Data Science R Basics

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

Learning Objectives

- Learn to read, extract, and create datasets in R
- Learn to perform a variety of operations on datasets using R
- Learn to write your own functions/sub-routines in R

Course Overview

Section 1: R Basics, Functions, Data types

You will get started with R, learn about its functions and data types.

Section 2: Vectors, Sorting

You will learn to operate on vectors and advanced functions such as sorting.

Section 3: Indexing, Data Manipulation, Plots

You will learn to wrangle and visualize data.

Section 4: Programming Basics

You will learn to use general programming features like 'if-else', and 'for loop' commands, and write your own functions to perform various operations on datasets.

Section 1 Overview

Section 1 introduces you to R Basics, Functions and Datatypes.

In Section 1, you will learn to:

- Appreciate the rationale for data analysis using R
- Define objects and perform basic arithmetic and logical operations
- Use pre-defined functions to perform operations on objects
- Distinguish between various data types

The textbook for this section is available here

Motivation

Here is a link to the textbook section on the motivation for this course.

Getting started

Here is a link to the textbook section on Getting Started with R.

Key Points

- R was developed by statisticians and data analysts as an interactive environment for data analysis.
- Some of the advantages of R are that (1) it is free and open source, (2) it has the capability to save scripts, (3) there are numerous resources for learning, and (4) it is easy for developers to share software implementation.
- Expressions are evaluated in the R console when you type the expression into the console and hit Return.
- A great advantage of R over point and click analysis software is that you can save your work as scripts.
- "Base R" is what you get after you first install R. Additional components are available via packages.

```
# installing the dslabs package
if(!require(dslabs)) install.packages("dslabs")
```

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

```
# loading the dslabs package into the R session
library(dslabs)
```

Installing R and R Studio

Installing R

To install R to work on your own computer, you can download it freely from the Comprehensive R Archive Network (CRAN). Note that CRAN makes several versions of R available: versions for multiple operating systems and releases older than the current one. You want to read the CRAN instructions to assure you download the correct version. If you need further help, you read the walkthrough in this Chapter of the textbook.

Installing RStudio

RStudio is an integrated development environment (IDE). We highly recommend installing and using RStudio to edit and test your code. You can install RStudio through the RStudio website. Their cheatsheet is a great resource. You must install R before installing RStudio.

Textbook Link

Here is a link to the textbook section on Installing R and RStudio.

R Basics - Objects

Here is a link to the textbook section on objects in R.

Key Points

- To define a variable, we may use the assignment symbol "<-".
- There are two ways to see the value stored in a variable: (1) type the variable into the console and hit Return, or (2) type print("variable name") and hit Return.
- Objects are stuff that is stored in R. They can be variables, functions, etc.
- The ls() function shows the names of the objects saved in your workspace.

Solving the equation x2+x−1=0

```
# assigning values to variables
a <- 1
b <- 1
c <- -1

# solving the quadratic equation
(-b + sqrt(b^2 - 4*a*c) ) / ( 2*a )
```

```
## [1] 0.618034
```

```
(-b - sqrt(b^2 - 4*a*c) ) / ( 2*a )
```

```
## [1] -1.618034
```

R Basics - Functions

Here is a link to the textbook section on functions.

Key points

- In general, to evaluate a function we need to use parentheses. If we type a function without parenthesis, R shows us the code for the function. Most functions also require an argument, that is, something to be written inside the parenthesis.
- To access help files, we may use the help function help("function name"), or write the question mark followed by the function name.
- The help file shows you the arguments the function is expecting, some of which are required and some are optional. If an argument is optional, a default value is assigned with the equal sign. The args() function also shows the arguments a function needs.
- To specify arguments, we use the equals sign. If no argument name is used, R assumes you're entering arguments in the order shown in the help file.
- Creating and saving a script makes code much easier to execute.
- To make your code more readable, use intuitive variable names and include comments (using the "#" symbol) to remind yourself why you wrote a particular line of code.

Assessment - R Basics

1. What is the sum of the first n positive integers? We can use the formula $n(n+1)/2$ to quickly compute this quantity.

```
# Here is how you compute the sum for the first 20 integers
20*(20+1)/2
```

```
## [1] 210
```

```
# However, we can define a variable to use the formula for other values of n
n <- 20
n*(n+1)/2
```

```
## [1] 210
```

```
n <- 25
n*(n+1)/2
```

```
## [1] 325
```

```
# Below, write code to calculate the sum of the first 100 integers
n<-100
n*(n+1)/2
```

```
## [1] 5050
```

2. What is the sum of the first 1000 positive integers? We can use the formula $n(n+1)/2$ to quickly compute this quantity.

```
# Below, write code to calculate the sum of the first 1000 integers
n<-1000
n*(n+1)/2
```

```
## [1] 500500
```

3. Run the following code in the R console.

```
n <- 1000
x <- seq(1, n)
sum(x)
```

```
## [1] 500500
```

Based on the result, what do you think the functions `seq` and `sum` do?

- ☐ A. sum creates a list of numbers and seq adds them up.
- ☒ B. seq creates a list of numbers and sum adds them up.
- ☐ C. seq computes the difference between two arguments and sum computes the sum of 1 through 1000.

☐ D. sum always returns the same number.

4. In math and programming we say we evaluate a function when we replace arguments with specific values. So if we type `log2(16)` we evaluate the `log2` function to get the log base 2 of `16` which is `4`.

In R it is often useful to evaluate a function inside another function. For example, `sqrt(log2(16))` will calculate the log to the base 2 of 16 and then compute the square root of that value. So the first evaluation gives a 4 and this gets evaluated by `sqrt` to give the final answer of 2.

```
# log to the base 2
log2(16)
```

```
## [1] 4
```

```
# sqrt of the log to the base 2 of 16:
sqrt(log2(16))
```

```
## [1] 2
```

```
# Compute log to the base 10 (log10) of the sqrt of 100. Do not use variables.
log10(sqrt(100))
```

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

5. Which of the following will always return the numeric value stored in `x`? You can try out examples and use the help system in the R console.

☐ A. log(10^x)
☐ B. log10(x^10)
☒ C. log(exp(x))
☐ D. exp(log(x, base = 2))

Data Types

You can find the section of the textbook on data types here.

Key Points

- The function "class" helps us determine the type of an object.
- Data frames can be thought of as tables with rows representing observations and columns representing different variables.
- To access data from columns of a data frame, we use the dollar sign symbol, which is called the accessor.
- A vector is an object consisting of several entries and can be a numeric vector, a character vector, or a logical vector.
- We use quotes to distinguish between variable names and character strings.
- Factors are useful for storing categorical data, and are more memory efficient than storing characters.

Code

```r
# loading the the murders dataset
data(murders)

# determining that the murders dataset is of the "data frame" class
class(murders)
```

```
## [1] "data.frame"
```

```r
# finding out more about the structure of the object
str(murders)
```

```
## 'data.frame':    51 obs. of  5 variables:
##  $ state     : chr  "Alabama" "Alaska" "Arizona" "Arkansas" ...
##  $ abb       : chr  "AL" "AK" "AZ" "AR" ...
##  $ region    : Factor w/ 4 levels "Northeast","South",..: 2 4 4 2 4 4 1 2 2 2 ...
##  $ population: num  4779736 710231 6392017 2915918 37253956 ...
##  $ total     : num  135 19 232 93 1257 ...
```

```r
# showing the first 6 lines of the dataset
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
```

```r
# using the accessor operator to obtain the population column
murders$population
```

```
##  [1]  4779736   710231  6392017  2915918 37253956  5029196  3574097   897934
##  [9]   601723 19687653  9920000  1360301  1567582 12830632  6483802  3046355
## [17]  2853118  4339367  4533372  1328361  5773552  6547629  9883640  5303925
## [25]  2967297  5988927   989415  1826341  2700551  1316470  8791894  2059179
## [33] 19378102  9535483   672591 11536504  3751351  3831074 12702379  1052567
## [41]  4625364   814180  6346105 25145561  2763885   625741  8001024  6724540
## [49]  1852994  5686986   563626
```

```r
# displaying the variable names in the murders dataset
names(murders)
```

```
## [1] "state"      "abb"        "region"     "population" "total"
```

```r
# determining how many entries are in a vector
pop <- murders$population
length(pop)
```

```
## [1] 51
```

```
# vectors can be of class numeric and character
class(pop)
```

```
## [1] "numeric"
```

```
class(murders$state)
```

```
## [1] "character"
```

```
# logical vectors are either TRUE or FALSE
z <- 3 == 2
z
```

```
## [1] FALSE
```

```
class(z)
```

```
## [1] "logical"
```

```
# factors are another type of class
class(murders$region)
```

```
## [1] "factor"
```

```
# obtaining the levels of a factor
levels(murders$region)
```

```
## [1] "Northeast"     "South"         "North Central" "West"
```

Assessment - Data Types

1. We're going to be using the following dataset for this module. Run this code in the console.

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

Next, use the function `str` to examine the structure of the `murders` object. We can see that this object is a data frame with 51 rows and five columns.

```
str(murders)
```

```
## 'data.frame':    51 obs. of  5 variables:
##  $ state     : chr  "Alabama" "Alaska" "Arizona" "Arkansas" ...
##  $ abb       : chr  "AL" "AK" "AZ" "AR" ...
##  $ region    : Factor w/ 4 levels "Northeast","South",..: 2 4 4 2 4 4 1 2 2 2 ...
##  $ population: num  4779736 710231 6392017 2915918 37253956 ...
##  $ total     : num  135 19 232 93 1257 ...
```

Which of the following best describes the variables represented in this data frame?

- ☐ A. The 51 states.
- ☐ B. The murder rates for all 50 states and DC.
- ☒ C. The state name, the abbreviation of the state name, the state's region, and the state's population and total number of murders for 2010.
- ☐ D. str shows no relevant information.

2. In the previous question, we saw the different variables that are a part of this dataset from the output of the `str()` function. The function `names()` is specifically designed to extract the column names from a data frame.

```
# Load package and data
library(dslabs)
data(murders)
```

```
# Use the function names to extract the variable names
names(murders)
```

```
## [1] "state"      "abb"        "region"     "population" "total"
```

3. In this module we have learned that every variable has a class. For example, the class can be a *character*, *numeric* or *logical*. The function `class()` can be used to determine the class of an object.

Here we are going to determine the class of one of the variables in the `murders` data frame. To extract variables from a data frame we use `$`, referred to as the accessor.

```
# To access the population variable from the murders dataset use this code:
p <- murders$population

# To determine the class of object `p` we use this code:
class(p)
```

```
## [1] "numeric"
```

```
# Use the accessor to extract state abbreviations and assign it to a
a <- murders$abb

# Determine the class of a
class(a)
```

```
## [1] "character"
```

4. An important lesson you should learn early on is that there are multiple ways to do things in R. For example, to generate the first five integers we note that `1:5` and `seq(1,5)` return the same result.

There are also multiple ways to access variables in a data frame. For example we can use the square brackets `[[` instead of the accessor `$`.

If you instead try to access a column with just one bracket,

```
murders["population"]
```

R returns a subset of the original data frame containing just this column. This new object will be of class `data.frame` rather than a vector. To access the column itself you need to use either the `$` accessor or the double square brackets `[[`.

Parentheses, in contrast, are mainly used alongside functions to indicate what argument the function should be doing something to. For example, when we did `class(p)` in the last question, we wanted the function `class` to do something related to the argument `p`.

This is an example of how R can be a bit idiosyncratic sometimes. It is very common to find it confusing at first.

```
# We extract the population like this:
p <- murders$population

# This is how we do the same with the square brackets:
o <- murders[["population"]]

# We can confirm these two are the same
identical(o, p)
```

```
## [1] TRUE
```

```
# Use square brackets to extract `abb` from `murders` and assign it to b
b <- murders[["abb"]]

# Check if `a` and `b` are identical
identical(a, b)
```

```
## [1] TRUE
```

5. Using the `str()` command, we saw that the *region* column stores a factor. You can corroborate this by using the `class` command on the *region* column.

The function `levels` shows us the categories for the factor.

```
# We can see the class of the region variable using class
class(murders$region)
```

```
## [1] "factor"
```

```
# Determine the number of regions included in this variable
length(levels(murders$region))
```

```
## [1] 4
```

6. The function `table` takes a vector as input and returns the frequency of each unique element in the vector.

```r
# Here is an example of what the table function does
x <- c("a", "a", "b", "b", "b", "c")
table(x)
```

```
## x
## a b c
## 2 3 1
```

```r
# Write one line of code to show the number of states per region
table(murders$region)
```

```
##
##     Northeast         South North Central          West
##             9            17            12            13
```

Section 1 Assessment

1. To find the solutions to an equation of the format $ax^2 + bx + c$, use the quadratic equation: $x = \frac{-b \pm \sqrt{(b^2 - 4ac)}}{2a}$.

What are the two solutions to $2x^2 - x - 4 = 0$? Use the quadratic equation. (Report the greater of the two solutions first, using 3 significant digits for both solutions)

```r
options(digits = 3)
a <- 2
b <- -1
c <- -4
(-b+sqrt(b^2-4*a*c))/(2*a)
```

```
## [1] 1.69
```

```r
(-b-sqrt(b^2-4*a*c))/(2*a)
```

```
## [1] -1.19
```

2. Use R to compute log base 4 of 1024. You can use the `help` function to learn how to use arguments to change the base of the `log` function.

```r
log(1024, base = 4)
```

```
## [1] 5
```

3. Load the `movielens` dataset

```r
data(movielens)
str(movielens)
```

```
## 'data.frame':    100004 obs. of  7 variables:
##  $ movieId  : int  31 1029 1061 1129 1172 1263 1287 1293 1339 1343 ...
##  $ title    : chr  "Dangerous Minds" "Dumbo" "Sleepers" "Escape from New York" ...
##  $ year     : int  1995 1941 1996 1981 1989 1978 1959 1982 1992 1991 ...
##  $ genres   : Factor w/ 901 levels "(no genres listed)",..: 762 510 899 120 762 836 81 762 844 899 .
##  $ userId   : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ rating   : num  2.5 3 3 2 4 2 2 2 3.5 2 ...
##  $ timestamp: int  1260759144 1260759179 1260759182 1260759185 1260759205 1260759151 1260759187 1260
```

How many rows are in the dataset? `100004`

How many different variables are in the dataset? `7`

What is the variable type of `title`?

- ☐ A. It is a text (txt) variable
- ☐ B. It is a chronological (chr) variable
- ☐ C. It is a string (str) variable
- ☐ D. It is a numeric (num) variable
- ☐ E. It is an integer (int) variable
- ☐ F. It is a factor (Factor) variable
- ☒ G. It is a character (chr) variable

What is the variable type of `genres`?

- ☐ A. It is a text (txt) variable
- ☐ B. It is a chronological (chr) variable
- ☐ C. It is a string (str) variable
- ☐ D. It is a numeric (num) variable
- ☐ E. It is an integer (int) variable
- ☒ F. It is a factor (Factor) variable
- ☐ G. It is a character (chr) variable

4. We already know we can use the `levels()` function to determine the levels of a factor. A different function, `nlevels()`, may be used to determine the number of levels of a factor.

Use this function to determine how many levels are in the factor `genres` in the `movielens` data frame.

```
nlevels(movielens$genres)
```

```
## [1] 901
```

Section 2 Overview

In Section 2.1, you will:

- Create numeric and character vectors.
- Name the columns of a vector.
- Generate numeric sequences.
- Access specific elements or parts of a vector.
- Coerce data into different data types as needed.

In Section 2.2, you will:

- Sort vectors in ascending and descending order.
- Extract the indices of the sorted elements from the original vector.
- Find the maximum and minimum elements, as well as their indices, in a vector.
- Rank the elements of a vector in increasing order.

In Section 2.3, you will:

- Perform arithmetic between a vector and a single number.
- Perform arithmetic between two vectors of same length.

Vectors

The textbook for this section is available here

Key Points

- The function `c()`, which stands for concatenate, is useful for creating vectors.
- Another useful function for creating vectors is the `seq()` function, which generates sequences.
- Subsetting lets us access specific parts of a vector by using square brackets to access elements of a vector.

Code

```
# We may create vectors of class numeric or character with the concatenate function
codes <- c(380, 124, 818)
country <- c("italy", "canada", "egypt")

# We can also name the elements of a numeric vector
# Note that the two lines of code below have the same result
codes <- c(italy = 380, canada = 124, egypt = 818)
codes <- c("italy" = 380, "canada" = 124, "egypt" = 818)

# We can also name the elements of a numeric vector using the names() function
codes <- c(380, 124, 818)
country <- c("italy","canada","egypt")
names(codes) <- country

# Using square brackets is useful for subsetting to access specific elements of a vector
codes[2]
```

```
## canada
##    124
```

```
codes[c(1,3)]
```

```
## italy egypt
##   380   818
```

```r
codes[1:2]
```

```
##  italy canada
##    380    124
```

```r
# If the entries of a vector are named, they may be accessed by referring to their name
codes["canada"]
```

```
## canada
##    124
```

```r
codes[c("egypt","italy")]
```

```
## egypt italy
##   818   380
```

Vectors - Vector Coercion

The textbook for this section is available here

Key Points

- In general, *coercion* is an attempt by R to be flexible with data types by guessing what was meant when an entry does not match the expected. For example, when defining x as

x <- c(1, "canada", 3)

R *coerced* the data into characters. It guessed that because you put a character string in the vector, you meant the 1 and 3 to actually be character strings "1" and "3".

- The function `as.character()` turns numbers into characters.
- The function `as.numeric()` turns characters into numbers.
- In R, missing data is assigned the value NA.

Assessment - Vectors

1. A vector is a series of values, all of the same type. They are the most basic data type in R and can hold numeric data, character data, or logical data. In R, you can create a vector with the concatenate (or combine) function `c()`

You place the vector elements separated by a comma between the parentheses. For example a numeric vector would look something like this:

```r
cost <- c(50, 75, 90, 100, 150)
```

```r
# Here is an example creating a numeric vector named cost
cost <- c(50, 75, 90, 100, 150)

# Create a numeric vector to store the temperatures listed in the instructions into a vector named temp
# Make sure to follow the same order in the instructions
temp <- c("Beijing"=35, "Lagos"=88, "Paris"=42, "Rio de Janeiro"=84, "San Juan"=81, "Toronto"=30)
cost
```

```
## [1]  50  75  90 100 150
```

```
temp
```

```
##        Beijing          Lagos          Paris Rio de Janeiro       San Juan
##             35             88             42             84             81
##        Toronto
##             30
```

```
class(temp)
```

```
## [1] "numeric"
```

2. As in the previous question, we are going to create a vector. Only this time, we learn to create *character* vectors. The main difference is that these have to be written as strings and so the names are enclosed within double quotes.

A *character* vector would look something like this:

```
food <- c("pizza", "burgers", "salads", "cheese", "pasta")
```

```
# here is an example of how to create a character vector
food <- c("pizza", "burgers", "salads", "cheese", "pasta")

# Create a character vector called city to store the city names
# Make sure to follow the same order as in the instructions
city <- c("Beijing", "Lagos", "Paris", "Rio de Janeiro", "San Juan", "Toronto")
```

3. We have successfully assigned the temperatures as *numeric* values to `temp` and the `city` names as character values to city. But can we associate the temperature to its related city? Yes! We can do so using a code we already know - `names`. We assign names to the *numeric* values.

It would look like this:

```
cost <- c(50, 75, 90, 100, 150)
food <- c("pizza", "burgers", "salads", "cheese", "pasta")
names(cost) <- food
```

```
# Associate the cost values with its corresponding food item
cost <- c(50, 75, 90, 100, 150)
food <- c("pizza", "burgers", "salads", "cheese", "pasta")
names(cost) <- food

# You already wrote this code
temp <- c(35, 88, 42, 84, 81, 30)
city <- c("Beijing", "Lagos", "Paris", "Rio de Janeiro", "San Juan", "Toronto")

# Associate the temperature values with its corresponding city
names(temp) <- city
temp
```

```
##        Beijing          Lagos          Paris Rio de Janeiro       San Juan
##             35             88             42             84             81
##        Toronto
##             30
```

4. If we want to display only selected values from the object, R can help us do that easily.

For example, if we want to see the cost of the last 3 items in our food list, we would type:

```
cost[3:5]
```

Note here, that we could also type `cost[c(3,4,5)]` and get the same result. The `:` operator helps us condense the code and get consecutive values.

```
# cost of the last 3 items in our food list:
cost[3:5]
```

```
## salads cheese  pasta
##     90    100    150
```

```
# temperatures of the first three cities in the list:
temp[1:3]
```

```
## Beijing   Lagos   Paris
##      35      88      42
```

5. In the previous question, we accessed the temperature for consecutive cities (1st three). But what if we want to access the temperatures for any 2 specific cities?

An example: To access the cost of `pizza` (1st) and `pasta` (5th food item) in our list, the code would be:

```
cost[c(1,5)]
```

```
# Access the cost of pizza and pasta from our food list
cost[c(1,5)]
```

```
## pizza pasta
##    50   150
```

```
# Define temp
temp <- c(35, 88, 42, 84, 81, 30)
city <- c("Beijing", "Lagos", "Paris", "Rio de Janeiro", "San Juan", "Toronto")
names(temp) <- city

# Access the temperatures of Paris and San Juan
temp[c(3,5)]
```

```
##    Paris San Juan
##       42       81
```

6. The `:` operator helps us create sequences of numbers. For example, `32:99` would create a list of numbers from 32 to 99.

Then, if we want to know the length of this sequence, all we need to do is use the `length` command.

```
# Create a vector m of integers that starts at 32 and ends at 99.
m <- 32:99

# Determine the length of object m.
length(m)
```

```
## [1] 68
```

```
# Create a vector x of integers that starts at 12 and ends at 73.
x <- 12:73

# Determine the length of object x.
length(x)
```

```
## [1] 62
```

7. We can also create different types of sequences in R. For example, in `seq(7, 49, 7)`, the first argument defines the start, and the second the end. The default is to go up in increments of 1, but a third argument lets us tell it by what interval.

```
# Create a vector with the multiples of 7, smaller than 50.
seq(7, 49, 7)
```

```
## [1]  7 14 21 28 35 42 49
```

```
# Create a vector containing all the positive odd numbers smaller than 100.
# The numbers should be in ascending order
seq(1,99,2)
```

```
##  [1]  1  3  5  7  9 11 13 15 17 19 21 23 25 27 29 31 33 35 37 39 41 43 45 47 49
## [26] 51 53 55 57 59 61 63 65 67 69 71 73 75 77 79 81 83 85 87 89 91 93 95 97 99
```

8. The second argument of the function `seq` is actually a maximum, not necessarily the end.

So if we type

```
seq(7, 50, 7)
```

we actually get the same vector of integers as if we type

```
seq(7, 49, 7)
```

This can be useful because sometimes all we want are sequential numbers that are smaller than some value. Let's look at an example.

```
# We can create a vector with the multiples of 7, smaller than 50 like this
seq(7, 49, 7)
```

```
## [1]  7 14 21 28 35 42 49
```

```
# But note that the second argument does not need to be the last number
# It simply determines the maximum value permitted
# so the following line of code produces the same vector as seq(7, 49, 7)
seq(7, 50, 7)
```

```
## [1]  7 14 21 28 35 42 49
```

```
# Create a sequence of numbers from 6 to 55, with 4/7 increments and determine its length
length(seq(6,55,4/7))
```

```
## [1] 86
```

9. The `seq()` function has another useful argument. The argument *length.out*. This argument lets us generate sequences that are increasing by the same amount but are of the prespecified length.

For example, this line of code

```
x <- seq(0, 100, length.out = 5)
produces the numbers 0, 25, 50, 75, 100.
```

Let's create a vector and see what is the class of the object produced.

```
# Store the sequence in the object a
a <- seq(1, 10, length.out = 100)

# Determine the class of a
class(a)
```

```
## [1] "numeric"
```

10. We have discussed the numeric class. We just saw that the `seq` function can generate objects of this class.

For another example, type

```
class(seq(1, 10, 0.5))
```

into the console and note that the `class` is *numeric*. R has another type of vector we have not described, the *integer* class. You can create an *integer* by adding the letter `L` after a whole number. If you type

```
class(3L)
```

in the console, you see this is an *integer* and not a *numeric*. For most practical purposes, integers and numerics are indistinguishable. For example 3, the integer, minus 3 the numeric is 0. To see this type this in the console

```
3L - 3
```

The main difference is that integers occupy less space in the computer memory, so for big computations using integers can have a substantial impact.

```
# Store the sequence in the object a
a <- seq(1,10)

# Determine the class of a
class(a)
```

```
## [1] "integer"
```

11. Let's confirm that `1L` is an *integer* not a *numeric*.

```
# Check the class of 1, assigned to the object a
class(1)
```

```
## [1] "numeric"
```

```
# Confirm the class of 1L is integer
class(1L)
```

```
## [1] "integer"
```

12. The concept of coercion is a very important one. Watching the video, we learned that when an entry does not match what an R function is expecting, R tries to guess what we meant before throwing an error. This might get confusing at times.

As we've discussed in earlier questions, there are numeric and character vectors. The character vectors are placed in quotes and the numerics are not.

We can avoid issues with coercion in R by changing characters to numerics and vice-versa. This is known as typecasting. The code, `as.numeric(x)` helps us convert character strings to numbers. There is an equivalent function that converts its argument to a string, `as.character(x)`.

Let's practice doing this!

```
# Define the vector x
x <- c(1, 3, 5,"a")

# Note that the x is character vector
x
```

```
## [1] "1" "3" "5" "a"
```

```
# Typecast the vector to get an integer vector
# You will get a warning but that is ok
x <- as.numeric(x)
```

```
## Warning: NAs introduced by coercion
```

```
x
```

```
## [1]  1  3  5 NA
```

Sorting

The textbook for this section is available here

Key Points

- The function `sort()` sorts a vector in increasing order.
- The function `order()` produces the indices needed to obtain the sorted vector, e.g. a result of 2 3 1 5 4 means the sorted vector will be produced by listing the 2nd, 3rd, 1st, 5th, and then 4th item of the original vector.
- The function `rank()` gives us the ranks of the items in the original vector.
- The function `max()` returns the largest value while `which.max()` returns the index of the largest value. The functions `min()` and `which.min()` work similarly for minimum values.

Assessment - Sorting

1. When looking at a dataset, we may want to sort the data in an order that makes more sense for analysis. Let's learn to do this using the `murders` dataset as an example

```
# Access the `state` variable and store it in an object
states <- murders$state

# Sort the object alphabetically and redefine the object
states <- sort(states)

# Report the first alphabetical value
states[1]
```

```
## [1] "Alabama"
```

```
# Access population values from the dataset and store it in pop
pop <- murders$population

# Sort the object and save it in the same object
pop <- sort(pop)

# Report the smallest population size
pop[1]
```

```
## [1] 563626
```

2. The function `order()` returns the index vector needed to sort the vector. This implies that `sort(x)` and `x[order(x)]` give the same result.

This can be useful for finding row numbers with certain properties such as "the row for the state with the smallest population". Remember that when we extract a variable from a data frame the order of the resulting vector is the same as the order of the rows of the data frame. So for example, the entries of the vector `murders$state` are ordered in the same way as the states if you go down the rows of `murders`.

```r
# Access population from the dataset and store it in pop
pop <- murders$population

# Use the command order to find the vector of indexes that order pop and store in object ord
ord <- order(pop)

# Find the index number of the entry with the smallest population size
ord[1]
```

```
## [1] 51
```

3. We can actually perform the same operation as in the previous exercise using the function `which.min`. It basically tells us which is the minimum value.

```r
# Find the index of the smallest value for variable total
which.min(murders$total)
```

```
## [1] 46
```

```r
# Find the index of the smallest value for population
which.min(murders$population)
```

```
## [1] 51
```

4. Now we know how small the smallest state is and we know which row represents it. However, which state is it?

```r
# Define the variable i to be the index of the smallest state
i <- which.min(murders$population)

# Define variable states to hold the states
states <- murders$state

# Use the index you just defined to find the state with the smallest population
states[i]
```

```
## [1] "Wyoming"
```

5. You can create a data frame using the data.frame function.

Here is a quick example:

```r
temp <- c(35, 88, 42, 84, 81, 30)
city <- c("Beijing", "Lagos", "Paris", "Rio de Janeiro", "San Juan", "Toronto")
city_temps <- data.frame(name = city, temperature = temp)
```

```r
# Store temperatures in an object
temp <- c(35, 88, 42, 84, 81, 30)

# Store city names in an object
city <- c("Beijing", "Lagos", "Paris", "Rio de Janeiro", "San Juan", "Toronto")

# Create data frame with city names and temperature
city_temps <- data.frame(name = city, temperature = temp)

# Define a variable states to be the state names
states <- murders$state

# Define a variable ranks to determine the population size ranks
ranks <- rank(murders$population)

# Create a data frame my_df with the state name and its rank
my_df <- data.frame(name = states, rank = ranks)
```

6. This exercise is somewhat more challenging. We are going to repeat the previous exercise but this time order ‘`my_df` so that the states are ordered from least populous to most.

```r
# Define a variable states to be the state names from the murders data frame
states <- murders$state

# Define a variable ranks to determine the population size ranks
ranks <- rank(murders$population)

# Define a variable ind to store the indexes needed to order the population values
ind <- order(murders$population)

# Create a data frame my_df with the state name and its rank and ordered from least populous to most
my_df <- data.frame(states = states[ind], ranks = ranks[ind])
```

7. The `na_example` dataset represents a series of counts. It is included in the *dslabs* package.

You can quickly examine the object using

```r
library(dslabs)
data(na_example)
str(na_example)
```

However, when we compute the average we obtain an `NA`. You can see this by typing

```r
mean(na_example)
```

```r
# Using new dataset
library(dslabs)
data(na_example)

# Checking the structure
str(na_example)
```

```
##  int [1:1000] 2 1 3 2 1 3 1 4 3 2 ...
```

```r
# Find out the mean of the entire dataset
mean(na_example)
```

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

```r
# Use is.na to create a logical index ind that tells which entries are NA
ind <- is.na(na_example)

# Determine how many NA ind has using the sum function
sum(ind)
```

```
## [1] 145
```

8. We previously computed the average of `na_example` using `mean(na_example)` and obtain `NA`. This is because the function `mean` returns `NA` if it encounters at least one `NA`. A common operation is therefore removing the entries that are NA and after that perform operations on the rest.

```r
# Note what we can do with the ! operator
x <- c(1, 2, 3)
ind <- c(FALSE, TRUE, FALSE)
x[!ind]
```

```
## [1] 1 3
```

```r
# Create the ind vector
library(dslabs)
data(na_example)
ind <- is.na(na_example)

# We saw that this gives an NA
mean(na_example)
```

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

```r
# Compute the average, for entries of na_example that are not NA
mean(na_example[!ind])
```

```
## [1] 2.3
```

Vector arithmetic

The textbook for this section is available here

Key Points

- In R, arithmetic operations on vectors occur element-wise.

Code

```r
# The name of the state with the maximum population is found by doing the following
murders$state[which.max(murders$population)]
```

```
## [1] "California"
```

```r
# how to obtain the murder rate
murder_rate <- murders$total / murders$population * 100000

# ordering the states by murder rate, in decreasing order
murders$state[order(murder_rate, decreasing=TRUE)]
```

```
##  [1] "District of Columbia" "Louisiana"            "Missouri"
##  [4] "Maryland"             "South Carolina"       "Delaware"
##  [7] "Michigan"             "Mississippi"          "Georgia"
## [10] "Arizona"              "Pennsylvania"         "Tennessee"
## [13] "Florida"              "California"           "New Mexico"
## [16] "Texas"                "Arkansas"             "Virginia"
## [19] "Nevada"               "North Carolina"       "Oklahoma"
## [22] "Illinois"             "Alabama"              "New Jersey"
## [25] "Connecticut"          "Ohio"                 "Alaska"
## [28] "Kentucky"             "New York"             "Kansas"
## [31] "Indiana"              "Massachusetts"        "Nebraska"
## [34] "Wisconsin"            "Rhode Island"         "West Virginia"
## [37] "Washington"           "Colorado"             "Montana"
## [40] "Minnesota"            "South Dakota"         "Oregon"
## [43] "Wyoming"              "Maine"                "Utah"
## [46] "Idaho"                "Iowa"                 "North Dakota"
## [49] "Hawaii"               "New Hampshire"        "Vermont"
```

Assessment - Vector Arithmetic

1. Previously we created this data frame.

{r, eval=FALSE, echo=TRUE temp <- c(35, 88, 42, 84, 81, 30) city <- c("Beijing", "Lagos", "Paris", "Rio de Janeiro", "San Juan", "Toronto") city_temps <- data.frame(name = city, temperature = temp)

```r
# Assign city names to `city`
city <- c("Beijing", "Lagos", "Paris", "Rio de Janeiro", "San Juan", "Toronto")

# Store temperature values in `temp`
temp <- c(35, 88, 42, 84, 81, 30)

# Convert temperature into Celsius and overwrite the original values of 'temp' with these Celsius value
temp <- 5/9 * (temp -32)

# Create a data frame `city_temps`
city_temps <- data.frame(name = city, temperature = temp)
```

2. We can use some of what we have learned to perform calculations that would otherwise be quite complicated. Let's see an example.

```r
# Define an object `x` with the numbers 1 through 100
x <- seq(1,100)

# Compute the sum
sum((1/x)^2)
```

```
## [1] 1.63
```

3. 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?

```r
# Store the per 100,000 murder rate for each state in murder_rate
murder_rate <- murders$total / murders$population * 100000

# Calculate the average murder rate in the US
mean(murder_rate)
```

```
## [1] 2.78
```

Section 2 Assessment

1. Consider the vector `x <- c(2, 43, 27, 96, 18)`.

Match the following outputs to the function which produces that output. Options include `sort(x)`, `order(x)`, `rank(x)` and none of these.

```r
x <- c(2, 43, 27, 96, 18)
sort(x)
```

```
## [1]  2 18 27 43 96
```

```r
order(x)
```

```
## [1] 1 5 3 2 4
```

```r
rank(x)
```

```
## [1] 1 4 3 5 2
```

`1, 2, 3, 4, 5` none of these

`1, 5, 3, 2, 4` order(x)

`1, 4, 3, 5, 2` rank(x)

`2, 18, 27, 43, 96` sort(x)

2. Continue working with the vector `x <- c(2, 43, 27, 96, 18)`.

```
x <- c(2, 43, 27, 96, 18)
min(x)
```

```
## [1] 2
```

```
which.min(x)
```

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

```
max(x)
```

```
## [1] 96
```

```
which.max(x)
```

```
## [1] 4
```

`min(x)` 2

`which.min(x)` 1

`max(x)` none of these

`which.max(x)` 4

3. Mandi, Amy, Nicole, and Olivia all ran different distances in different time intervals. Their distances (in miles) and times (in minutes) are as follows:

```
name <- c("Mandi", "Amy", "Nicole", "Olivia")
distance <- c(0.8, 3.1, 2.8, 4.0)
time <- c(10, 30, 40, 50)
```

Write a line of code to convert time to hours. Remember there are 60 minutes in an hour. Then write a line of code to calculate the speed of each runner in miles per hour. Speed is distance divided by time.

How many hours did Olivia run?

```
hours <- time/60
hours[4]
```

```
## [1] 0.833
```

What was Mandi's speed in miles per hour?

```
speed <- distance/hours
speed[1]
```

```
## [1] 4.8
```

Which runner had the fastest speed?

```
name[which.max(speed)]
```

```
## [1] "Amy"
```

Section 3 Overview

Section 3 introduces to the R commands and techniques that help you wrangle, analyze, and visualize data.

In Section 3.1, you will:

- Subset a vector based on properties of another vector.
- Use multiple logical operators to index vectors.
- Extract the indices of vector elements satisfying one or more logical conditions.
- Extract the indices of vector elements matching with another vector.
- Determine which elements in one vector are present in another vector.

In Section 3.2, you will:

- Wrangle data tables using the functions in 'dplyr' package.
- Modify a data table by adding or changing columns.
- Subset rows in a data table.
- Subset columns in a data table.
- Perform a series of operations using the pipe operator.
- Create data frames.

In Section 3.3, you will:

- Plot data in scatter plots, box plots and histograms.

Indexing

The textbook for this section is available here

Key Points

- We can use logicals to index vectors.
- Using the function >sum()on a logical vector returns the number of entries that are true.
- The logical operator "&" makes two logicals true only when they are both true.

Code

```
# defining murder rate as before
murder_rate <- murders$total / murders$population * 100000
# creating a logical vector that specifies if the murder rate in that state is less than or equal to 0.
index <- murder_rate <= 0.71
# determining which states have murder rates less than or equal to 0.71
murders$state[index]
```

```
## [1] "Hawaii"        "Iowa"          "New Hampshire" "North Dakota"
## [5] "Vermont"
```

```
# calculating how many states have a murder rate less than or equal to 0.71
sum(index)
```

```
## [1] 5
```

```
# creating the two logical vectors representing our conditions
west <- murders$region == "West"
safe <- murder_rate <= 1
# defining an index and identifying states with both conditions true
index <- safe & west
murders$state[index]
```

```
## [1] "Hawaii"  "Idaho"   "Oregon"  "Utah"    "Wyoming"
```

Indexing - Indexing Functions

The textbook for this section is available here

Key Points

- The function which() gives us the entries of a logical vector that are true.
- The function match() looks for entries in a vector and returns the index needed to access them.
- We use the function %in% if we want to know whether or not each element of a first vector is in a second vector.

Code

```
# to determine the murder rate in Massachusetts we may do the following
ind <- which(murders$state == "Massachusetts")
murder_rate[ind]
```

```
## [1] 1.8
```

```
# to obtain the indices and subsequent murder rates of New York, Florida, Texas, we do:
ind <- match(c("New York", "Florida", "Texas"), murders$state)
ind
```

```
## [1] 33 10 44
```

```
murder_rate[ind]
```

```
## [1] 2.67 3.40 3.20
```

```
# to see if Boston, Dakota, and Washington are states
c("Boston", "Dakota", "Washington") %in% murders$state
```

```
## [1] FALSE FALSE  TRUE
```

Assessment - Indexing

1. Here we will be using logical operators to create a logical vector. Compute the per 100,000 murder rate for each state and store it in an object called `murder_rate`. Then use logical operators to create a logical vector named `low` that tells us which entries of `murder_rate` are lower than 1.

```
# Store the murder rate per 100,000 for each state, in `murder_rate`
murder_rate <- murders$total / murders$population * 100000

# Store the `murder_rate < 1` in `low`
low <- murder_rate < 1
```

2. The function 'which() helps us know directly, which values are low or high, etc. Let's use it in this question.

```
# Store the murder rate per 100,000 for each state, in murder_rate
murder_rate <- murders$total/murders$population*100000

# Store the murder_rate < 1 in low
low <- murder_rate < 1

# Get the indices of entries that are below 1
ind <- which(low)
ind
```

```
##  [1] 12 13 16 20 24 30 35 38 42 45 46 51
```

3. Note that if we want to know which entries of a vector are lower than a particular value we can use code like this.

```
small <- murders$population < 1000000
murders$state[small]
```

The code above shows us the states with populations smaller than one million.

```
# Store the murder rate per 100,000 for each state, in murder_rate
murder_rate <- murders$total/murders$population*100000

# Store the murder_rate < 1 in low
low <- murder_rate < 1

# Names of states with murder rates lower than 1
murders$state[low]
```

```
##  [1] "Hawaii"        "Idaho"         "Iowa"          "Maine"
##  [5] "Minnesota"     "New Hampshire" "North Dakota"  "Oregon"
##  [9] "South Dakota"  "Utah"          "Vermont"       "Wyoming"
```

4. Now we will extend the code from the previous exercises to report the states in the Northeast with a murder rate lower than 1.

```r
# Store the murder rate per 100,000 for each state, in `murder_rate`
murder_rate <- murders$total/murders$population*100000

# Store the `murder_rate < 1` in `low`
low <- murder_rate < 1

# Create a vector ind for states in the Northeast and with murder rates lower than 1.
northeast <- murders$region == "Northeast"
ind <- low & northeast

# Names of states in `ind`
murders$state[ind]
```

```
## [1] "Maine"         "New Hampshire" "Vermont"
```

5. In a previous exercise we computed the murder rate for each state and the average of these numbers. How many states are below the average?

```r
# Store the murder rate per 100,000 for each state, in murder_rate
murder_rate <- murders$total/murders$population*100000


# Compute the average murder rate using `mean` and store it in object named `avg`
avg <- mean(murder_rate)

# How many states have murder rates below avg ? Check using sum
ind <- murder_rate < avg
sum(ind)
```

```
## [1] 27
```

6. In this exercise we use the `match` function to identify the states with abbreviations AK, MI, and IA.

```r
# Store the 3 abbreviations in a vector called `abbs` (remember that they are character vectors and nee
abbs <- c("AK", "MI", "IA")

# Match the abbs to the murders$abb and store in ind
ind <- match(abbs, murders$abb)

# Print state names from ind
murders$state[ind]
```

```
## [1] "Alaska"   "Michigan" "Iowa"
```

7. If rather than an index we want a logical that tells us whether or not each element of a first vector is in a second, we can use the function `%in%`.

For example:

```
x <- c(2, 3, 5)
y <- c(1, 2, 3, 4)
x%in%y
```

Gives us two `TRUE` followed by a `FALSE` because 2 and 3 are in `y` but 5 is not.

```
# Store the 5 abbreviations in `abbs`. (remember that they are character vectors)
abbs <- c("MA", "ME", "MI", "MO", "MU")

# Use the %in% command to check if the entries of abbs are abbreviations in the the murders data frame
abbs%in%murders$abb
```

```
## [1]  TRUE  TRUE  TRUE  TRUE FALSE
```

8. In a previous exercise we computed the index `abbs%in%murders$abb`. Based on that, and using the `which` function and the `!` operator, get the index of the entries of `abbs` that are **not** abbreviations.

```
# Store the 5 abbreviations in abbs. (remember that they are character vectors)
abbs <- c("MA", "ME", "MI", "MO", "MU")

# Use the `which` command and `!` operator to find out which index abbreviations are not actually part
ind <- which(!abbs%in%murders$abb)

# Names of abbreviations in `ind`
abbs[ind]
```

```
## [1] "MU"
```

Basic Data Wrangling

The textbook for this section is available here and here

In the textbook, the dplyr package is introduced in the context of the tidyverse, a collection of R packages

Key Points

- To change a data table by adding a new column, or changing an existing one, we use the `mutate` function.
- To filter the data by subsetting rows, we use the function `filter`.
- To subset the data by selecting specific columns, we use the `select` function.
- We can perform a series of operations by sending the results of one function to another function using what is called the pipe operator, `%>%`.

Code

```
# installing and loading the dplyr package
if(!require(dplyr)) install.packages("dplyr")
```

```
## Loading required package: dplyr
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(dplyr)

# adding a column with mutate
library(dslabs)
data("murders")
murders <- mutate(murders, rate = total / population * 100000)

# subsetting with filter
filter(murders, rate <= 0.71)
```

```
##           state abb        region population total  rate
## 1        Hawaii  HI          West    1360301     7 0.515
## 2          Iowa  IA North Central    3046355    21 0.689
## 3 New Hampshire  NH     Northeast    1316470     5 0.380
## 4  North Dakota  ND North Central     672591     4 0.595
## 5       Vermont  VT     Northeast     625741     2 0.320
```

```
# selecting columns with select
new_table <- select(murders, state, region, rate)

# using the pipe
murders %>% select(state, region, rate) %>% filter(rate <= 0.71)
```

```
##           state        region  rate
## 1        Hawaii          West 0.515
## 2          Iowa North Central 0.689
## 3 New Hampshire     Northeast 0.380
## 4  North Dakota North Central 0.595
## 5       Vermont     Northeast 0.320
```

Basic Data Wrangling - Creating Data Frames

Key Points

- We can use the `data.frame()` function to create data frames.
- By default, the `data.frame()` function turns characters into factors. To avoid this, we utilize the `stringsAsFactors` argument and set it equal to false.

Code

```r
# creating a data frame with stringAsFactors = FALSE
grades <- data.frame(names = c("John", "Juan", "Jean", "Yao"),
                     exam_1 = c(95, 80, 90, 85),
                     exam_2 = c(90, 85, 85, 90),
                     stringsAsFactors = FALSE)
```

Assessment - Basic Data Wrangling

1. You can add columns using the `dplyr` function `mutate`.

This function is aware of the column names and inside the function you can call them unquoted. Like this:

```r
murders <- mutate(murders, population_in_millions = population / 10^6)
```

Note that we can write `population` rather than `murders$population`. The function `mutate` knows we are grabing columns from `murders`.

```r
# Redefine murders so that it includes a column named rate with the per 100,000 murder rates
murders <- mutate(murders, rate = total / population * 100000)
```

2. Note that if `rank(x)` gives you the ranks of `x` from lowest to highest, `rank(-x)` gives you the ranks from highest to lowest.

```r
# Note that if you want ranks from highest to lowest you can take the negative and then compute the ran
x <- c(88, 100, 83, 92, 94)
rank(-x)
```

```
## [1] 4 1 5 3 2
```

```r
# Defining rate
rate <-  murders$total/ murders$population * 100000

# Redefine murders to include a column named rank
# with the ranks of rate from highest to lowest
murders <- mutate(murders, rank = rank(-rate))
```

3. With `dplyr` we can use `select` to show only certain columns. For example with this code we would only show the states and population sizes:

```r
select(murders, state, population)
```

```r
# Use select to only show state names and abbreviations from murders
select(murders, state, abb)
```

```
##                  state abb
## 1              Alabama  AL
## 2               Alaska  AK
## 3              Arizona  AZ
## 4             Arkansas  AR
```

```
## 5            California  CA
## 6              Colorado  CO
## 7           Connecticut  CT
## 8              Delaware  DE
## 9  District of Columbia  DC
## 10              Florida  FL
## 11              Georgia  GA
## 12               Hawaii  HI
## 13                Idaho  ID
## 14             Illinois  IL
## 15              Indiana  IN
## 16                 Iowa  IA
## 17               Kansas  KS
## 18             Kentucky  KY
## 19            Louisiana  LA
## 20                Maine  ME
## 21             Maryland  MD
## 22        Massachusetts  MA
## 23             Michigan  MI
## 24            Minnesota  MN
## 25          Mississippi  MS
## 26             Missouri  MO
## 27              Montana  MT
## 28             Nebraska  NE
## 29               Nevada  NV
## 30        New Hampshire  NH
## 31           New Jersey  NJ
## 32           New Mexico  NM
## 33             New York  NY
## 34       North Carolina  NC
## 35         North Dakota  ND
## 36                 Ohio  OH
## 37             Oklahoma  OK
## 38               Oregon  OR
## 39         Pennsylvania  PA
## 40         Rhode Island  RI
## 41       South Carolina  SC
## 42         South Dakota  SD
## 43            Tennessee  TN
## 44                Texas  TX
## 45                 Utah  UT
## 46              Vermont  VT
## 47             Virginia  VA
## 48           Washington  WA
## 49        West Virginia  WV
## 50            Wisconsin  WI
## 51              Wyoming  WY
```

4. The `dplyr` function `filter` is used to choose specific rows of the data frame to keep. Unlike `select` which is for columns, `filter` is for rows.

For example you can show just the New York row like this:

```
filter(murders, state == "New York")
```

You can use other logical vectors to filter rows.

```
# Add the necessary columns
murders <- mutate(murders, rate = total/population * 100000, rank = rank(-rate))

# Filter to show the top 5 states with the highest murder rates
filter(murders, rank <= 5)
```

```
##                  state abb        region population total  rate rank
## 1 District of Columbia  DC         South     601723    99 16.45    1
## 2            Louisiana  LA         South    4533372   351  7.74    2
## 3             Maryland  MD         South    5773552   293  5.07    4
## 4             Missouri  MO North Central    5988927   321  5.36    3
## 5       South Carolina  SC         South    4625364   207  4.48    5
```

5. We can remove rows using the `!=` operator.

For example to remove Florida we would do this:

```
no_florida <- filter(murders, state != "Florida")
```

```
# Use filter to create a new data frame no_south
no_south <- filter(murders, region != "South")

# Use nrow() to calculate the number of rows
nrow(no_south)
```

```
## [1] 34
```

6. We can also use the `%in%` to filter with `dplyr`.

For example you can see the data from New York and Texas like this:

```
filter(murders, state %in% c("New York", "Texas"))
```

```
# Create a new data frame called murders_nw with only the states from the northeast and the west
murders_nw <- filter(murders, region %in% c("Northeast", "West"))

# Number of states (rows) in this category
nrow(murders_nw)
```

```
## [1] 22
```

7. Suppose you want to live in the Northeast or West **and** want the murder rate to be less than 1.

We want to see the data for the states satisfying these options. Note that you can use logical operators with `filter`:

```
filter(murders, population < 5000000 & region == "Northeast")
```

```
# add the rate column
murders <- mutate(murders, rate =  total / population * 100000, rank = rank(-rate))

# Create a table, call it my_states, that satisfies both the conditions
my_states <- filter(murders, rate < 1 & region %in% c("Northeast", "West"))

# Use select to show only the state name, the murder rate and the rank
select(my_states, state, rate, rank)
```

```
##           state  rate rank
## 1        Hawaii 0.515   49
## 2         Idaho 0.766   46
## 3         Maine 0.828   44
## 4 New Hampshire 0.380   50
## 5        Oregon 0.940   42
## 6          Utah 0.796   45
## 7       Vermont 0.320   51
## 8       Wyoming 0.887   43
```

8. The pipe %>% can be used to perform operations sequentially without having to define intermediate objects.

After redefining murder to include rate and rank.

```
library(dplyr)
murders <- mutate(murders, rate = total / population * 100000, rank = (-rate))
```

in the solution to the previous exercise we did the following:

```
# Created a table
my_states <- filter(murders, region %in% c("Northeast", "West") & rate < 1)

# Used select to show only the state name, the murder rate and the rank
select(my_states, state, rate, rank)
```

The pipe %>% permits us to perform both operation sequentially and without having to define an intermediate variable `my_states`

For example we could have mutated and selected in the same line like this:

```
mutate(murders, rate = total / population * 100000, rank = (-rate)) %>% select(state, rate, rank)
```

Note that `select` no longer has a data frame as the first argument. The first argument is assumed to be the result of the operation conducted right before the %>%

```
## Define the rate column
murders <- mutate(murders, rate =  total / population * 100000, rank = rank(-rate))

# show the result and only include the state, rate, and rank columns, all in one line
filter(murders, region %in% c("Northeast", "West") & rate < 1) %>% select(state, rate, rank)
```

```
##           state  rate rank
## 1        Hawaii 0.515   49
## 2         Idaho 0.766   46
## 3         Maine 0.828   44
## 4 New Hampshire 0.380   50
## 5        Oregon 0.940   42
## 6          Utah 0.796   45
## 7       Vermont 0.320   51
## 8       Wyoming 0.887   43
```

9. Now we will reset murders to the original table by using `data(murders)`.

```
# Loading the table
data(murders)

# Create new data frame called my_states (with specifications in the instructions)
my_states <- murders %>% mutate(rate =  total / population * 100000, rank = rank(-rate)) %>% filter(reg
```

Basic Plots

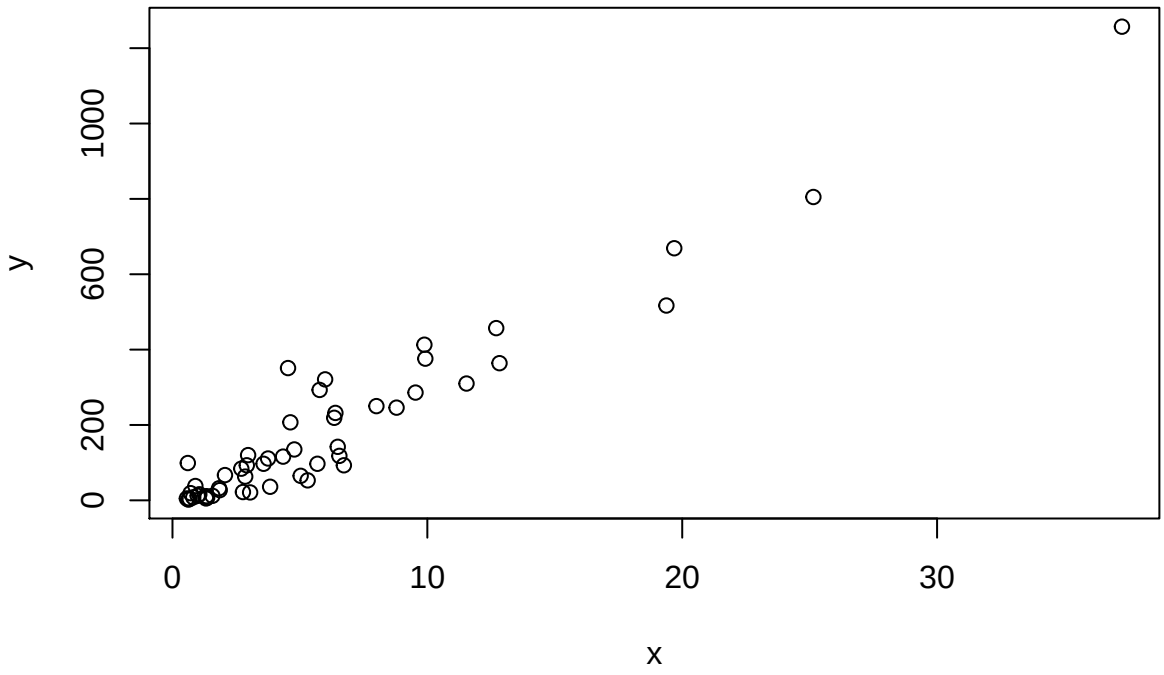
Here is a link to the textbook section on basic plots

Key Points

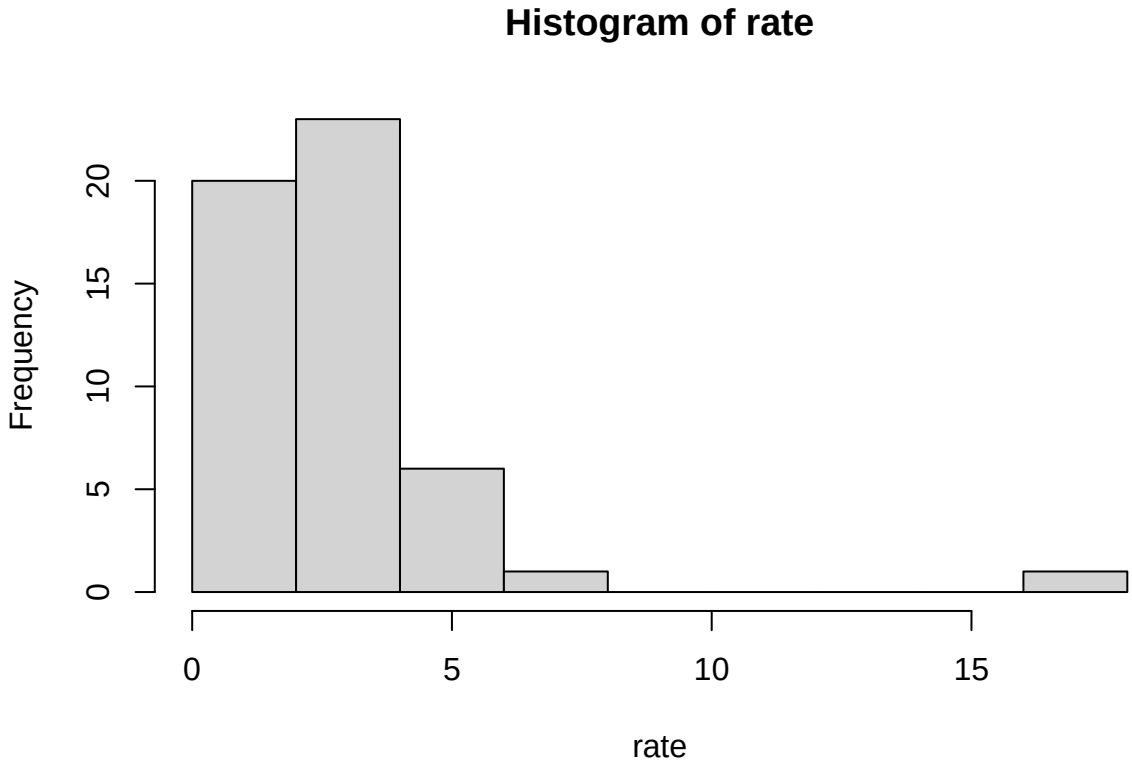
- We can create a simple scatterplot using the function `plot()`.
- Histograms are graphical summaries that give you a general overview of the types of values you have. In R, they can be produced using the `hist()` function.
- Boxplots provide a more compact summary of a distribution than a histogram and are more useful for comparing distributions. They can be produced using the "'boxplot() function.

Code

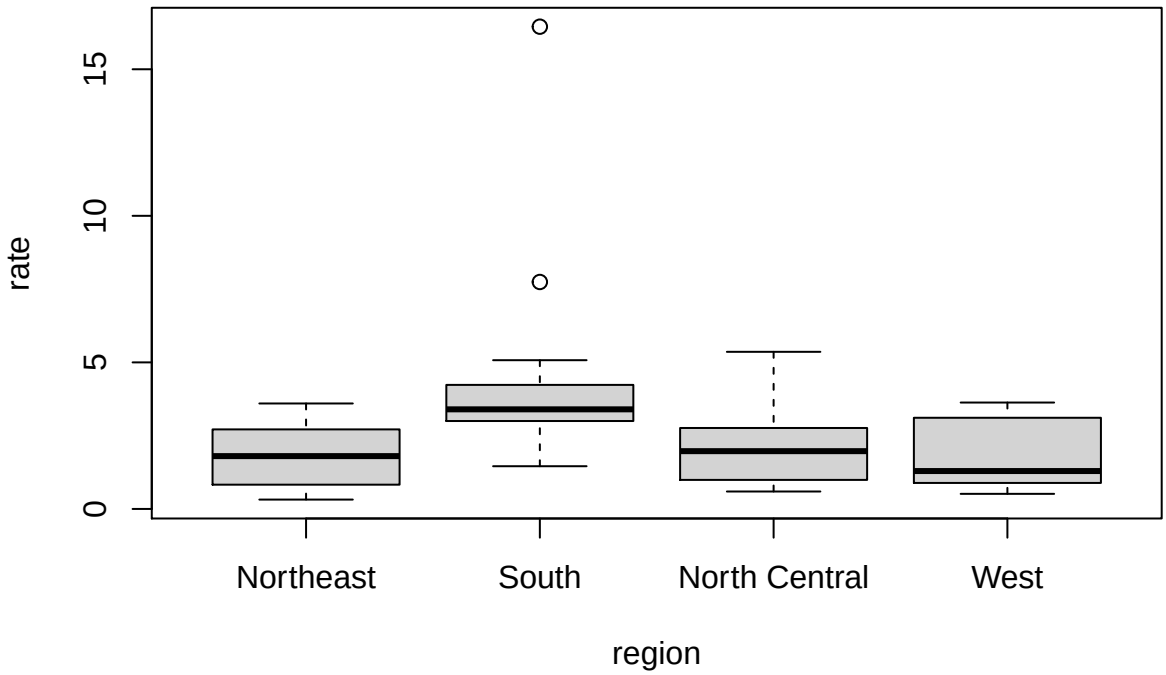
```
# a simple scatterplot of total murders versus population
x <- murders$population / 10^6
y <- murders$total
plot(x, y)
```




```
# a histogram of murder rates
hist(rate)
```




```
# boxplots of murder rates by region
boxplot(rate~region, data = murders)
```



Assessment - Basic Plots

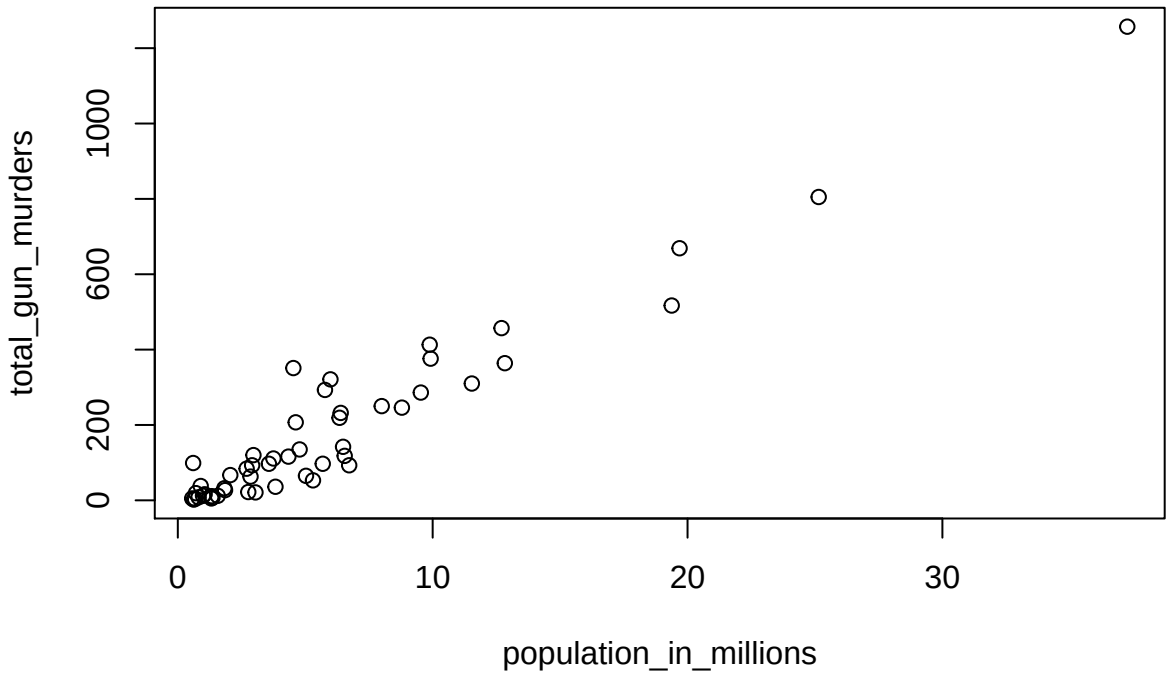
1. We made a plot of total murders versus population and noted a strong relationship: not surprisingly, states with larger populations had more murders.

You can run the code in the console to get the plot.

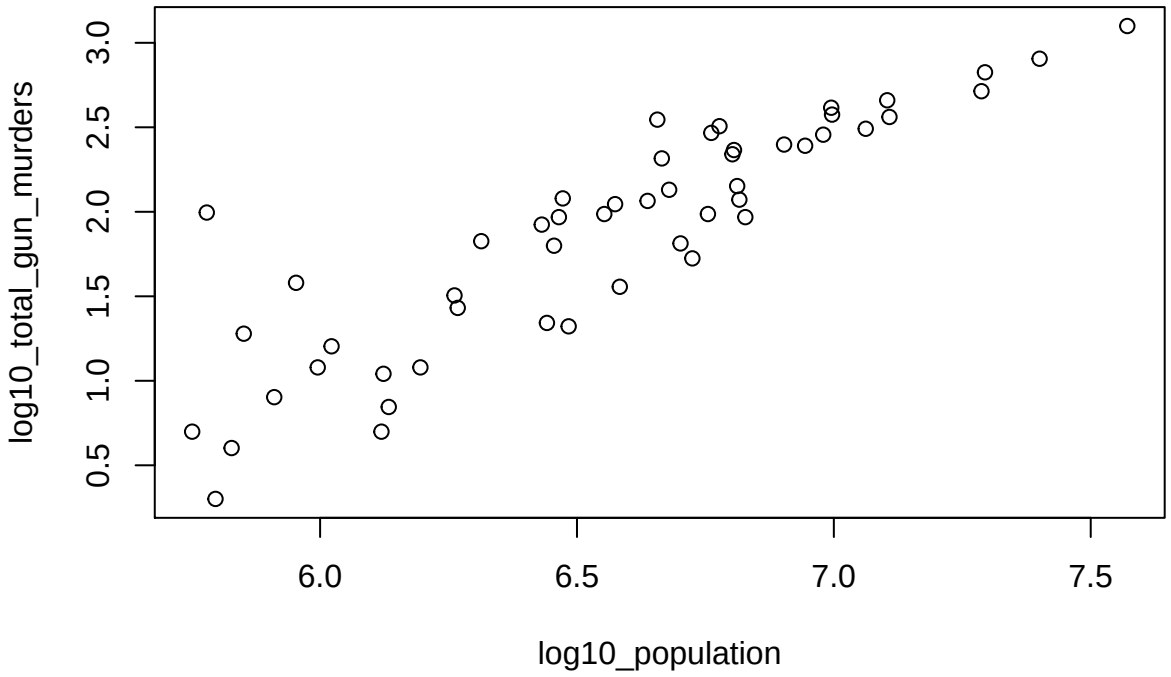
```
library(dslabs)
data(murders)

population_in_millions <- murders$population/10^6
total_gun_murders <- murders$total

plot(population_in_millions, total_gun_murders)
```

Note that many states have populations below 5 million and are bunched up in the plot. We may gain further insights from making this plot in the log scale.

```
population_in_millions <- murders$population/10^6
total_gun_murders <- murders$total

plot(population_in_millions, total_gun_murders)
```

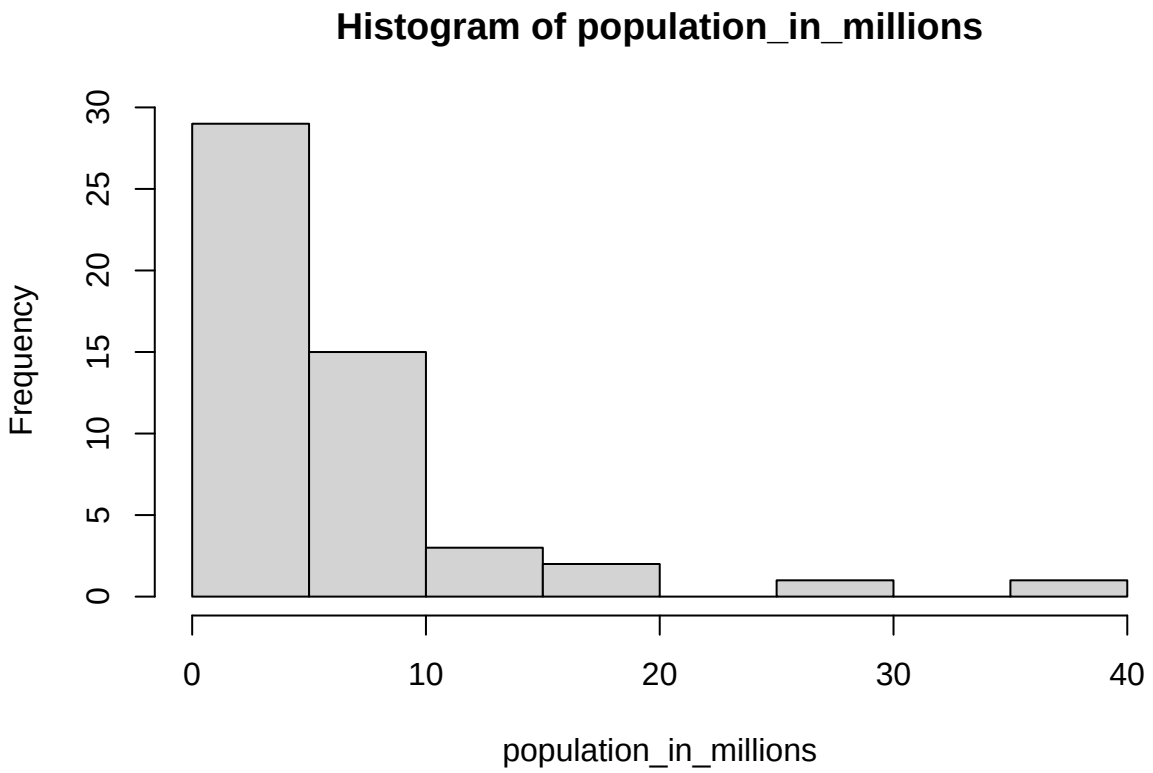



```
# Transform population using the log10 transformation and save to object log10_population
log10_population <- log10(murders$population)

# Transform total gun murders using log10 transformation and save to object log10_total_gun_murders
log10_total_gun_murders <- log10(total_gun_murders)

# Create a scatterplot with the log scale transformed population and murders
plot(log10_population, log10_total_gun_murders)
```



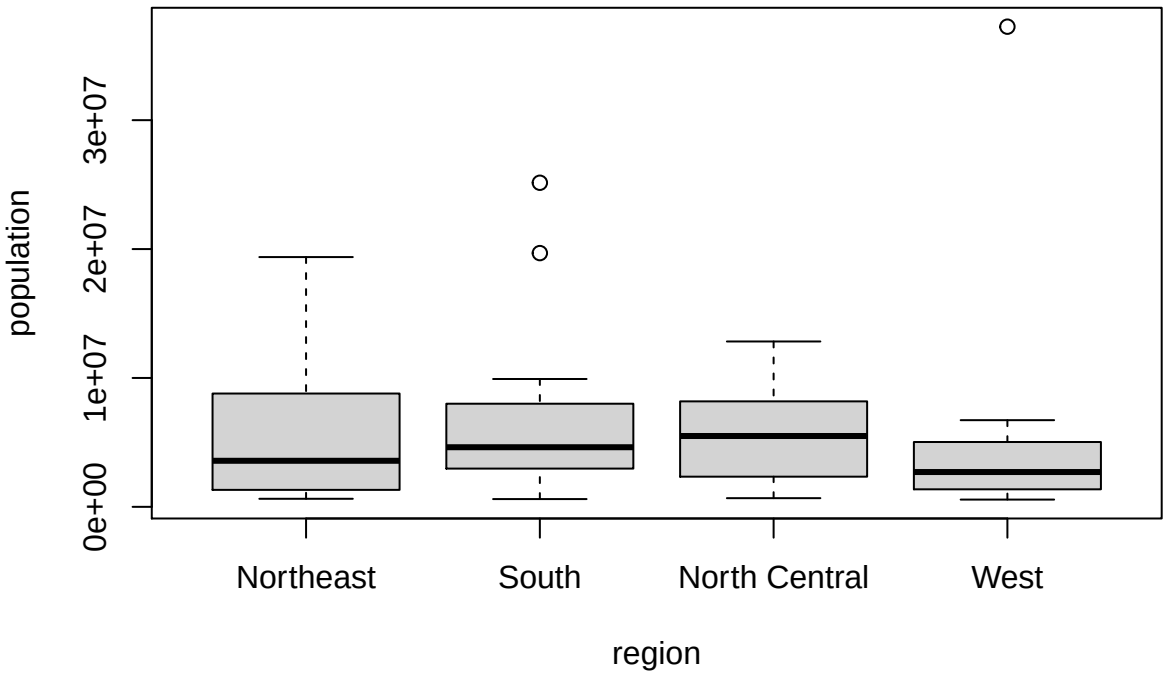
2. Now we are going to make a histogram.

```r
# Store the population in millions and save to population_in_millions
population_in_millions <- murders$population/10^6

# Create a histogram of this variable
hist(population_in_millions)
```



3. Now we are going to make boxplots. Boxplots are useful when we want a summary of several variables or several strata of the same variables. Making too many histograms can become too cumbersome.

```r
# Create a boxplot of state populations by region for the murders dataset
boxplot(population~region, data = murders)
```



Section 3 Assessment

```
data(heights)
options(digits = 3)    # report 3 significant digits for all answers
```

1. First, determine the average height in this dataset. Then create a logical vector `ind` with the indices for those individuals who are above average height.

How many individuals in the dataset are above average height?

```
ind <- heights$height > mean(heights$height)
sum(ind)
```

```
## [1] 532
```

2. How many individuals in the dataset are above average height and are female?

```
sum(ind & heights$sex=="Female")
```

```
## [1] 31
```

3. If you use `mean` on a logical (TRUE/FALSE) vector, it returns the proportion of observations that are TRUE.

What proportion of individuals in the dataset are female?

```
mean(heights$sex == "Female")
```

```
## [1] 0.227
```

4. This question takes you through three steps to determine the sex of the individual with the minimum height.

Determine the minimum height in the `heights` dataset.

```
min(heights$height)
```

```
## [1] 50
```

Use the `match()` function to determine the index of the individual with the minimum height.

```
match(50,heights$height)
```

```
## [1] 1032
```

Subset the `sex` column of the dataset by the index above to determine the individual's sex. `Male`

```
heights$sex[1032]
```

```
## [1] Male
## Levels: Female Male
```

5. This question takes you through three steps to determine how many of the integer height values between the minimum and maximum heights are not actual heights of individuals in the heights dataset.

Determine the maximum height.

```
max(heights$height)
```

```
## [1] 82.7
```

Which integer values are between the maximum and minimum heights? For example, if the minimum height is 10.2 and the maximum height is 20.8, your answer should be `x <- 11:20` to capture the integers in between those values. (If either the maximum or minimum height are integers, include those values too.)

Write code to create a vector x that includes the *integers* between the minimum and maximum heights.

```
x <- 50:82
```

How many of the integers in x are NOT heights in the dataset?

```
sum(!(x %in% heights$height))
```

```
## [1] 3
```

6. Using the `heights` dataset, create a new column of heights in centimeters named `ht_cm`. Recall that 1 inch = 2.54 centimeters. Save the resulting dataset as `heights2`.

What is the height in centimeters of the 18th individual (index 18)?

```
heights2 <- mutate(heights, ht_cm = height*2.54)

# Then we subset the new heights2 dataset:

heights2$ht_cm[18]
```

```
## [1] 163
```

What is the mean height in centimeters?

```
mean(heights2$ht_cm)
```

```
## [1] 174
```

Create a data frame `females` by filtering the `heights2` data to contain only female individuals.

How many females are in the heights2 dataset?

```
females <- filter(heights2, sex == "Female")
nrow(females)
```

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

What is the mean height of the females in centimeters?

```
mean(females$ht_cm)
```

```
## [1] 165
```

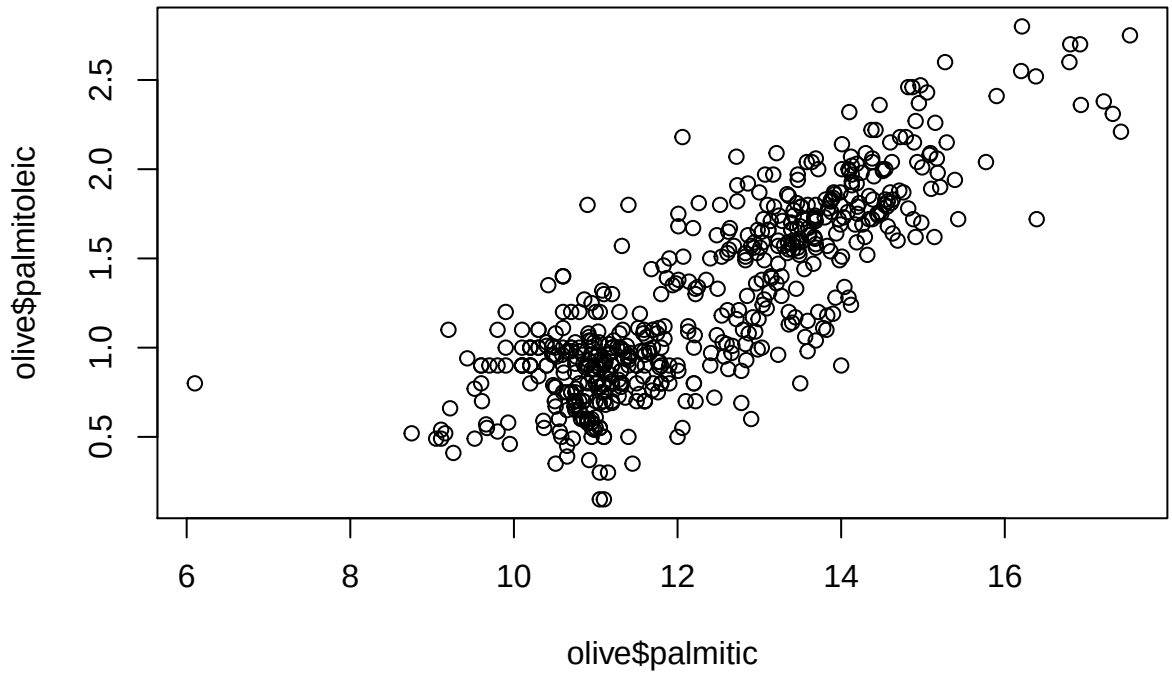
8. The `olive` dataset in **dslabs** contains composition in percentage of eight fatty acids found in the lipid fraction of 572 Italian olive oils:

```
data(olive)
head(olive)
```

```
##           region         area palmitic palmitoleic stearic oleic linoleic
## 1 Southern Italy North-Apulia    10.75        0.75    2.26  78.2     6.72
## 2 Southern Italy North-Apulia    10.88        0.73    2.24  77.1     7.81
## 3 Southern Italy North-Apulia     9.11        0.54    2.46  81.1     5.49
## 4 Southern Italy North-Apulia     9.66        0.57    2.40  79.5     6.19
## 5 Southern Italy North-Apulia    10.51        0.67    2.59  77.7     6.72
## 6 Southern Italy North-Apulia     9.11        0.49    2.68  79.2     6.78
##   linolenic arachidic eicosenoic
## 1      0.36      0.60       0.29
## 2      0.31      0.61       0.29
## 3      0.31      0.63       0.29
## 4      0.50      0.78       0.35
## 5      0.50      0.80       0.46
## 6      0.51      0.70       0.44
```

Plot the percent palmitic acid versus palmitoleic acid in a scatterplot. What relationship do you see?

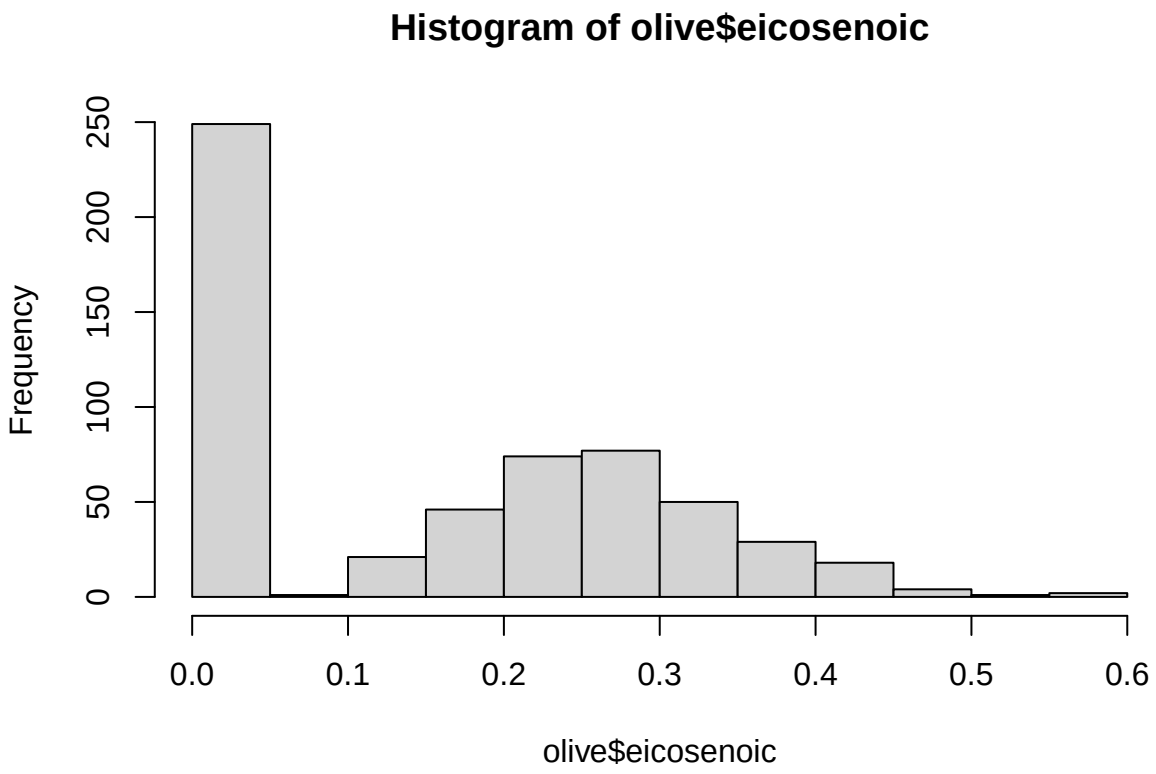
```
plot(olive$palmitic, olive$palmitoleic)
```



- ☐ A. There is no relationship between palmitic and palmitoleic.
- ☒ B. There is a positive linear relationship between palmitic and palmitoleic.
- ☐ C. There is a negative linear relationship between palmitic and palmitoleic.
- ☐ D. There is a positive exponential relationship between palmitic and palmitoleic.
- ☐ E. There is a negative exponential relationship between palmitic and palmitoleic.

9. Create a histogram of the percentage of eicosenoic acid in `olive`. Which of the following is true?

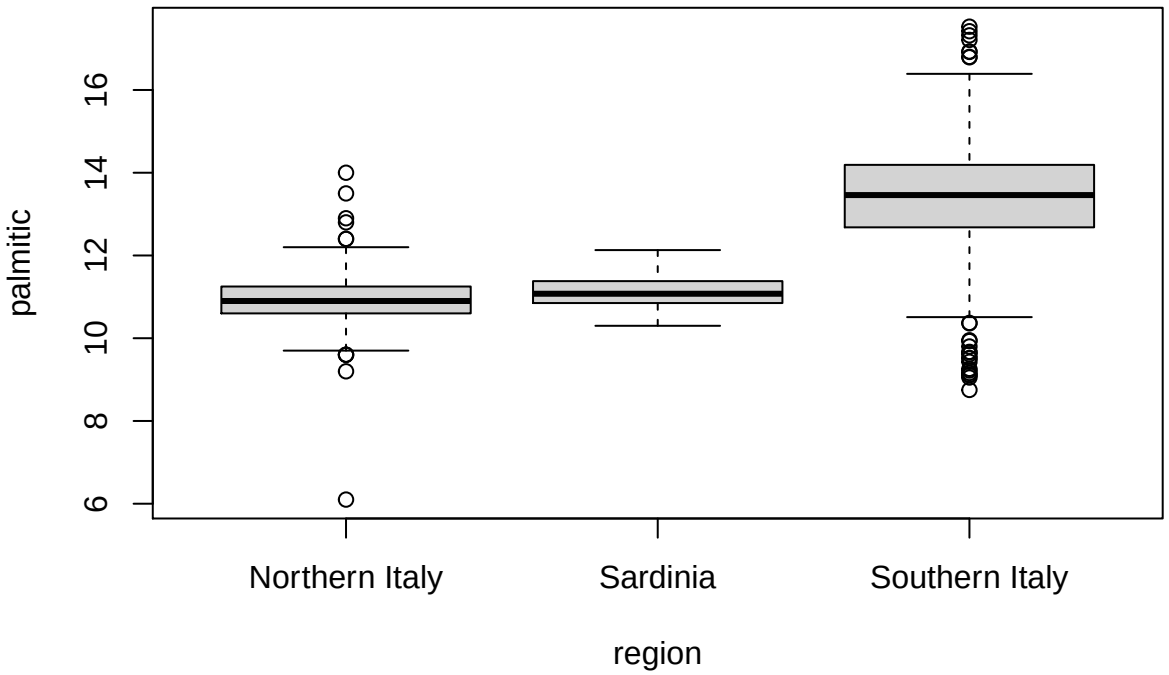
```
hist(olive$eicosenoic)
```



- ☒ A. The most common value of eicosenoic acid is below 0.05%.
- ☐ B. The most common value of eicosenoic acid is greater than 0.5%.
- ☐ C. The most common value of eicosenoic acid is around 0.3%.
- ☐ D. There are equal numbers of olive oils with eicosenoic acid below 0.05% and greater than 0.5%.

10. Make a boxplot of palmitic acid percentage in `olive` with separate distributions for each region.

```
boxplot(palmitic ~ region, data = olive)
```



Which region has the highest median palmitic acid percentage? `Southern Italy`

Which region has the most variable palmitic acid percentage? `Southern Italy`

Section 4 Overview

Section 4 introduces you to general programming features like 'if-else', and 'for loop' commands so that you can write your own functions to perform various operations on datasets.

In Section 4.1, you will:

- Understand some of the programming capabilities of R.

In Section 4.2, you will:

- Use basic conditional expressions to perform different operations.
- Check if any or all elements of a logical vector are TRUE.

In Section 4.3, you will:

- Define and call functions to perform various operations.
- Pass arguments to functions, and return variables/objects from functions.

In Section 4.4, you will:

- Use 'for' loop to perform repeated operations.
- Articulate in-built functions of R that you could try for yourself.

Programming Basics - Introduction to Programming in R

The textbook for this section is available here

Basic Conditionals

The textbook for this section is available here

Key Points

- The most common conditional expression in programming is an if-else statement, which has the form "if [condition], perform [expression], else perform [alternative expression]".
- The `ifelse()` function works similarly to an if-else statement, but it is particularly useful since it works on vectors by examining each element of the vector and returning a corresponding answer accordingly.
- The `any()` function takes a vector of logicals and returns true if any of the entries are true.
- The `all()` function takes a vector of logicals and returns true if all of the entries are true.

Code

```
# an example showing the general structure of an if-else statement
a <- 0
if(a!=0){
  print(1/a)
} else{
  print("No reciprocal for 0.")
}
```

```
## [1] "No reciprocal for 0."
```

```
# an example that tells us which states, if any, have a murder rate less than 0.5
library(dslabs)
data(murders)
murder_rate <- murders$total / murders$population*100000
ind <- which.min(murder_rate)
if(murder_rate[ind] < 0.5){
  print(murders$state[ind])
} else{
  print("No state has murder rate that low")
}
```

```
## [1] "Vermont"
```

```
# changing the condition to < 0.25 changes the result
if(murder_rate[ind] < 0.25){
  print(murders$state[ind])
} else{
  print("No state has a murder rate that low.")
}
```

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

```
# the ifelse() function works similarly to an if-else conditional
a <- 0
ifelse(a > 0, 1/a, NA)
```

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

```r
# the ifelse() function is particularly useful on vectors
a <- c(0,1,2,-4,5)
result <- ifelse(a > 0, 1/a, NA)

# the ifelse() function is also helpful for replacing missing values
data(na_example)
no_nas <- ifelse(is.na(na_example), 0, na_example)
sum(is.na(no_nas))
```

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

```r
# the any() and all() functions evaluate logical vectors
z <- c(TRUE, TRUE, FALSE)
any(z)
```

```
## [1] TRUE
```

```r
all(z)
```

```
## [1] FALSE
```

Functions

The textbook for this section is available here

Key points

- The R function, called `function()` tells R you are about to define a new function.
- Functions are objects, so must be assigned a variable name with the arrow operator.
- The general way to define functions is: (1) decide the function name, which will be an object, (2) type `function()` with your function's arguments in parentheses, (3) write all the operations inside brackets.
- Variables defined inside a function are not saved in the workspace.

Code

```r
# example of defining a function to compute the average of a vector x
avg <- function(x){
  s <- sum(x)
  n <- length(x)
  s/n
}

# we see that the above function and the pre-built R mean() function are identical
x <- 1:100
identical(mean(x), avg(x))
```

```
## [1] TRUE
```

```r
# variables inside a function are not defined in the workspace
s <- 3
avg(1:10)
```

```
## [1] 5.5
```

```r
s
```

```
## [1] 3
```

```r
# the general form of a function
my_function <- function(VARIABLE_NAME){
  perform operations on VARIABLE_NAME and calculate VALUE
  VALUE
}
```

```r
# functions can have multiple arguments as well as default values
avg <- function(x, arithmetic = TRUE){
  n <- length(x)
  ifelse(arithmetic, sum(x)/n, prod(x)^(1/n))
}
```

For Loops

The textbook for this section is available here

Key points

- For-loops perform the same task over and over while changing the variable. They let us define the range that our variable takes, and then changes the value with each loop and evaluates the expression every time inside the loop.
- The general form of a for-loop is: "For i in [some range], do operations". This i changes across the range of values and the operations assume i is a value you're interested in computing on.
- At the end of the loop, the value of i is the last value of the range.

Code

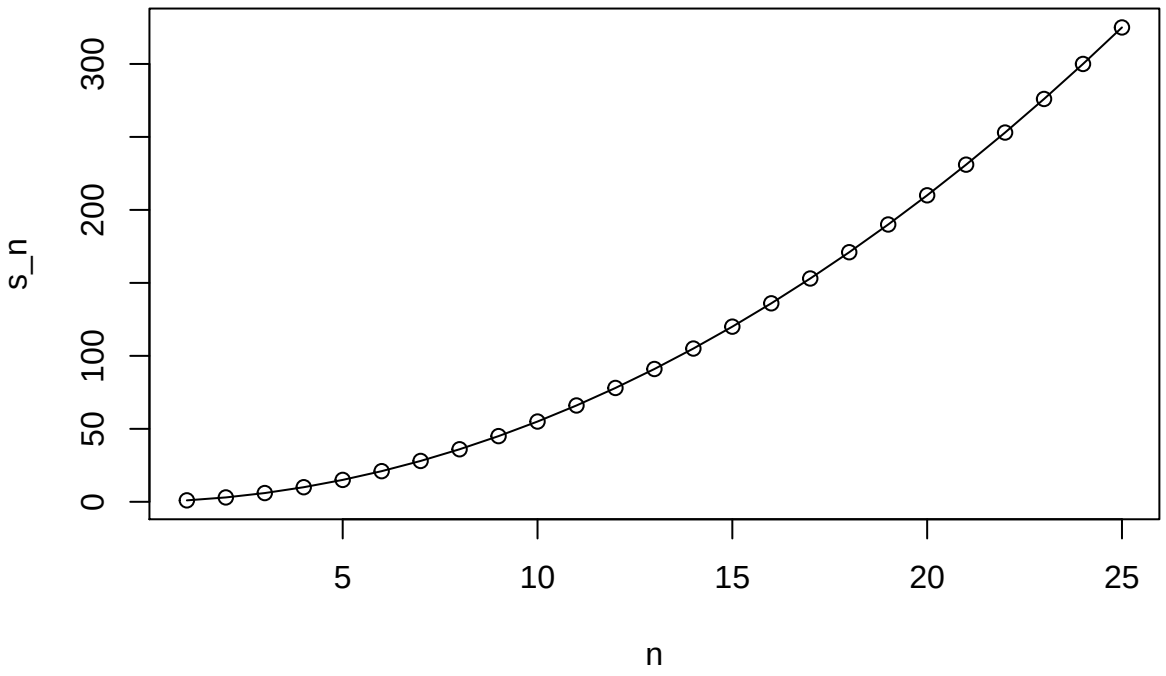
```r
# creating a function that computes the sum of integers 1 through n
compute_s_n <- function(n){
  x <- 1:n
  sum(x)
}

# a very simple for-loop
for(i in 1:5){
  print(i)
}
```

```
## [1] 1
## [1] 2
## [1] 3
## [1] 4
## [1] 5
```

```r
# a for-loop for our summation
m <- 25
s_n <- vector(length = m) # create an empty vector
for(n in 1:m){
  s_n[n] <- compute_s_n(n)
}

# creating a plot for our summation function
n <- 1:m
plot(n, s_n)

# a table of values comparing our function to the summation formula
head(data.frame(s_n = s_n, formula = n*(n+1)/2))
```

```
##   s_n formula
## 1   1       1
## 2   3       3
## 3   6       6
## 4  10      10
## 5  15      15
## 6  21      21
```

```r
# overlaying our function with the summation formula
plot(n, s_n)
lines(n, n*(n+1)/2)
```



Assessment - Programming Basics

1. What will this conditional expression return?

```r
x <- c(1,2,-3,4)
if(all(x>0)){
print("All Postives")
} else{
print("Not all positives")
}
```

```
## [1] "Not all positives"
```

- ☐ A. All Positives
- ☒ B. Not All Positives
- ☐ C. N/A
- ☐ D. None of the above

2. Which of the following expressions is always `FALSE` when at least one entry of a logical vector x is 'TRUE?

- ☐ A. all(x)
- ☐ B. any(x)
- ☐ C. any(!x)
- ☒ D. all(!x)

3. The function '`nchar` tells you how many characters long a character vector is.

For example:

```r
char_len <- nchar(murders$state)
head(char_len)
```

The function `ifelse` is useful because you convert a vector of logicals into something else. For example, some datasets use the number -999 to denote NA. A bad practice! You can convert the -999 in a vector to NA using the following `ifelse` call:

```r
x <- c(2, 3, -999, 1, 4, 5, -999, 3, 2, 9)
ifelse(x == -999, NA, x)
```

If the entry is -999 it returns NA, otherwise it returns the entry.

```r
# Assign the state abbreviation when the state name is longer than 8 characters
char_len <- nchar(murders$state)
new_names <- ifelse(char_len > 8, murders$abb, murders$state)
```

4. You will encounter situations in which the function you need does not already exist. R permits you to write your own.

Let's practice one such situation, in which you first need to define the function to be used. The functions you define can have multiple arguments as well as default values.

To define functions we use `function`. For example the following function adds 1 to the number it receives as an argument:

```
{r, eval=FALSE, echo=TRUE my_func <- function(x){     y <- x + 1     y }
```

The last value in the function, in this case that stored in `y`, gets returned.

If you run the code above R does not show anything. This means you defined the function. You can test it out like this:

```
my_func(5)
```

```
# Create function called `sum_n`
sum_n <- function(n){
    x <- 1:n
    sum(x)
}

# Use the function to determine the sum of integers from 1 to 5000
sum_n(5000)
```

```
## [1] 12502500
```

5. We will make another function for this exercise. We will define a function `altman_plot` that takes two arguments `x` and `y` and plots the difference `y-x` in the y-axis against the sum `x+y` in the x-axis.

You can define functions with as many variables as you want. For example, here we need at least two, `x` and `y`. The following function plots log transformed values:

```
log_plot <- function(x, y){
    plot(log10(x), log10(y))
}
```

This function does not return anything. It just makes a plot.

```
# Create `altman_plot`
altman_plot <- function(x, y) {
  plot(x+y, y-x)
}
```

6. Lexical scoping is a convention used by many languages that determine when an object is available by its name.

When you run the code below you will see which `x` is available at different points in the code.

```
x <- 8
my_func <- function(y){
    x <- 9
    print(x)
    y + x
}
my_func(x)
print(x)
```

Note that when we define `x` as 9, this is inside the function, but it is 8 after you run the function. The `x` changed inside the function but not outside.

```r
# Run this code
x <- 3
    my_func <- function(y){
    x <- 5
    y+5
}

# Print the value of x
x <- 3
my_func <- function(y){
    x <- 5
    y
    print(x)
}
my_func(x)
```

```
## [1] 5
```

```r
print(x)
```

```
## [1] 3
```

7. In the next exercise we are going to write a for-loop. In that for-loop we are going to call a function. We define that function here.

```r
# Here is an example of a function that adds numbers from 1 to n
example_func <- function(n){
    x <- 1:n
    sum(x)
}

# Here is the sum of the first 100 numbers
example_func(100)
```

```
## [1] 5050
```

```r
# Write a function compute_s_n with argument n that for any given n computes the sum of 1 + 2^2 + ...+ 
compute_s_n <- function(n){
    x <- 1:n
    sum(x^2)
}

# Report the value of the sum when n=10
compute_s_n(10)
```

```
## [1] 385
```

8. Now we are going to compute the sum of the squares for several values of n. We will use a for-loop for this.

Here is an example of a for-loop:

```
results <- vector("numeric", 10)
n <- 10
for(i in 1:n){
    x <- 1:i
    results[i] <- sum(x)
}
```

Note that we start with a call to `vector` which constructs an empty vector that we will fill while the loop runs.

```
# Define a function and store it in `compute_s_n`
compute_s_n <- function(n){
  x <- 1:n
  sum(x^2)
}

# Create a vector for storing results
s_n <- vector("numeric", 25)

# write a for-loop to store the results in s_n
for(n in 1:length(s_n)){
  s_n[n] <- compute_s_n(n)
}
```

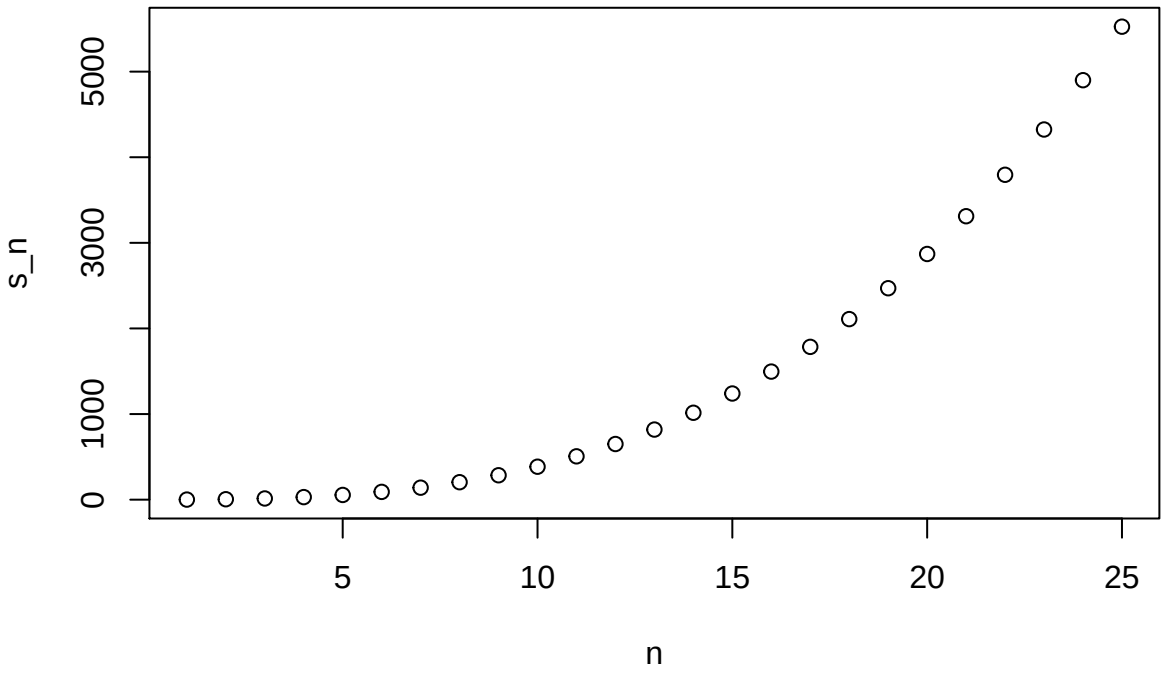
9. If we do the math, we can show that $S_n = 1^2 + 2^2 + 3^2 + \cdots + n^2 = n(n+1)(2n+1)/6$

We have already computed the values of S_n from 1 to 25 using a for loop.

If the formula is correct then a plot of S_n versus n should look cubic.

Let's make this plot.

```
# Define the function
compute_s_n <- function(n){
  x <- 1:n
  sum(x^2)
}

# Define the vector of n
n <- 1:25

# Define the vector to store data
s_n <- vector("numeric", 25)
for(i in n){
  s_n[i] <- compute_s_n(i)
}

#  Create the plot
plot(n,s_n)
```



10. Now let's actually check if we get the exact same answer.

```
# Define the function
compute_s_n <- function(n){
  x <- 1:n
  sum(x^2)
}

# Define the vector of n
n <- 1:25

# Define the vector to store data
s_n <- vector("numeric", 25)
for(i in n){
  s_n[i] <- compute_s_n(i)
}

# Check that s_n is identical to the formula given in the instructions.
identical(s_n,(n*(n+1)*(2*n+1))/6)
```

```
## [1] TRUE
```

Section 4 Assessment

1. Load the **heights** dataset from dslabs:

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

Write an `ifelse` statement that returns 1 if the sex is Female and 2 if the sex is Male.

What is the sum of the resulting vector?

```
sum(ifelse(heights$sex == "Female", 1, 2))
```

```
## [1] 1862
```

2. Write an `ifelse` statement that takes the height column and returns the height if it is greater than 72 inches and returns 0 otherwise.

What is the mean of the resulting vector?

```
mean(ifelse(heights$height > 72, heights$height, 0))
```

```
## [1] 9.65
```

3. Write a function `inches_to_ft` that takes a number of inches x and returns the number of feet. One foot equals 12 inches.

What is `inches_to_ft(144)`?

```
inches_to_ft <- function(x){x/12}
inches_to_ft(144)
```

```
## [1] 12
```

How many individuals in the heights dataset have a height less than 5 feet?

```
sum(inches_to_ft(heights$height) < 5)
```

```
## [1] 20
```

4. Which of the following are TRUE?

Select ALL that apply.

- ☒ A. any(TRUE, TRUE, TRUE)
- ☒ B. any(TRUE, TRUE, FALSE)
- ☒ C. any(TRUE, FALSE, FALSE)
- ☐ D. any(FALSE, FALSE, FALSE)
- ☒ E. all(TRUE, TRUE, TRUE)
- ☐ F. all(TRUE, TRUE, FALSE)
- ☐ G. all(TRUE, FALSE, FALSE)
- ☐ H. all(FALSE, FALSE, FALSE)

5. Given an integer x, the factorial of x is called x! and is the product of all integers up to and including x. The `factorial()` function computes factorials in R. For example, `factorial(4)` returns $4! = 4 \times 3 \times 2 \times 1 = 24$.

Complete the code below to generate a vector of length m where the first entry is 1!, the second entry is 2!, and so on up to m!.

```r
# define a vector of length m
m <- 10
f_n <- vector(length = m)

# make a vector of factorials
for(n in 1:m){
f_n[n] <- factorial(n)
}

# inspect f_n
f_n
```

```
##  [1]       1       2       6      24     120     720    5040   40320  362880
## [10] 3628800
```

- ☐ A. function(n)
- ☐ B. if(n < m)
- ☒ C. for(n in 1:m)
- ☐ D. function(m,n)
- ☐ E. if(m < n)
- ☐ F. for(m in 1:n)