the first question.

The normal distribution was a useful approximation for this case. However, the approximation is not always useful. An example is for the more extreme values, often called the "tails" of the distribution. Let's look at an example. We can compute the proportion of heights between 79 and 81.

```
library(dslabs)
data(heights)
x <- heights$height[heights$sex == "Male"]
mean(x > 79 & x <= 81)
```

```
x <- heights$height[heights$sex == "Male"]
avg <- mean(x)
stdev <- sd(x)
exact <- mean(x > 79 & x <= 81)
approx <- pnorm(81, avg, stdev) - pnorm(79, avg, stdev)
exact
```

```
## [1] 0.004926108
```

```
approx
```

```
## [1] 0.003051617
```

```
exact/approx
```

```
## [1] 1.614261
```

4. Someone asks you what percent of seven footers are in the National Basketball Association (NBA). Can you provide an estimate? Let's try using the normal approximation to answer this question.

First, we will estimate the proportion of adult men that are 7 feet tall or taller.

Assume that the distribution of adult men in the world as normally distributed with an average of 69 inches and a standard deviation of 3 inches.

```
# use pnorm to calculate the proportion over 7 feet (7*12 inches)
1 - pnorm(7*12, 69, 3)
```

```
## [1] 2.866516e-07
```

5. Now we have an approximation for the proportion, call it `p`, of men that are 7 feet tall or taller.

We know that there are about 1 billion men between the ages of 18 and 40 in the world, the age range for the NBA.

Can we use the normal distribution to estimate how many of these 1 billion men are at least seven feet tall?

```
p <- 1 - pnorm(7*12, 69, 3)
round(p*10^9)
```

```
## [1] 287
```

6. There are about 10 National Basketball Association (NBA) players that are 7 feet tall or higher.

```
p <- 1 - pnorm(7*12, 69, 3)
N <- round(p*10^9)
10/N
```

```
## [1] 0.03484321
```

7. In the previous exerceise we estimated the proportion of seven footers in the NBA using this simple code:

```
p <- 1 - pnorm(7*12, 69, 3)
N <- round(p * 10^9)
10/N
```

Repeat the calculations performed in the previous question for Lebron James' height: 6 feet 8 inches. There are about 150 players, instead of 10, that are at least that tall in the NBA.

```
## Change the solution to previous answer
p <- 1 - pnorm(7*12, 69, 3)
N <- round(p * 10^9)
10/N
```

```
## [1] 0.03484321
```

```
p <- 1 - pnorm(6*12+8, 69, 3)
N <- round(p * 10^9)
150/N
```

```
## [1] 0.001220842
```

8. In answering the previous questions, we found that it is not at all rare for a seven footer to become an NBA player.

What would be a fair critique of our calculations?

- ☐ A. Practice and talent are what make a great basketball player, not height.
- ☐ B. The normal approximation is not appropriate for heights.
- ☒ C. As seen in exercise 3, the normal approximation tends to underestimate the extreme values. It's possible that there are more seven footers than we predicted.
- ☐ D. As seen in exercise 3, the normal approximation tends to overestimate the extreme values. It's possible that there are less seven footers than we predicted.

Quantile-Quantile Plots

The textbook for this section is available here

Key points

- Quantile-quantile plots, or QQ-plots, are used to check whether distributions are well-approximated by a normal distribution.
- Given a proportion p, the quantile q is the value such that the proportion of values in the data below q is p.
- In a QQ-plot, the sample quantiles in the observed data are compared to the theoretical quantiles expected from the normal distribution. If the data are well-approximated by the normal distribution, then the points on the QQ-plot will fall near the identity line (sample = theoretical).
- Calculate sample quantiles (observed quantiles) using the `quantile` function.
- Calculate theoretical quantiles with the `qnorm` function. `qnorm` will calculate quantiles for the standard normal distribution ($\mu = 0$, $\sigma = 1$) by default, but it can calculate quantiles for any normal distribution given mean and `sd` arguments. We will learn more about `qnorm` in the probability course.
- Note that we will learn alternate ways to make QQ-plots with less code later in the series.

Code

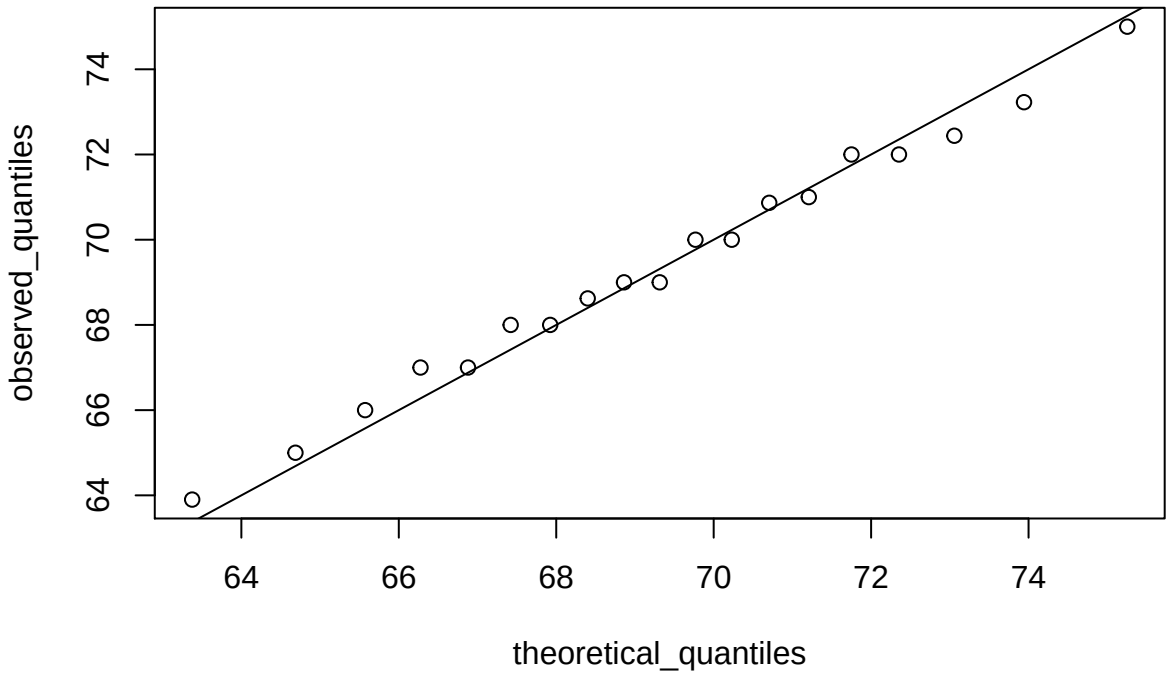
```
# define x and z
index <- heights$sex=="Male"
x <- heights$height[index]
z <- scale(x)

# proportion of data below 69.5
mean(x <= 69.5)
```

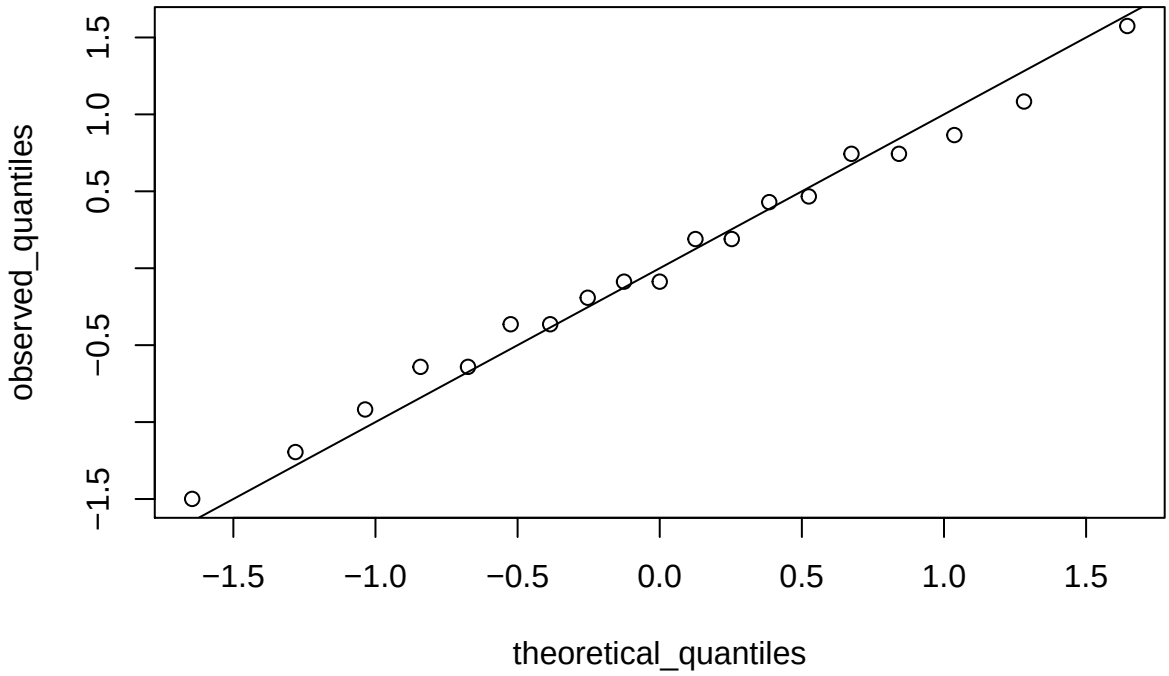
```
## [1] 0.5147783
```

```
# calculate observed and theoretical quantiles
p <- seq(0.05, 0.95, 0.05)
observed_quantiles <- quantile(x, p)
theoretical_quantiles <- qnorm(p, mean = mean(x), sd = sd(x))

# make QQ-plot
plot(theoretical_quantiles, observed_quantiles)
abline(0,1)
```




```r
# make QQ-plot with scaled values
observed_quantiles <- quantile(z, p)
theoretical_quantiles <- qnorm(p)
plot(theoretical_quantiles, observed_quantiles)
abline(0,1)
```



Percentiles

The textbook for this section is available here

Key points

- *Percentiles* are the quantiles obtained when defining p as `0.01,0.02,...,0.99`. They summarize the values at which a certain percent of the observations are equal to or less than that value.
- The 50th percentile is also known as the *median*.
- The *quartiles* are the 25th, 50th and 75th percentiles.

Boxplots

The textbook for this section is available here

Key points

- When data do not follow a normal distribution and cannot be succinctly summarized by only the mean and standard deviation, an alternative is to report a five-number summary: range (ignoring outliers) and the quartiles (25th, 50th, 75th percentile).
- In a *boxplot*, the box is defined by the 25th and 75th percentiles and the median is a horizontal line through the box. The whiskers show the range excluding outliers, and outliers are plotted separately as individual points.
- The *interquartile* range is the distance between the 25th and 75th percentiles.
- Boxplots are particularly useful when comparing multiple distributions.
- We discuss outliers later.

Assessment - Quantiles, percentiles, and boxplots

1. When analyzing data it's often important to know the number of measurements you have for each category.

```
male <- heights$height[heights$sex=="Male"]
female <- heights$height[heights$sex=="Female"]
length(male)
```

```
## [1] 812
```

```
length(female)
```

```
## [1] 238
```

2. Suppose we can't make a plot and want to compare the distributions side by side. If the number of data points is large, listing all the numbers is inpractical. A more practical approach is to look at the percentiles. We can obtain percentiles using the `quantile` function like this

```
library(dslabs)
data(heights)
quantile(heights$height, seq(.01, 0.99, 0.01))
```

```
male <- heights$height[heights$sex=="Male"]
female <- heights$height[heights$sex=="Female"]
female_percentiles <- quantile(female, seq(0.1, 0.9, 0.2))
male_percentiles <- quantile(male, seq(0.1, 0.9, 0.2))
df <- data.frame(female = (female_percentiles), male = (male_percentiles))
df
```

```
##       female     male
## 10% 61.00000 65.00000
## 30% 63.00000 68.00000
## 50% 64.98031 69.00000
## 70% 66.46417 71.00000
## 90% 69.00000 73.22751
```

3. Study the boxplots summarizing the distributions of populations sizes by country.

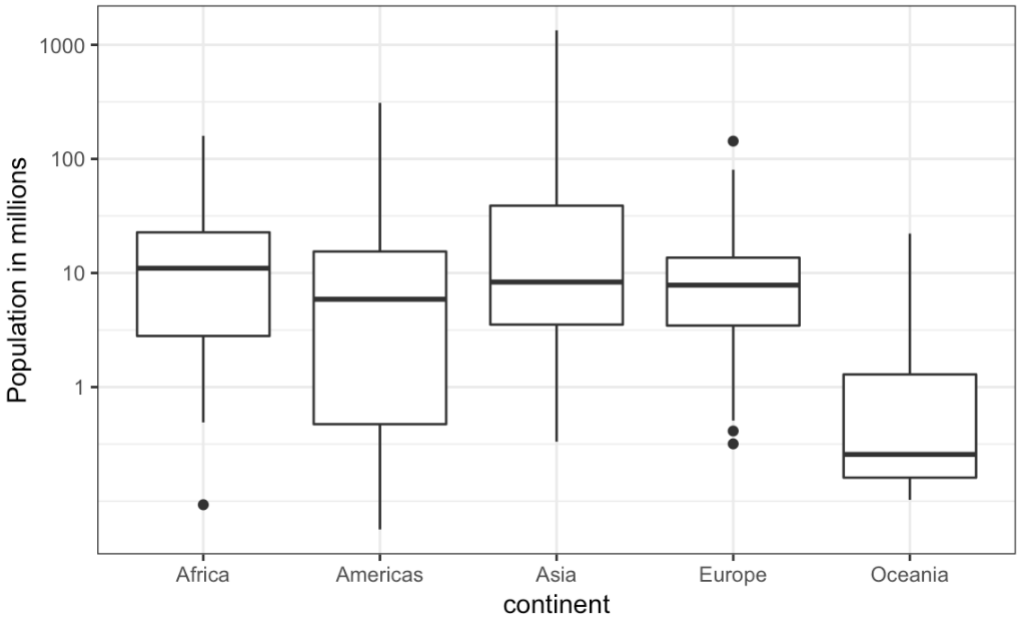


Figure 7: Continent vs Population

Which continent has the country with the largest population size?

- ☐ A. Africa
- ☐ B. Americas
- ☒ C. Asia
- ☐ D. Europe
- ☐ E. Oceania

4. Study the boxplots summarizing the distributions of populations sizes by country.

Which continent has median country with the largest population?

- ☒ A. Africa
- ☐ B. Americas
- ☐ C. Asia
- ☐ D. Europe
- ☐ E. Oceania

5. Again, look at the boxplots summarizing the distributions of populations sizes by country.

To the nearest million, what is the median population size for Africa?

☐ A. 100 million
☐ B. 25 million
☒ C. 10 million
☐ D. 5 million
☐ E. 1 million

6. Examine the following boxplots and report approximately what proportion of countries in Europe have populations below 14 million?

☒ A. 0.75
☐ B. 0.50
☐ C. 0.25
☐ D. 0.01

7. Based on the boxplot, if we use a log transformation, which continent shown below has the largest interquartile range?

☐ A. Africa
☒ B. Americas
☐ C. Asia
☐ D. Europe
☐ E. Oceania

Distribution of Female Heights

The textbook for this section is available here

Key points

- If a distribution is not normal, it cannot be summarized with only the mean and standard deviation. Provide a histogram, smooth density or boxplot instead.
- A plot can force us to see unexpected results that make us question the quality or implications of our data.

Assessment - Robust Summaries With Outliers

1. For this chapter, we will use height data collected by Francis Galton for his genetics studies. Here we just use height of the children in the dataset:

```
library(HistData)
data(Galton)
x <- Galton$child
```

```
if(!require(HistData)) install.packages("HistData")
```

```
## Loading required package: HistData
```

```
## Warning: package 'HistData' was built under R version 4.0.2
```

```
library(HistData)
data(Galton)
x <- Galton$child
mean(x)
```

```
## [1] 68.08847
```

```
median(x)
```

```
## [1] 68.2
```

2. Now for the same data compute the standard deviation and the median absolute deviation (MAD).

```
x <- Galton$child
sd(x)
```

```
## [1] 2.517941
```

```
mad(x)
```

```
## [1] 2.9652
```

3. In the previous exercises we saw that the mean and median are very similar and so are the standard deviation and MAD. This is expected since the data is approximated by a normal distribution which has this property.

Now suppose that suppose Galton made a mistake when entering the first value, forgetting to use the decimal point. You can imitate this error by typing:

```
library(HistData)
data(Galton)
x <- Galton$child
x_with_error <- x
x_with_error[1] <- x_with_error[1]*10
```

The data now has an outlier that the normal approximation does not account for. Let's see how this affects the average.

```
x <- Galton$child
x_with_error <- x
x_with_error[1] <- x_with_error[1]*10
gem <- mean(x)
gem_error <- mean(x_with_error)
gem_error - gem
```

```
## [1] 0.5983836
```

4. In the previous exercise we saw how a simple mistake in 1 out of over 900 observations can result in the average of our data increasing more than half an inch, which is a large difference in practical terms.

Now let's explore the effect this outlier has on the standard deviation.

```
x_with_error <- x
x_with_error[1] <- x_with_error[1]*10
sd(x_with_error)- sd(x)
```

```
## [1] 15.6746
```

5. In the previous exercises we saw how one mistake can have a substantial effect on the average and the standard deviation.

Now we are going to see how the median and MAD are much more resistant to outliers. For this reason we say that they are *robust* summaries.

```
x_with_error <- x
x_with_error[1] <- x_with_error[1]*10
mediaan <- median(x)
mediaan_error <- median(x_with_error)
mediaan_error - mediaan
```

```
## [1] 0
```

6. We saw that the median barely changes. Now let's see how the MAD is affected.

We saw that the median barely changes. Now let's see how the MAD is affected.

```
x_with_error <- x
x_with_error[1] <- x_with_error[1]*10
mad_normal <- mad(x)
mad_error <- mad(x_with_error)
mad_error - mad_normal
```

```
## [1] 0
```

7. How could you use exploratory data analysis to detect that an error was made?

☐ A. Since it is only one value out of many, we will not be able to detect this.
☐ B. We would see an obvious shift in the distribution.
☒ C. A boxplot, histogram, or qq-plot would reveal a clear outlier.
☐ D. A scatter plot would show high levels of measurement error.

8. We have seen how the average can be affected by outliers.

But how large can this effect get? This of course depends on the size of the outlier and the size of the dataset.

To see how outliers can affect the average of a dataset, let's write a simple function that takes the size of the outlier as input and returns the average.

```
x <- Galton$child
error_avg <- function(k){
x[1] = k
mean(x)
}
error_avg(10000)
```

```
## [1] 78.79784
```

```
error_avg(-10000)
```

```
## [1] 57.24612
```

Section 2 Overview

In Section 2, you will learn how to create data visualizations in R using ggplot2.

After completing Section 2, you will:

- be able to use ggplot2 to create data visualizations in R.
- be able to explain what the data component of a graph is.
- be able to identify the geometry component of a graph and know when to use which type of geometry.
- be able to explain what the aesthetic mapping component of a graph is.
- be able to understand the scale component of a graph and select an appropriate scale component to use.

Note that it can be hard to memorize all of the functions and arguments used by ggplot2, so we recommend that you have a cheat sheet handy to help you remember the necessary commands.

ggplot

The textbook for this section is available here

Key points

- Throughout the series, we will create plots with the **ggplot2** package. ggplot2 is part of the tidyverse, which you can load with `library(tidyverse)`.
- Note that you can also load ggplot2 alone using the command `library(ggplot2)`, instead of loading the entire tidyverse.
- ggplot2 uses a *grammar of graphics* to break plots into building blocks that have intuitive syntax, making it easy to create relatively complex and aesthetically pleasing plots with relatively simple and readable code.
- ggplot2 is designed to work exclusively with tidy data (rows are observations and columns are variables).

Graph Components

The textbook for this section is available here

Key points

- Plots in ggplot2 consist of 3 main components:
  - Data: The dataset being summarized
  - Geometry: The type of plot (scatterplot, boxplot, barplot, histogram, qqplot, smooth density, etc.)
  - Aesthetic mapping: Variables mapped to visual cues, such as x-axis and y-axis values and color
- There are additional components:
  - Scale
  - Labels, Title, Legend
  - Theme/Style

Creating a New Plot

The textbook for this section is available here

Key points

- You can associate a dataset x with a ggplot object with any of the 3 commands:
  - `ggplot(data = x)`
  - `ggplot(x)`
  - `x %>% ggplot()`
- You can assign a ggplot object to a variable. If the object is not assigned to a variable, it will automatically be displayed.
- You can display a ggplot object assigned to a variable by printing that variable.

Code

```
ggplot(data = murders)

murders %>% ggplot()
```

```
p <- ggplot(data = murders)
class(p)
```

```
## [1] "gg"     "ggplot"
```

```
print(p)    # this is equivalent to simply typing p
```

The functions above render a plot, in this case a blank slate since no geometry has been defined. The only style choice we see is a grey background.

Layers

The textbook for this section is available:

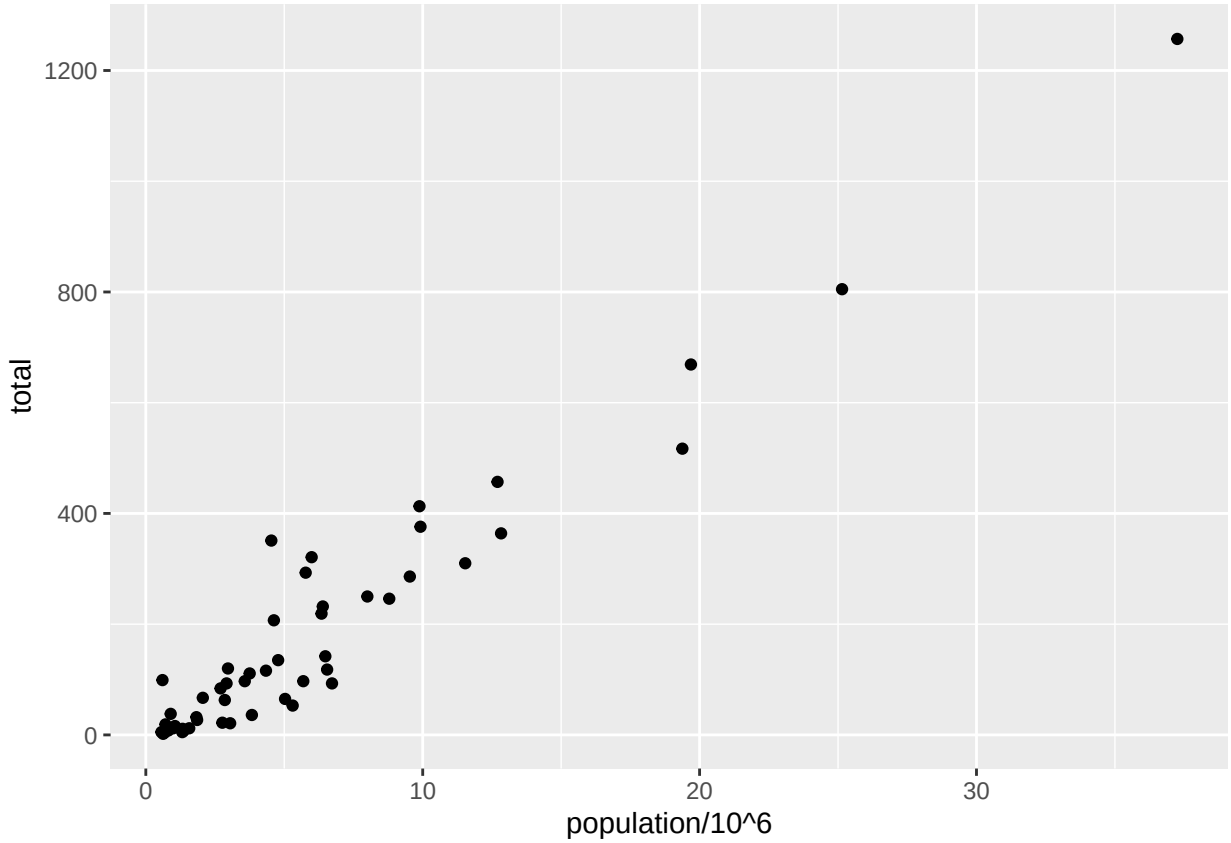
- Geometries
- Aesthetic mappings
- Layers

Key points

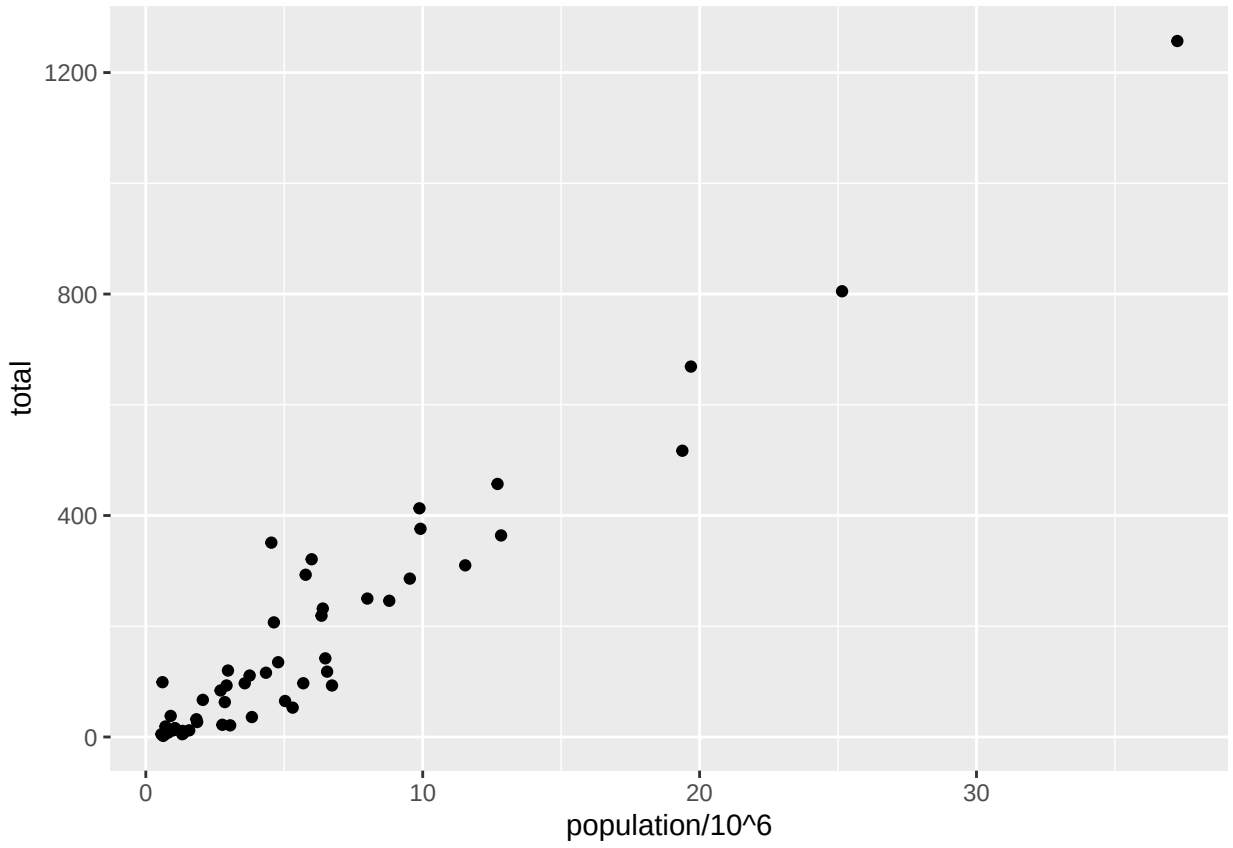
- In ggplot2, graphs are created by adding *layers* to the ggplot object: `DATA %>% ggplot() + LAYER_1 + LAYER_2 + ... + LAYER_N`
- The *geometry layer* defines the plot type and takes the format `geom_X` where X is the plot type.
- *Aesthetic mappings* describe how properties of the data connect with features of the graph (axis position, color, size, etc.) Define aesthetic mappings with the `aes` function.
- aes uses variable names from the object component (for example, `total` rather than `murders$total`).
- `geom_point` creates a scatterplot and requires x and y aesthetic mappings.
- `geom_text` and `geom_label` add text to a scatterplot and require x, y, and label aesthetic mappings.
- To determine which aesthetic mappings are required for a geometry, read the help file for that geometry.
- You can add layers with different aesthetic mappings to the same graph.

Code: Adding layers to a plot

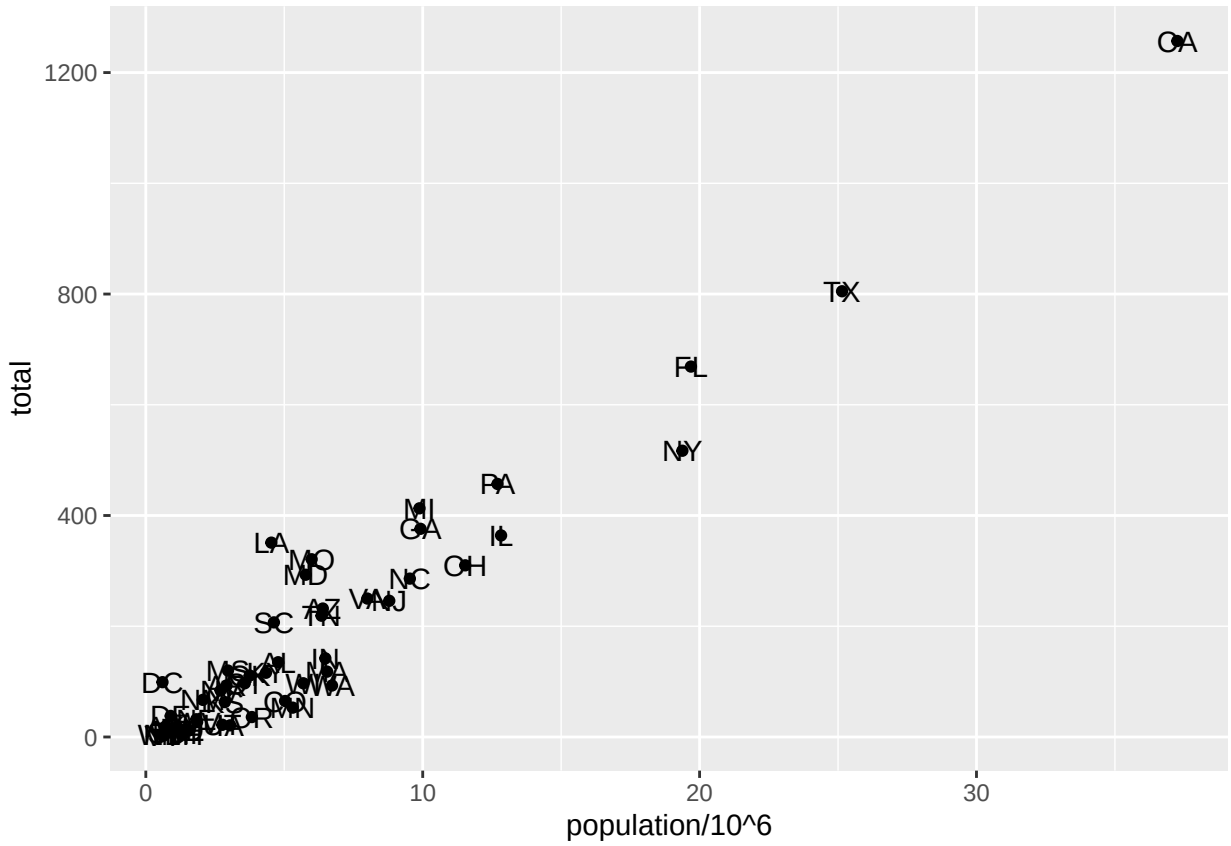
```
murders %>% ggplot() +
    geom_point(aes(x = population/10^6, y = total))
```




```
# add points layer to predefined ggplot object
p <- ggplot(data = murders)
p + geom_point(aes(population/10^6, total))
```




```
# add text layer to scatterplot
p + geom_point(aes(population/10^6, total)) +
    geom_text(aes(population/10^6, total, label = abb))
```



Code: Example of ***aes*** *behavior*

```
# no error from this call
p_test <- p + geom_text(aes(population/10^6, total, label = abb))
```

```
# error - "abb" is not a globally defined variable and cannot be found outside of aes
p_test <- p + geom_text(aes(population/10^6, total), label = abb)
```

Tinkering

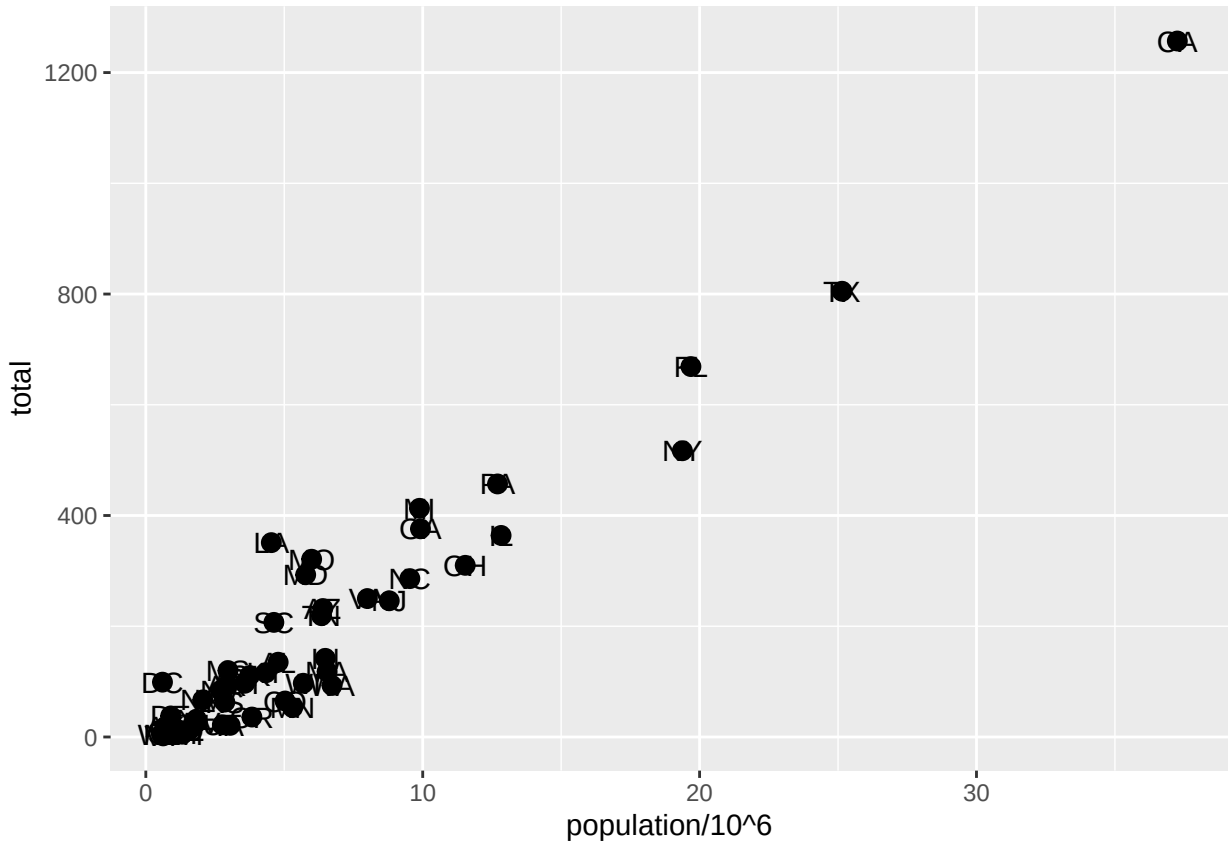
The textbook for this section is available here and here

Key points

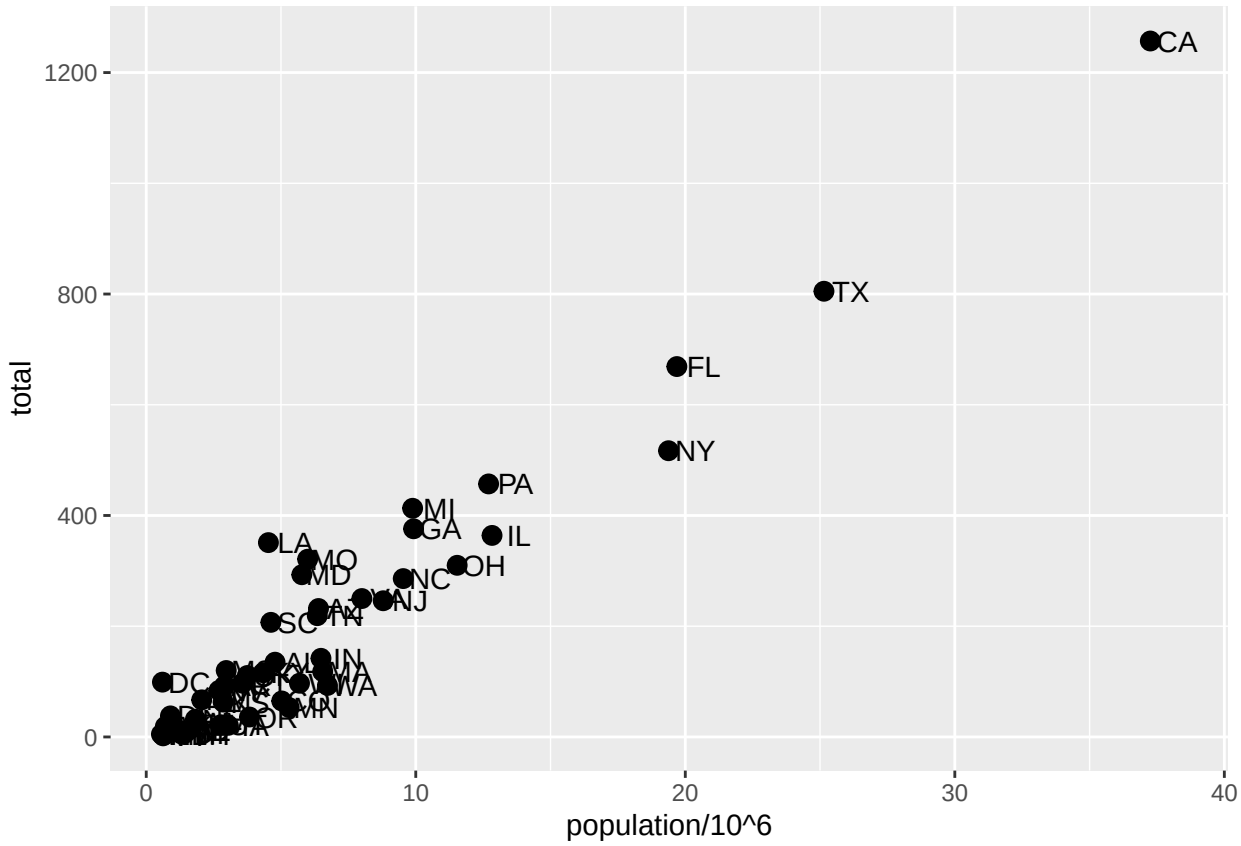
- You can modify arguments to geometry functions other than aes and the data. Additional arguments can be found in the documentation for each geometry.
- These arguments are not aesthetic mappings: they affect all data points the same way.
- *Global aesthetic mappings* apply to all geometries and can be defined when you initially call `ggplot`. All the geometries added as layers will default to this mapping. Local aesthetic mappings add additional information or override the default mappings.

Code

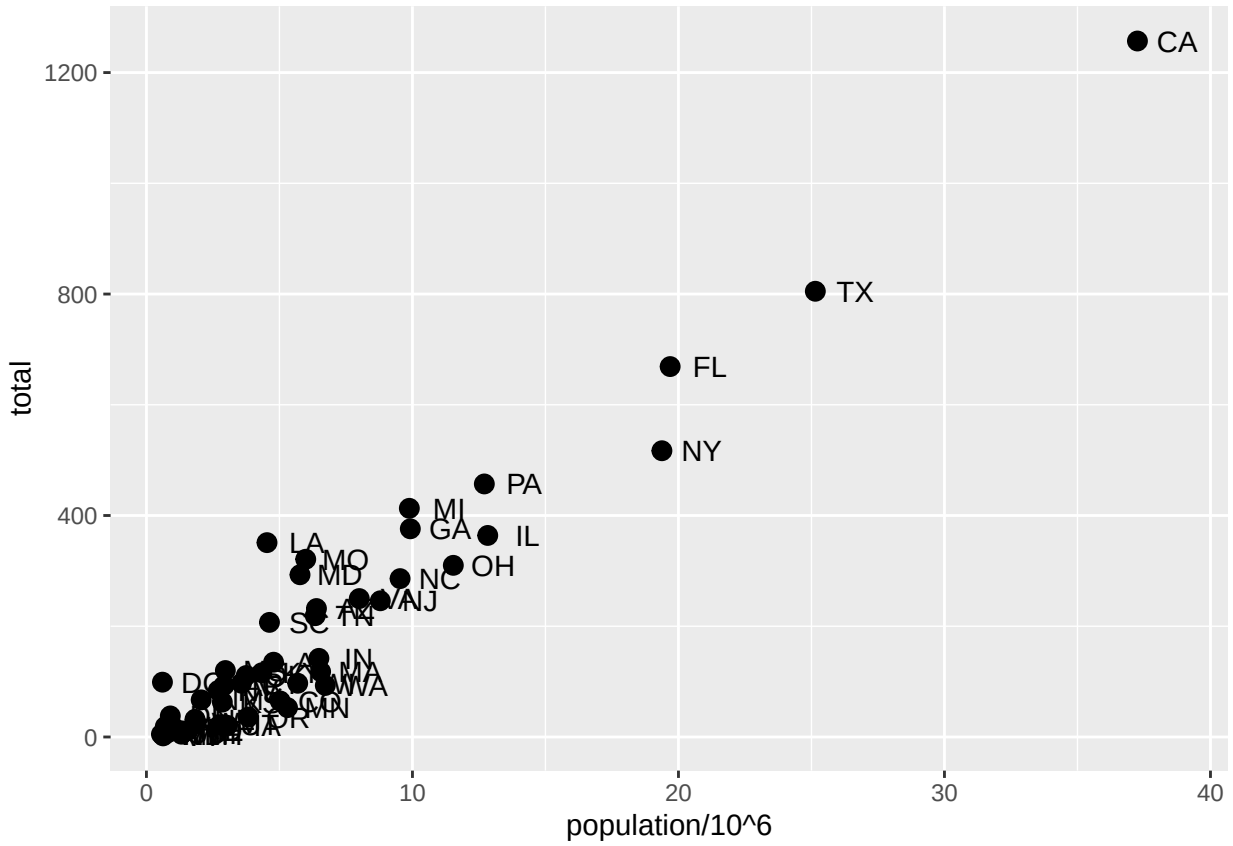
```
# change the size of the points
p + geom_point(aes(population/10^6, total), size = 3) +
    geom_text(aes(population/10^6, total, label = abb))
```



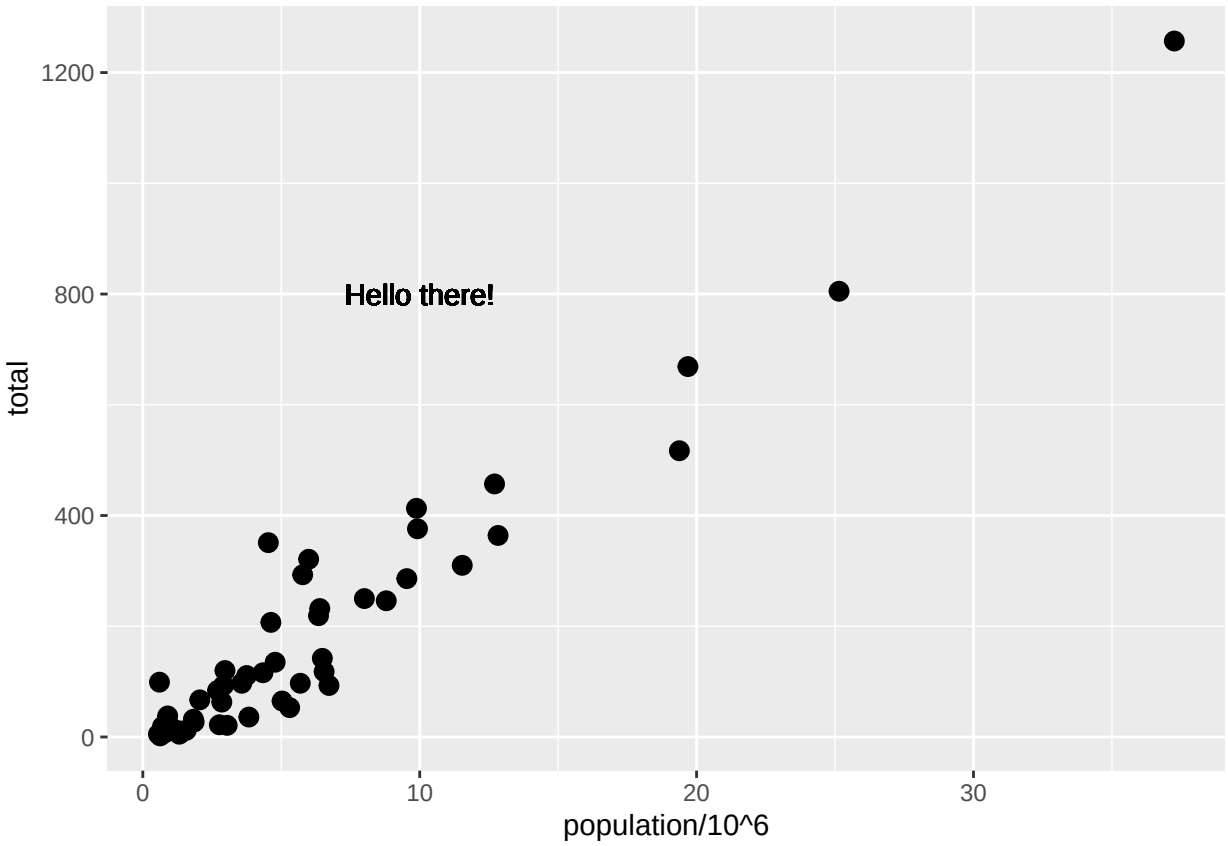

```
# move text labels slightly to the right
p + geom_point(aes(population/10^6, total), size = 3) +
    geom_text(aes(population/10^6, total, label = abb), nudge_x = 1)
```




```
# simplify code by adding global aesthetic
p <- murders %>% ggplot(aes(population/10^6, total, label = abb))
p + geom_point(size = 3) +
    geom_text(nudge_x = 1.5)
```




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



Scales, Labels, and Colors

The textbook for this section is available:

- Scales
- Labels and titles
- Categories as colors
- Annotation, shapes and adjustments

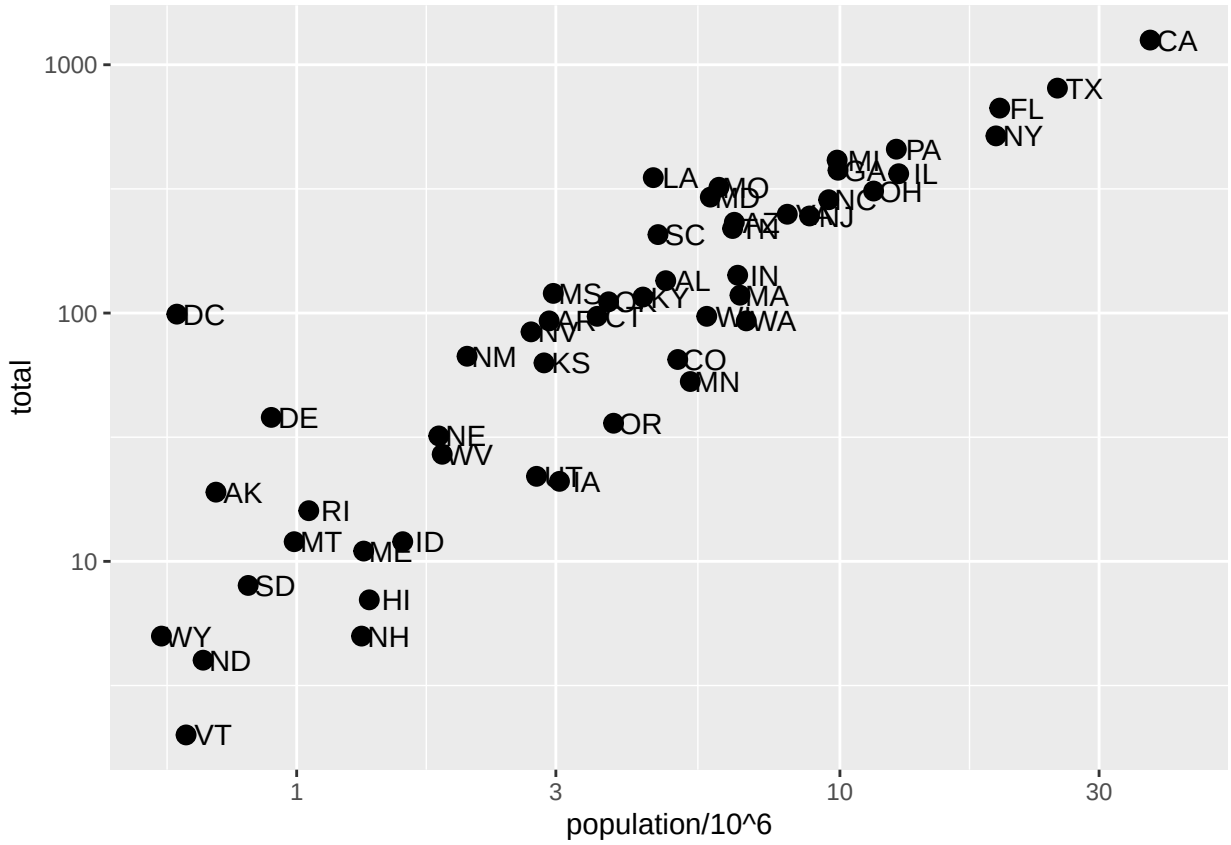
Key points

- Convert the x-axis to log scale with `scale_x_continuous(trans = "log10")` or `scale_x_log10`. Similar functions exist for the y-axis.
- Add axis titles with `xlab` and `ylab` functions. Add a plot title with the `ggtitle` function.
- Add a color mapping that colors points by a variable by defining the `col` argument within `aes`. To color all points the same way, define `col` outside of `aes`.
- Add a line with the `geom_abline` geometry. `geom_abline` takes arguments `slope` (default = 1) and `intercept` (default = 0). Change the color with `col` or `color` and line type with `lty`.
- Placing the line layer after the point layer will overlay the line on top of the points. To overlay points on the line, place the line layer before the point layer.
- There are many additional ways to tweak your graph that can be found in the ggplot2 documentation, cheat sheet, or on the internet. For example, you can change the legend title with `scale_color_discrete`.

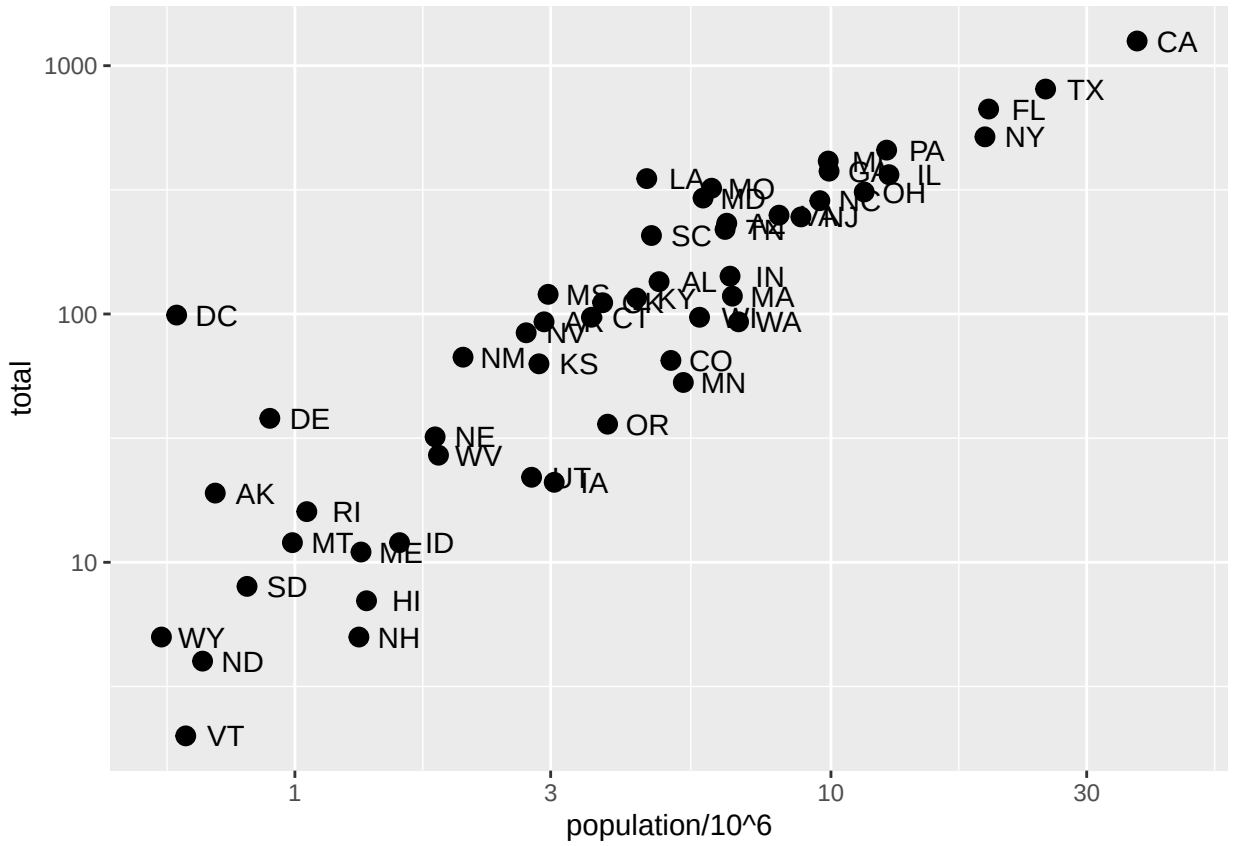
Code: Log-scale the x- and y-axis

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

# log base 10 scale the x-axis and y-axis
p + geom_point(size = 3) +
    geom_text(nudge_x = 0.05) +
    scale_x_continuous(trans = "log10") +
    scale_y_continuous(trans = "log10")
```

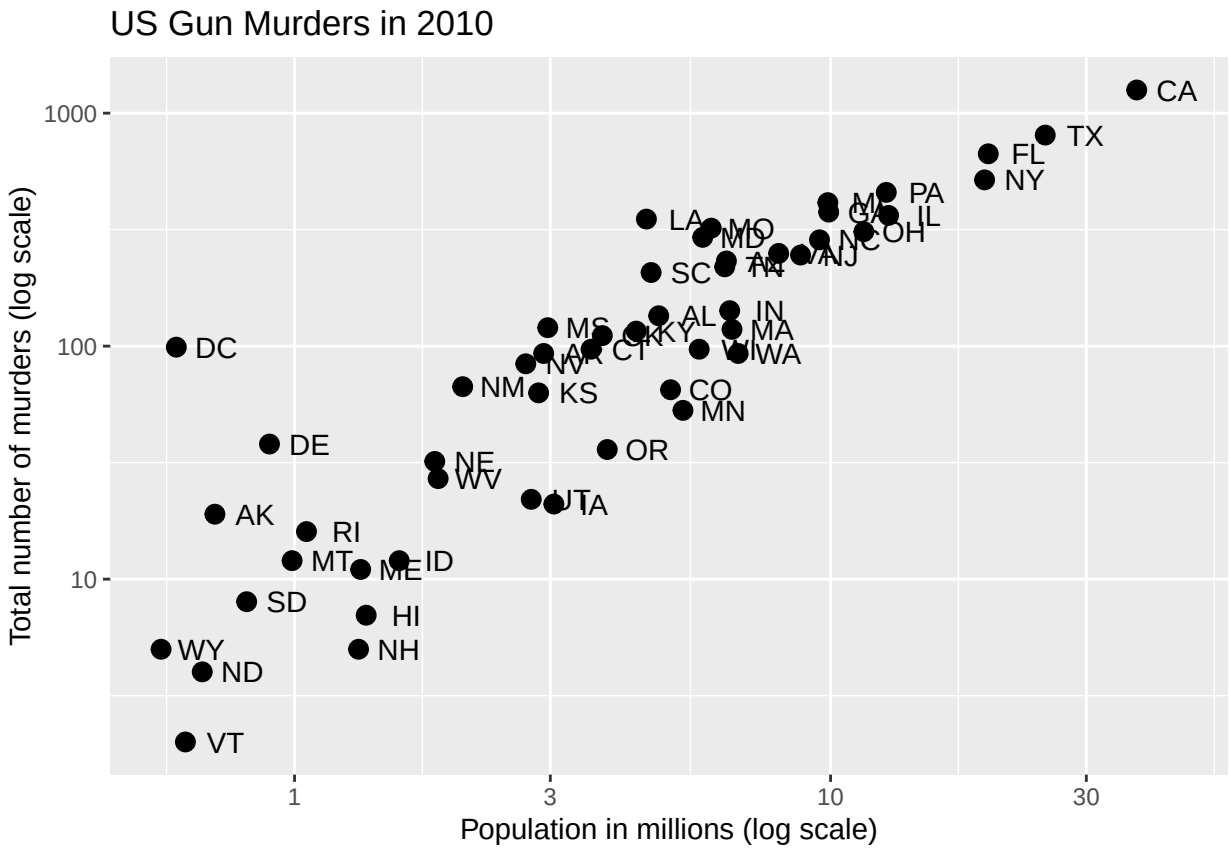



```
# efficient log scaling of the axes
p + geom_point(size = 3) +
    geom_text(nudge_x = 0.075) +
    scale_x_log10() +
    scale_y_log10()
```



Code: Add labels and title

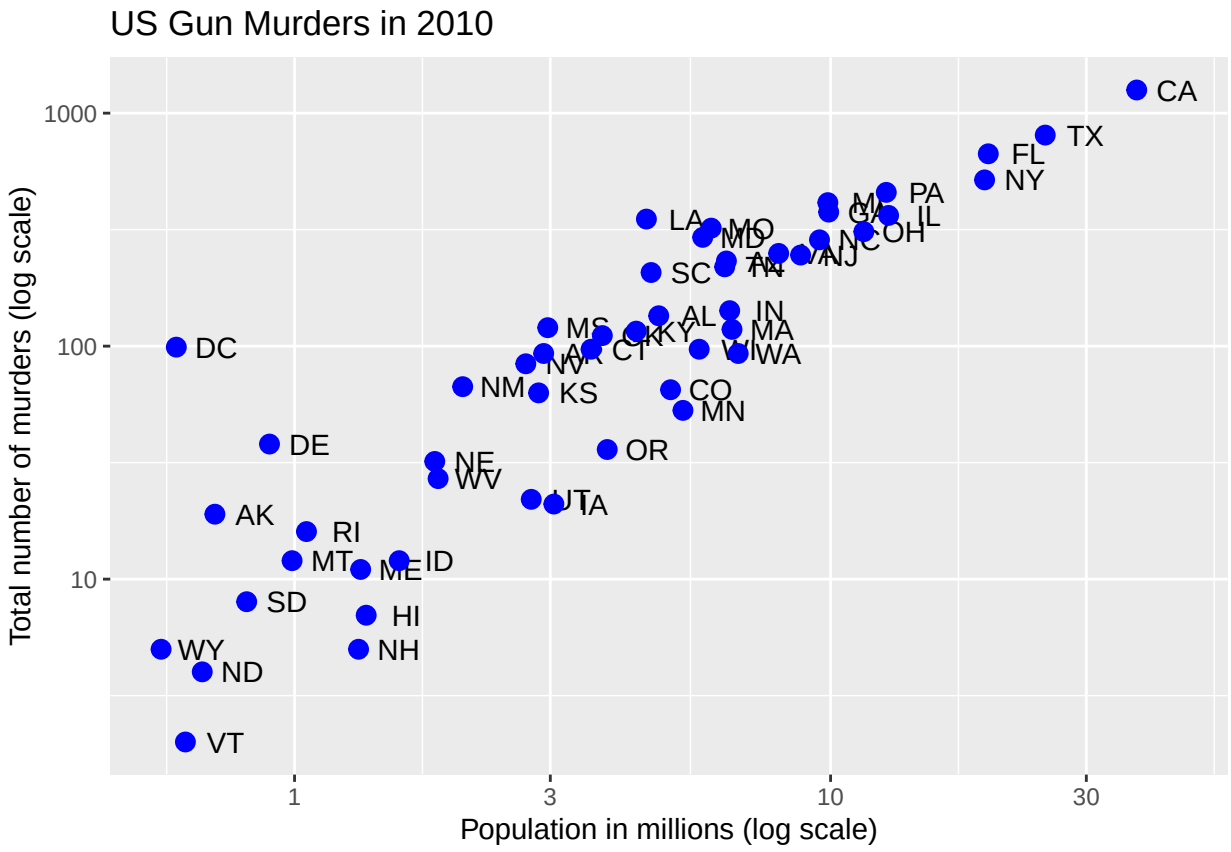
```
p + geom_point(size = 3) +
    geom_text(nudge_x = 0.075) +
    scale_x_log10() +
    scale_y_log10() +
    xlab("Population in millions (log scale)") +
    ylab("Total number of murders (log scale)") +
    ggtitle("US Gun Murders in 2010")
```



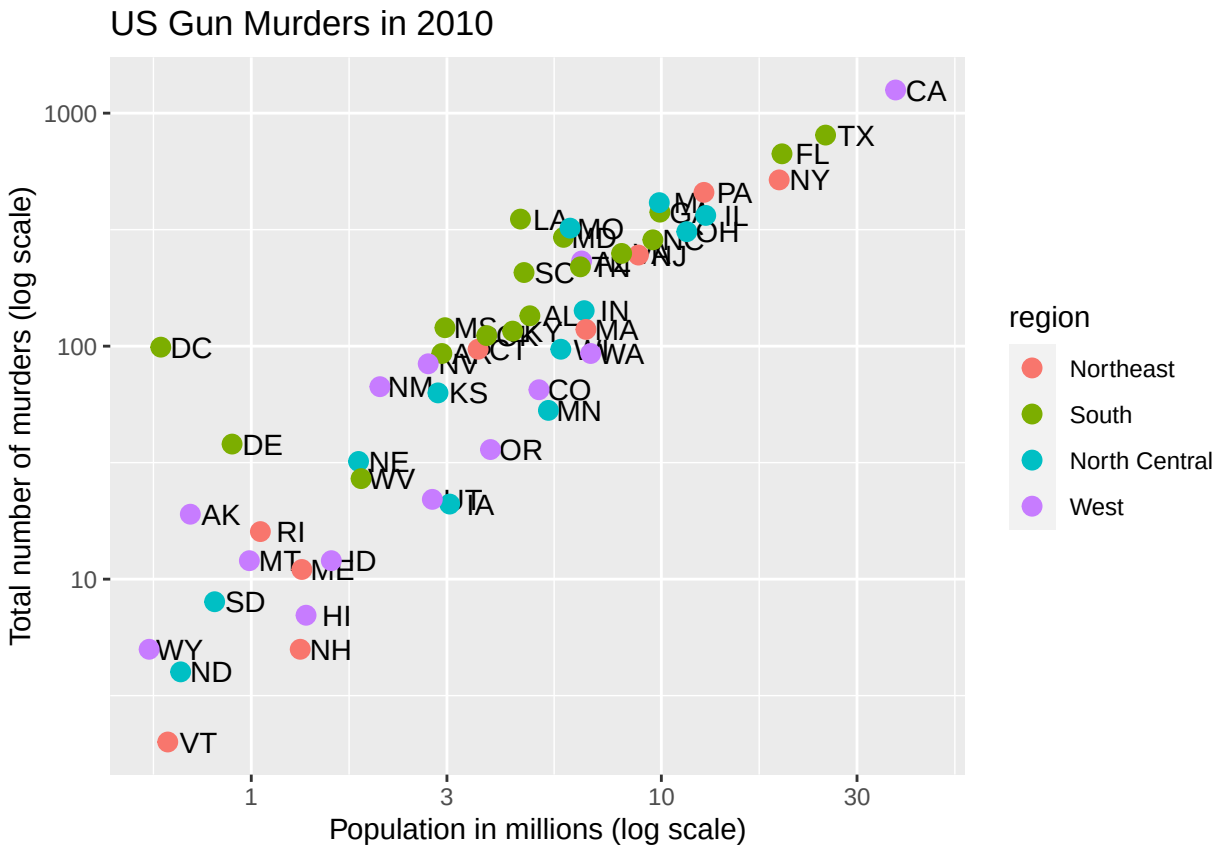
Code: Change color of the points

```
# redefine p to be everything except the points layer
p <- murders %>%
    ggplot(aes(population/10^6, total, label = abb)) +
    geom_text(nudge_x = 0.075) +
    scale_x_log10() +
    scale_y_log10() +
    xlab("Population in millions (log scale)") +
    ylab("Total number of murders (log scale)") +
    ggtitle("US Gun Murders in 2010")

# make all points blue
p + geom_point(size = 3, color = "blue")
```



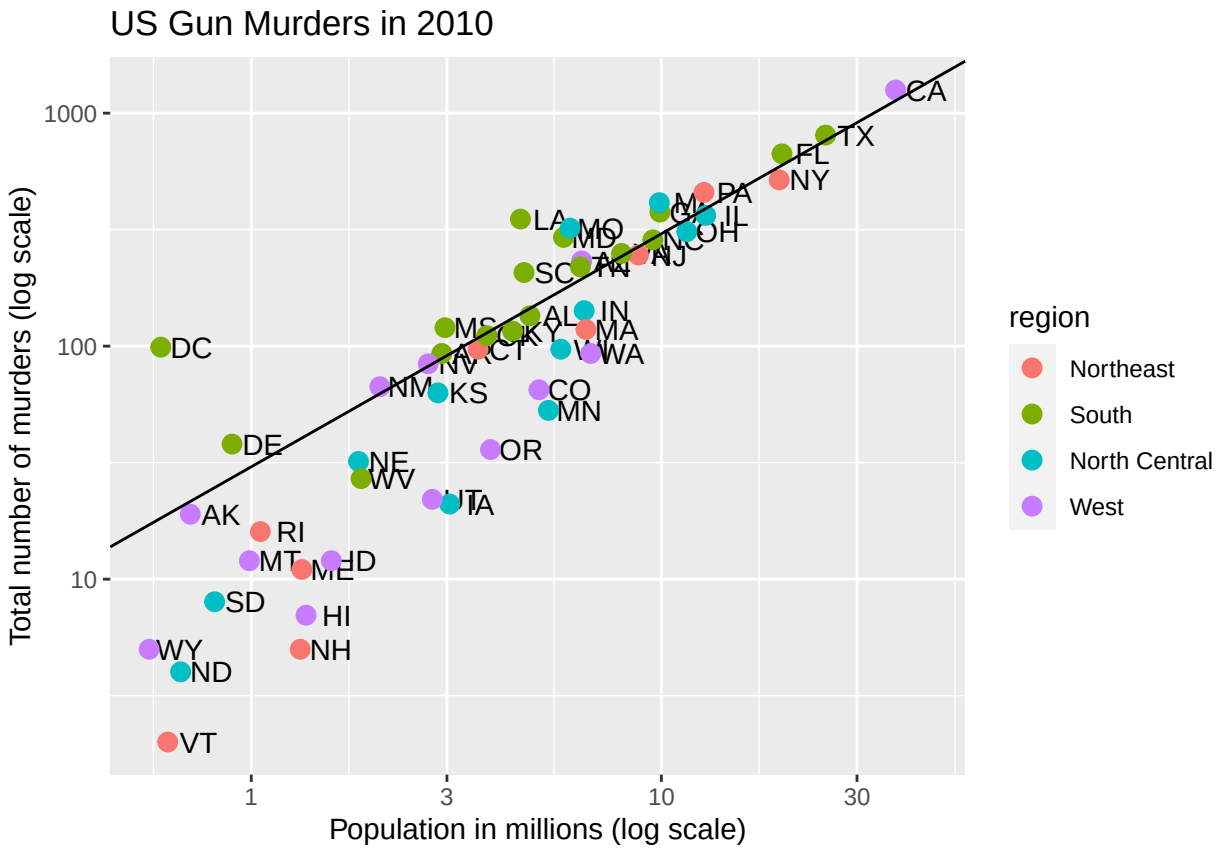

```
# color points by region
p + geom_point(aes(col = region), size = 3)
```



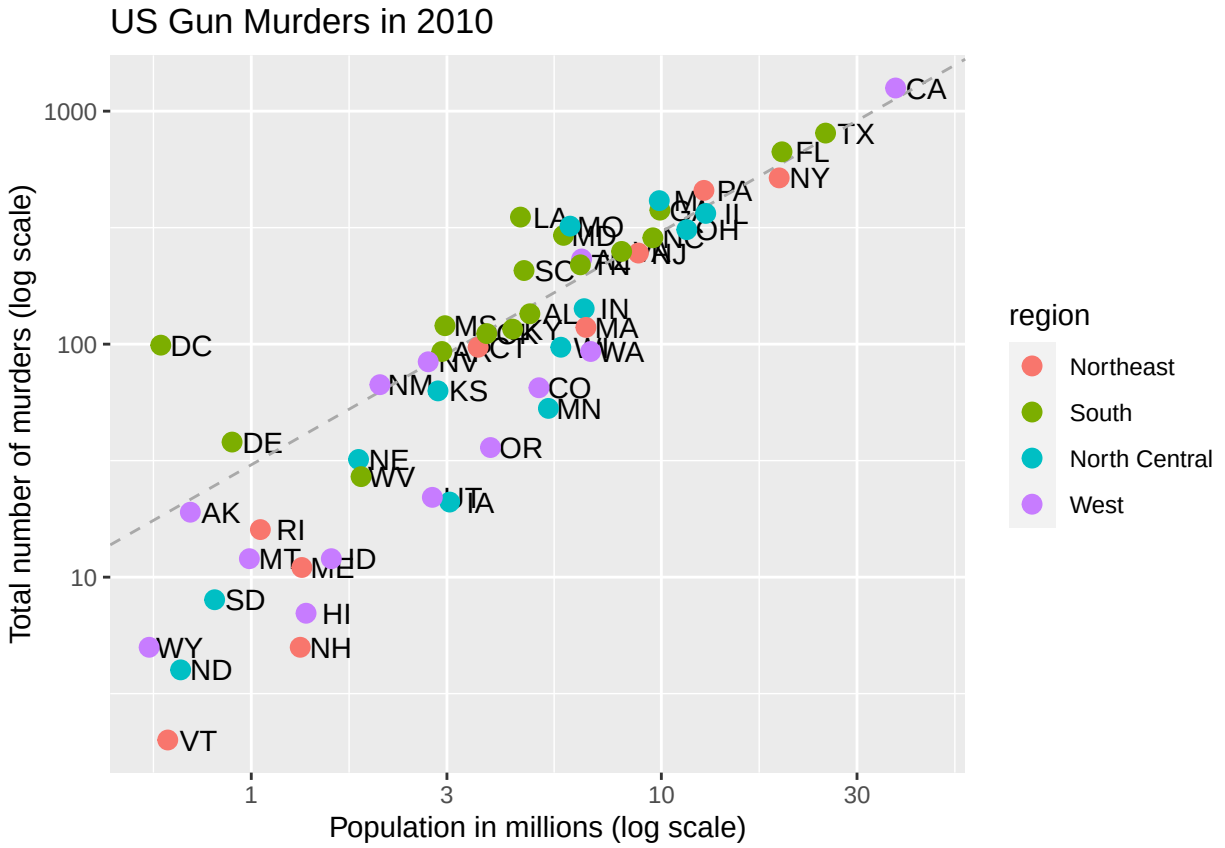
Code: Add a line with average murder rate

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

# basic line with average murder rate for the country
p + geom_point(aes(col = region), size = 3) +
    geom_abline(intercept = log10(r))    # slope is default of 1
```




```
# change line to dashed and dark grey, line under points
p +
    geom_abline(intercept = log10(r), lty = 2, color = "darkgrey") +
    geom_point(aes(col = region), size = 3)
```



Code: Change legend title

```
p <- p + scale_color_discrete(name = "Region")    # capitalize legend title
```

Add-on Packages

The textbook for this section is available here and here

Key points

- The style of a ggplot graph can be changed using the `theme` function.
- The **ggthemes** package adds additional themes.
- The **ggrepel** package includes a geometry that repels text labels, ensuring they do not overlap with each other: `geom_text_repel`.

Code: Adding themes

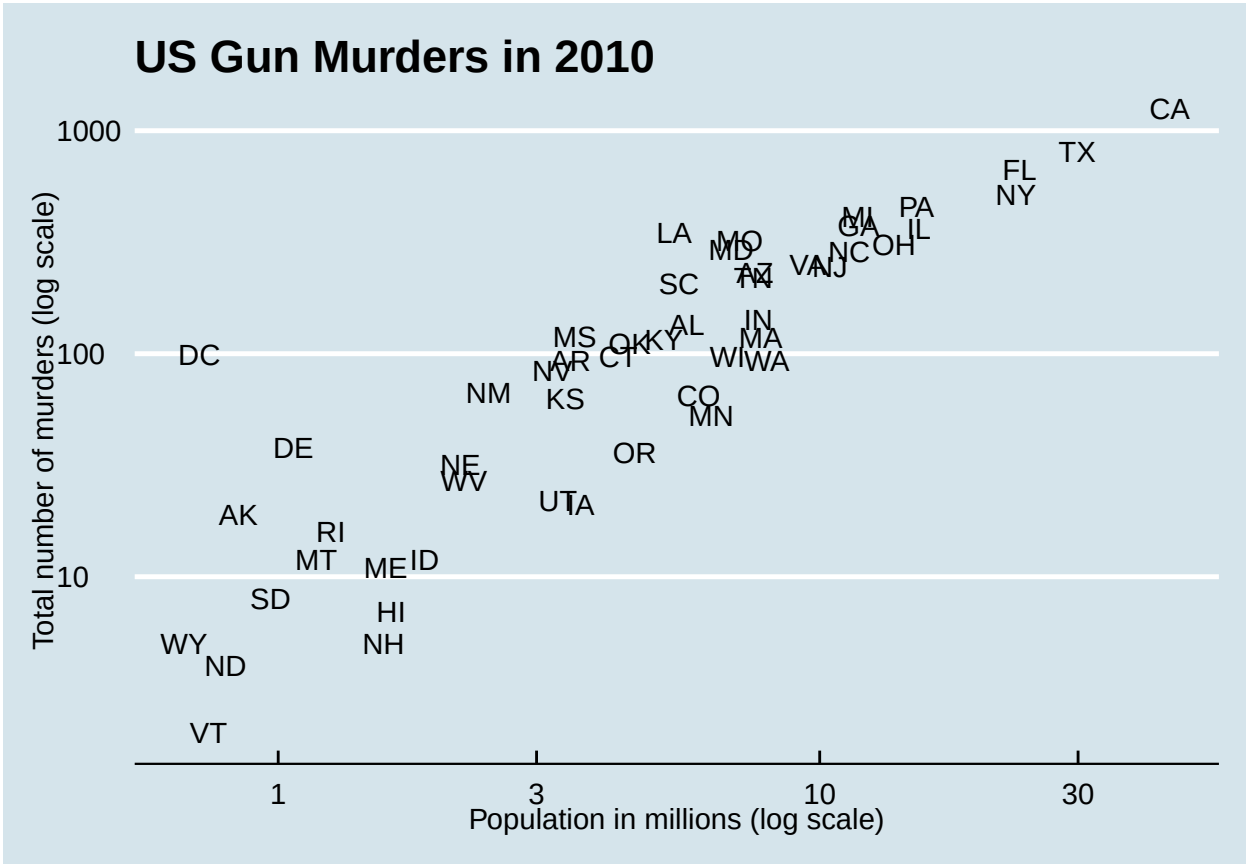
```
if(!require(ggthemes)) install.packages("ggthemes")
```

```
## Loading required package: ggthemes
```

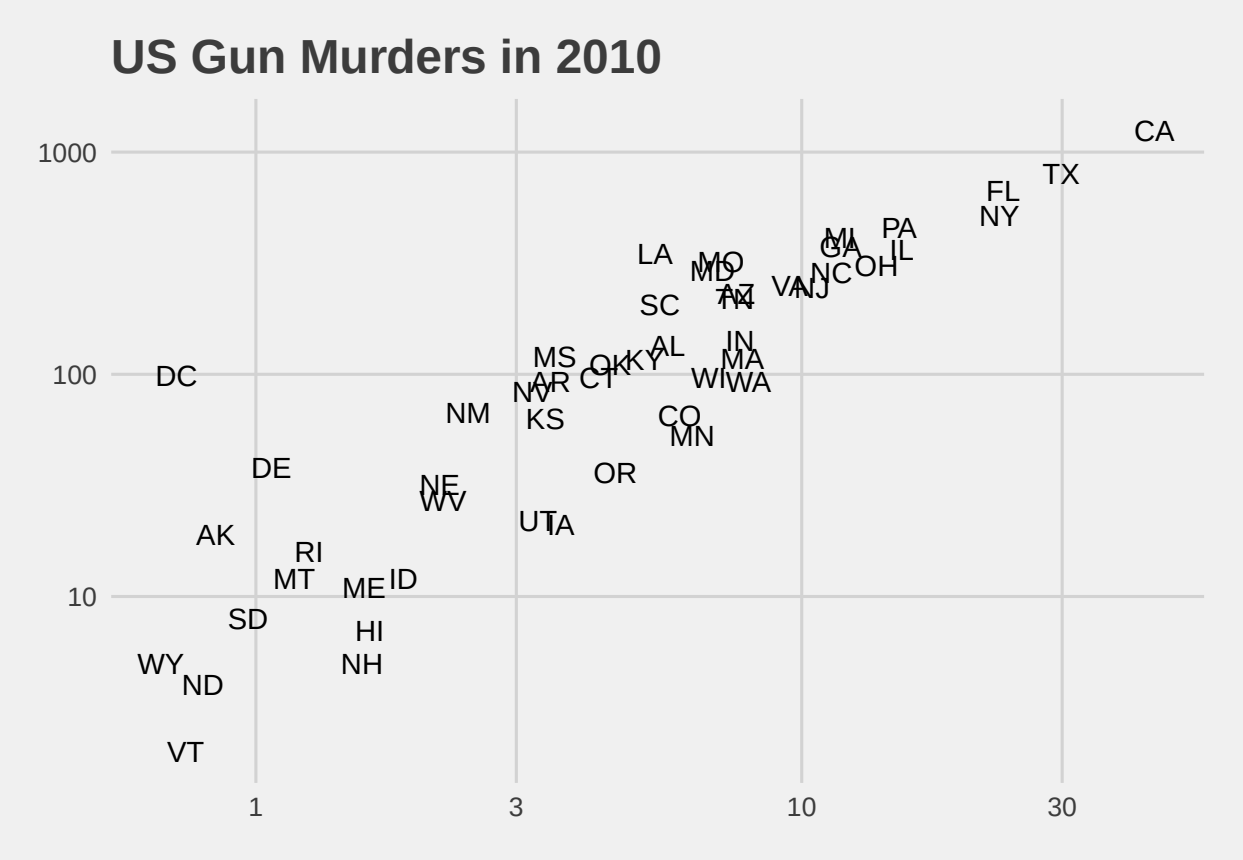
```
## Warning: package 'ggthemes' was built under R version 4.0.2
```

```
# theme used for graphs in the textbook and course
ds_theme_set()

# themes from ggthemes
library(ggthemes)
p + theme_economist()    # style of the Economist magazine
```




```
p + theme_fivethirtyeight()    # style of the FiveThirtyEight website
```



Code: Putting it all together to assemble the plot

```
if(!require(ggrepel)) install.packages("ggrepel")
```

```
## Loading required package: ggrepel
```

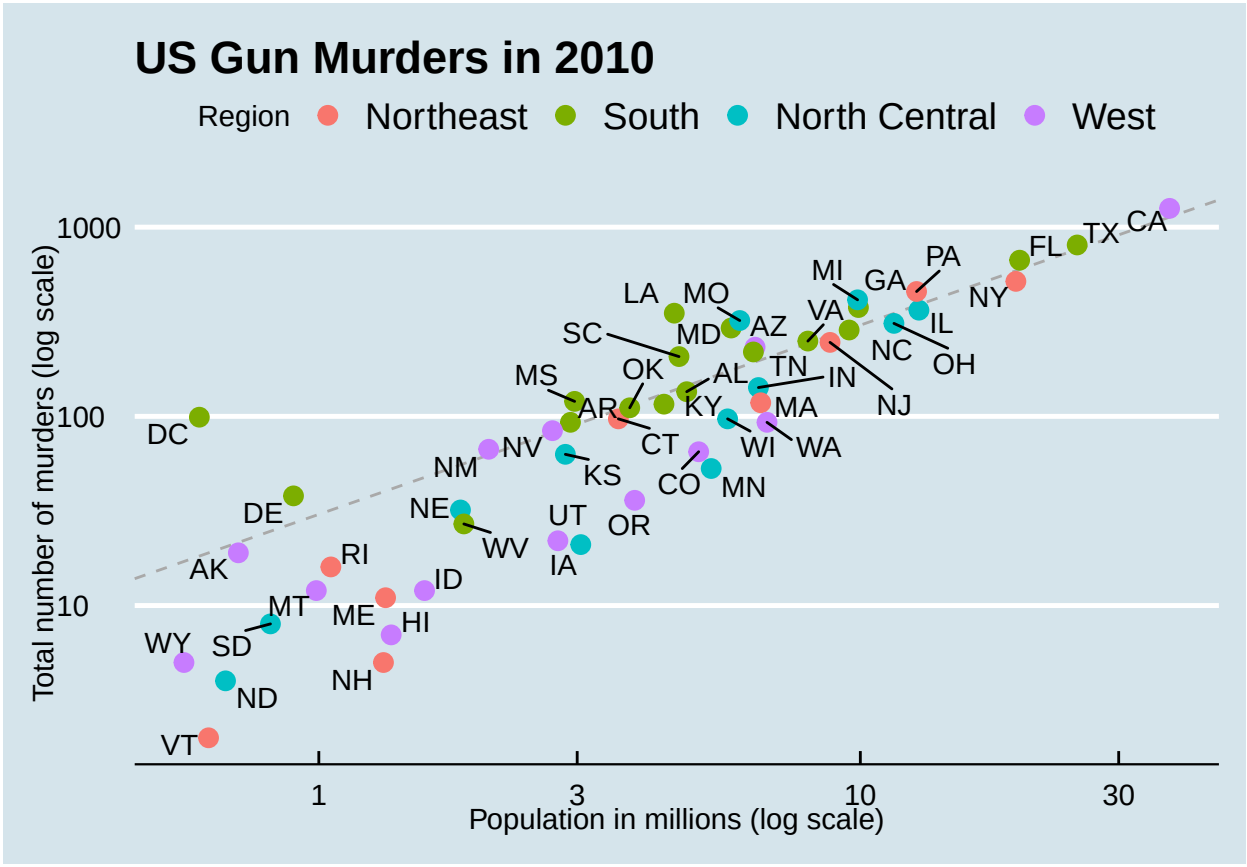
```
## Warning: package 'ggrepel' was built under R version 4.0.2
```

```
# load libraries
library(ggrepel)

# define the intercept
r <- murders %>%
    summarize(rate = sum(total) / sum(population) * 10^6) %>%
    .$rate

# make the plot, combining all elements
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("Population in millions (log scale)") +
```

```
  ylab("Total number of murders (log scale)") +
  ggtitle("US Gun Murders in 2010") +
  scale_color_discrete(name = "Region") +
  theme_economist()
```



Other Examples

The textbook for this section is available:

- Histograms
- Density plots
- QQ-plots
- Grids of plots

Key points

- `geom_histogram` creates a histogram. Use the `binwidth` argument to change the width of bins, the `fill` argument to change the bar fill color, and the `col` argument to change bar outline color.
- `geom_density` creates smooth density plots. Change the fill color of the plot with the `fill` argument.
- `geom_qq` creates a quantile-quantile plot. This geometry requires the `sample` argument. By default, the data are compared to a standard normal distribution with a mean of 0 and standard deviation of 1. This can be changed with the `dparams` argument, or the sample data can be scaled.

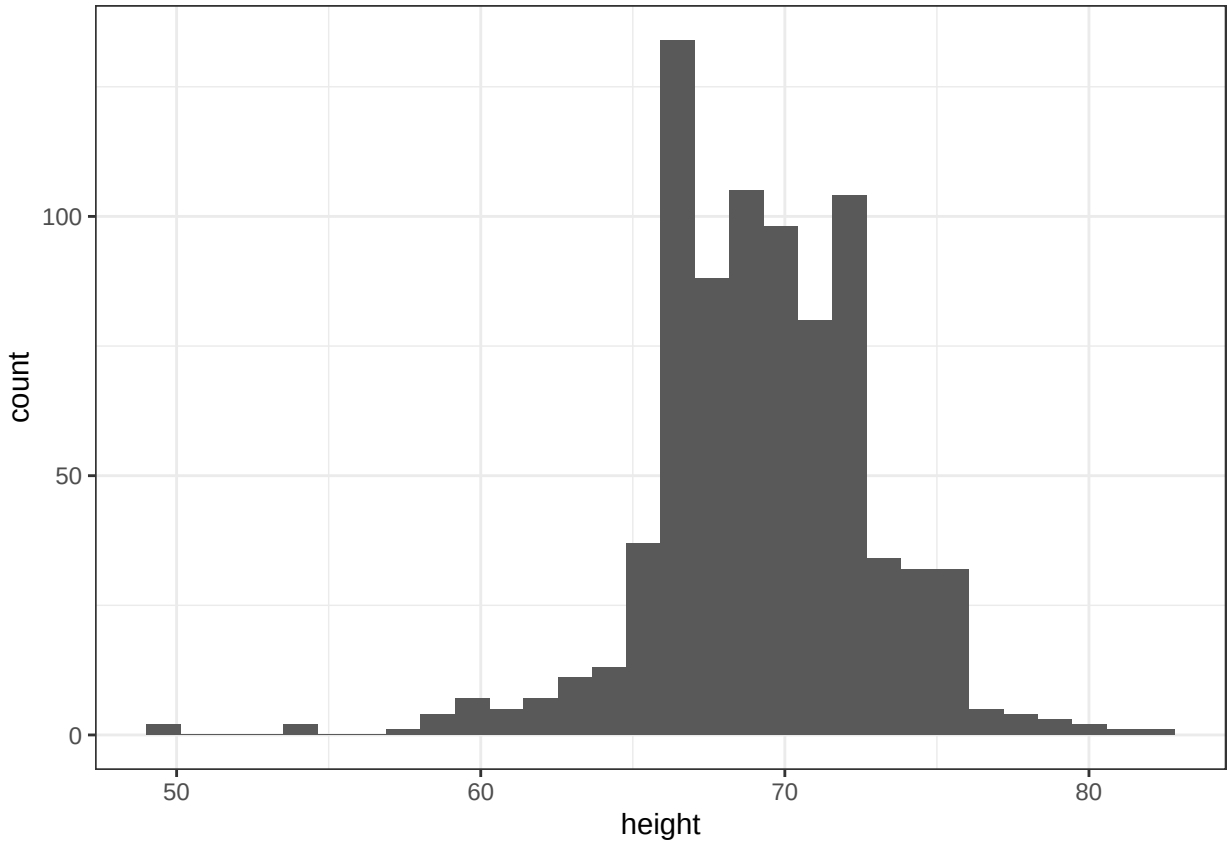
- Plots can be arranged adjacent to each other using the `grid.arrange` function from the `gridExtra` package. First, create the plots and save them to objects (p1, p2, …). Then pass the plot objects to `grid.arrange`.

Code: Histograms in ggplot2

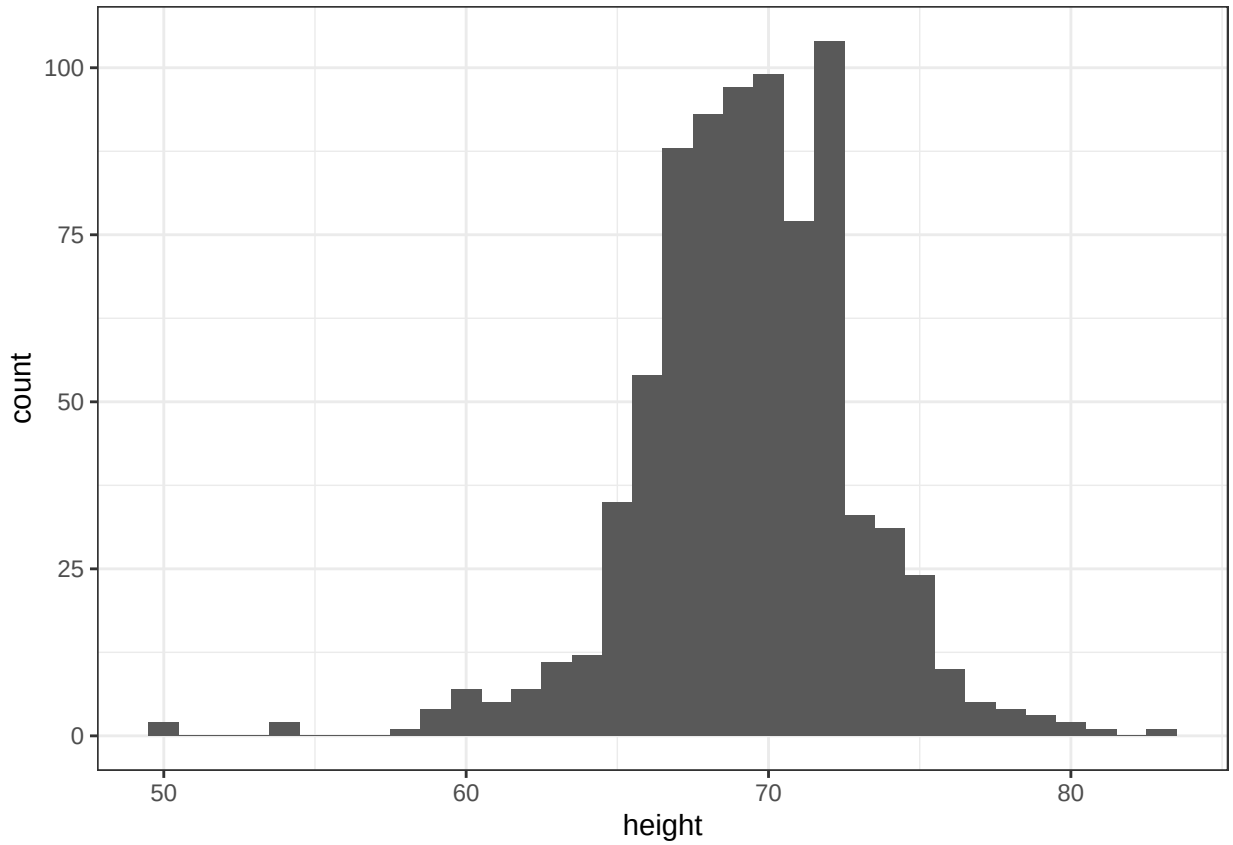
```
# define p
p <- heights %>%
    filter(sex == "Male") %>%
    ggplot(aes(x = height))

# basic histograms
p + geom_histogram()
```

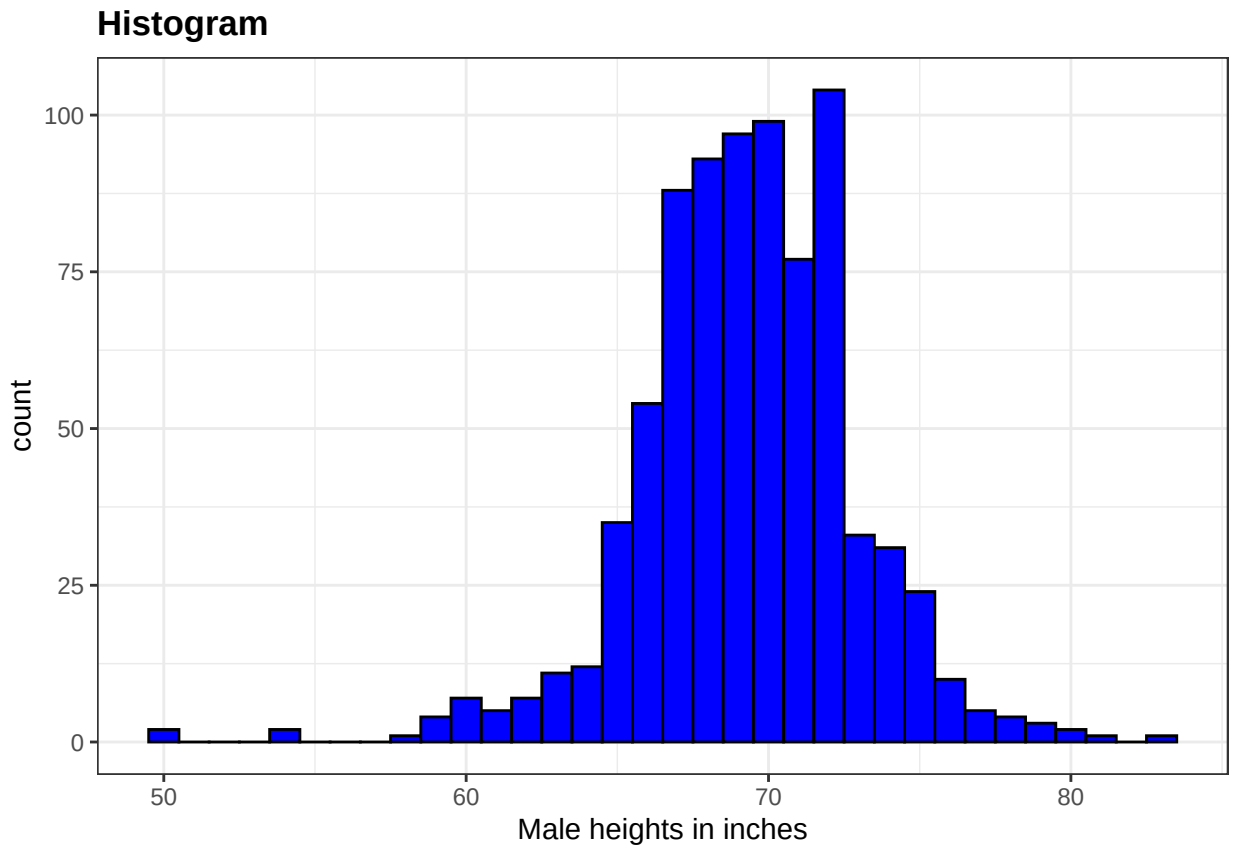
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```




```
p + geom_histogram(binwidth = 1)
```

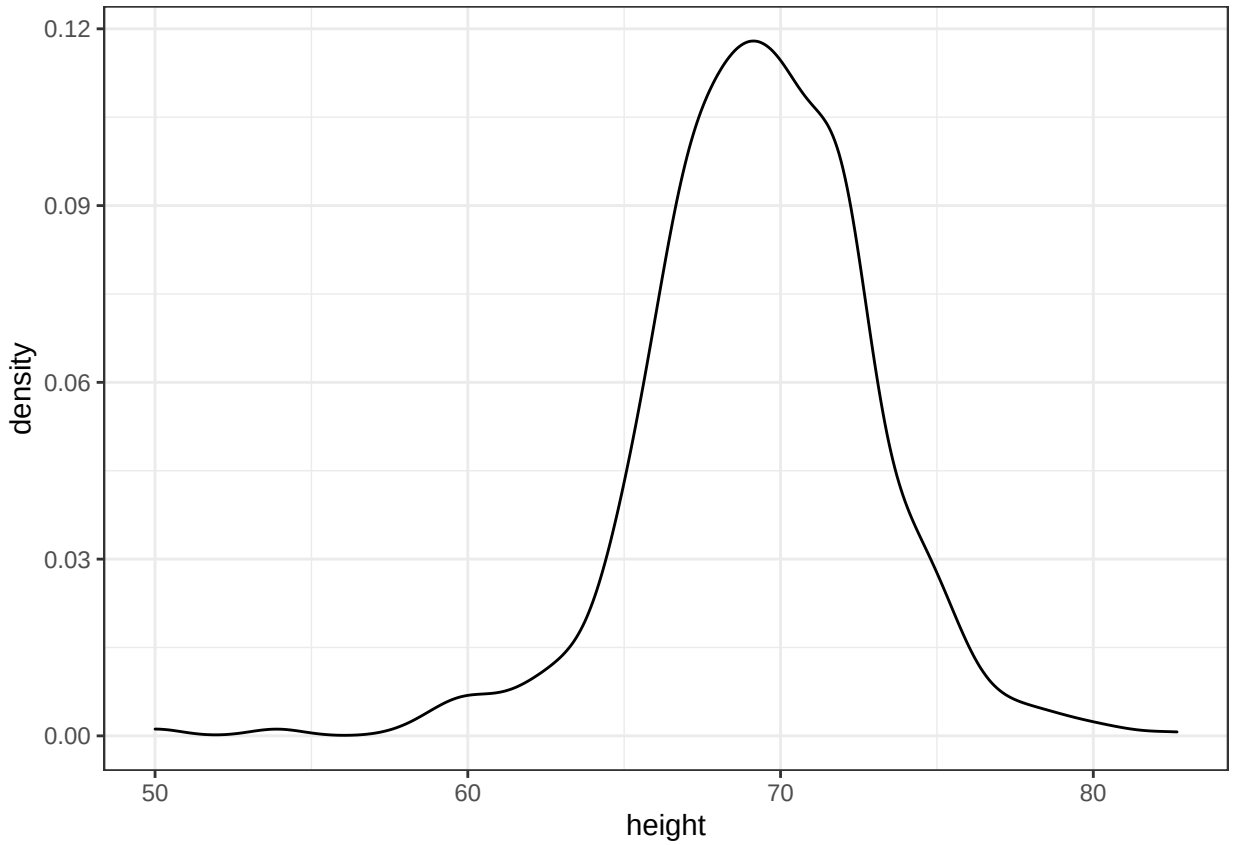



```
# histogram with blue fill, black outline, labels and title
p + geom_histogram(binwidth = 1, fill = "blue", col = "black") +
    xlab("Male heights in inches") +
    ggtitle("Histogram")
```

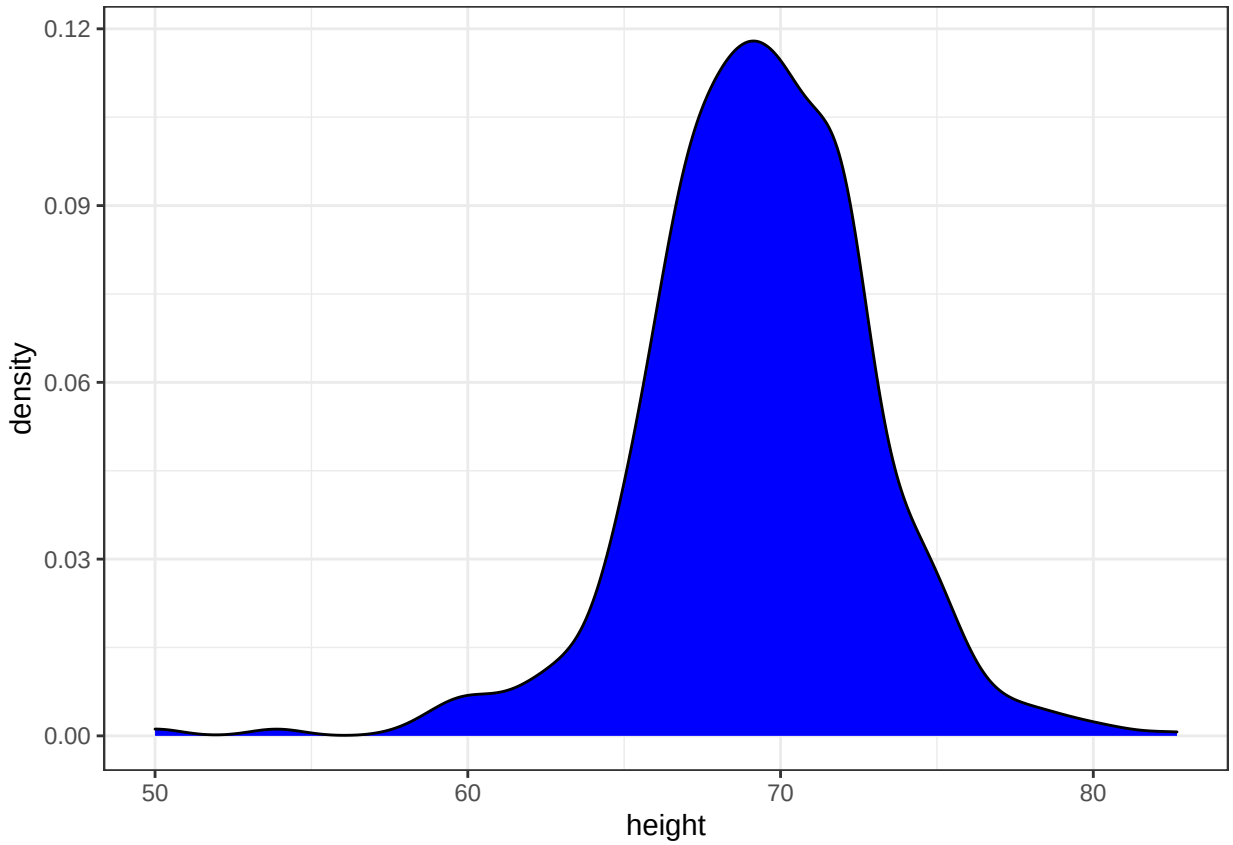


Code: Smooth density plots in ggplot2

```
p + geom_density()
```

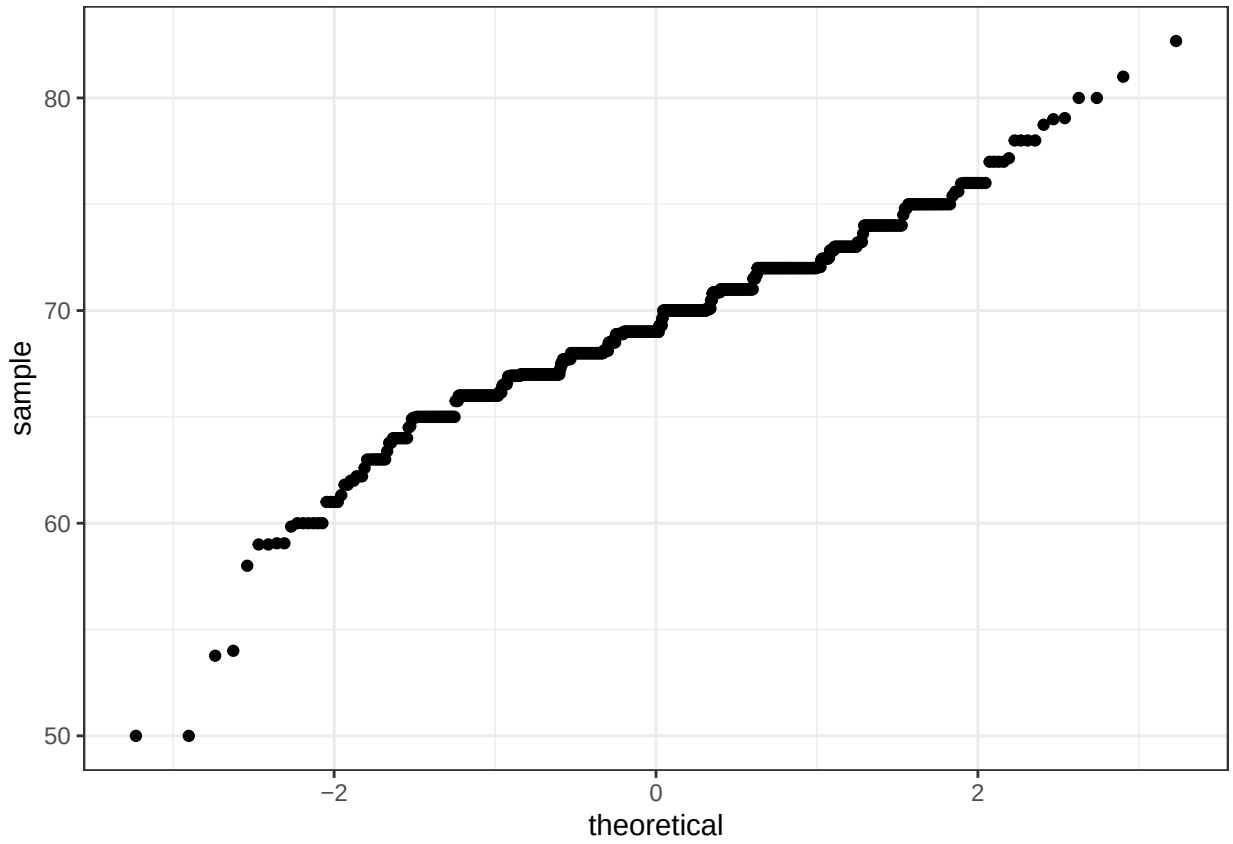



```
p + geom_density(fill = "blue")
```

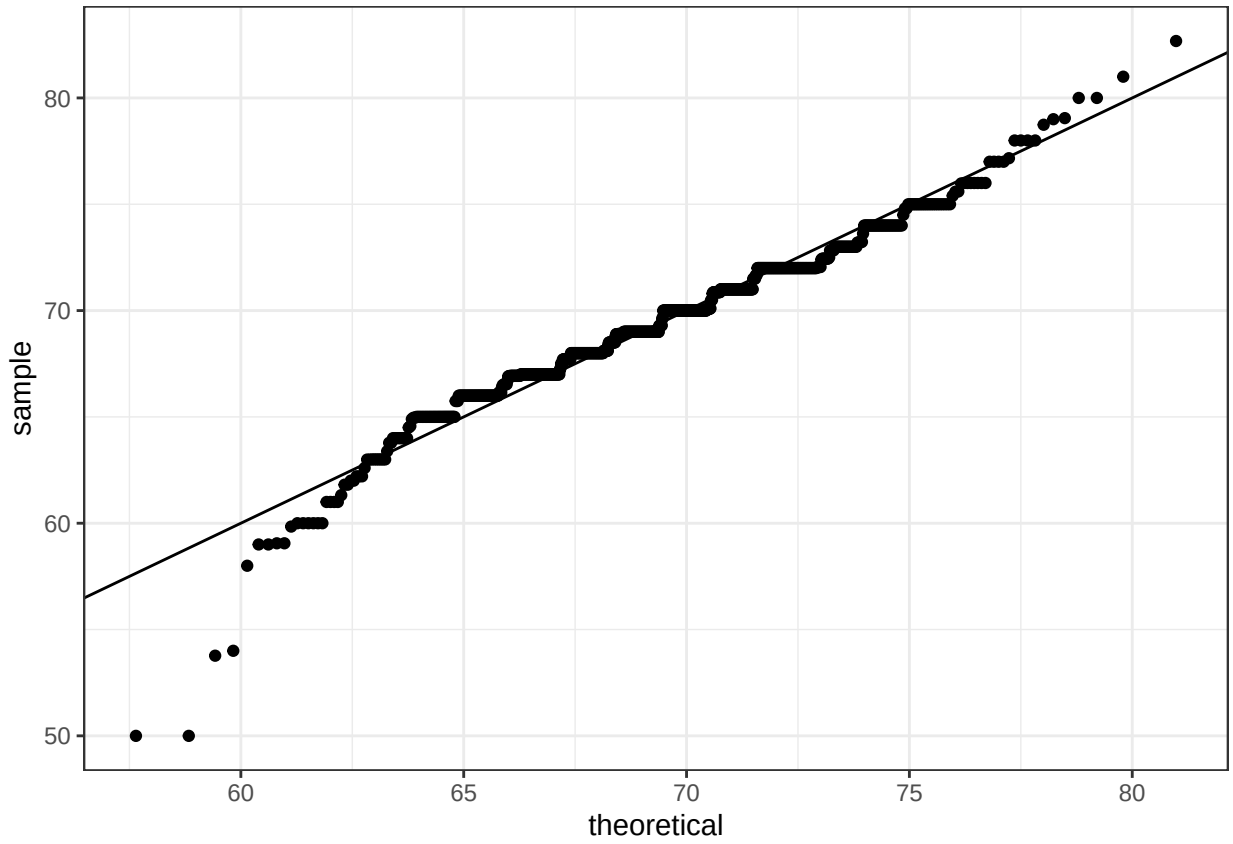


Code: Quantile-quantile plots in ggplot2

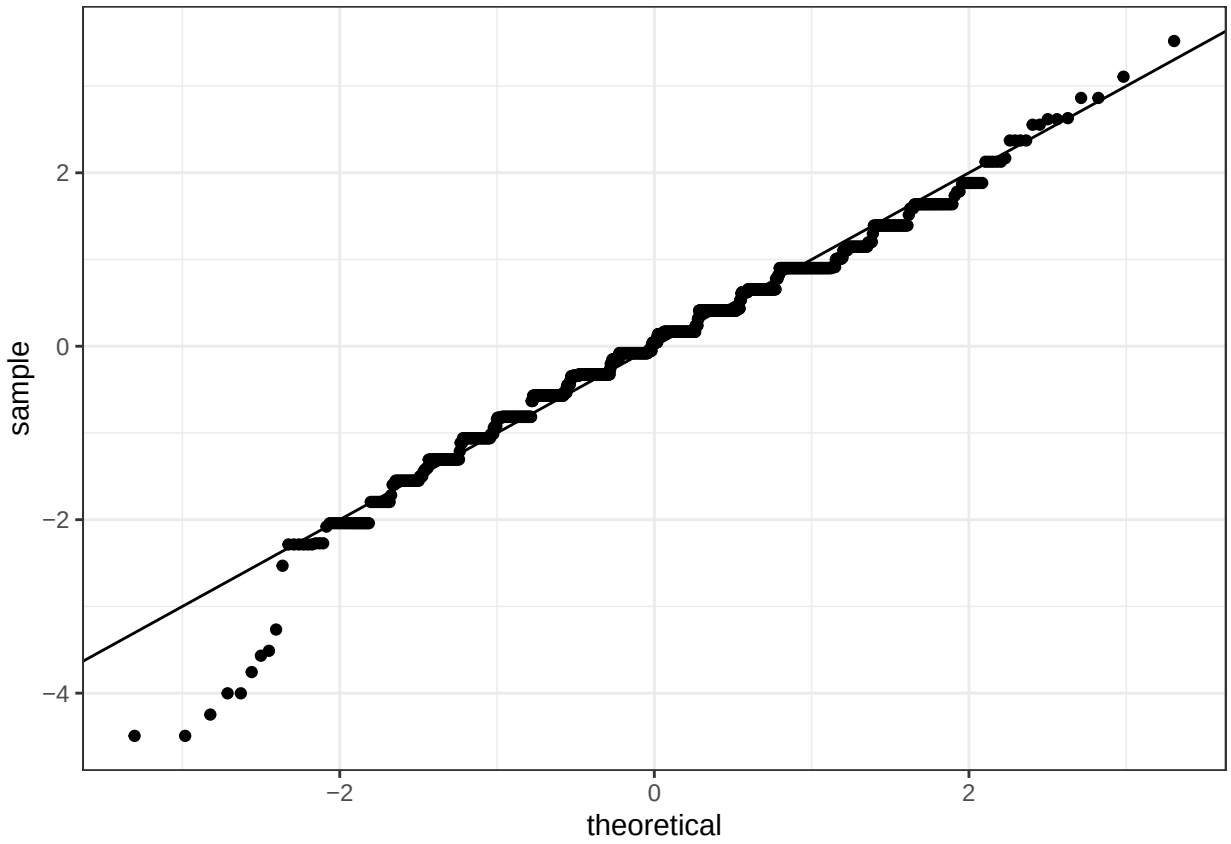
```
# basic QQ-plot
p <- heights %>% filter(sex == "Male") %>%
    ggplot(aes(sample = height))
p + geom_qq()
```




```
# QQ-plot against a normal distribution with same mean/sd as data
params <- heights %>%
    filter(sex == "Male") %>%
    summarize(mean = mean(height), sd = sd(height))
p + geom_qq(dparams = params) +
    geom_abline()
```




```
# QQ-plot of scaled data against the standard normal distribution
heights %>%
    ggplot(aes(sample = scale(height))) +
    geom_qq() +
    geom_abline()
```



Code: Grids of plots with the grid.extra package

```
if(!require(gridExtra)) install.packages("gridExtra")
```

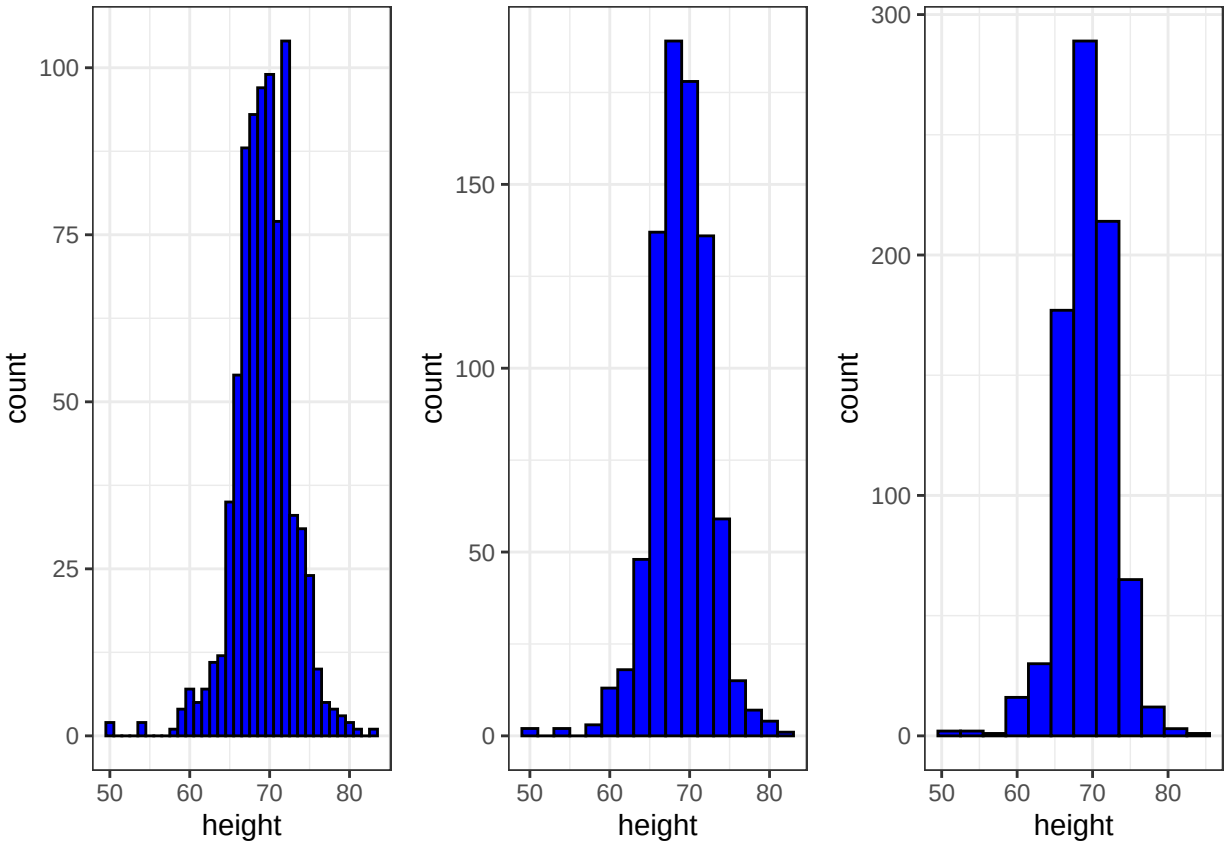
```
## Loading required package: gridExtra
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
# define plots p1, p2, p3
p <- heights %>% filter(sex == "Male") %>% ggplot(aes(x = height))
p1 <- p + geom_histogram(binwidth = 1, fill = "blue", col = "black")
p2 <- p + geom_histogram(binwidth = 2, fill = "blue", col = "black")
p3 <- p + geom_histogram(binwidth = 3, fill = "blue", col = "black")

# arrange plots next to each other in 1 row, 3 columns
library(gridExtra)
grid.arrange(p1, p2, p3, ncol = 3)
```



Assessment - ggplot2

1. Start by loading the dplyr and ggplot2 libraries as well as the `murders` data.

```
library(dplyr)
library(ggplot2)
library(dslabs)
data(murders)
```

Note that you can load both dplyr and ggplot2, as well as other packages, by installing and loading the tidyverse package.

With ggplot2 plots can be saved as objects. For example we can associate a dataset with a plot object like this

```
p <- ggplot(data = murders)
```

Because `data` is the first argument we don't need to spell it out. So we can write this instead:

```
p <- ggplot(murders)
```

or, if we load `dplyr`, we can use the pipe:

```
p <- murders %>% ggplot()
```

Remember the pipe sends the object on the left of `%>%` to be the first argument for the function the right of `%>%`.

Now let's get an introduction to `ggplot`.

```
if(!require(dplyr)) install.packages("dplyr")

library(dplyr)
p <- ggplot(murders)
class(p)
```

```
## [1] "gg"     "ggplot"
```

2. Remember that to print an object you can use the command `print` or simply type the object. For example, instead of

```
x <- 2
print(x)
```

you can simply type

```
x <-2
x
```

Print the object `p` defined in exercise one

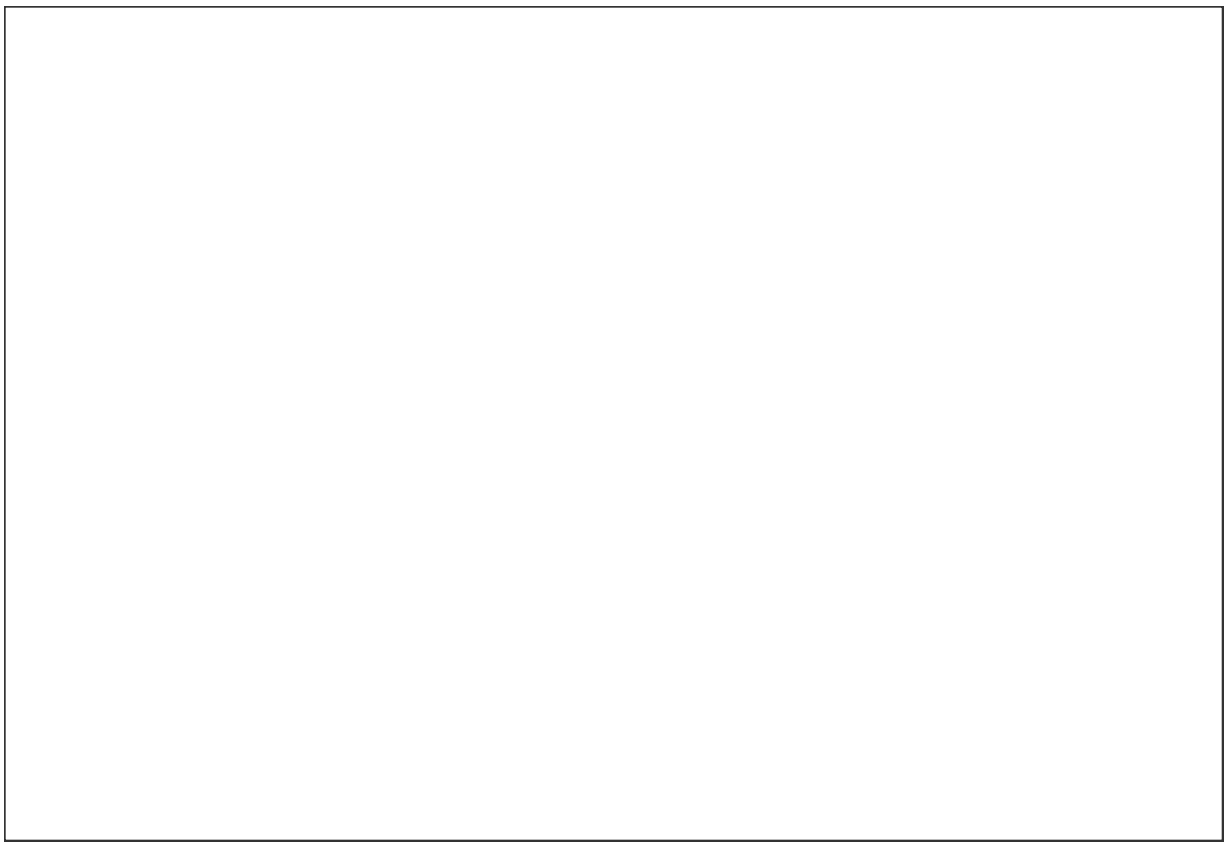
```
p <- ggplot(murders)
```

and describe what you see.

- ☐ A. Nothing happens.
- ☒ B. A blank slate plot.
- ☐ C. A scatter plot.
- ☐ D. A histogram.

3. Now we are going to review the use of pipes by seeing how they can be used with `ggplot`.

```
# define ggplot object called p like in the previous exercise but using a pipe
p <- heights %>% ggplot()
p # a blank slate plot
```



4. Now we are going to add layers and the corresponding aesthetic mappings. For the murders data, we plotted total murders versus population sizes in the videos.

Explore the `murders` data frame to remind yourself of the names for the two variables (total murders and population size) we want to plot and select the correct answer.

- ☐ A. state and abb.
- ☐ B. total_murders and population_size.
- ☒ C. total and population.
- ☐ D. murders and size.

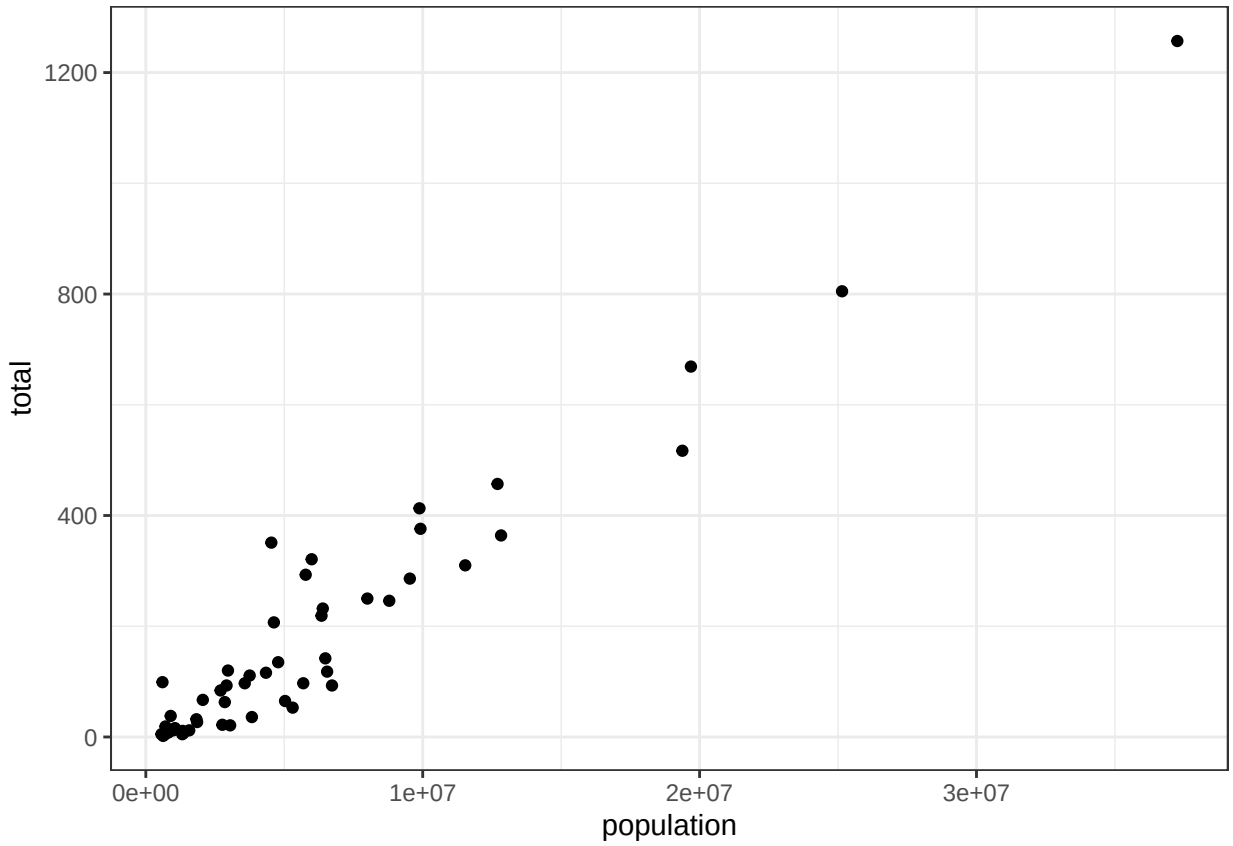
5. To create a scatter plot, we add a layer with the function `geom_point`.

The aesthetic mappings require us to define the x-axis and y-axis variables respectively. So the code looks like this:

```
murders %>% ggplot(aes(x = , y = )) +
  geom_point()
```

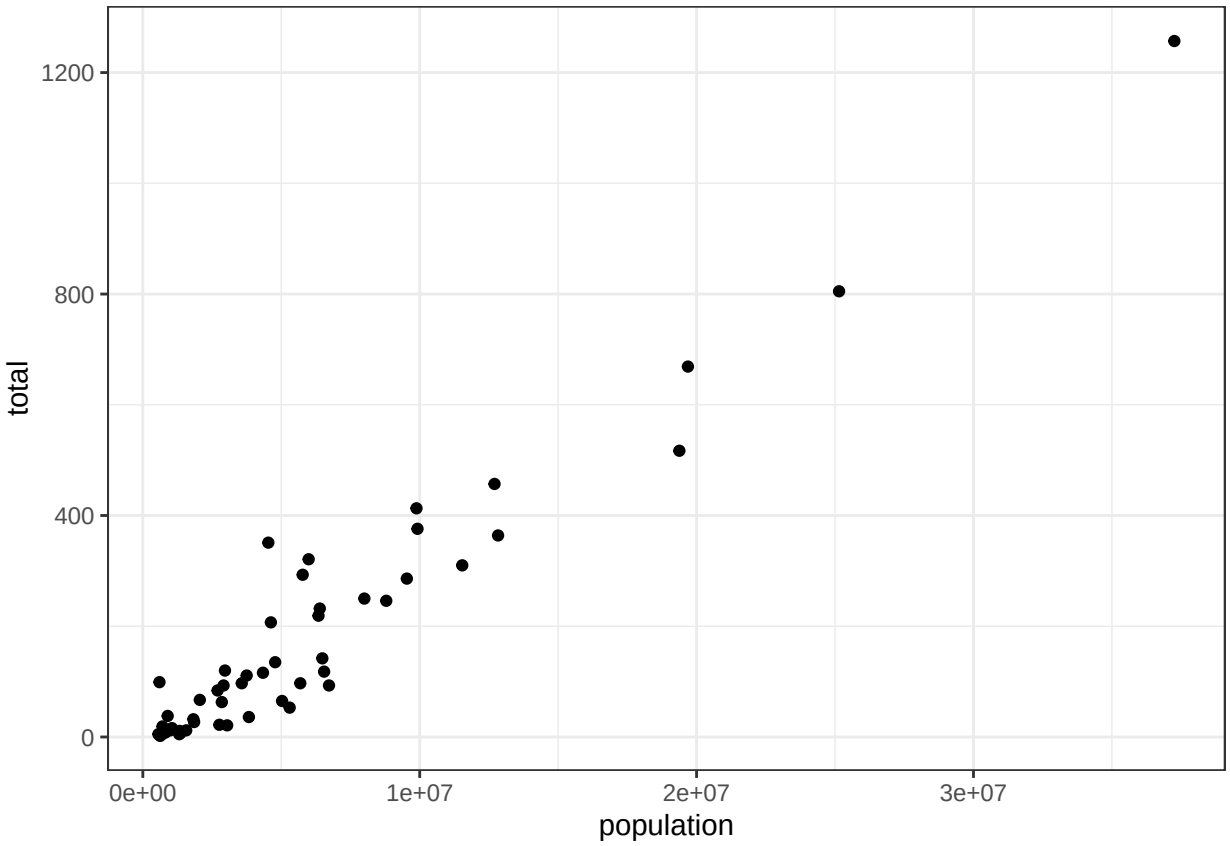
except we have to fill in the blanks to define the two variables `x` and `y`.

```
## Fill in the blanks
murders %>% ggplot(aes(x =population , y =total )) +
  geom_point()
```



6. Note that if we don't use argument names, we can obtain the same plot by making sure we enter the variable names in the desired order.

```
murders %>% ggplot(aes(population, total)) +
  geom_point()
```



7. If instead of points we want to add text, we can use the geom_text() or geom_label() geometries.

However, note that the following code

```
murders %>% ggplot(aes(population, total)) +
  geom_label()
```

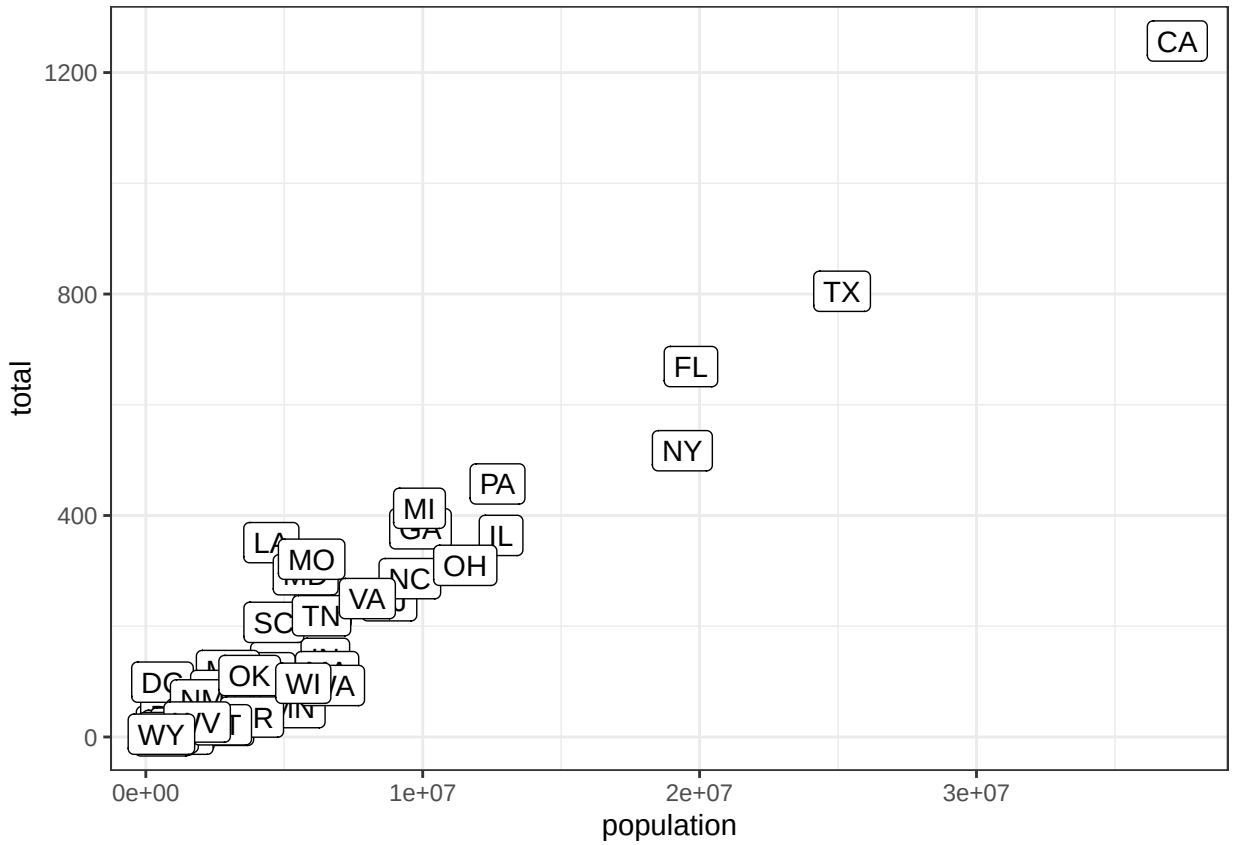
will give us the error message: `Error: geom_label requires the following missing aesthetics: label`

Why is this?

☒ A. We need to map a character to each point through the label argument in aes.
☐ B. We need to let geom_label know what character to use in the plot.
☐ C. The geom_label geometry does not require x-axis and y-axis values.
☐ D. geom_label is not a ggplot2 command.

8. You can also add labels to the points on a plot.

```
## edit the next line to add the label
murders %>% ggplot(aes(population, total, label = abb)) + geom_label()
```



9. Now let's change the color of the labels to blue. How can we do this?

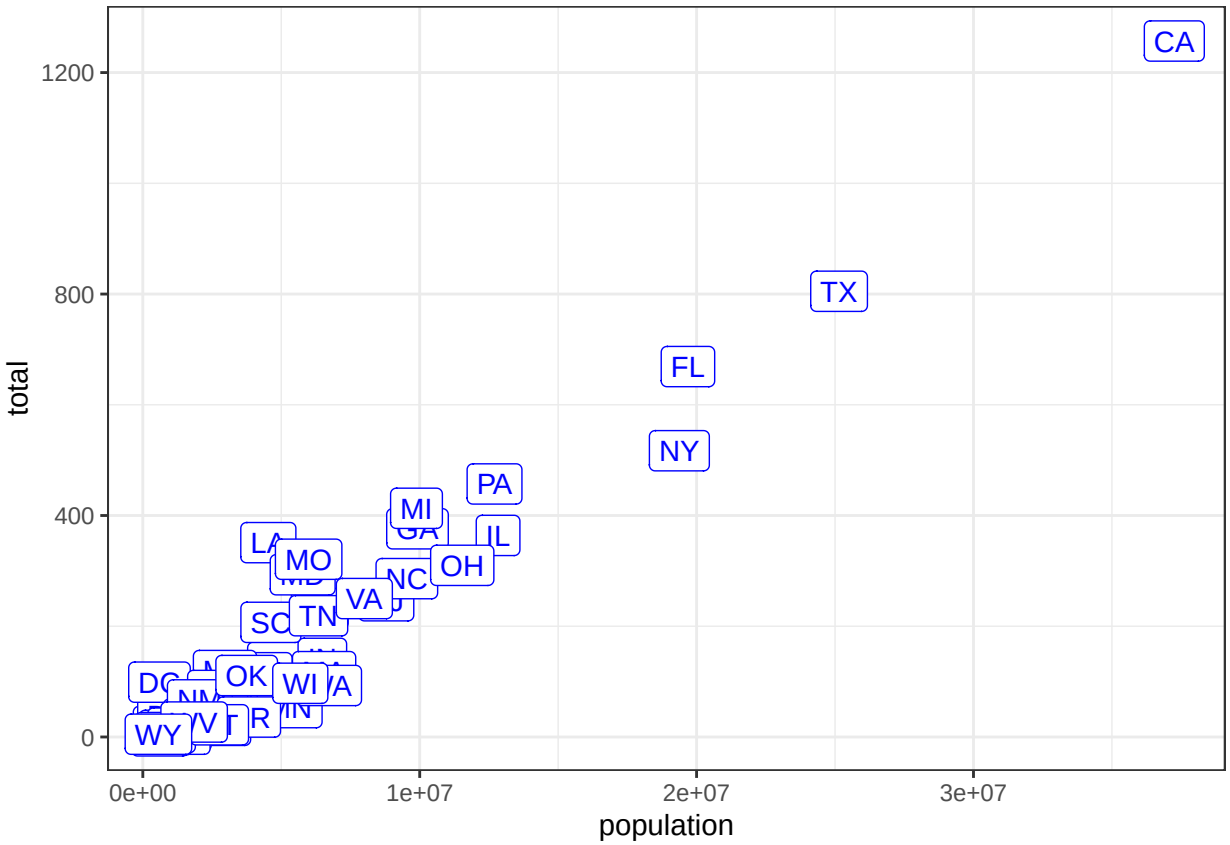
☐ A. By adding a column called blue to murders
☐ B. By mapping the colors through aes because each label needs a different color
☐ C. By using the color argument in ggplot
☒ D. By using the color argument in geom_label because we want all colors to be blue so we do not need to map colors

10. Now let's go ahead and make the labels blue. We previously wrote this code to add labels to our plot:

```
murders %>% ggplot(aes(population, total, label= abb)) +
  geom_label()
```

Now we will edit this code.

```
murders %>% ggplot(aes(population, total,label= abb)) +
  geom_label(color="blue")
```



11. Now suppose we want to use color to represent the different regions.

So the states from the West will be one color, states from the Northeast another, and so on.

In this case, which of the following is most appropriate:

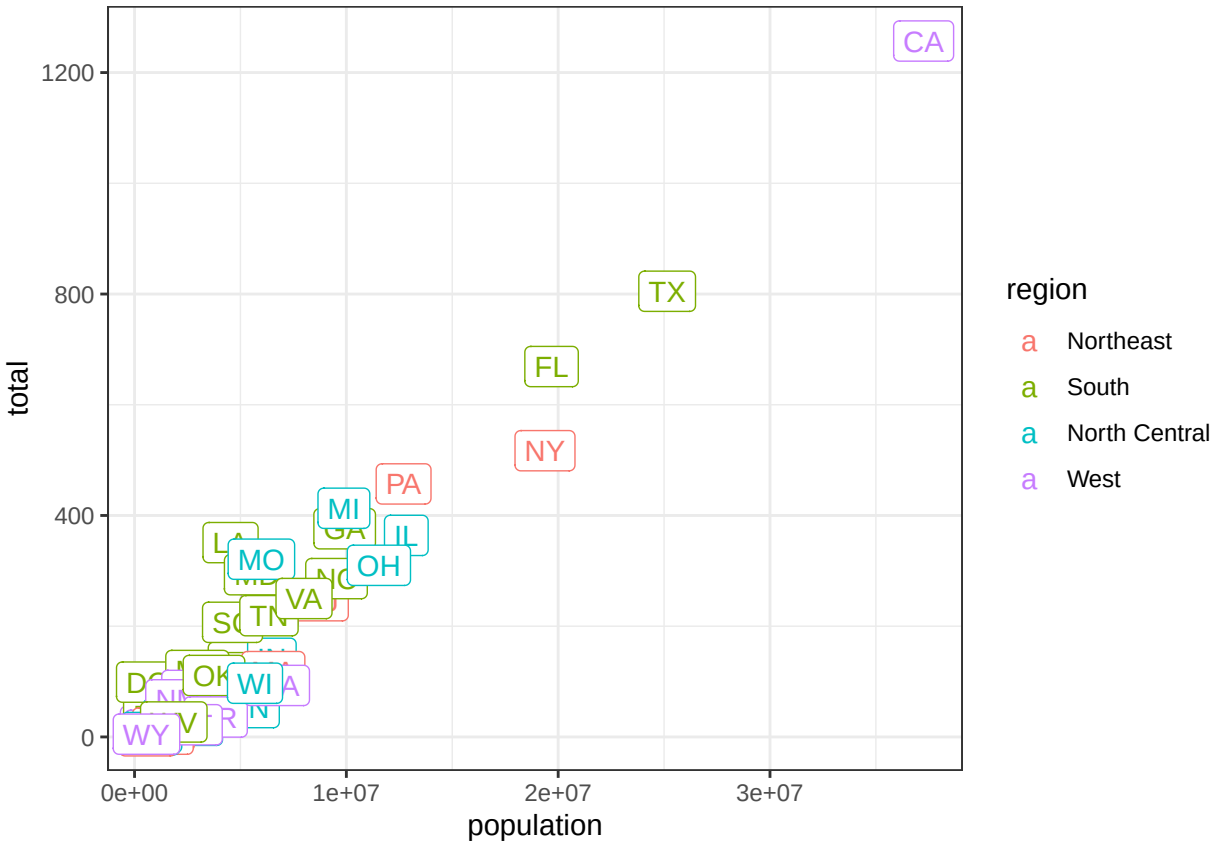
- ☐ A. Adding a column called color to murders with the color we want to use
- ☒ B. Mapping the colors through the color argument of aes because each label needs a different color
- ☐ C. Using the color argument in ggplot
- ☐ D. Using the color argument in geom_label because we want all colors to be blue so we do not need to map colors

12. We previously used this code to make a plot using the state abbreviations as labels:

```
murders %>% ggplot(aes(population, total, label = abb)) +
  geom_label()
```

We are now going to add color to represent the region.

```
## edit this code
murders %>% ggplot(aes(population, total, label = abb, color=region)) +
  geom_label()
```



13. Now we are going to change the axes to log scales to account for the fact that the population distribution is skewed.

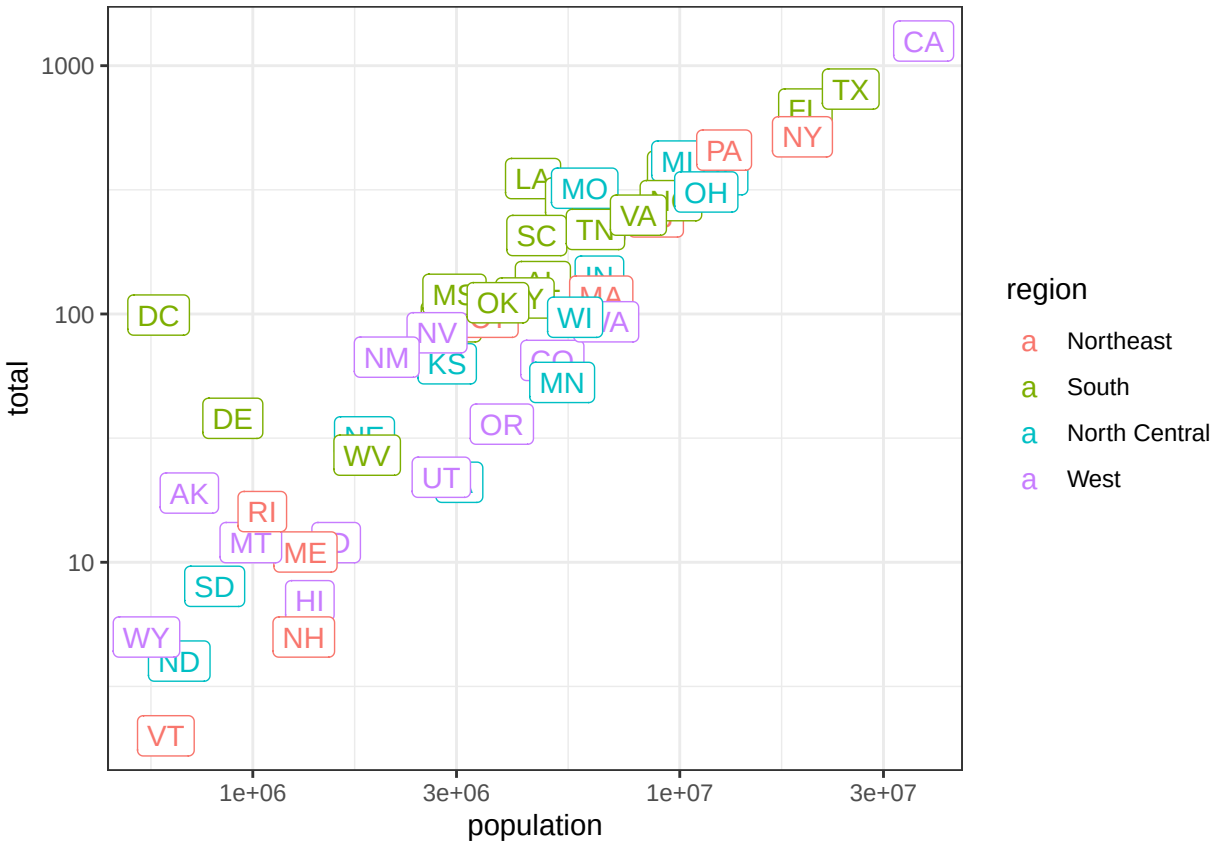
Let's start by defining an object `p` that holds the plot we have made up to now:

```
p <- murders %>% ggplot(aes(population, total, label = abb, color = region)) +
  geom_label()
```

To change the x-axis to a log scale we learned about the `scale_x_log10()` function. We can change the axis by adding this layer to the object `p` to change the scale and render the plot using the following code:

```
p + scale_x_log10()
```

```
p <- murders %>% ggplot(aes(population, total, label = abb, color = region)) + geom_label()
## add layers to p here
p + scale_x_log10() + scale_y_log10()
```

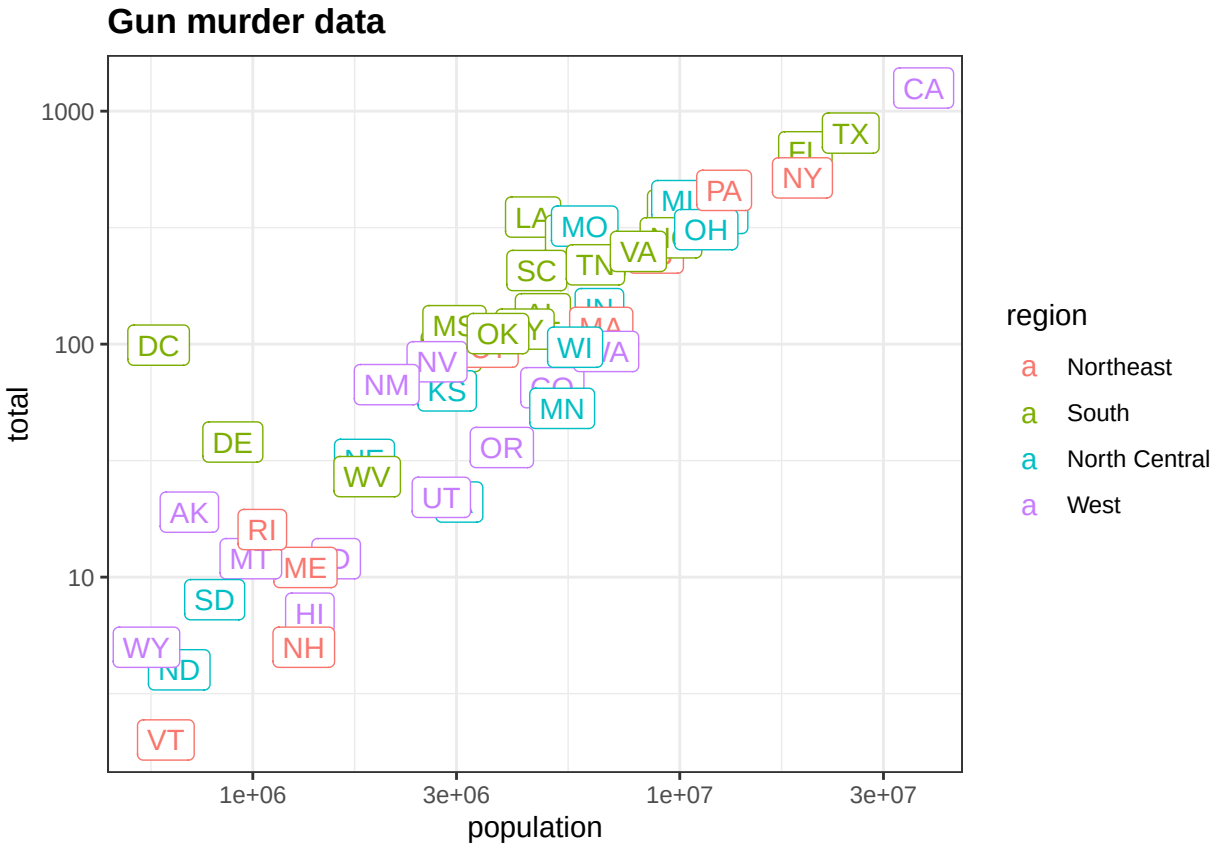


14. In the previous exercises we created a plot using the following code:

```
library(dplyr)
library(ggplot2)
library(dslabs)
data(murders)
p<- murders %>% ggplot(aes(population, total, label = abb, color = region)) +
  geom_label()
p + scale_x_log10() + scale_y_log10()
```

We are now going to add a title to this plot. We will do this by adding yet another layer, this time with the function `ggtitle`.

```
p <- murders %>% ggplot(aes(population, total, label = abb, color = region)) + geom_label()
# add a layer to add title to the next line
p + scale_x_log10() + scale_y_log10() + ggtitle("Gun murder data")
```



15. We are going to shift our focus from the `murders` dataset to explore the `heights` dataset.

We use the `geom_histogram` function to make a histogram of the heights in the `heights` data frame. When reading the documentation for this function we see that it requires just one mapping, the values to be used for the histogram.

What is the variable containing the heights in inches in the `heights` data frame?

- ☐ A. sex
- ☐ B. heights
- ☒ C. height
- ☐ D. heights$height

16. We are now going to make a histogram of the heights so we will load the heights dataset.

The following code has been pre-run for you to load the heights dataset:

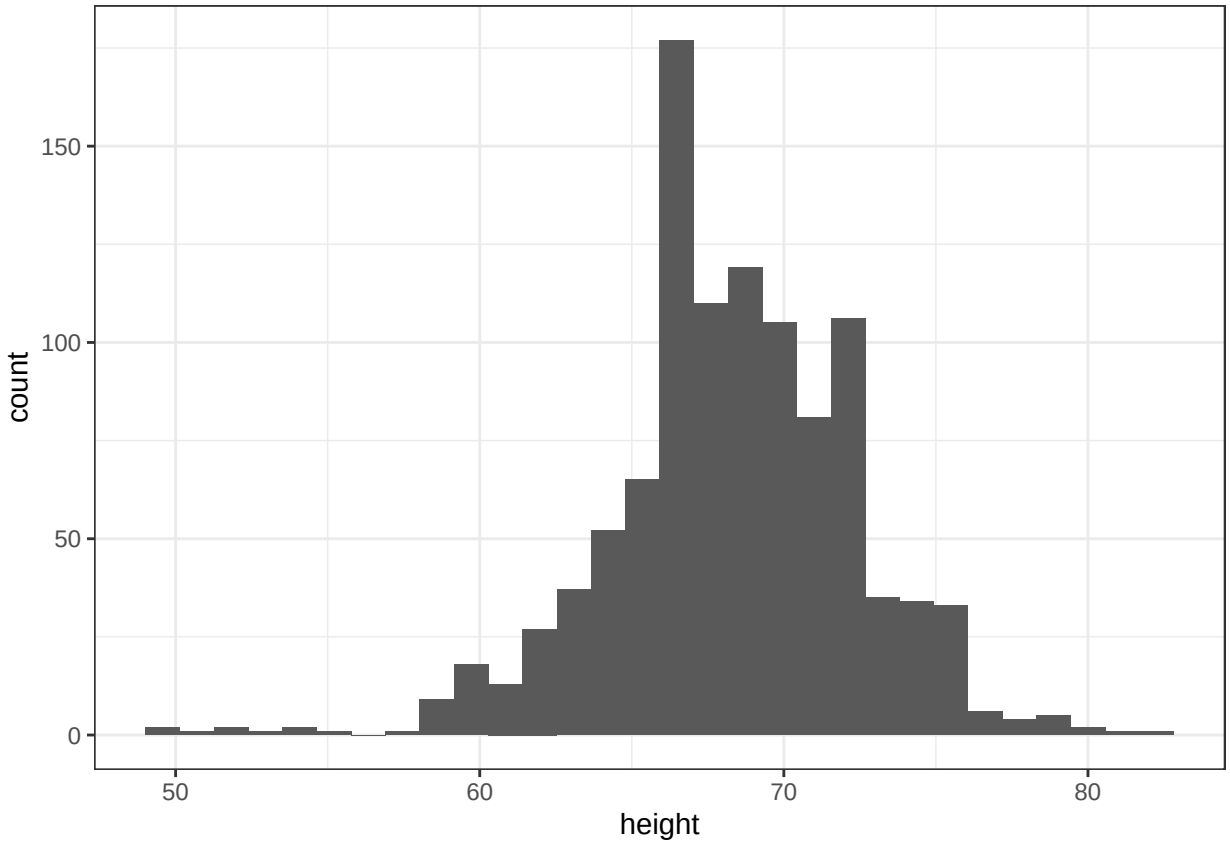
```
library(dplyr)
library(ggplot2)
library(dslabs)
data(heights)
```

```
# define p here
p <- heights %>% ggplot(aes(height))
```

17. Now we are ready to add a layer to actually make the histogram.

```
p <- heights %>%
  ggplot(aes(height))
## add a layer to p
p + geom_histogram()
```

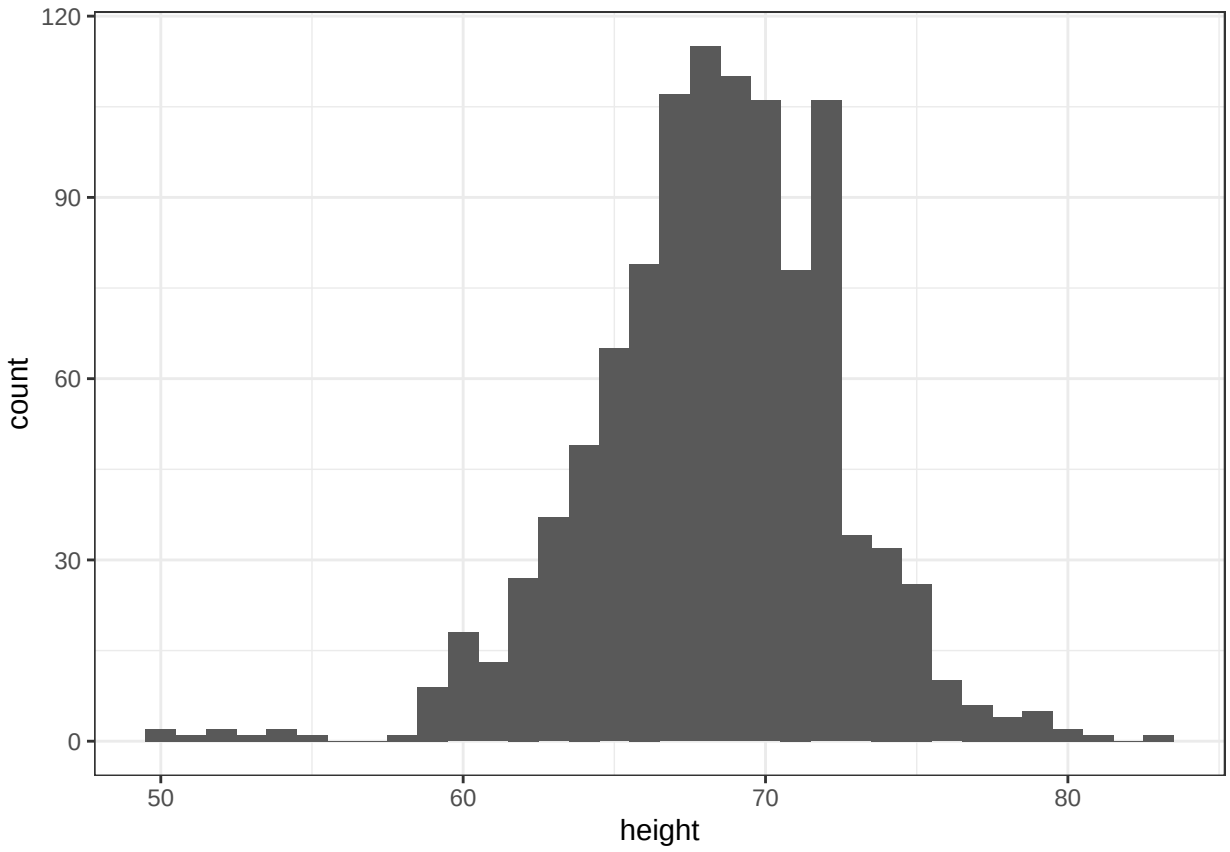
```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



18. Note that when we run the code from the previous exercise we get the following warning:

```
stat_bin() using bins = 30. Pick better value with binwidth.
```

```
p <- heights %>%
  ggplot(aes(height))
## add the geom_histogram layer but with the requested argument
p + geom_histogram(binwidth = 1)
```

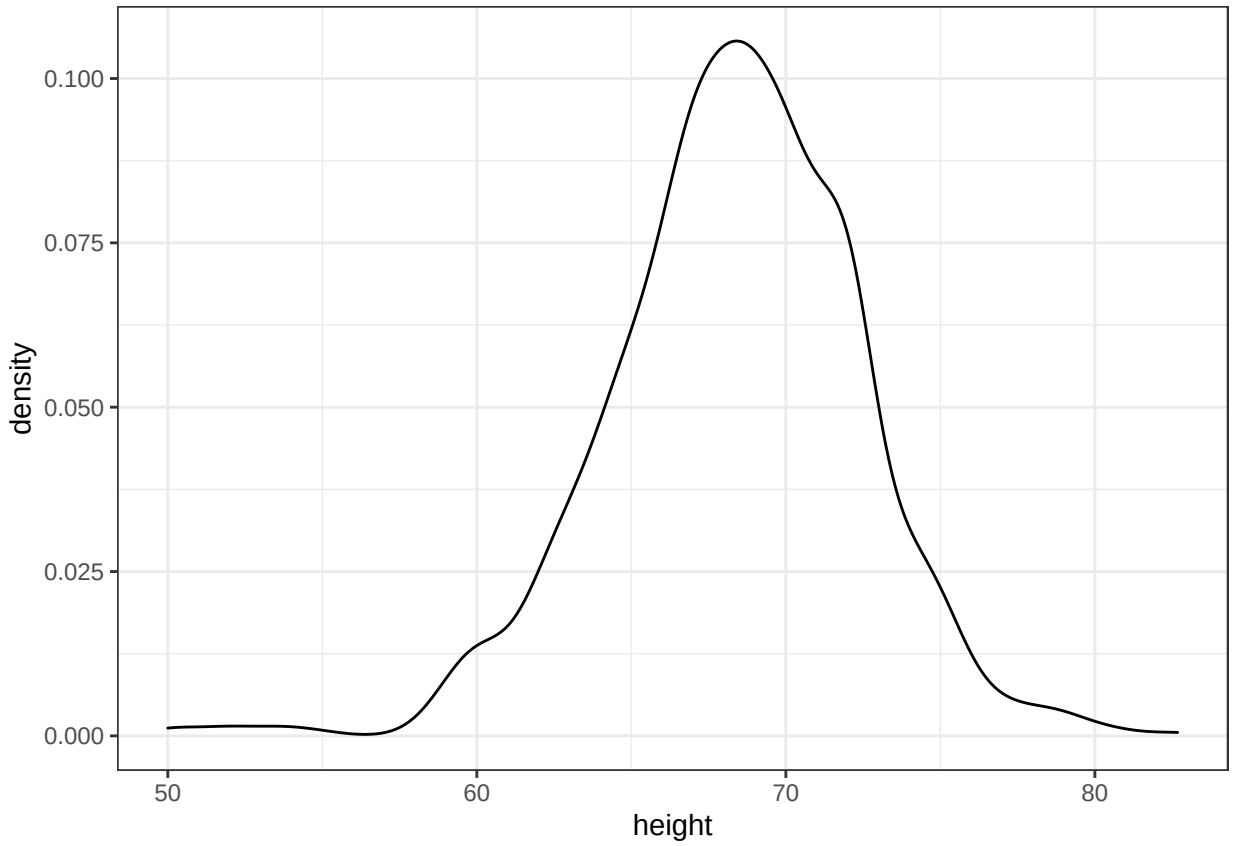


19. Now instead of a histogram we are going to make a smooth density plot.

In this case, we will not make an object `p`. Instead we will render the plot using a single line of code. In the previous exercise, we could have created a histogram using one line of code like this:

```
heights %>%
  ggplot(aes(height)) +
  geom_histogram()
```

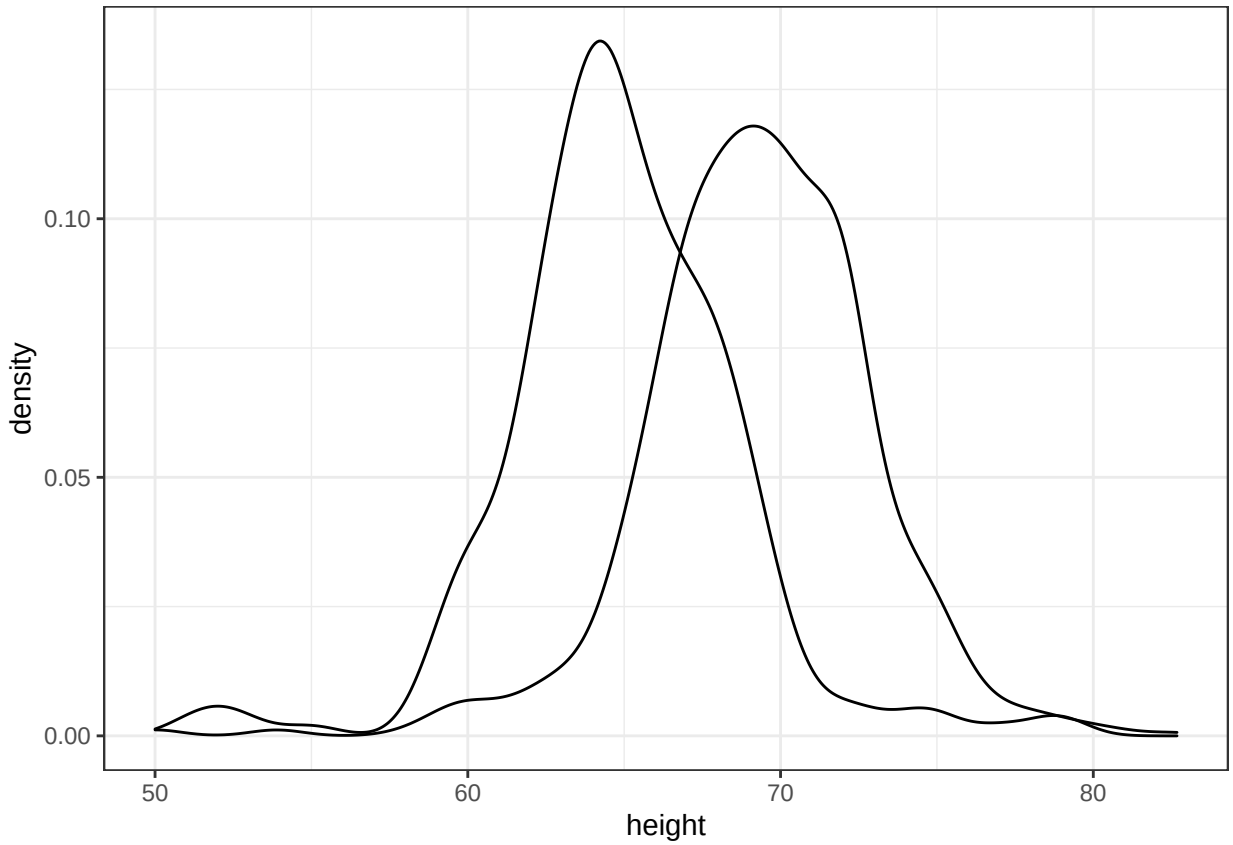
```
## add the correct layer using +
heights %>%
  ggplot(aes(height)) + geom_density()
```



20. Now we are going to make density plots for males and females separately.

We can do this using the `group` argument within the `aes` mapping. Because each point will be assigned to a different density depending on a variable from the dataset, we need to map within `aes`.

```
## add the group argument then a layer with +
heights %>%
  ggplot(aes(height, group = sex)) + geom_density()
```

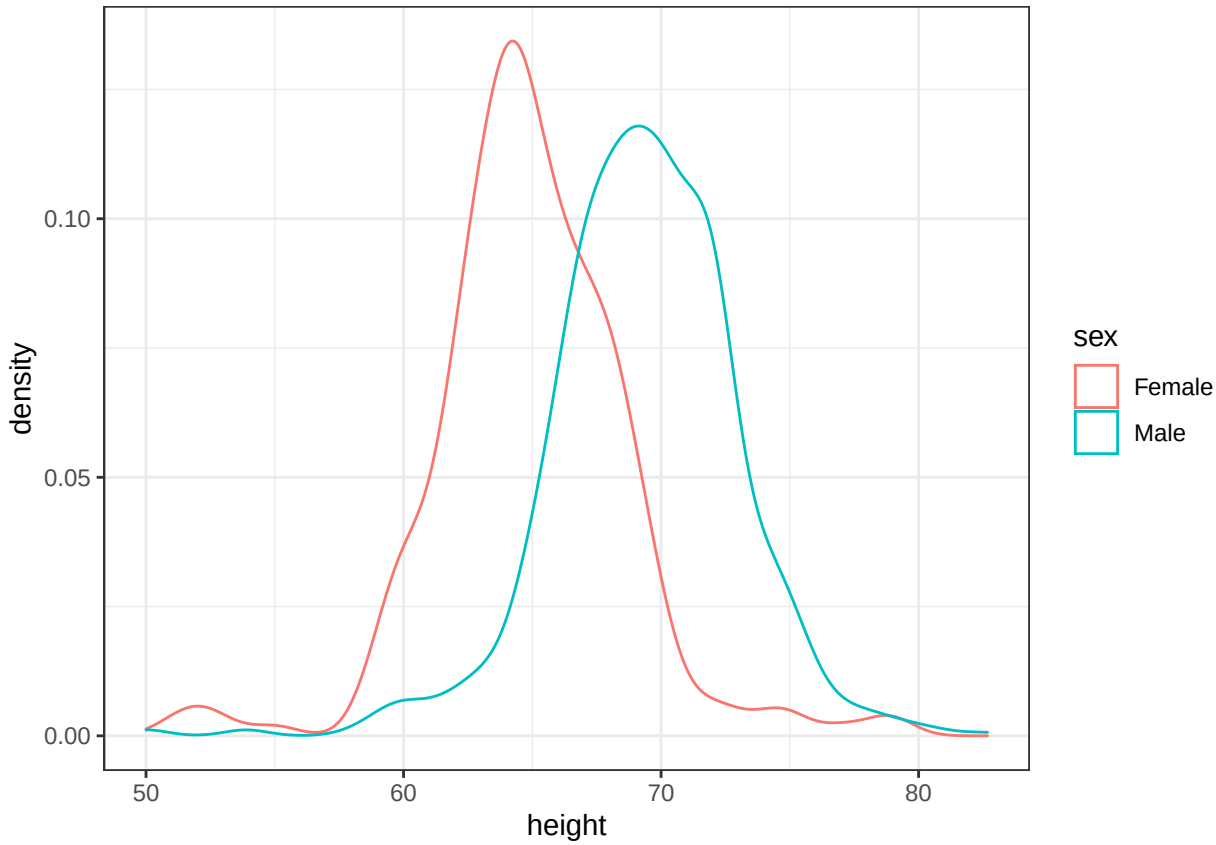


21. In the previous exercise we made the two density plots, one for each sex, using:

```
heights %>%
  ggplot(aes(height, group = sex)) +
  geom_density()
```

We can also assign groups through the `color` or `fill` argument. For example, if you type `color = sex` ggplot knows you want a different color for each sex. So two densities must be drawn. You can therefore skip the `group = sex` mapping. Using `color` has the added benefit that it uses color to distinguish the groups. Change the density plots from the previous exercise to add color.

```
## edit the next line to use color instead of group then add a density layer
heights %>%
  ggplot(aes(height, color = sex)) + geom_density()
```



22. We can also assign groups using the `fill` argument.

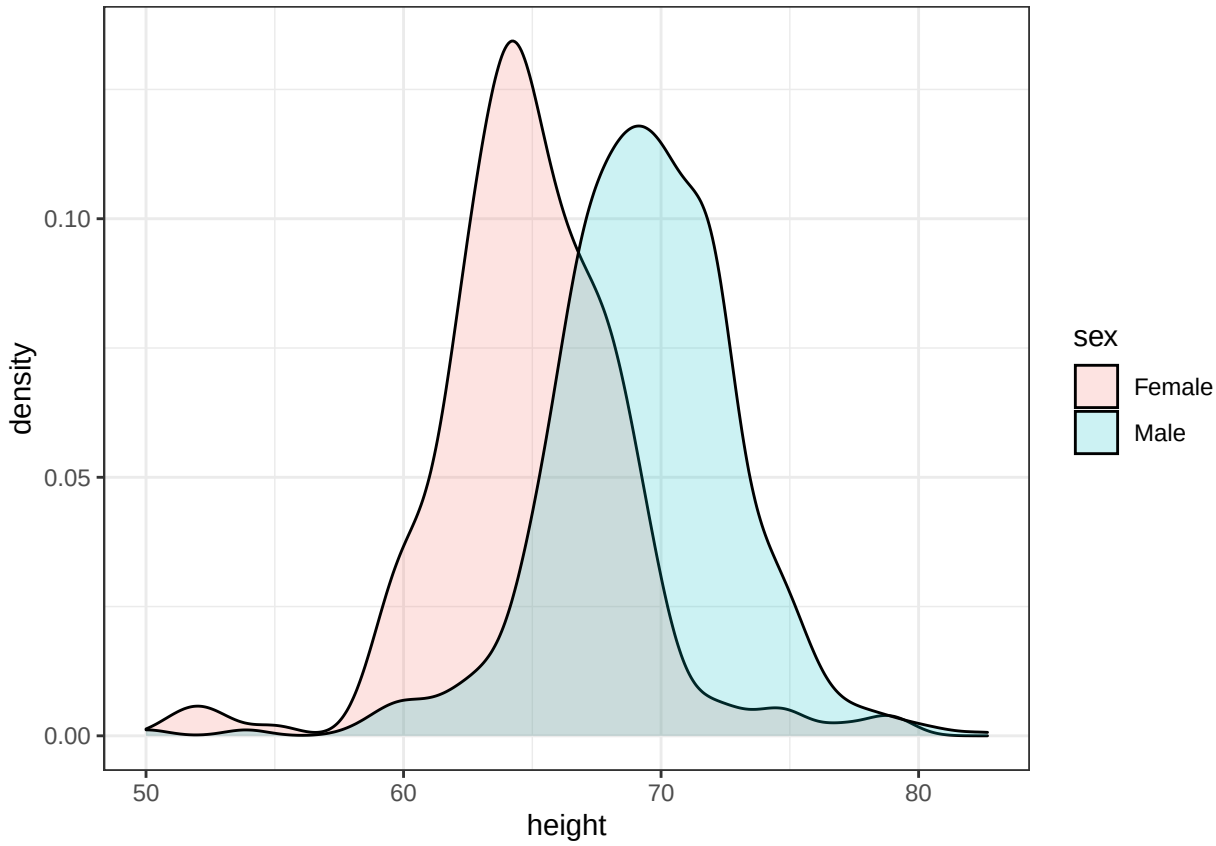
When using the `geom_density` geometry, `color` creates a colored line for the smooth density plot while `fill` colors in the area under the curve.

We can see what this looks like by running the following code:

```
heights %>%
  ggplot(aes(height, fill = sex)) +
  geom_density()
```

However, here the second density is drawn over the other. We can change this by using something called *alpha blending*.

```
heights %>%
  ggplot(aes(height, fill = sex)) +
  geom_density(alpha=0.2)
```



Section 3 Overview

Section 3 introduces you to summarizing with dplyr.

After completing Section 3, you will:

- understand the importance of summarizing data in exploratory data analysis.
- be able to use the "summarize" verb in dplyr to facilitate summarizing data.
- be able to use the "group_by" verb in dplyr to facilitate summarizing data.
- be able to access values using the dot placeholder.
- be able to use "arrange" to examine data after sorting.

dplyr

The textbook for this section is available here

Key points

- `summarize` from the dplyr/tidyverse package computes summary statistics from the data frame. It returns a data frame whose column names are defined within the function call.
- `summarize` can compute any summary function that operates on vectors and returns a single value, but it cannot operate on functions that return multiple values.
- Like most dplyr functions, `summarize` is aware of variable names within data frames and can use them directly.

Code

```
# compute average and standard deviation for males
s <- heights %>%
    filter(sex == "Male") %>%
    summarize(average = mean(height), standard_deviation = sd(height))

# access average and standard deviation from summary table
s$average
```

```
## [1] 69.31475
```

```
s$standard_deviation
```

```
## [1] 3.611024
```

```
# compute median, min and max
heights %>%
    filter(sex == "Male") %>%
    summarize(median = median(height),
                        minimum = min(height),
                        maximum = max(height))
```

```
##   median minimum  maximum
## 1     69      50 82.67717
```

```
# alternative way to get min, median, max in base R
quantile(heights$height, c(0, 0.5, 1))
```

```
##       0%      50%     100%
## 50.00000 68.50000 82.67717
```

```
# generates an error: summarize can only take functions that return a single value
heights %>%
    filter(sex == "Male") %>%
    summarize(range = quantile(height, c(0, 0.5, 1)))
```

The Dot Placeholder

The textbook for this section is available here

Note that a common replacement for the dot operator is the pull function. Here is the textbook section on the pull function.

Key points

- The dot operator allows you to access values stored in data that is being piped in using the `%>%` character. The dot is a placeholder for the data being passed in through the pipe.
- The dot operator allows `dplyr` functions to return single vectors or numbers instead of only data frames.
- `us_murder_rate %>% .$rate` is equivalent to `us_murder_rate$rate`.

- Note that an equivalent way to extract a single column using the pipe is `us_murder_rate %>% pull(rate)`. The pull function will be used in later course material.

Code

```
murders <- murders %>% mutate(murder_rate = total/population*100000)
summarize(murders, mean(murder_rate))
```

```
##   mean(murder_rate)
## 1          2.779125
```

```
# calculate US murder rate, generating a data frame
us_murder_rate <- murders %>%
    summarize(rate = sum(total) / sum(population) * 100000)
us_murder_rate
```

```
##       rate
## 1 3.034555
```

```
# extract the numeric US murder rate with the dot operator
us_murder_rate %>% .$rate
```

```
## [1] 3.034555
```

```
# calculate and extract the murder rate with one pipe
us_murder_rate <- murders %>%
    summarize(rate = sum(total) / sum(population * 100000)) %>%
    .$rate
```

Group By

The textbook for this section is available here

Key points

- The `group_by` function from **dplyr** converts a data frame to a grouped data frame, creating groups using one or more variables.
- `summarize` and some other **dplyr** functions will behave differently on grouped data frames.
- Using `summarize` on a grouped data frame computes the summary statistics for each of the separate groups.

Code

```
# compute separate average and standard deviation for male/female heights
heights %>%
    group_by(sex) %>%
    summarize(average = mean(height), standard_deviation = sd(height))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 2 x 3
##   sex    average standard_deviation
##   <fct>    <dbl>              <dbl>
## 1 Female    64.9               3.76
## 2 Male      69.3               3.61
```

```
# compute median murder rate in 4 regions of country
murders <- murders %>%
    mutate(murder_rate = total/population * 100000)
murders %>%
    group_by(region) %>%
    summarize(median_rate = median(murder_rate))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)

## # A tibble: 4 x 2
##   region        median_rate
##   <fct>               <dbl>
## 1 Northeast            1.80
## 2 South                3.40
## 3 North Central        1.97
## 4 West                 1.29
```

Sorting Data Tables

The textbook for this section is available here

Key points

- The `arrange` function from **dplyr** sorts a data frame by a given column.
- By default, `arrange` sorts in ascending order (lowest to highest). To instead sort in descending order, use the function `desc` inside of `arrange`.
- You can `arrange` by multiple levels: within equivalent values of the first level, observations are sorted by the second level, and so on.
- The `top_n` function shows the top results ranked by a given variable, but the results are not ordered. You can combine `top_n` with `arrange` to return the top results in order.

Code

```
# set up murders object
murders <- murders %>%
    mutate(murder_rate = total/population * 100000)

# arrange by population column, smallest to largest
murders %>% arrange(population) %>% head()
```

```
##                  state abb        region population total murder_rate
## 1              Wyoming  WY          West     563626     5   0.8871131
## 2 District of Columbia  DC         South     601723    99  16.4527532
## 3              Vermont  VT     Northeast     625741     2   0.3196211
## 4         North Dakota  ND North Central     672591     4   0.5947151
## 5               Alaska  AK          West     710231    19   2.6751860
## 6         South Dakota  SD North Central     814180     8   0.9825837
```

```
# arrange by murder rate, smallest to largest
murders %>% arrange(murder_rate) %>% head()
```

```
##           state abb        region population total murder_rate
## 1       Vermont  VT     Northeast     625741     2   0.3196211
## 2 New Hampshire  NH     Northeast    1316470     5   0.3798036
## 3        Hawaii  HI          West    1360301     7   0.5145920
## 4  North Dakota  ND North Central     672591     4   0.5947151
## 5          Iowa  IA North Central    3046355    21   0.6893484
## 6         Idaho  ID          West    1567582    12   0.7655102
```

```
# arrange by murder rate in descending order
murders %>% arrange(desc(murder_rate)) %>% head()
```

```
##                  state abb        region population total murder_rate
## 1 District of Columbia  DC         South     601723    99   16.452753
## 2            Louisiana  LA         South    4533372   351    7.742581
## 3             Missouri  MO North Central    5988927   321    5.359892
## 4             Maryland  MD         South    5773552   293    5.074866
## 5       South Carolina  SC         South    4625364   207    4.475323
## 6             Delaware  DE         South     897934    38    4.231937
```

```
# arrange by region alphabetically, then by murder rate within each region
murders %>% arrange(region, murder_rate) %>% head()
```

```
##           state abb    region population total murder_rate
## 1       Vermont  VT Northeast     625741     2   0.3196211
## 2 New Hampshire  NH Northeast    1316470     5   0.3798036
## 3         Maine  ME Northeast    1328361    11   0.8280881
## 4  Rhode Island  RI Northeast    1052567    16   1.5200933
## 5 Massachusetts  MA Northeast    6547629   118   1.8021791
## 6      New York  NY Northeast   19378102   517   2.6679599
```

```
# show the top 10 states with highest murder rate, not ordered by rate
murders %>% top_n(10, murder_rate)
```

```
##                  state abb        region population total murder_rate
## 1              Arizona  AZ          West    6392017   232    3.629527
## 2             Delaware  DE         South     897934    38    4.231937
## 3  District of Columbia  DC         South     601723    99   16.452753
## 4              Georgia  GA         South    9920000   376    3.790323
## 5            Louisiana  LA         South    4533372   351    7.742581
## 6             Maryland  MD         South    5773552   293    5.074866
## 7             Michigan  MI North Central    9883640   413    4.178622
## 8          Mississippi  MS         South    2967297   120    4.044085
## 9             Missouri  MO North Central    5988927   321    5.359892
## 10      South Carolina  SC         South    4625364   207    4.475323
```

```
# show the top 10 states with highest murder rate, ordered by rate
murders %>% arrange(desc(murder_rate)) %>% top_n(10)
```

```
## Selecting by murder_rate
```

```
##                   state abb        region population total murder_rate
## 1  District of Columbia  DC         South     601723    99   16.452753
## 2             Louisiana  LA         South    4533372   351    7.742581
## 3              Missouri  MO North Central    5988927   321    5.359892
## 4              Maryland  MD         South    5773552   293    5.074866
## 5        South Carolina  SC         South    4625364   207    4.475323
## 6              Delaware  DE         South     897934    38    4.231937
## 7              Michigan  MI North Central    9883640   413    4.178622
## 8           Mississippi  MS         South    2967297   120    4.044085
## 9               Georgia  GA         South    9920000   376    3.790323
## 10              Arizona  AZ          West    6392017   232    3.629527
```

Assessment - Summarizing with dplyr

To practice our dplyr skills we will be working with data from the survey collected by the United States National Center for Health Statistics (NCHS). This center has conducted a series of health and nutrition surveys since the 1960's.

Starting in 1999, about 5,000 individuals of all ages have been interviewed every year and then they complete the health examination component of the survey. Part of this dataset is made available via the NHANES package which can be loaded this way:

```
if(!require(NHANES)) install.packages("NHANES")
```

```
## Loading required package: NHANES
```

```
## Warning: package 'NHANES' was built under R version 4.0.2
```

```
library(NHANES)
data(NHANES)
```

The NHANES data has many missing values. Remember that the main summarization function in R will return `NA` if any of the entries of the input vector is an `NA`. Here is an example:

```
data(na_example)
mean(na_example)
```

```
## [1] NA
```

```
sd(na_example)
```

```
## [1] NA
```

To ignore the `NA`s, we can use the `na.rm` argument:

```
mean(na_example, na.rm = TRUE)
```

```
## [1] 2.301754
```

```r
sd(na_example, na.rm = TRUE)
```

```
## [1] 1.22338
```

Try running this code, then let us know you are ready to proceed with the analysis.

1. Let's explore the `NHANES` data. We will be exploring blood pressure in this dataset.

First let's select a group to set the standard. We will use 20-29 year old females. Note that the category is coded with `20-29`, with a space in front of the 20! The `AgeDecade` is a categorical variable with these ages.

To know if someone is female, you can look at the `Gender` variable.

```r
## fill in what is needed
tab <- NHANES %>% filter(AgeDecade == " 20-29" & Gender == "female")
head(tab)
```

```
## # A tibble: 6 x 76
##      ID SurveyYr Gender   Age AgeDecade AgeMonths Race1 Race3 Education
##   <int> <fct>    <fct>  <int> <fct>         <int> <fct> <fct> <fct>
## 1 51710 2009_10  female    26 " 20-29"        319 White <NA>  College ~
## 2 51731 2009_10  female    28 " 20-29"        346 Black <NA>  High Sch~
## 3 51741 2009_10  female    21 " 20-29"        253 Black <NA>  Some Col~
## 4 51741 2009_10  female    21 " 20-29"        253 Black <NA>  Some Col~
## 5 51760 2009_10  female    27 " 20-29"        334 Hisp~ <NA>  9 - 11th~
## 6 51764 2009_10  female    29 " 20-29"        357 White <NA>  College ~
## # ... with 67 more variables: MaritalStatus <fct>, HHIncome <fct>,
## #   HHIncomeMid <int>, Poverty <dbl>, HomeRooms <int>, HomeOwn <fct>,
## #   Work <fct>, Weight <dbl>, Length <dbl>, HeadCirc <dbl>, Height <dbl>,
## #   BMI <dbl>, BMICatUnder20yrs <fct>, BMI_WHO <fct>, Pulse <int>,
## #   BPSysAve <int>, BPDiaAve <int>, BPSys1 <int>, BPDia1 <int>, BPSys2 <int>,
## #   BPDia2 <int>, BPSys3 <int>, BPDia3 <int>, Testosterone <dbl>,
## #   DirectChol <dbl>, TotChol <dbl>, UrineVol1 <int>, UrineFlow1 <dbl>,
## #   UrineVol2 <int>, UrineFlow2 <dbl>, Diabetes <fct>, DiabetesAge <int>,
## #   HealthGen <fct>, DaysPhysHlthBad <int>, DaysMentHlthBad <int>,
## #   LittleInterest <fct>, Depressed <fct>, nPregnancies <int>, nBabies <int>,
## #   Age1stBaby <int>, SleepHrsNight <int>, SleepTrouble <fct>,
## #   PhysActive <fct>, PhysActiveDays <int>, TVHrsDay <fct>, CompHrsDay <fct>,
## #   TVHrsDayChild <int>, CompHrsDayChild <int>, Alcohol12PlusYr <fct>,
## #   AlcoholDay <int>, AlcoholYear <int>, SmokeNow <fct>, Smoke100 <fct>,
## #   Smoke100n <fct>, SmokeAge <int>, Marijuana <fct>, AgeFirstMarij <int>,
## #   RegularMarij <fct>, AgeRegMarij <int>, HardDrugs <fct>, SexEver <fct>,
## #   SexAge <int>, SexNumPartnLife <int>, SexNumPartYear <int>, SameSex <fct>,
## #   SexOrientation <fct>, PregnantNow <fct>
```

2. Now we will compute the average and standard deviation for the subgroup we defined in the previous exercise (20-29 year old females), which we will use reference for what is typical.

You will determine the average and standard deviation of systolic blood pressure, which are stored in the `BPSysAve` variable in the NHANES dataset.

```
## complete this line of code.
ref <- NHANES %>% filter(AgeDecade == " 20-29" & Gender == "female") %>% summarize(average = mean(BPSys
ref
```

```
## # A tibble: 1 x 2
##   average standard_deviation
##     <dbl>              <dbl>
## 1    108.               10.1
```

3. Now we will repeat the exercise and generate only the average blood pressure for 20-29 year old females.

For this exercise, you should review how to use the place holder `.` in dplyr or the `pull` function.

```
## modify the code we wrote for previous exercise.
ref_avg <- NHANES %>%
  filter(AgeDecade == " 20-29" & Gender == "female") %>%
  summarize(average = mean(BPSysAve, na.rm = TRUE),
            standard_deviation = sd(BPSysAve, na.rm=TRUE)) %>% .$average
ref_avg
```

```
## [1] 108.4224
```

4. Let's continue practicing by calculating two other data summaries: the minimum and the maximum.

Again we will do it for the `BPSysAve` variable and the group of 20-29 year old females.

```
## complete the line
NHANES %>%
      filter(AgeDecade == " 20-29"  & Gender == "female") %>% summarize(minbp = min(BPSysAve, na.rm = T
            maxbp = max(BPSysAve, na.rm=TRUE))
```

```
## # A tibble: 1 x 2
##   minbp maxbp
##   <int> <int>
## 1    84   179
```

5. Now let's practice using the `group_by` function.

What we are about to do is a very common operation in data science: you will split a data table into groups and then compute summary statistics for each group.

We will compute the average and standard deviation of systolic blood pressure for females for each age group separately. Remember that the age groups are contained in `AgeDecade`.

```
##complete the line with group_by and summarize
NHANES %>%
      filter(Gender == "female") %>% group_by(AgeDecade) %>% summarize(average = mean(BPSysAve, na.rm =
            standard_deviation = sd(BPSysAve, na.rm=TRUE))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 9 x 3
##   AgeDecade average standard_deviation
##   <fct>       <dbl>              <dbl>
## 1 " 0-9"       100.               9.07
## 2 " 10-19"     104.               9.46
## 3 " 20-29"     108.              10.1
## 4 " 30-39"     111.              12.3
## 5 " 40-49"     115.              14.5
## 6 " 50-59"     122.              16.2
## 7 " 60-69"     127.              17.1
## 8 " 70+"       134.              19.8
## 9  <NA>        142.              22.9
```

6. Now let's practice using `group_by` some more.

We are going to repeat the previous exercise of calculating the average and standard deviation of systolic blood pressure, but for males instead of females.

This time we will not provide much sample code. You are on your own!

```
NHANES %>%
      filter(Gender == "male") %>% group_by(AgeDecade) %>% summarize(average = mean(BPSysAve, na.rm = TR
            standard_deviation = sd(BPSysAve, na.rm=TRUE))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 9 x 3
##   AgeDecade average standard_deviation
##   <fct>       <dbl>              <dbl>
## 1 " 0-9"       97.4               8.32
## 2 " 10-19"    110.               11.2
## 3 " 20-29"    118.               11.3
## 4 " 30-39"    119.               12.3
## 5 " 40-49"    121.               14.0
## 6 " 50-59"    126.               17.8
## 7 " 60-69"    127.               17.5
## 8 " 70+"      130.               18.7
## 9  <NA>       136.               23.5
```

7. We can actually combine both of these summaries into a single line of code.

This is because `group_by` permits us to group by more than one variable.

We can use `group_by(AgeDecade, Gender)` to group by both age decades and gender.

```
NHANES %>% group_by(AgeDecade, Gender) %>% summarize(average = mean(BPSysAve, na.rm = TRUE),
            standard_deviation = sd(BPSysAve, na.rm=TRUE))
```

```
## `summarise()` regrouping output by 'AgeDecade' (override with `.groups` argument)
```

```
## # A tibble: 18 x 4
## # Groups:   AgeDecade [9]
```

```
##    AgeDecade Gender average standard_deviation
##    <fct>     <fct>    <dbl>              <dbl>
##  1 " 0-9"    female   100.                9.07
##  2 " 0-9"    male      97.4               8.32
##  3 " 10-19"  female   104.                9.46
##  4 " 10-19"  male     110.               11.2
##  5 " 20-29"  female   108.               10.1
##  6 " 20-29"  male     118.               11.3
##  7 " 30-39"  female   111.               12.3
##  8 " 30-39"  male     119.               12.3
##  9 " 40-49"  female   115.               14.5
## 10 " 40-49"  male     121.               14.0
## 11 " 50-59"  female   122.               16.2
## 12 " 50-59"  male     126.               17.8
## 13 " 60-69"  female   127.               17.1
## 14 " 60-69"  male     127.               17.5
## 15 " 70+"    female   134.               19.8
## 16 " 70+"    male     130.               18.7
## 17  <NA>     female   142.               22.9
## 18  <NA>     male     136.               23.5
```

8. Now we are going to explore differences in systolic blood pressure across races, as reported in the `Race1` variable.

We will learn to use the `arrange` function to order the outcome acording to one variable.

Note that this function can be used to order any table by a given outcome. Here is an example that arranges by systolic blood pressure.

```
NHANES %>% arrange(BPSysAve)
```

If we want it in descending order we can use the `desc` function like this:

```
NHANES %>% arrange(desc(BPSysAve))
```

In this example, we will compare systolic blood pressure across values of the `Race1` variable for males between the ages of 40-49.

```
NHANES %>% filter(AgeDecade == " 40-49" & Gender == "male") %>% group_by(Race1) %>% summarize(average =
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 5 x 3
##   Race1    average standard_deviation
##   <fct>      <dbl>              <dbl>
## 1 White       120.               13.4
## 2 Other       120.               16.2
## 3 Hispanic    122.               11.1
## 4 Mexican     122.               13.9
## 5 Black       126.               17.1
```