Chester Ismay and Albert Y. Kim

A MODERN DIVE into Data with R

Contents

1

Prerequisites

This book was written using the **bookdown** R package from Yihui Xie. In order to follow along and run the code in this book on your own, you'll need to have access to R and RStudio. You can find more information on both of these with a simple Google search for "R" and for "RStudio." An introduction to using R, RStudio, and R Markdown is also available in a free book here (Ismay, 2016). It is recommended that you refer back to this book frequently as it has GIF screen recordings that you can follow along with as you learn.

We will keep a running list of R packages you will need to have installed to complete the analysis as well here in the `needed_pkgs` character vector. You can check if you have all of the needed packages installed by running all of the lines below. The last lines including the `if` will install them as needed (i.e., download their needed files from the internet to your hard drive).

You can run the `library` function on them to load them into your current analysis. Prior to each analysis where a package is needed, you will see the corresponding `library` function in the text. Make sure to check the top of the chapter to see if a package was loaded there.

```
needed_pkgs <- c("nycflights13", "dplyr", "ggplot2", "knitr",
  "ggplot2movies", "dygraphs", "rmarkdown", "mosaic", "tibble")

new.pkgs <- needed_pkgs[!(needed_pkgs %in% installed.packages())]

if(length(new.pkgs)) {
  install.packages(new.pkgs, repos = "http://cran.rstudio.com")
}
```

Book was last updated:

```
## [1] "By cismay on Friday, December 02, 2016 17:01:55 PST"
```

Colophon

The source of the book is available here and was built with versions of R packages (and their dependent packages) given below. This may not be of importance for initial readers of this

book, but the hope is you can reproduce a duplicate of this book by installing these versions of the packages.

package	*	version	date	source
assertthat		0.1	2013-12-06	CRAN (R 3.3.0)
backports		1.0.4	2016-10-24	CRAN (R 3.3.0)
base64enc		0.1-3	2015-07-28	CRAN (R 3.3.0)
BH		1.62.0-1	2016-11-19	CRAN (R 3.3.2)
bitops		1.0-6	2013-08-17	CRAN (R 3.3.0)
caTools		1.17.1	2014-09-10	CRAN (R 3.3.0)
colorspace		1.3-1	2016-11-18	CRAN (R 3.3.2)
curl		2.3	2016-11-24	CRAN (R 3.3.2)
DBI		0.5-1	2016-09-10	CRAN (R 3.3.0)
dichromat		2.0-0	2013-01-24	CRAN (R 3.3.0)
digest		0.6.10	2016-08-02	CRAN (R 3.3.0)
dplyr		0.5.0	2016-06-24	CRAN (R 3.3.0)
dygraphs		1.1.1.3	2016-11-09	CRAN (R 3.3.2)
evaluate		0.10	2016-10-11	CRAN (R 3.3.0)
ggdendro		0.1-20	2016-04-27	CRAN (R 3.3.0)
ggplot2		2.2.0.9000	2016-11-29	Github (tidyverse/ggplot2@f6f9f9d)
ggplot2movies		0.0.1	2015-08-25	CRAN (R 3.3.0)
gridExtra		2.2.1	2016-02-29	CRAN (R 3.3.0)
gtable		0.2.0	2016-02-26	CRAN (R 3.3.0)
highr		0.6	2016-05-09	CRAN (R 3.3.0)
hms		0.3	2016-11-22	CRAN (R 3.3.2)
htmltools		0.3.5	2016-03-21	CRAN (R 3.3.0)
htmlwidgets		0.8	2016-11-09	CRAN (R 3.3.2)
jsonlite		1.1	2016-09-14	CRAN (R 3.3.0)
knitr		1.15.1	2016-11-22	CRAN (R 3.3.2)
labeling		0.3	2014-08-23	CRAN (R 3.3.0)
lattice		0.20-34	2016-09-06	CRAN (R 3.3.2)
latticeExtra		0.6-28	2016-02-09	CRAN (R 3.3.0)
lazyeval		0.2.0	2016-06-12	CRAN (R 3.3.0)
magrittr		1.5	2014-11-22	CRAN (R 3.3.0)
markdown		0.7.7	2015-04-22	CRAN (R 3.3.0)
MASS		7.3-45	2016-04-21	CRAN (R 3.3.2)
Matrix		1.2-7.1	2016-09-01	CRAN (R 3.3.2)
mime		0.5	2016-07-07	CRAN (R 3.3.0)
mosaic		0.14.4	2016-07-29	CRAN (R 3.3.0)
mosaicData		0.14.0	2016-06-17	CRAN (R 3.3.0)
munsell		0.4.3	2016-02-13	CRAN (R 3.3.0)

nycflights13	0.2.0	2016-04-30	CRAN (R 3.3.0)
plyr	1.8.4	2016-06-08	CRAN (R 3.3.0)
R6	2.2.0	2016-10-05	CRAN (R 3.3.0)
RColorBrewer	1.1-2	2014-12-07	CRAN (R 3.3.0)
Rcpp	0.12.8	2016-11-17	CRAN (R 3.3.2)
readr	1.0.0	2016-08-03	CRAN (R 3.3.0)
reshape2	1.4.2	2016-10-22	CRAN (R 3.3.0)
rmarkdown	1.2	2016-11-21	CRAN (R 3.3.2)
rprojroot	1.1	2016-10-29	CRAN (R 3.3.0)
scales	0.4.1	2016-11-09	CRAN (R 3.3.2)
stringi	1.1.2	2016-10-01	CRAN (R 3.3.0)
stringr	1.1.0	2016-08-19	CRAN (R 3.3.0)
tibble	1.2	2016-08-26	CRAN (R 3.3.0)
tidyr	0.6.0	2016-08-12	CRAN (R 3.3.0)
xts	0.9-7	2014-01-02	CRAN (R 3.3.0)
yaml	2.1.14	2016-11-12	CRAN (R 3.3.2)
zoo	1.7-13	2016-05-03	CRAN (R 3.3.0)

2

Introduction

2.1 Preamble

This book is inspired by three books:

- "Mathematical Statistics with Resampling and R" (Chihara and Hesterberg, 2011),
- "Intro Stat with Randomization and Simulation" (Diez et al., 2014), and
- "R for Data Science" (Grolemund and Wickham, 2016).

The first book, while designed for upper-level undergraduates and graduate students, provides an excellent resource on how to use resampling to build statistical concepts like normal distributions using computers instead of focusing on memorization of formulas. The last two books also provide a path towards free alternatives to the traditionally expensive introductory statistics textbook. When looking over the vast number of introductory statistics textbooks we found that there wasn't one that incorporated many of the new R packages directly into the text. Additionally, there wasn't an open-source, free textbook available that showed new learners all of the following

1. how to use R to explore and visualize data
2. how to use randomization and simulation to build inferential ideas
3. how to effectively create stories using these ideas to convey information to a lay audience.

We will introduce sometimes difficult statistics concepts through the medium of data visualization. In today's world, we are bombarded with graphics that attempt to convey ideas. We will explore what makes a good graphic and what the standard ways are to convey relationships with data. You'll also see the use of visualization to introduce concepts like mean, median, standard deviation, distributions, etc. In general, we'll use visualization as a way of building almost all of the ideas in this book.

Additionally, this book will focus on the triad of computational thinking, data thinking, and inferential thinking. We'll see throughout the book how these three modes of thinking can build effective ways to work with, describe, and convey statistical knowledge. In order to do so, you'll see the importance of literate programming to develop literate data science. In other

words, you'll see how to write code and descriptions that are useful not just for a computer to execute but also for readers to understand exactly what a statistical analysis is doing and how it works. Hal Abelson coined the phrase that we will follow throughout this book:

> "Programs must be written for people to read, and only incidentally for machines to execute."

2.2 Two driving data sources

Instead of hopping from one data set to the next, we've decided to focus throughout the book on two different data sources: flights leaving New York City in 2013 and IMDB (Internet Movie DataBase) ratings on movies. By focusing on just two large data sources, it is our hope that you'll be able to see how each of the chapters is interconnected. You'll see how the data being tidy leads into data visualization and manipulation and how those concepts tie into inference.

2.3 Data/science pipeline

You may think of statistics as just being a bunch of numbers. We commonly hear the phrase "statistician" when listening to broadcasts of sporting events. Statistics (in particular, data analysis), in addition to describing numbers like with baseball batting averages, plays a vital role in all of the sciences. You'll commonly hear the phrase "statistically significant" thrown around in the media. You'll see things that say "Science now shows that chocolate is good for you." Underpinning these claims is data analysis. By the end of this book, you'll be able to better understand whether these claims should be trusted or whether we should be weary. Inside data analysis are many sub-fields that we will discuss throughout this book (not necessarily in this order):

- data collection
- data manipulation
- data visualization
- data modeling
- inference
- interpretation of results
- data storytelling

This can be summarized in a graphic that is commonly used by Hadley Wickham:

We will begin with a discussion on what is meant by tidy data and then dig into the gray **Understand** portion of the cycle and conclude by talking about interpretting and discussing the results of our models via **Communication**. These steps are vital to any statistical analysis. But why should you care about statistics? "Why did they make me take this class?"

There's a reason so many fields require a statistics course. Scientific knowledge grows through an understanding of statistical significance and data analysis. You needn't be intimidated by statistics. It's not the beast that it used to be and paired with computation you'll see how reproducible research in the sciences particularly increases scientific knowledge.

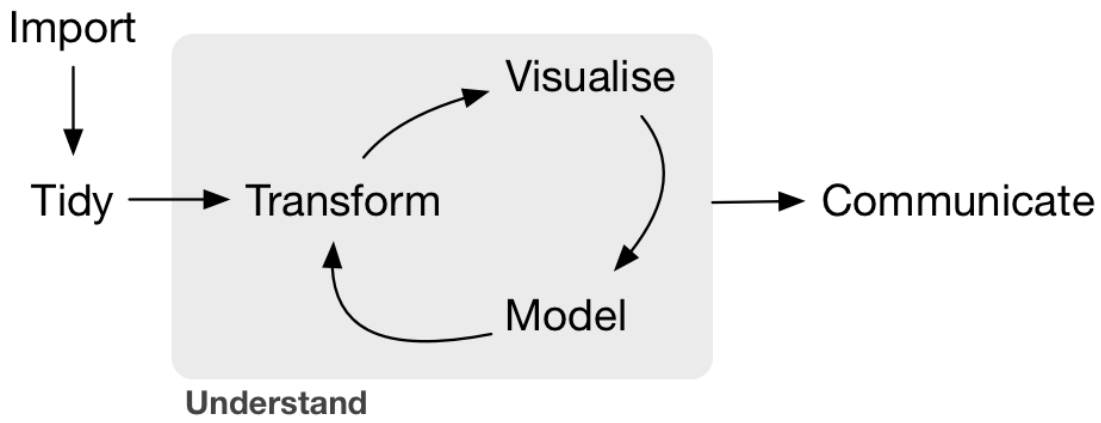


Figure 2.1: Hadley's workflow graphic

2.4 Reproducibility

> "The most important tool is the *mindset*, when starting, that the end product will be reproducible." – Keith Baggerly

Another large goal of this book is to help readers understand the importance of reproducible analyses. The hope is to get readers into the habit of making their analyses reproducible from the very beginning. This means we'll be trying to help you build new habits. This will take practice and be difficult at times. You'll see just why it is so important for you to keep track of your code and well-document it to help yourself later and any potential collaborators as well.

Copying and pasting is not the way that efficient and effective scientific research is conducted. It's much more important for time to be spent on data collection and data analysis and not on copying and pasting plots back and forth across a variety of programs.

In a traditional analyses if an error was made with the original data, we'd need to step through the entire process again: recreate the plots and copy and paste all of the new plots and our statistical analsis into your document. This is error prone and a frustrating use of time. We'll see how to use R Markdown to get away from this tedious activity so that we can spend more time doing science.

> "We are talking about *computational* reproducibility." - Yihui Xie

Reproducibility means a lot of things in terms of different scientific fields. Are experiments conducted in a way that another researcher could follow the steps and get similar results? In this book, we will focus on what is known as **computational reproducibility**. This refers to being able to pass all of one's data analysis and conclusions to someone else and have them get exactly the same results on their machine. This allows for time to be spent doing actual science and interpretting of results and assumptions instead of the more error prone way of starting from scratch or follow a list of steps that may be different from machine to machine.

2.5 Who is this book for?

This book is targetted at students taking a traditional intro stats class in a small college environment using RStudio and preferably RStudio Server. We assume no prerequisites: no calculus and no prior programming experience. This is intended to be a gentle and nice introduction to the practice of statistics in terms of how data scientists, statisticians, and other scientists analyze data and write stories about data. We have intentionally avoided the use of throwing formulas at you and instead have focused on developing statistical concepts via data visualization and statistical computing. We hope this is a more intuitive experience than the way statistics has traditionally been taught in the past (and how it is commonly perceived from the outside). We additionally hope that you see the value of reproducible research via R as you continue in your studies. We understand that there will initially be growing pains in learning to program but we are here to help you and you should know that there is a huge community of R users that are always happy to help newbies along.

Now let's get into learning about how to create good stories about and with data!

Part I

Data Exploration

3

Tidy Data

In this chapter, we'll discuss the importance of tidy data. You may think that this means just having your data in a spreadsheet, but you'll see that it is actually more specific than that. Data actually comes to us in a variety of formats from pictures to text and to just numbers. We'll focus on datasets that can be stored in a spreadsheet throughout this book as that is the most common way data is collected in the sciences.

Having tidy data will allow us to more easily create data visualizations as we will see in Chapter 4. It will also help us with manipulating data in Chapter 5 and in all subsequent chapters when we discuss statistical inference. You may not necessarily understand the importance for **tidy data** but it will become more and more apparent as we proceed through the book.

3.1 What is tidy data?

You have surely heard the word "tidy" in your life:

- "Tidy up your room!"
- "Please write your homework in a tidy way so that it is easier to grade and to provide feedback."
- Marie Kondo's best-selling book *The Life-Changing Magic of Tidying Up: The Japanese Art of Decluttering and Organizing*
- "I am not by any stretch of the imagination a tidy person, and the piles of unread books on the coffee table and by my bed have a plaintive, pleading quality to me - 'Read me, please!' " - Linda Grant

So what does it mean for your data to be **tidy**? Put simply: it means that your data is organized. But it's more than just that. It means that your data follows the same standard format making it easy for others to find elements of your data, to manipulate and transform your data, and for our purposes continuing with the common theme: it makes it easier to visualize your data and the relationships between different variables in your data.

We will follow Hadley Wickham's definition of **tidy data** here (Wickham, 2014):

> A dataset is a collection of values, usually either numbers (if quantitative) or strings (if qualita-

tive). Values are organised in two ways. Every value belongs to a variable and an observation. A variable contains all values that measure the same underlying attribute (like height, temperature, duration) across units. An observation contains all values measured on the same unit (like a person, or a day, or a race) across attributes.

Tidy data is a standard way of mapping the meaning of a dataset to its structure. A dataset is messy or tidy depending on how rows, columns and tables are matched up with observations, variables and types. In **tidy data**:

1. Each variable forms a column.
2. Each observation forms a row.
3. Each type of observational unit forms a table.

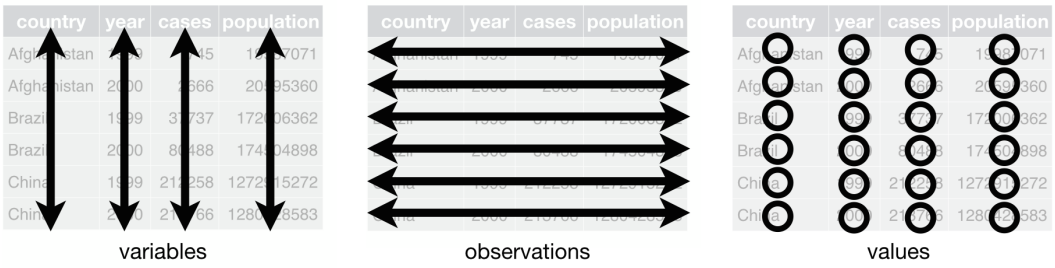


Figure 3.1: Tidy data graphic from http://r4ds.had.co.nz/tidy-data.html

Reading over this definition, you can begin to think about datasets that won't follow this nice format.

Learning check

(LC3.1) Give an example dataset that doesn't follow this format.

- What features of this dataset might make it difficult to visualize?
- How could the dataset be tweaked to make it **tidy**?

3.2 The `nycflights13` datasets

We likely have all flown on airplanes or know someone that has. Air travel has become an ever-present aspect of our daily lives. If you live in or are visiting a relatively large city and

you walk around that city's airport, you see gates showing flight information from many different airlines. And you will frequently see that some flights are delayed because of a variety of conditions. Are there ways that we can avoid having to deal with these flight delays?

We'd all like to arrive at our destinations on time whenever possible. (Unless you secretly love hanging out at airports. If you are one of these people, pretend for the moment that you are very much anticipating being at your final destination.) Hadley Wickham (herein just referred to as "Hadley") created multiple datasets containing information about departing flights from the New York City area in 2013 (Wickham, 2016). We will begin by loading in one of these datasets, the `flights` dataset, and getting an idea of its structure:

```
library(nycflights13)
data(flights)
```

The `library` function here loads the R package `nycflights13` into the current R environment in which you are working. The `data(flights)` loads in the `flights` dataset that is stored in the `nycflights13` package. Note that you'll get an error if you try to load this package in and it hasn't been downloaded and installed. You can ensure it is installed by running the code below:

```
if(!require(nycflights13))
  install.packages("nycflights13", repos = "http://cran.rstudio.org")
```

This code checks to see if `nycflights13` is installed and, if not, then goes to the specified repository of "`http://cran.rstudio.org`" and downloads the package from there and installs it. If it is already installed you can see it listed in the **Packages** tab in the bottom right portion of RStudio and the code will not install the package again since this is redundant and you won't need to do it over and over again.

This dataset and most others presented in this book will be in the `data.frame` format in R. Data frames are ways to look at collections of variables that are tightly coupled together. Frequently, the best way to get a feel for a data frame is to use the `View` function in RStudio. This command will be given throughout the book as a reminder, but the actual output will be hidden.

```
View(flights)
```

Learning check

(LC3.2) What does any *ONE* row in this `flights` dataset refer to?

- A. Data on an airline

- B. Data on a flight
- C. Data on an airport
- D. Data on multiple flights

By running `View(flights)`, we see the different **variables** listed in the columns and we see that there are different types of variables. Some of the variables like `distance`, `day`, and `arr_delay` are what we will call **quantitative** variables. These variables vary in a numerical way. Other variables here are **categorical**.

Note that if you look in the leftmost column of the `View(flights)` output, you will see a column of numbers. These are the row numbers of the dataset. If you glance across a row with the same number, say row 5, you can get an idea of what each row corresponds to. In other words, this will allow you to identify what object is being referred to in a given row. This is often called the **observational unit**. The **observational unit** in this example is an individual flight departing New York City in 2013.

Note: Frequently the first thing you should do when given a dataset is to

- identify the observation unit,
- specify the variables, and
- give the types of variables you are presented with.

```
str(flights)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    336776 obs. of  19 variables:
##  $ year          : int  2013 2013 2013 2013 2013 2013 2013 2013 2013 2013 ...
##  $ month         : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ day           : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ dep_time      : int  517 533 542 544 554 554 555 557 557 558 ...
##  $ sched_dep_time: int  515 529 540 545 600 558 600 600 600 600 ...
##  $ dep_delay     : num  2 4 2 -1 -6 -4 -5 -3 -3 -2 ...
##  $ arr_time      : int  830 850 923 1004 812 740 913 709 838 753 ...
##  $ sched_arr_time: int  819 830 850 1022 837 728 854 723 846 745 ...
##  $ arr_delay     : num  11 20 33 -18 -25 12 19 -14 -8 8 ...
##  $ carrier       : chr  "UA" "UA" "AA" "B6" ...
##  $ flight        : int  1545 1714 1141 725 461 1696 507 5708 79 301 ...
##  $ tailnum       : chr  "N14228" "N24211" "N619AA" "N804JB" ...
##  $ origin        : chr  "EWR" "LGA" "JFK" "JFK" ...
##  $ dest          : chr  "IAH" "IAH" "MIA" "BQN" ...
##  $ air_time      : num  227 227 160 183 116 150 158 53 140 138 ...
##  $ distance      : num  1400 1416 1089 1576 762 ...
##  $ hour          : num  5 5 5 5 6 5 6 6 6 6 ...
##  $ minute        : num  15 29 40 45 0 58 0 0 0 0 ...
##  $ time_hour     : POSIXct, format: "2013-01-01 05:00:00" ...
```

Learning check

(LC3.3) What are some examples in this dataset of **categorical** variables? What makes them different than **quantitative** variables?

(LC3.4) What does `int`, `num`, and `chr` mean in the output above?

(LC3.5) How many different columns are in this dataset?

(LC3.6) How many different rows are in this dataset?

Another way to view the properties of a dataset is to use the `str` function ("str" is short for "structure"). The `str` function is expecting an object for its argument. In this case, the object is a data frame named `flights`. You can use the `str` function on other objects and data frames using the syntax `str(object)` where `object` is the name of an object in R. This will give you the first few entries of each variable in a row after the variable. In addition, the type of the variable is given immediately after the `:` following each variable's name. Here, `int` and `num` refer to quantitative variables. In contrast, `chr` refers to categorical variables. One more type of variable is given here with the `time_hour` variable: **POSIXct**. As you may suspect, this variable corresponds to a specific date and time of day.

Another nice feature of R is the help system. You can get help in R by simply entering a question mark before the name of a function or an object and you will be presented with a page showing the documentation. Note that this output help file is omitted here but can be accessed here on page 3 of the PDF document.

```
?str
?flights
```

Another aspect of tidy data is a description of what each variable in the dataset represents. This helps others to understand what your variable names mean and what they correspond to. If we look at the output of `?flights`, we can see that a description of each variable by name is given.

An important feature to **ALWAYS** include with your data is the appropriate units of measurement. We'll see this further when we work with the `dep_delay` variable in Chapter 4. (It's in minutes, but you'd get some really strange interpretations if you thought it was in hours or seconds. UNITS MATTER!)

3.3 How is `flights` tidy?

We see that `flights` has a rectangular shape with each row corresponding to a different flight and each column corresponding to a characteristic of that flight. This matches exactly with how Hadley defined tidy data:

1. Each variable forms a column.
2. Each observation forms a row.

But what about the third property?

3. Each type of observational unit forms a table.

We identified earlier that the observational unit in the `flights` dataset is an individual flight. And we have shown that this dataset consists of 336,776 flights with 19 variables. In other words, some rows of this dataset don't refer to a measurement on an airline or on an airport. They specifically refer to characteristics/measurements on a given **flight** from New York City in 2013.

By contrast, also included in the `nycflights13` package are datasets with different observational units (Wickham, 2016):

- `weather`: hourly meteorological data for each airport
- `planes`: construction information about each plane
- `airports`: airport names and locations
- `airlines`: translation between two letter carrier codes and names

You may have been asking yourself what `carrier` refers to in the `str(flights)` output above. The `airlines` dataset provides a description of this with each airline being the observational unit:

```
data(airlines)
airlines
```

```
##    carrier                        name
## 1       9E           Endeavor Air Inc.
## 2       AA      American Airlines Inc.
## 3       AS        Alaska Airlines Inc.
## 4       B6             JetBlue Airways
## 5       DL        Delta Air Lines Inc.
## 6       EV    ExpressJet Airlines Inc.
## 7       F9      Frontier Airlines Inc.
## 8       FL AirTran Airways Corporation
## 9       HA      Hawaiian Airlines Inc.
## 10      MQ                  Envoy Air
```

```
## 11      OO       SkyWest Airlines Inc.
## 12      UA       United Air Lines Inc.
## 13      US             US Airways Inc.
## 14      VX              Virgin America
## 15      WN      Southwest Airlines Co.
## 16      YV          Mesa Airlines Inc.
```

As can be seen here when you just enter the name of an object in R, by default it will print the contents of that object to the screen. Be careful! It's usually better to use the `View()` function in RStudio since larger objects may take awhile to print to the screen and it likely won't be helpful to you to have hundreds of lines outputted.

3.4 Normal forms of data

The datasets included in the `nycflights13` package are in a form that minimizes redundancy of data. We will see that there are ways to *merge* (or *join*) the different tables together easily. We are capable of doing so because each of the tables have *keys* in common to relate one to another. This is an important property of **normal forms** of data. The process of decomposing data frames into less redundant tables without losing information is called **normalization**. More information is available on Wikipedia.

We saw an example of this above with the `airlines` dataset. While the `flights` data frame could also include a column with the names of the airlines instead of the carrier code, this would be repetitive since there is a unique mapping of the carrier code to the name of the airline/carrier.

Below an example is given showing how to **join** the `airlines` data frame together with the `flights` data frame by linking together the two datasets via a common **key** of `"carrier"`. Note that this "joined" data frame is assigned to a new data frame called `joined_flights`.

```
if(!require(nycflights13))
  install.packages("nycflights13", repos = "http://cran.rstudio.org")
library(dplyr)
joined_flights <- inner_join(x = flights, y = airlines, by = "carrier")
```

```
View(joined_flights)
```

If we `View` this dataset, we see a new variable has been created called (We will see in Subsection 5.1.1 ways to change `name` to a more descriptive variable name.)

More discussion about joining data frames together will be given in Chapter 5. We will see there that the names of the columns to be linked need not match as they did here with `"carrier"`.

Review questions

(RQ3.1) What are common characteristics of "tidy" datasets?

(RQ3.2) What makes "tidy" datasets useful for organizing data?

(RQ3.3) How many variables are presented in the table below? What does each row correspond to? (**Hint:** You may not be able to answer both of these questions immediately but take your best guess.)

students	faculty
4	2
6	3

(RQ3.4) The confusion you may have encountered in Question 4 is a common one those that work with data are commonly presented with. This dataset is not tidy. Actually, the dataset in Question 4 has three variables not the two that were presented. Make a guess as to what these variables are and present a tidy dataset instead of this untidy one given in Question 4.

(RQ3.5) The actual data presented in Question 4 is given below in tidy data format:

role	Sociology?	Type of School
student	TRUE	Public
student	TRUE	Public
student	TRUE	Public
student	TRUE	Public
student	FALSE	Public
student	FALSE	Public
student	FALSE	Private
student	FALSE	Private
student	FALSE	Private
student	FALSE	Private
faculty	TRUE	Public
faculty	TRUE	Public
faculty	FALSE	Public
faculty	FALSE	Private
faculty	FALSE	Private

- What does each row correspond to?
- What are the different variables in this data frame?
- The `Sociology?` variable is known as a logical variable. What types of values does a logical variable take on?

(RQ3.6) What are some advantages of data in normal forms? What are some disadvantages?

3.5 What's to come?

In Chapter 4, we will further explore the distribution of a variable in a related dataset to `flights`: the `temp` variable in the `weather` dataset. We'll be interested in understanding how this variable varies in relation to the values of other variables in the dataset. We will see that visualization is often a powerful tool in helping us see what is going on in a dataset. It will be a useful way to expand on the `str` function we have seen here for tidy data.

4
Visualizing Data

In Chapter 3, we discussed the importance of datasets being **tidy**. You will see in examples here why having a tidy dataset helps us immensely with plotting our data. In plotting our data, we will be able to gain valuable insights from our data that we couldn't initially see from just looking at the raw tidy data. We will focus on using Hadley's `ggplot2` package in doing so, which was developed to work specifically on datasets that are **tidy**. It provides an easy way to customize your plots and is based on data visualization theory given in *The Grammar of Graphics* (Wilkinson, 2005).

At the most basic level, graphics/plots/charts provide a nice way for us to get a sense for how quantitative variables compare in terms of their center and their spread. The most important thing to know about graphics is that they should be created to make it obvious for your audience to see the findings you want to get across. This requires a balance on not including too much in your plots, but also including enough so that relationships and interesting findings can be easily seen. As we will see, plots/graphics also help us to identify patterns and outliers in our data. We will see that a common extension of these ideas is to compare the distribution of one quantitative variable (i.e., what the spread of a variable looks like) as we go across the levels of a different categorical variable.

4.1 Five Named Graphs - The 5NG

For our purposes here, we will be working with five different types of graphs. (Note that we will use a lot of different words here in regards to plotting - "graphs", "plots", and "charts" are all ways to discuss a resulting graphic. You can think of them as all being synonyms.) These five plots are:

- histograms
- boxplots
- barplots
- scatter-plots
- line-graphs

With this toolbox of plots, you can visualize just about any type of variable thrown at you. We

will discuss some other variations of these but with the 5NG in your repertoire you can do big things! Something we will also stress here is that certain plots only work for categorical/logical variables and others only for quantitative variables. You'll want to quiz yourself often on which plot makes sense with a given problem set-up.

We now introduce another dataframe in the `nycflights13` package introduced in Chapter 3.

```
if(!require("nycflights13"))
  install.packages("nycflights13", repos = "http://cran.rstudio.org")
library(nycflights13)
data(weather)
```

4.2 Histograms

Our focus turns to the `temp` variable in this `weather` dataset. We would like to visualize what the 26130 temperatures look like. Looking over the `weather` dataset[1] and running `?weather`, we can see that the `temp` variable corresponds to hourly temperature (in Fahrenheit) recordings at weather stations near airports in New York City. We could just produce points where each of the different values appear on something similar to a number line:

[1] Recall that to view a dataset in spreadsheet format in RStudio, you can run the `View()` function with the dataframe as its argument.

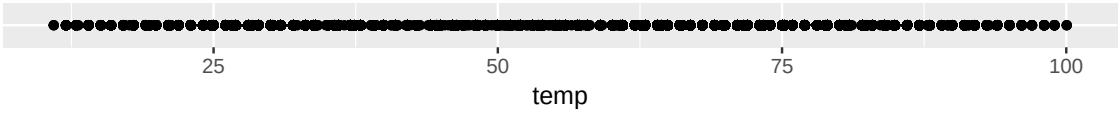


Figure 4.1: Strip Plot of Hourly Temperature Recordings from NYC in 2013

This gives us a general idea of how the values of `temp` differ. We see that temperatures vary from around 11 up to 100 degrees Fahrenheit. The area between 40 and 60 degrees appears to have more points plotted than outside that range.

What is commonly produced instead of this strip plot is a plot known as a **histogram**. The **histogram** shows how many elements of the variable fall in specified **bins**. These **bins** may correspond to between 0-10°F, 10-20°F, etc. To produce a histogram, we introduce Hadley's `ggplot2` package (Wickham and Chang, 2016). We will use the `ggplot` function which expects at a bare minimal as arguments

- the dataframe where the variables exist (the `data` argument) and
- the names of the variables to be plotted (the `mapping` argument).

The names of the variables will be entered into the `aes` function as arguments where `aes` stands for "aesthetics".

```
if(!require("ggplot2"))
  install.packages("ggplot2", repos = "http://cran.rstudio.org")
library(ggplot2)
ggplot(data = weather, mapping = aes(x = temp))
```

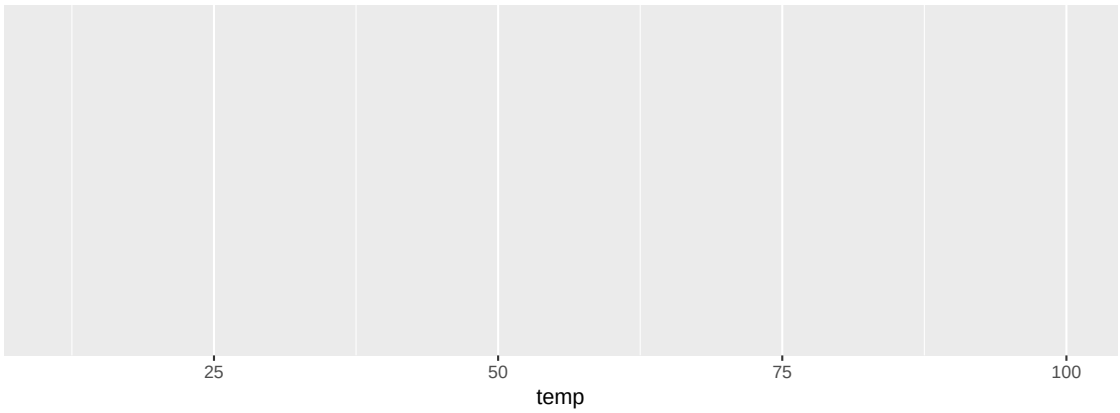


Figure 4.2: ggplot backdrop

The plot given above is not a histogram, but the output does show us a bit of what is going on with `ggplot(data = weather, mapping = aes(x = temp))`. It is producing a backdrop onto which we will "paint" elements. We next proceed by adding a layer—hence, the use of the `+` symbol—to the plot to produce a histogram. (Note also here that we don't have to specify the `data =` and `mapping =` text in our function calls. This is covered in more detail in Chapter 5 of the "Getting Used to R, RStudio, and R Markdown" book (Ismay, 2016)).

You are encouraged to enter **Return** on your keyboard after entering the `+`. As we add more and more elements, it will be nice to keep them indented as you see below. Note that this will not work if you begin the line with the `+`.

```
ggplot(data = weather, mapping = aes(x = temp)) +
  geom_histogram()
```

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

```
## Warning: Removed 1 rows containing non-finite values (stat_bin).
```

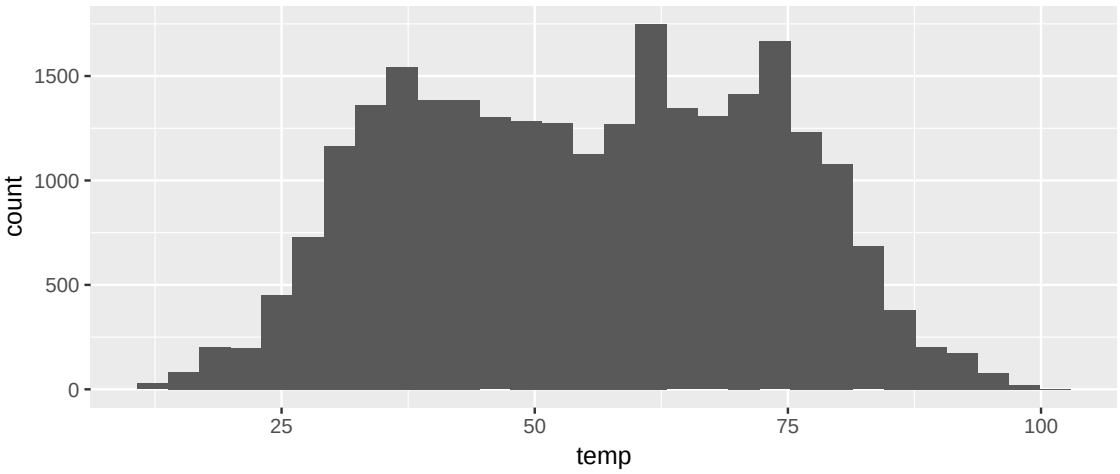


Figure 4.3: Histogram of Hourly Temperature Recordings from NYC in 2013

We have the power to specify how many bins we would like to put the data into as an argument in the `geom_histogram` function. By default, this is chosen to be 30 somewhat arbitrarily and we have received a warning above our plot that this was done. We also notice here that another warning about 1 missing value is given. This value is omitted from the plot. This warning is ignored for future customizations of the plot.

Missing values are a common problem when working with data and there are entire fields of study on how to work with missing data. Frequently what is done is to remove instances from the data set that are missing. This is certainly the easy way to deal with them, but not necessarily the correct decision in all cases. For our purposes, we will usually ignore potential warnings about missing data since R can usually handle them by ignoring them.

```
ggplot(data = weather, mapping = aes(x = temp)) +
  geom_histogram(bins = 60)
```

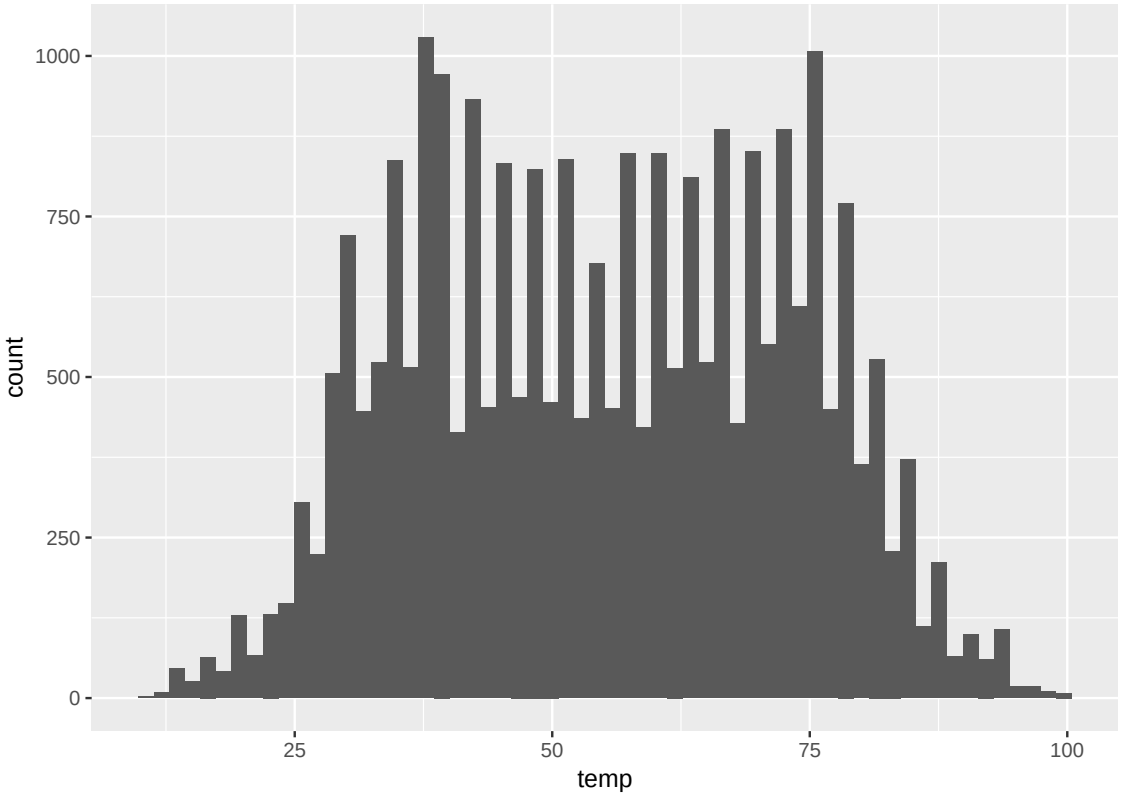


Figure 4.4: Histogram of Hourly Temperature Recordings from NYC in 2013 - 60 Bins

We can tweak the plot a little more by specifying the width of the bins (instead of how many bins to divide the variable into) by using the `binwidth` argument in the `geom_histogram` function. We can also add some color to the plot by invoking the `fill` and `color` arguments. A listing of all of the built-in colors to R by name and color is available here. You are encouraged to play around with tweaking this plot by changing the arguments to help you understand how you could go about making your own histograms.

```
ggplot(data = weather, mapping = aes(x = temp)) +
  geom_histogram(binwidth = 10, color = "white", fill = "forestgreen")
```

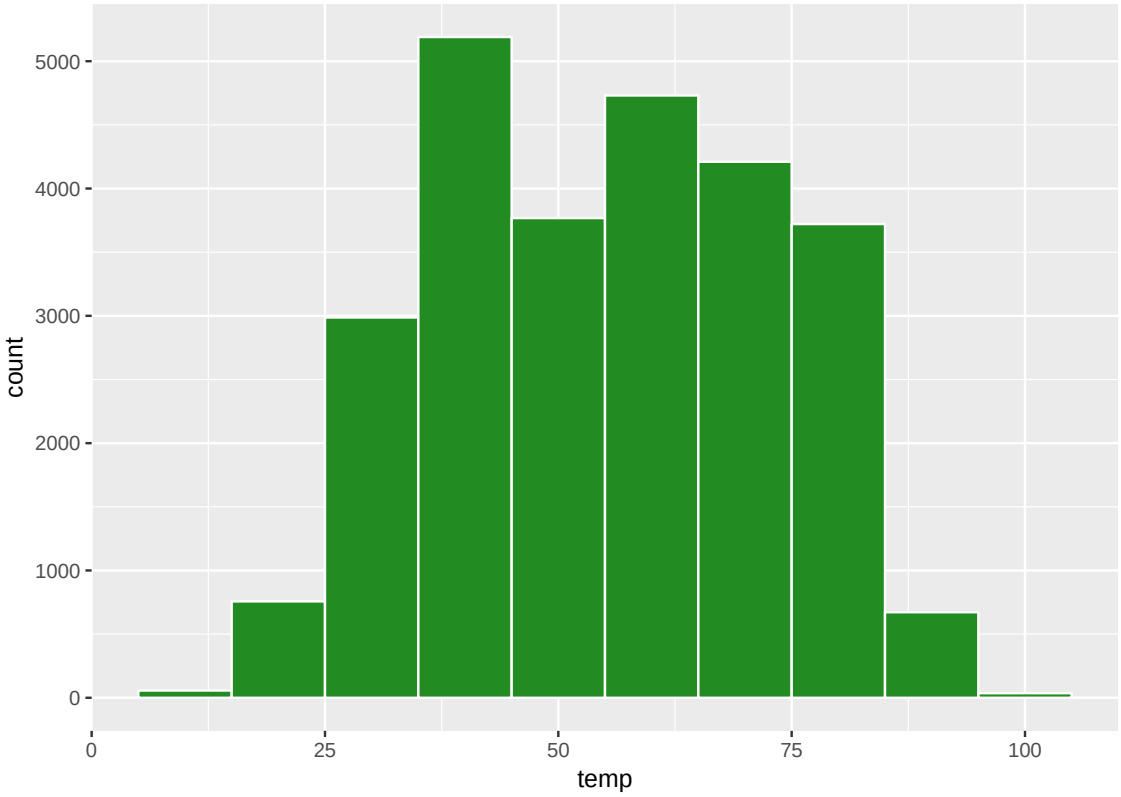


Figure 4.5: Histogram of Hourly Temperature Recordings from NYC in 2013 - Binwidth = 10

Learning check

(LC4.1) What does changing the number of bins from 30 to 60 tell us about the distribution of temperatures?

(LC4.2) Would you classify the distribution of temperatures as symmetric or skewed?

(LC4.3) What would you guess is the "center" value in this distribution? Why did you make that choice?

(LC4.4) Is this data spread out greatly from the center or is it close? Why?

4.2.1 Continuous data summaries

The `temp` variable is a **continuous** quantitative variable (frequently just called a **continuous variable**). "A variable is **continuous** if you can arrange its values in order and an infinite number of unique values can exist between any two values of the variable" (Grolemund and Wickham, 2016). Some common examples of continuous variables are time and height. Between any two times there are an infinitely many number of time units that fall between them. It is often easier to think about quantitative variables that are not continuous to help us better understand continuity. The best example is counts. If we are looking to count the number of flights that depart on a given day from New York City, this variable would not be continuous. It falls on a **discrete** scale.

We can examine some summary information about this `temp` variable. To do so, we introduce the `summary` function. (We will see in Chapter 5 how to use the `summarize` function in the `dplyr` package to produce similar results.) The syntax here is a little different than what we have seen before. (A further discussion about R syntax is available in Chapter 5 of the "R basics" book (Ismay, 2016)). Here, `summary` is the function and it is expecting an object to be summarized as its argument. The object here is the `temp` variable in the `weather` dataframe. To focus on just this one variable `temp` in `weather`, we separate them by the dollar sign symbol `$`. Order matters here: the dataframe comes before the `$` and the variable/column name comes after.

```
summary(weather$temp)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##   10.94   39.92   55.04   55.20   69.98  100.00       1
```

This tells us what is known as the **five-number summary** for our variable, the **mean** value of the variable, and how many missing values `NA`'s appear in this column of the `weather` data frame. More information on the concepts of five-number summary and mean is given in Appendix B.

This `summary` gives us some numerical summaries of our temperature variable. The minimum recorded temperature is 10.94 degrees Fahrenheit and the maximum is 100.04 degrees Fahrenheit. We have one missing value denoted as an `NA` in the observations of this variable. The median Fahrenheit temperature of 55.04 and mean of 55.2035149 are quite close. This is a property of symmetric distributions.

The last two entries given by `summary` correspond to the 25^{th} percentile and the 75^{th} percentile. If we sorted all of the temperatures in increasing order, we would see that 25% of them would fall below 39.92 and that 75% of them would fall below 69.98. This implies that the middle 50% of data values lie between 39.92 and 69.98 degrees Fahrenheit.

Another common measure to determine the variability of a data set is the **standard deviation**. You can read further about the mathematical details of standard deviation in Appendix B, but you can think of it as being a measure of how far the data is, on average, from the mean. Let's investigate this further by calculating the standard deviation of our temperature variable:

```
sd(weather$temp)
```

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

Remember that there were some missing values in our temperature data when we plotted it earlier. By default, the `sd` function that computes standard deviation of a variable will give the value of `NA` if any of the data is missing. To further understand this, you can look at the help of the `sd` function in the R Console:

```
?sd
```

Under **Usage** you can see that `na.rm` is set to `FALSE` by default. We'd like for missing values to be removed from our analysis so we set that value to `TRUE`:

```
sd(weather$temp, na.rm = TRUE)
```

```
## [1] 17.78212
```

Standard deviation is always in the same units as our original data set. So in this case the standard deviation is in degrees Fahrenheit. Thus, for a randomly selected element in our temperature column, we can expect it to be about 17.7821236 degrees Fahrenheit from our mean value of 55.2035149. By combining this knowledge with the plots above, we can have a good idea for whether this data is very spread out from its center or if it is tightly bunched.

4.2.2 Summary

Histograms provide a useful way of looking at how ONE continuous variable varies. They allow us to answer questions such as

- Are there values far away from the center? These are commonly called **outliers** and can frequently be easily identified on a histogram.
- Are most values close to the center? If so, the spread of the variable is small. If not, the spread is large.
- How spread out are the values? One measure of this spread is **standard deviation** discussed above.

The histogram shows how many entries fall in different groupings of this variable. Another common property of distributions is symmetry and as we saw it is quite easily identified by looking over the histogram produced from the variable's values.

4.3 Boxplots

Histograms can also be produced to compare the distribution of a variable over another variable. Suppose we were interested in looking at how the temperature recordings we saw in the

last section varied by month. This is what is meant by "the distribution of a variable over another variable": `temp` is one variable and `month` is the other variable.

Before we introduce the concept of **boxplots**, we'll begin with an exploration into **faceting**. We will see that this is a powerful way to look at the relationships of two variables. Specifically this is nice in comparing the distribution of a quantitative variable over different levels of a categorical variable. It is often recommended that you create a faceted histogram and a boxplot in situations such as this. By looking at both of them together, you'll be able to identify patterns that you may miss by looking at only one of them. As you read through this next section, think about how you might use faceting to look at the relationships between other types of variables using the different types of plots we explore throughout this chapter.

4.3.1 Faceting

In order to look at histograms of `temp` for each month, we introduce a new concept called **faceting**. Faceting is used when we'd like to create small multiples of the same plot over a different categorical variable. By default, all of the small multiples will have the same vertical axis. An example will help here. We will discuss the concept of faceting in further detail in Section 4.4.

```
ggplot(data = weather, mapping = aes(x = temp)) +
  geom_histogram(binwidth = 5, color = "white", fill = "firebrick") +
  facet_wrap(~ month)
```

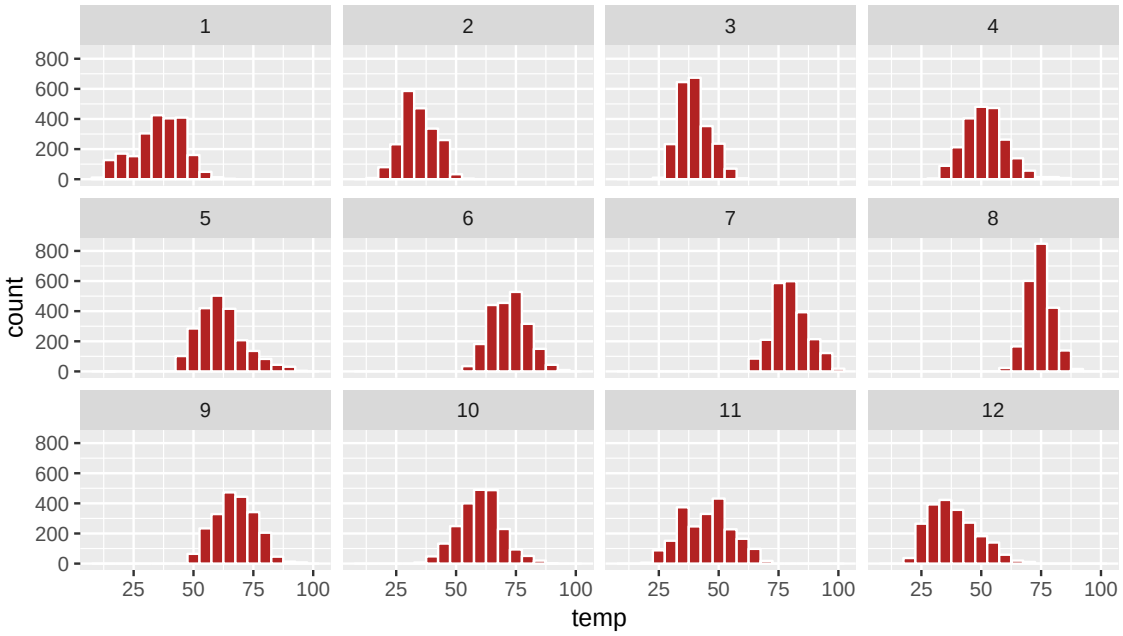


Figure 4.6: Faceted histogram

As we might expect, the temperature tends to increase as summer approaches and then decrease as winter approaches.

Learning check

(LC4.5) What other things do you notice about the faceted plot above? How does a faceted plot help us see how relationships between two variables?

(LC4.6) What do the numbers 1-12 correspond to in the plot above? What about 25, 50, 75, 100?

(LC4.7) What could be done to make the faceted plot above more readable? (Focus on tweaking the histograms and not on making a different type of plot here.)

(LC4.8) For which types of datasets would these types of faceted plots not work well in comparing relationships between variables? Give an example describing the variability of the variables and other important characteristics.

(LC4.9) Does the `temp` variable in the `weather` data set have a lot of variability? Why do you say that?

Histograms can provide a way to compare distributions across groups as we see above when we looked at temperature over months. Frequently, a plot called a **boxplot** (also called a **side-by-side boxplot**) is done instead. The **boxplot** uses the information provided in the **five-number summary** referred to in the previous section when we used the `summary` function. It gives a way to compare this summary information across the different levels of a group. Let's create a boxplot to compare the monthly temperatures as we did above with the faceted histograms.

```
ggplot(data = weather, mapping = aes(x = month, y = temp)) +
  geom_boxplot()
```

```
## Warning: Continuous x aesthetic -- did you forget aes(group=...)?
```

```
## Warning: Removed 1 rows containing non-finite values (stat_boxplot).
```

Note the first warning that is given here. (The second one corresponds to missing values in the dataframe and it is turned off on subsequent plots.) Observe that this plot does not look like what we were expecting. We were expecting to see the distribution of temperatures for each month (so 12 different boxplots). This gives us the overall boxplot without any other groupings. We can get around this by introducing a new function for our `x` variable.

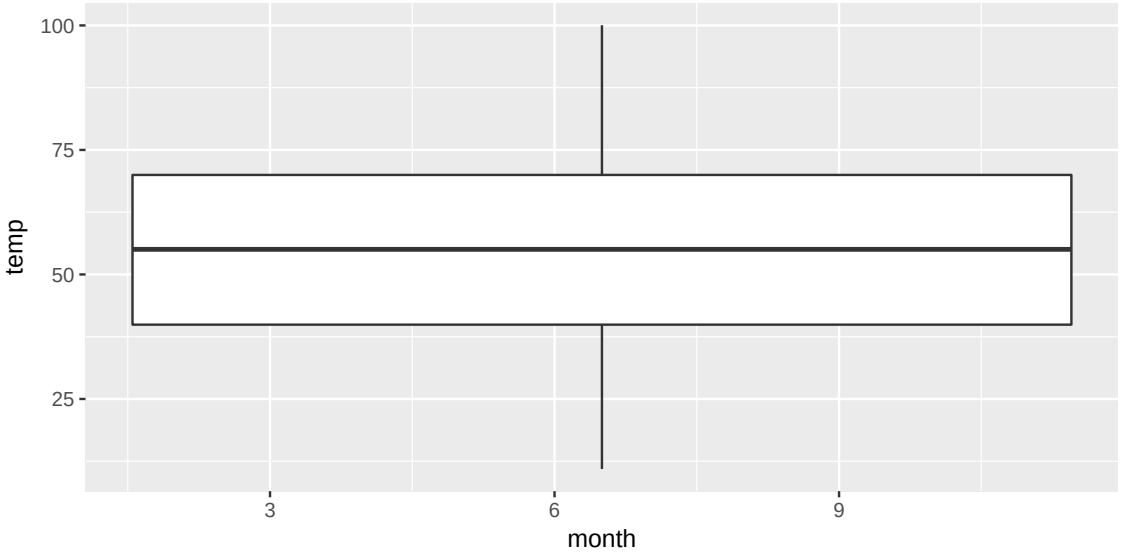


Figure 4.7: Invalid boxplot specification

```
ggplot(data = weather, mapping = aes(x = factor(month), y = temp)) +
  geom_boxplot()
```

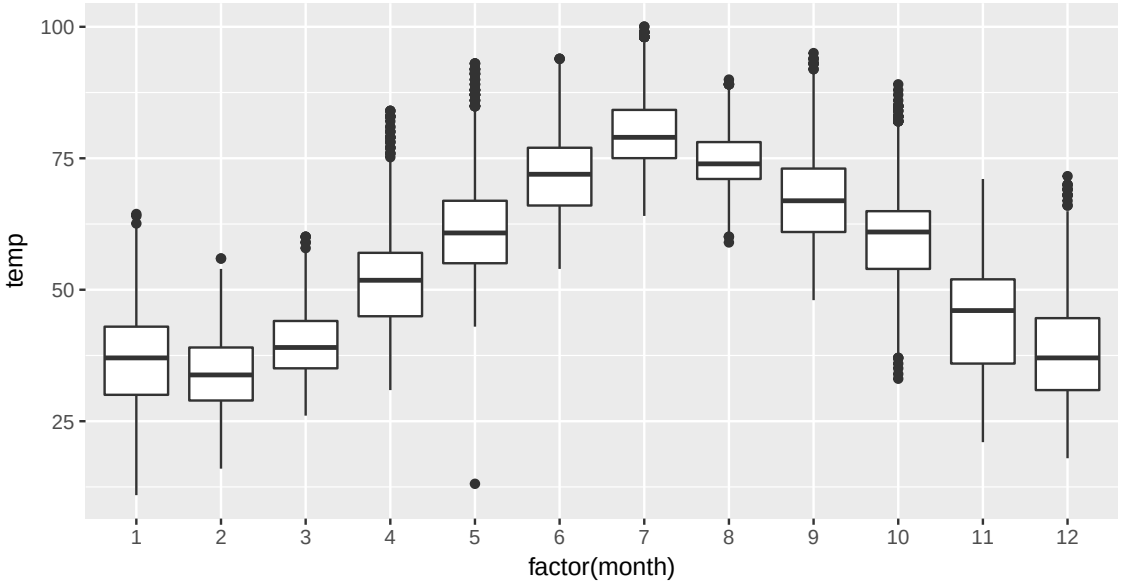


Figure 4.8: Month by temp boxplot

We have introduced a new function called `factor()` here. One of the things this function does is to convert a discrete value like `month` (1, 2, ..., 12) into a categorical variable. The "box" part of this plot represents the 25^{th} percentile, the median (50^{th} percentile), and the 75^{th} percentile. The dots correspond to **outliers**. (The specific formulation for these outliers is discussed in Appendix B.) The lines show how the data varies that is not in the center 50% defined by the first and third quantiles. Longer lines correspond to more variability and shorter lines correspond to less variability.

Learning check

(LC4.10) What does the dot at the bottom of the plot for May correspond to? Explain what might have occurred in May to produce this point.

(LC4.11) Which months have the highest variability in temperature? What reasons do you think this is?

(LC4.12) We looked at the distribution of a continuous variable over a categorical variable here with this boxplot. Why can't we look at the distribution of one continuous variable over the distribution of another continuous variable? Say temperature across pressure, for example?

(LC4.13) Boxplots provide a simple way to identify outliers. Why may outliers be easier to identify when looking at a boxplot instead of a faceted histogram?

4.3.2 Summary

Boxplots provide a way to compare and contrast the distribution of ONE quantitative variable across multiple levels of ONE categorical variable. One can easily look to see where the median falls across the different groups by looking at the center line in the box. You can also see how spread out the variable is across the different groups by looking at the width of the box and also how far out the lines stretch from the box. If the lines stretch far from the box but the box has a small width, the variability of the values closer to the center is much smaller than the variable of the outer ends of the variable. Lastly, outliers are even more easily identified when looking at a boxplot than when looking at a histogram.

4.4 Barplots

Both histograms and boxplots represent ways to visualize the variability of continuous variables. Another common task is to present the distribution of a categorical variable. This is a simpler task since we will be interested in how many elements from our data fall into the different categories of the categorical variable. We need not bin the data or identify the different quantiles for categorical variables.

Frequently, the best way to visualize these different counts (also known as **frequencies**) is via a barplot. Consider the distribution of airlines that flew out of New York City in 2013. Here we explore the number of flights from each airline/`carrier`. This can be plotted by invoking the `geom_bar` function in `ggplot2`:

```
ggplot(data = flights, mapping = aes(x = carrier)) +
  geom_bar()
```

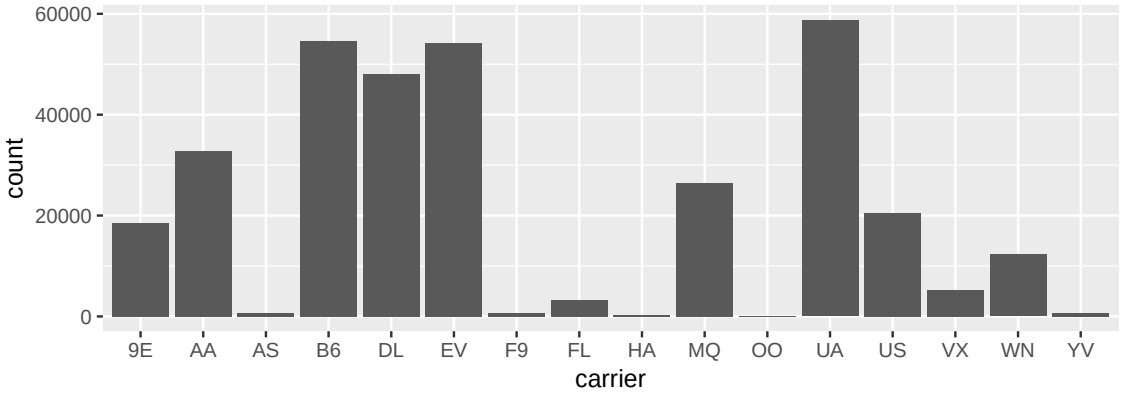


Figure 4.9: Number of flights departing NYC in 2013 by airline

Recall the `airlines` dataset discussed in Chapter 3.

```
if(!require("nycflights13"))
  install.packages("nycflights13", repos = "http://cran.rstudio.org")
library(nycflights13)
data(airlines)
airlines
```

```
## # A tibble: 16 × 2
##    carrier                        name
##      <chr>                       <chr>
## 1       9E           Endeavor Air Inc.
## 2       AA      American Airlines Inc.
## 3       AS        Alaska Airlines Inc.
## 4       B6             JetBlue Airways
## 5       DL        Delta Air Lines Inc.
## 6       EV    ExpressJet Airlines Inc.
## 7       F9      Frontier Airlines Inc.
## 8       FL AirTran Airways Corporation
## 9       HA      Hawaiian Airlines Inc.
## 10      MQ                   Envoy Air
## 11      OO       SkyWest Airlines Inc.
## 12      UA       United Air Lines Inc.
## 13      US             US Airways Inc.
## 14      VX              Virgin America
## 15      WN      Southwest Airlines Co.
## 16      YV          Mesa Airlines Inc.
```

We see that United Air Lines, JetBlue Airways, and ExpressJet Airlines had the most flights

depart New York City in 2013. To get the actual number of flights by each airline we can use the `count` function in the `dplyr` package on the `carrier` variable in `flights`:

```
if(!require("dplyr"))
  install.packages("dplyr", repos = "http://cran.rstudio.org")
library(dplyr)
flights_table <- count(x = flights, vars = carrier)
flights_table
```

```
## # A tibble: 16 × 2
##     vars     n
##    <chr> <int>
## 1     9E 18460
## 2     AA 32729
## 3     AS   714
## 4     B6 54635
## 5     DL 48110
## 6     EV 54173
## 7     F9   685
## 8     FL  3260
## 9     HA   342
## 10    MQ 26397
## 11    OO    32
## 12    UA 58665
## 13    US 20536
## 14    VX  5162
## 15    WN 12275
## 16    YV   601
```

Learning check

(LC4.14) Why are histograms inappropriate for visualizing categorical variables?

(LC4.15) What is the difference between histograms and barplots?

(LC4.16) How many Envoy Air flights departed NYC in 2013?

(LC4.17) What was the seventh highest airline in terms of departed flights from NYC in 2013?

4.4.1 Must avoid pie charts!

Unfortunately, one of the most common plots seen today for categorical data is the pie chart. While they may see harmless enough, they actually present a problem in that humans are unable to judge angles well. As Naomi Robbins describes in her book "Creating More Effective Graphs" (Robbins, 2013), we overestimate angles greater than 90 degrees and we underestimate angles less than 90 degrees. In other words, it is difficult for us to determine relative size of one piece of the pie compared to another.

Let's examine our previous barplot example on the number of flights departing NYC by airline. This time we will use a pie chart. As you review this chart, try to identify

- how much larger the portion of the pie is for ExpressJet Airlines (`EV`) compared to US Airways (`US`),
- what the third largest carrier is in terms of departing flights, and
- how many carriers have fewer flights than United Airlines (`UA`)?

Figure 4.10: The dreaded pie chart

While it is quite easy to look back at the barplot to get the answer to these questions, it's

quite difficult to get the answers correct when looking at the pie graph. Barplots can always present the information in a way that is easier for the eye to determine relative position. There may be one exception from Nathan Yau at FlowingData.com but we will leave this for the reader to decide:

Figure 4.11: The only good pie chart

Learning check

(LC4.18) Why should pie charts be avoided and replaced by barplots?

(LC4.19) What is your opinion as to why pie charts continue to be used?

4.4.2 Using barplots to compare two variables

Barplots are the go-to way to visualize the frequency of different categories of a categorical variable. They make it easy to order the counts and to compare one group's frequency to another. Another use of barplots (unfortunately, sometimes inappropriately and confusingly) is to compare two categorical variables together. Let's examine the distribution of outgoing flights from NYC by `carrier` and `airport`.

We begin by getting the names of the airports in NYC that were included in the `flights` dataset. Remember from Chapter 3 that this can be done by using the `inner_join` function.

```
library(dplyr)
flights_namedports <- inner_join(flights, airports, by = c("origin" = "faa"))
```

After running `View(flights_namedports)`, we see that `name` now corresponds to the name of the airport as referenced by the `origin` variable. We will now plot `carrier` as the horizontal variable. When we specify `geom_bar`, it will specify `count` as being the vertical variable. A new addition here is `fill = name`. Look over what was produced from the plot to get an idea of what this argument gives.

```
ggplot(data = flights_namedports, mapping = aes(x = carrier, fill = name)) +
  geom_bar()
```

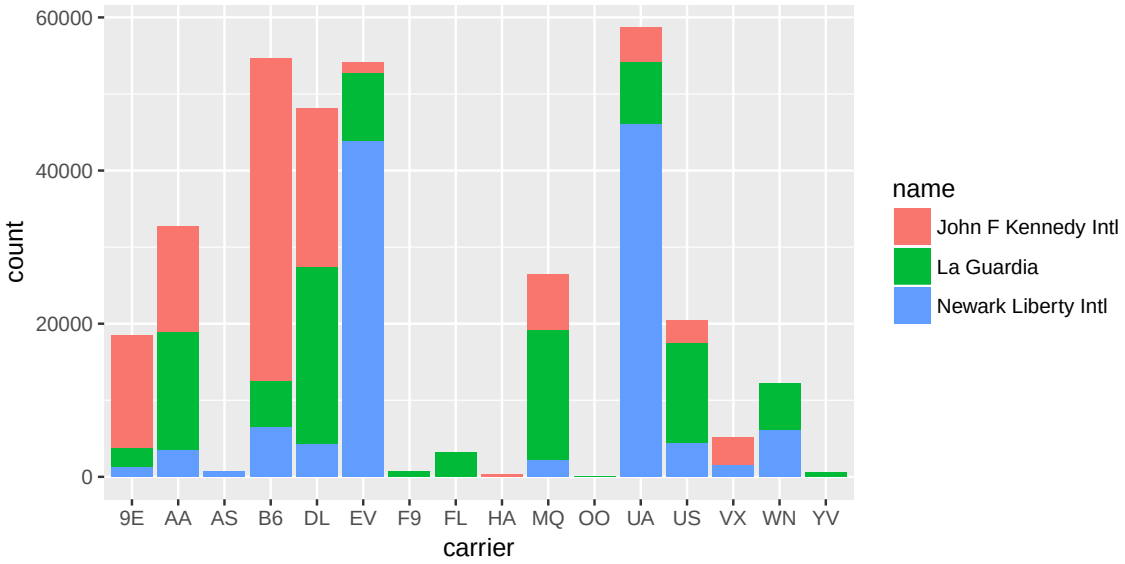


Figure 4.12: Stacked barplot comparing the number of flights by carrier and airport

This plot is what is known as a **stacked barplot**. While simple to make, it often leads to many problems.

Learning check

(LC4.20) What kinds of questions are not easily answered by looking at the above figure?

(LC4.21) What can you say, if anything, about the relationship between airline and airport in NYC in 2013 in regards to the number of departing flights?

Another variation on the **stacked barplot** is the **side-by-side barplot**.

```
ggplot(data = flights_namedports, mapping = aes(x = carrier, fill = name)) +
  geom_bar(position = "dodge")
```

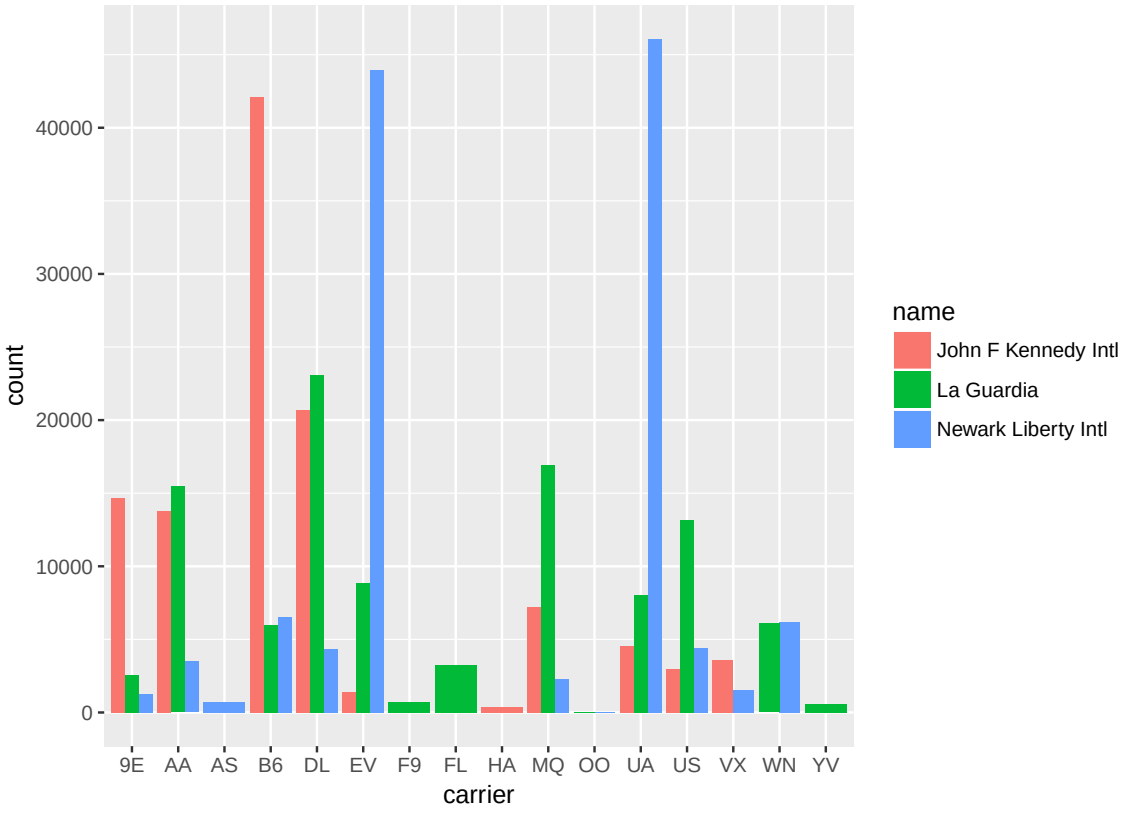


Figure 4.13: Side-by-side barplot comparing the number of flights by carrier and airport

---

Learning check

(LC4.22) Why might the side-by-side barplot be preferable to a stacked barplot in this case?

(LC4.23) What are the disadvantages of using a side-by-side barplot, in general?

Lastly, an often preferred type of barplot is the **faceted barplot**. We already saw this concept of faceting and small multiples in Subsection 4.3.1. This gives us a nicer way to compare the distributions across both `carrier` and airport/`name`.

```
ggplot(data = flights_namedports, mapping = aes(x = carrier, fill = name)) +
  geom_bar() +
  facet_grid(name ~ .)
```

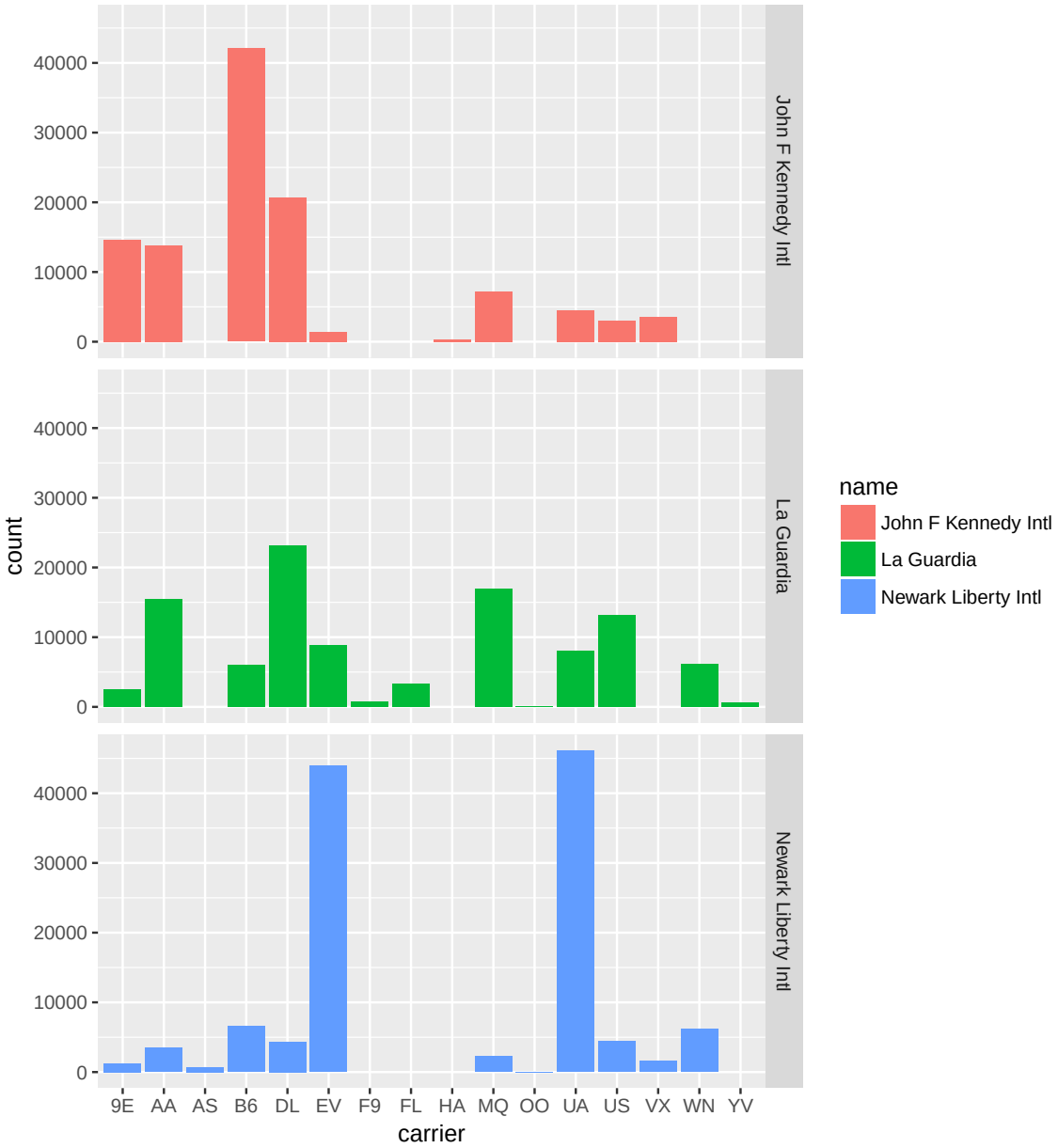


Figure 4.14: Faceted barplot comparing the number of flights by carrier and airport

Note how the `facet_grid` function arguments are written here. We are wanting the names of the airports vertically and the `carrier` listed horizontally. As you may have guessed, this argument and other *formulas* of this sort in R are in `y ~ x` order.

Learning check

(LC4.24) Why is the faceted barplot preferred to the side-by-side and stacked barplots in this case?

(LC4.25) What information about the different carriers at different airports is more easily seen in the faceted barplot?

4.4.3 Summary

Barplots are the preferred way of displaying categorical variables. They are easy-to-understand and to make comparisons across groups of a categorical variable. When dealing with more than one categorical variable, faceted barplots are frequently preferred over side-by-side or stacked barplots. Stacked barplots are sometimes nice to look at, but it is quite difficult to compare across the levels since the sizes of the bars are all of different sizes. Side-by-side barplots can provide an improvement on this, but the issue about comparing across groups still must be dealt with.

4.5 Scatter-plots

We have seen that boxplots are most appropriate when plotting the distribution of ONE continuous variable across different levels/groups of ONE categorical variable. Barplots (preferably the faceted type) are best when looking at the distribution of ONE categorical variable across different levels of another categorical variable. But what if we are looking to investigate the relationship between TWO continuous variables? What is commonly produced is the well-known **scatter-plot**, which shows the points corresponding to the values of each of the variables scattered around.

We will now investigate arrival delays (the vertical "y" axis variable) versus departure delays (the horizontal "x" axis variable) for Alaska Airlines flights leaving NYC in 2013. Notice the new function that is invoked here: `filter`, which resides in the `dplyr` package. You will see many more examples using this function in Chapter 5. The `filter` function goes through the dataframe specified (`flights` here) and selects only those rows which meet the condition given (`carrier == "AS"` here).

```
alaska_flights <- filter(flights, carrier == "AS")
ggplot(alaska_flights, aes(x = dep_delay, y = arr_delay)) +
  geom_point()
```

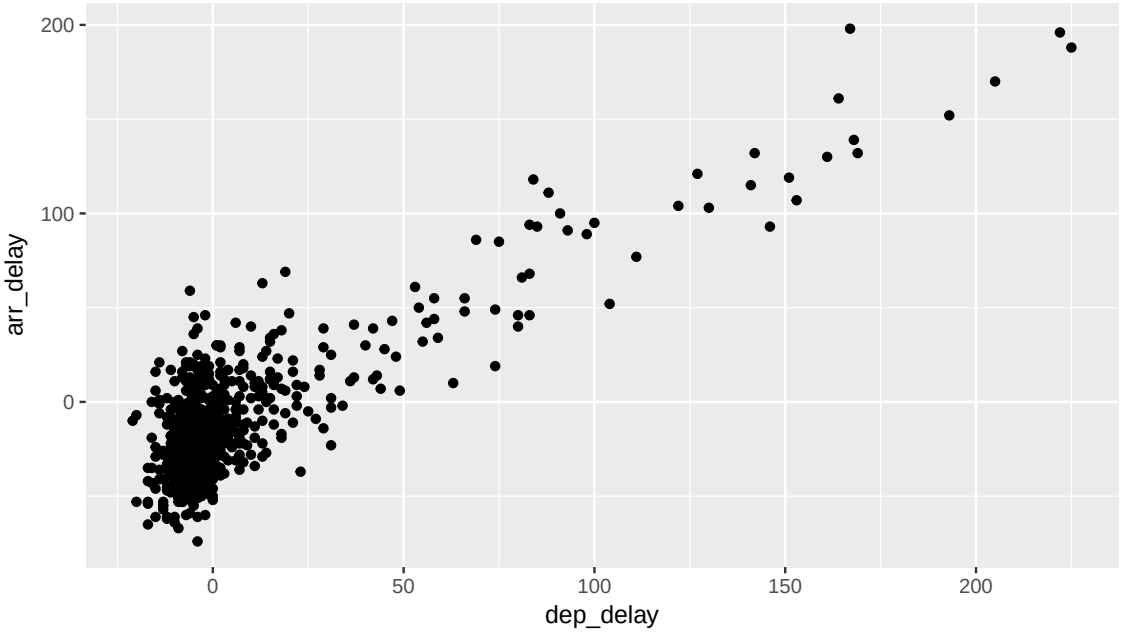


Figure 4.15: Arrival Delays vs Departure Delays for Alaska Airlines flights from NYC in 2013

We see that a positive relationship exists between `dep_delay` and `arr_delay`: as departure delays increase, arrival delays tend to also increase. We also note that the majority of points fall near the point (0, 0) here. There is a large mass of points clustered there.

Learning check

(LC4.26) What are some practical reasons why `dep_delay` and `arr_delay` have a positive relationship?

(LC4.27) What variables (not necessarily in the `flights` dataframe) would you expect to have a negative correlation (i.e. a negative relationship) with `dep_delay`? Why? Remember that we are focusing on continuous variables here.

(LC4.28) Why do you believe there is a cluster of points near (0, 0)?

- What does (0, 0) correspond to in terms of the Alaskan flights?

(LC4.29) What are some other features of the plot that stand out to you?

4.5.1 Jittering

The large mass of points near (0, 0) can cause some confusion. This is the result of a phenomenon called **over-plotting**. As one may guess, this corresponds to values being plotted on top of each other *over* and *over* again. It is often difficult to know just how many values are plotted in this way when looking at a basic scatter-plot as we have here.

One way of relieving this issue of **over-plotting** is to **jitter** the points a bit. In other words, we are going to add just a bit of random noise to the points to better see them and remove some of the over-plotting. You can think of "jittering" as shaking the points a bit on the plot. Instead of using `geom_point`, we use `geom_jitter` to perform this shaking and specify around how much jitter to add with the `width` and `height` arguments. This corresponds to how hard you'd like to shake the plot in units corresponding to those for both the horizontal and vertical variables (minutes here).

```
ggplot(alaska_flights, aes(x = dep_delay, y = arr_delay)) +
  geom_jitter(width = 30, height = 30)
```

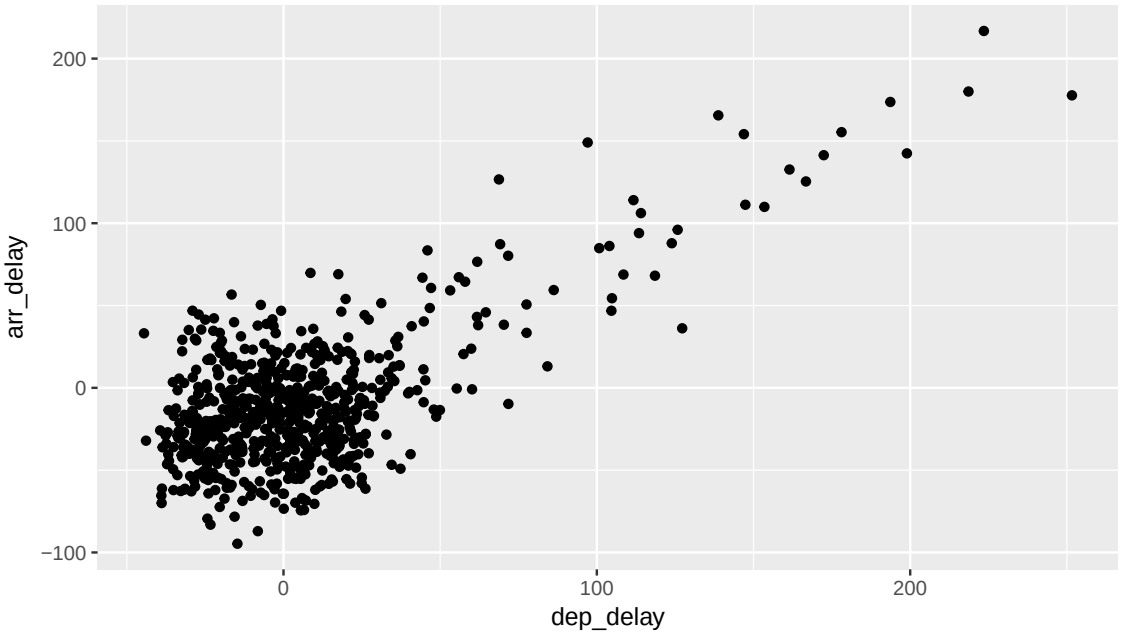


Figure 4.16: Jittered delay scatterplot

This helps us a little bit in getting a sense for the over-plotting, but with a relatively large dataset like this one (714 flights), it is often useful to change the transparency of the points as seen in the next section.

4.5.2 Setting transparency

One of the arguments that can be changed with `geom_point` is `alpha`. By default, this value is set to `1`. We can change this value to a smaller fraction to change the transparency of the points in the plot:

```
ggplot(alaska_flights, aes(x = dep_delay, y = arr_delay)) +
  geom_point(alpha = 0.2)
```

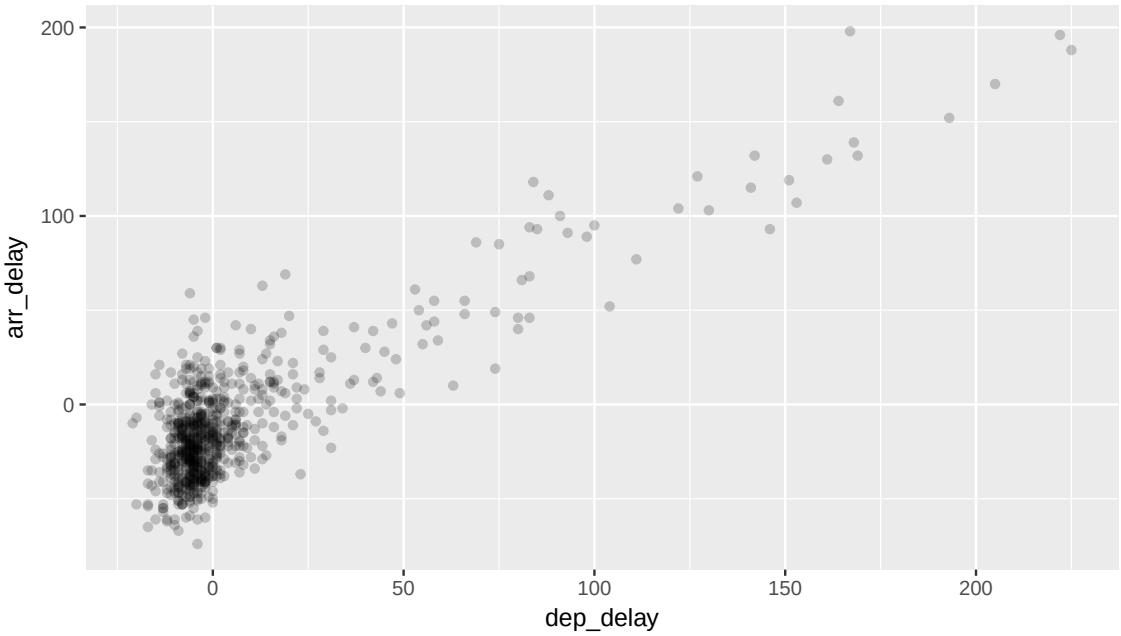


Figure 4.17: Arrival Delays vs Departure Delays for Alaska Airlines flights from NYC in 2013 - alpha=0.2 1

We can also specify the `alpha` argument in `geom_jitter`:

```
ggplot(alaska_flights, aes(x = dep_delay, y = arr_delay)) +
  geom_jitter(width = 30, height = 30, alpha = 0.3)
```

Learning check

(LC4.30) Why is setting the `alpha` argument value useful with scatter-plots?

- What further information does it give you that a regular scatter-plot cannot?

(LC4.31) After viewing the 4.17 above, give a range of arrival times and departure times that occur most frequently?

- How has that region changed compared to when you observed the same plot without the `alpha = 0.2` set in 4.15?

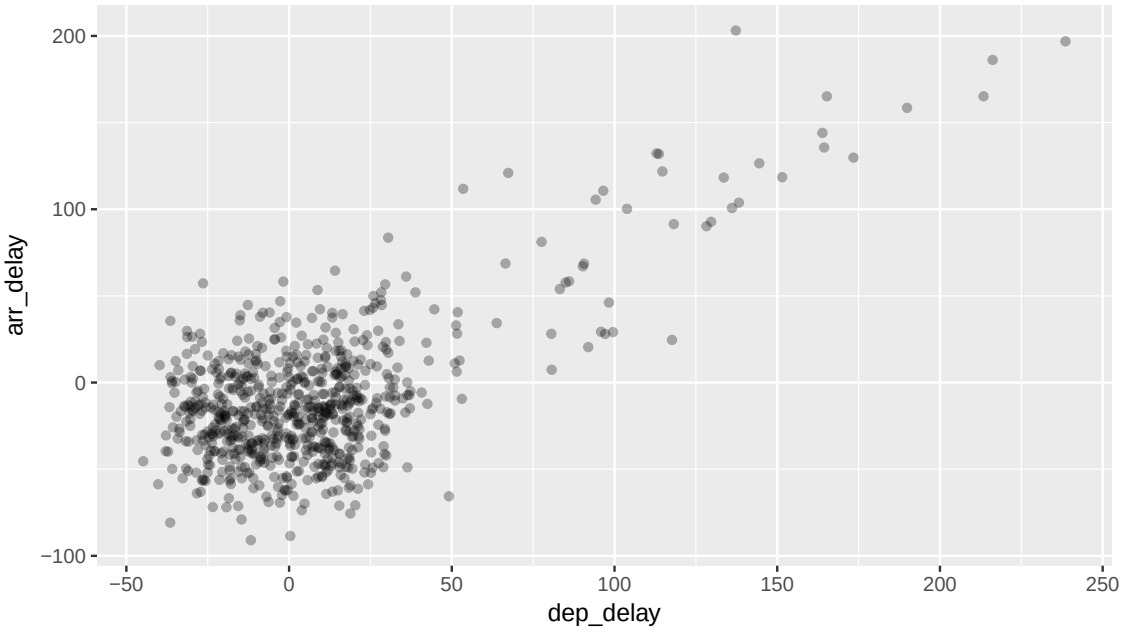


Figure 4.18: Arrival Delays vs Departure Delays for Alaska Airlines flights from NYC in 2013 - jitter and alpha added 1

4.5.3 Summary

Scatter-plots may be the most used plot today and they can provide an immediate way to see the trend in one variable versus another. Remember that they only make sense when plotting a continuous variable versus a continuous variable though. If you try to create a scatter-plot where either one of the two variables is not quantitative, you will get strange results. Be careful!

With medium to large datasets, you may need to tweak arguments in both `geom_jitter` and the `alpha` parameter in order to get a good feel for relationships in your data. This tweaking is often a fun part of data visualization since you'll have the chance to see different relationships come about as you make subtle changes to your plots.

4.6 Line-graphs

The last of the 5NG is a line-graph. They are most frequently used when the horizontal axis is time. Time represents a variable that is connected together by each day following the previous day. In other words, time has a natural ordering. Line-graphs should be avoided when there is not a clear ordering to the explanatory ("x" variable).

We are interested in exploring the arrival delays by day throughout the year of 2013 from outgoing flights from New York City. If we plotted all of these values, we obtain the following scatter-plot:

```
ggplot(flights, aes(x = time_hour, y = arr_delay)) +
  geom_point()
```

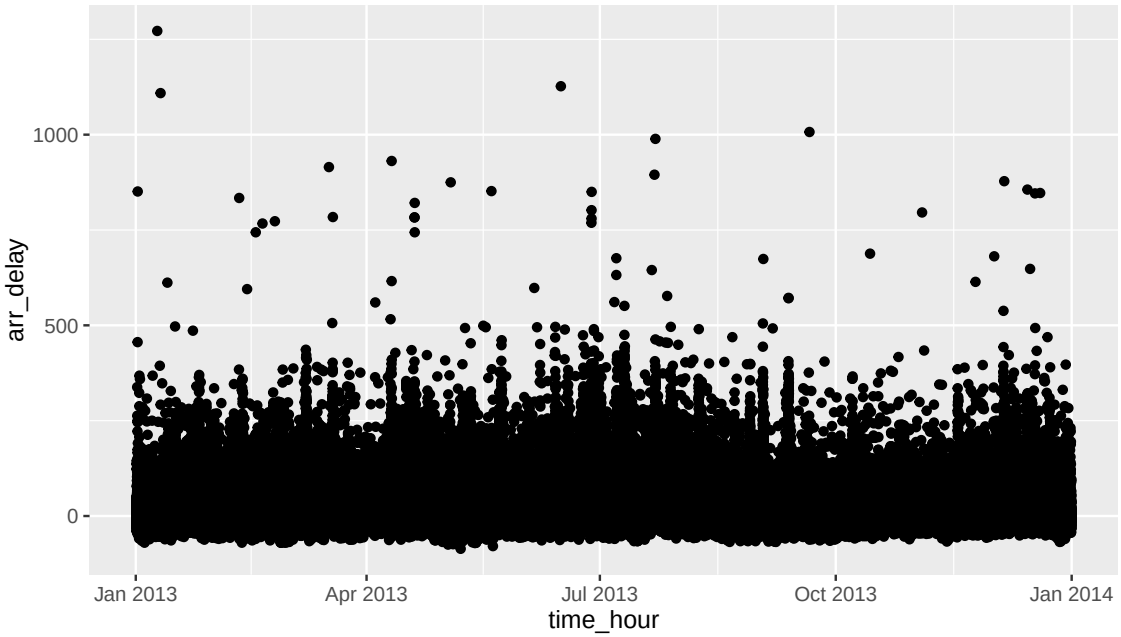


Figure 4.19: Hard to read scatterplot

We see that this plot is difficult to understand based on the sheer number of points plotted. We see some outlier points with more than 500 minutes of arrival delay, but even some jittering and transparency is not going to help us here.

Instead of plotting all of the values for each hour for all flights, it might make sense to plot the average value for each day in terms of arrival delays. Of course, we also need to address which average we should use: mean or median. With there being some outliers here, we have chosen to use the median arrival delay (since the mean is heavily influence by outliers).

You may think that this is a difficult task but the `group_by` and `summarize` functions make this a breeze. You'll see more examples using these two functions in Chapter 5. Here we will create a new variable, which corresponds to the month and day combined, from the `time_hour` column using the `mutate` function and create a new dataframe called `flights_day`. Notice from running `View(flights_day)` that the new variable added called `date` appears on the far right of the dataset.

```
flights_day <- mutate(flights, date = as.Date(time_hour))
```

```
flights_summarized <- flights_day %>% group_by(date) %>%
  summarize(median_arr_delay = median(arr_delay, na.rm = TRUE))
flights_summarized
```

```
## # A tibble: 365 × 2
##          date median_arr_delay
##        <date>            <dbl>
## 1  2013-01-01                3
## 2  2013-01-02                4
```

```
## 3  2013-01-03                1
## 4  2013-01-04               -8
## 5  2013-01-05               -7
## 6  2013-01-06               -1
## 7  2013-01-07              -10
## 8  2013-01-08               -7
## 9  2013-01-09               -6
## 10 2013-01-10              -11
## # ... with 355 more rows
```

You will see the "pipe" operator `%>%` explained in more detail in Chapter 5, but you can read it as "and then". Here, we take the `flights_day` dataframe that we just created and then group it together by `date`. This goes through the dataframe and puts together all rows that have `2013-01-01` together, all rows that have `2013-01-02` together, ..., and all rows that have `2013-12-31` together. And then it looks at the median value of `arr_delay` over each one of the days. You can get a glimpse of the first few rows of this new dataset above since we invoked the `head` function on it.

Note also that there are missing values in this data set so we need to exclude them from the analysis. This is why the `na.rm = TRUE` argument is invoked. Many functions require this extra specification so it's always a good idea to run a `?median` or `?mean` before you try to run the function. Or you can always run it afterwards as well when you get strange results.

Now getting back to our line-graph. We want to plot the median arrival delay over all airlines on all days in 2013 from departing flights in NYC. This syntax should look similar to what we have seen before with plots involving `ggplot`. Notice that we are using the `flights_summarized` dataset here and not the `flights_day` or `flights` dataframes.

```
ggplot(data = flights_summarized, aes(x = date, y = median_arr_delay)) +
  geom_line()
```

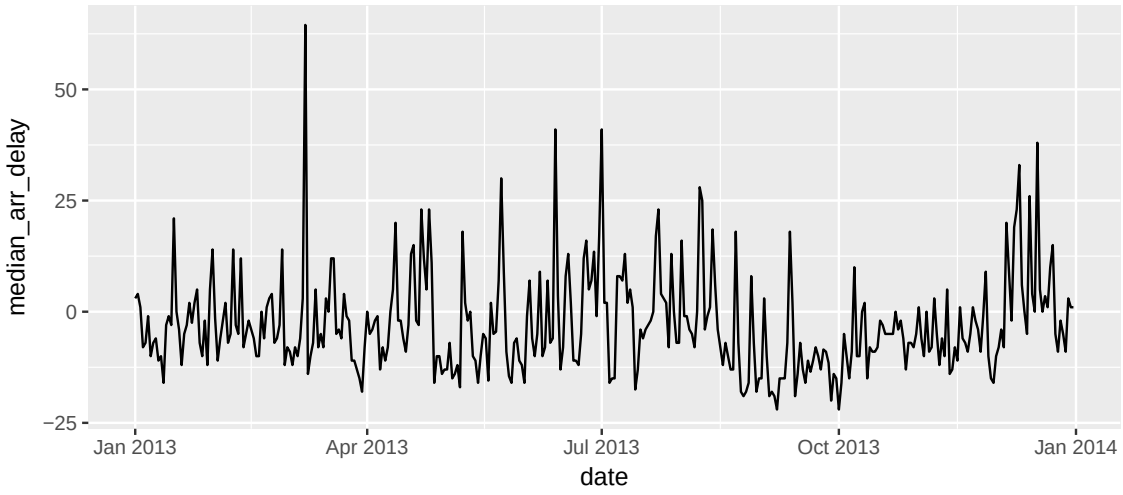


Figure 4.20: Line-graph of median arrival delay for flights leaving NYC in 2013 versus day of the year

---

Learning check

(LC4.32) Why should line-graphs be avoided when there is not a clear ordering of the horizontal axis?

(LC4.33) Why are line-graphs frequently used when time is the explanatory variable?

(LC4.34) Why did we use the `flights_summarized` dataframe to produce the line-graph in Figure 4.20 instead of `flights` or `flights_day`?

(LC4.35) Are the largest median arrival delays where you expected them to occur on the line-graph above in Figure 4.20? Why or why not?

4.6.1 Summary

Line-graphs provide a useful tool for viewing a continuous variable that is plotted versus time. We need to be careful to not be too entrenched in using line-graphs whenever we wish though. They only make sense when the explanatory variable (the one on the explanatory variable) has a natural ordering. We can mislead our audience if that isn't the case.

4.7 Brief Review of The Grammar of Graphics

The 5NG discussion above has introduced you to all of the major pieces behind "The Grammar of Graphics", which serves as the basis for the `ggplot2` package. This theoretical framework given by Leland Wilkinson (Wilkinson, 2005) helps us identify what the pieces are that make up a statistical graphic:

> In brief, the grammar tells us that a statistical graphic is a mapping from data to aesthetic attributes (color, shape, size) of geometric objects (points, lines, bars).

Specially, we can break a graphic into the following components:

- `aes`: mappings of data to *aesthetics* we can perceive on a graphic. These include x/y position, color, size, and shape. Each aesthetic can be mapped to a variable in our data set. If not assigned, they are set to defaults.
- `geom`: (geometric objects) This refers to our type of plot: points, lines, bars, etc.
- `stat`: (statistical transformations to summarize data) This includes smoothing, binning values into a histogram, or just itself `"identity"`.

- `facet`: how to break up data into subsets and display broken down plots as small multiples
- `scales` both
  - convert **data units** to **physical units** the computer can display
  - draw a legend and/or axes, which provide an inverse mapping to make it possible to read the original data values from the graph.
- `coord`: coordinate system for x/y values: typically cartesian.
- `position` adjustments

There are other extra attributes that can be tweaked as well including titles for the plot and each of the axes and also over-arching themes for the plot. In general, the Grammar of Graphics allows for customizability but also keeping with a consistent framework that allows the user to easily tweak their creations as they wish or need to in order to convey a message about their data.

We'll see (and have seen) that you don't necessarily need to include all of these in your code to produce a plot but each of the components are set by default and do exist with each plot produced using `ggplot2`.

An excellent resource as you begin to create plots using the `ggplot2` package is a cheatsheet that RStudio has put together entitled "Data Visualization with ggplot2" available here. This covers more than what we've discussed in this chapter but provides nice visual descriptions of what each function produces.

4.8 Script of R code

An R script file of all R code used in this chapter is available here.

4.9 What's to come?

In Chapter 5, we'll further explore data by grouping our data, creating summaries based on those groupings, filtering our data to match conditions, selecting specific columns of our data, and other manipulations with our data including defining new columns/variables. These data manipulation procedures will go hand-in-hand with the data visualizations you've produced here.

5

Manipulating Data

Let's briefly recap where we have been so far and where we are headed. In Chapter 3, we discussed what it means for data to be tidy. We saw that this refers to observational units corresponding to rows and variables being stored in columns. The entries in the data frame correspond to different combinations of observational units and variables. In the `flights` data frame, we saw that each row corresponded to a different flight leaving New York City. (In other words, the observational unit of that tidy data frame is a flight.) The variables are listed as columns and for `flights` they include both quantitative variables like `dep_delay` and `distance` but also categorical variables like `carrier` and `origin`. An entry in the table corresponds to a particular flight on a given day and a particular value of a given variable representing that flight.

We saw in Chapter 4 that organizing data in this tidy way makes it easy for us to produce graphics. We can simply specify what variable/column we would like on one axis, what variable we'd like on the other axis, and what type of plot we'd like to make. We can also do things such as changing the color by another variable or change the size of our points by a fourth variable given this tidy data set.

In Chapter 4, we also introduced some ways to summarize and manipulate data to suit your needs. This chapter focuses more on the details of this by giving a variety of examples using the five main verbs in the `dplyr` package (Wickham and Francois, 2016). There are more advanced operations that can be done than these and you'll see some examples of this near the end of the chapter.

As we saw with the RStudio cheatsheet on data visualization, RStudio has also created a cheatsheet for data manipulation entitled "Data Wrangling with dplyr and tidyr" available here. We will focus only on the `dplyr` functions in this book, but you are encouraged to also explore `tidyr` if you are presented with data that is not in the tidy format that we have specified as the preferred option for our purposes.

5.1 Five Main Verbs - The FMV

If you scan over the Data Wrangling cheatsheet, you may be initially overwhelmed by the amount of functions available. You'll see the use of all of these as you work more and more

with data frames in R. The `d` in `dplyr` stands for data frames so the functions here work when you are working with objects of the data frame type.

It's most important for you to focus on the five most commonly used functions that help us manipulate and summarize data. A description of these verbs follows with each subsection devoted to seeing an example of that verb in play (or a combination of a few verbs):

- `select`: Choose variables/columns by their names
- `filter`: Pick rows based on conditions about their values
- `summarize`: Create summary measures of variables (or groups of observations on variables using `group_by`)
- `mutate`: Make a new variable in the data frame
- `arrange`: Sort the rows based on one or more variables

Just as we had the 5NG (The Five Named Graphs in Chapter 4 using `ggplot2`), we have the FMV here (The Five Main Verbs in `dplyr`):

5.1.1 Select variables using `select`

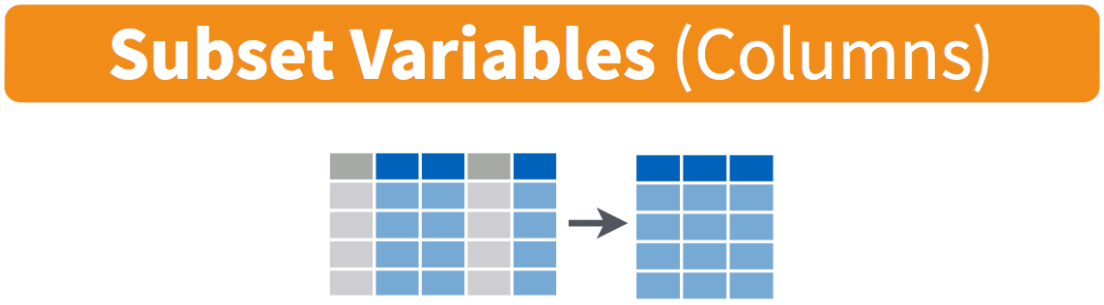


Figure 5.1: Select diagram from Data Wrangling with dplyr and tidyr cheatsheet

We've seen that the `flights` data frame in the `nycflights13` package contains many different variables (19 in fact). You can identify this by running the `dim` function or the `ncol` function:

```
library(nycflights13)
data(flights)
dim(flights)
```

```
## [1] 336776     19
```

```
ncol(flights)
```

```
## [1] 19
```

One of these variables is `year`. If you remember the original description of the `flights` data frame (or by running `?flights`), you'll remember that this data correspond to flights in 2013

departing New York City. The `year` variable isn't really a variable here in that it doesn't vary... `flights` actually comes from a larger data set that covers many years. We may want to remove the `year` variable from our data set since it won't be helpful for analysis in this case. To do so easily, we use the `select` variable:

```
if(!require(dplyr))
  install.packages("dplyr", repos = "http://cran.rstudio.org")
library(dplyr)
flights <- select(.data = flights, -year)
names(flights)
```

```
##  [1] "month"          "day"            "dep_time"       "sched_dep_time"
##  [5] "dep_delay"      "arr_time"       "sched_arr_time" "arr_delay"
##  [9] "carrier"        "flight"         "tailnum"        "origin"
## [13] "dest"           "air_time"       "distance"       "hour"
## [17] "minute"         "time_hour"
```

Here we have specified that the first argument to `select` is the `.data` argument. (Remember that you can get an idea for what arguments a function requires by using the `?` operator. In this case `?select` will show you information about the `select` function in the `dplyr` package.) We will likely avoid specifying this going forward since the `.data` argument is implied to be the first argument in many cases. The `names` function gives a listing of all the columns in a data frame. We see that `year` has been removed. This was done using a `-` in front of the name of the column we'd like to remove.

We could also select specific columns (instead of deselecting columns) by listing them out:

```
flight_dep_times <- select(flights, month, day, dep_time, sched_dep_time)
flight_dep_times
```

```
## # A tibble: 336,776 × 4
##    month   day dep_time sched_dep_time
##    <int> <int>    <int>          <int>
## 1      1     1      517            515
## 2      1     1      533            529
## 3      1     1      542            540
## 4      1     1      544            545
## 5      1     1      554            600
## 6      1     1      554            558
## 7      1     1      555            600
## 8      1     1      557            600
## 9      1     1      557            600
## 10     1     1      558            600
## # ... with 336,766 more rows
```

Or we could specify a ranges of columns:

```
flight_arr_times <- select(flights, month:day, arr_time:sched_arr_time)
flight_arr_times
```

```
## # A tibble: 336,776 × 4
##    month   day arr_time sched_arr_time
##    <int> <int>    <int>          <int>
## 1      1     1      830            819
## 2      1     1      850            830
## 3      1     1      923            850
## 4      1     1     1004           1022
## 5      1     1      812            837
## 6      1     1      740            728
## 7      1     1      913            854
## 8      1     1      709            723
## 9      1     1      838            846
## 10     1     1      753            745
## # ... with 336,766 more rows
```

The `select` function can also be used to reorder columns in combination with the `everything` helper function. Let's suppose we'd like the `hour`, `minute`, and `time_hour` variables, which appear at the end of the `flights` data set, to actually appear immediately after the `day` variable:

```
flights_reorder <- select(flights, month:day, hour:time_hour, everything())
names(flights_reorder)
```

```
##  [1] "month"          "day"            "hour"           "minute"
##  [5] "time_hour"      "dep_time"       "sched_dep_time" "dep_delay"
##  [9] "arr_time"       "sched_arr_time" "arr_delay"      "carrier"
## [13] "flight"         "tailnum"        "origin"         "dest"
## [17] "air_time"       "distance"
```

Lastly, the helper functions `starts_with`, `ends_with`, and `contains` can be used to choose column names that match those conditions:

```
flights_begin_a <- select(flights, starts_with("a"))
flights_begin_a
```

```
## # A tibble: 336,776 × 3
##    arr_time arr_delay air_time
##       <int>     <dbl>    <dbl>
## 1       830        11      227
## 2       850        20      227
```

```
## 3       923        33      160
## 4      1004       -18      183
## 5       812       -25      116
## 6       740        12      150
## 7       913        19      158
## 8       709       -14       53
## 9       838        -8      140
## 10      753         8      138
## # ... with 336,766 more rows
```

```
flights_delays <- select(flights, ends_with("delay"))
flights_delays
```

```
## # A tibble: 336,776 × 2
##    dep_delay arr_delay
##        <dbl>     <dbl>
## 1          2        11
## 2          4        20
## 3          2        33
## 4         -1       -18
## 5         -6       -25
## 6         -4        12
## 7         -5        19
## 8         -3       -14
## 9         -3        -8
## 10        -2         8
## # ... with 336,766 more rows
```

```
flights_time <- select(flights, contains("time"))
flights_time
```

```
## # A tibble: 336,776 × 6
##    dep_time sched_dep_time arr_time sched_arr_time air_time
##       <int>          <int>    <int>          <int>    <dbl>
## 1       517            515      830            819      227
## 2       533            529      850            830      227
## 3       542            540      923            850      160
## 4       544            545     1004           1022      183
## 5       554            600      812            837      116
## 6       554            558      740            728      150
## 7       555            600      913            854      158
## 8       557            600      709            723       53
## 9       557            600      838            846      140
## 10      558            600      753            745      138
```

```
## # ... with 336,766 more rows, and 1 more variables: time_hour <dttm>
```

Another useful function is `rename`, which as you may suspect renames one column to another name. Suppose we wanted `dep_time` and `arr_time` to be `departure_time` and `arrival_time` instead in the `flights_time` data frame:

```
flights_time <- rename(flights_time,
                       departure_time = dep_time,
                       arrival_time = arr_time)
names(flights_time)
```

```
## [1] "departure_time" "sched_dep_time" "arrival_time"   "sched_arr_time"
## [5] "air_time"       "time_hour"
```

It's easy to forget if the new name comes before or after the equals sign. I usually remember this as "New Before, Old After" or NBOA.

You'll receive an error if you try to do it the other way:

```
Error: Unknown variables: departure_time, arrival_time.
```

Learning check

(LC5.1) What are some ways to select all three of the `dest`, `air_time`, and `distance` variables from `flights`? Give the code showing how to do this in at least three different ways.

(LC5.2) How could one use `starts_with`, `ends_with`, and `contains` to select columns from the `flights` data frame? Provide three different examples in total: one for `starts_with`, one for `ends_with`, and one for `contains`.

(LC5.3) Why might we want to use the `select` function on a data frame?

5.1.2 Filter observations using `filter`

All of the FMVs follow the same syntax with the first argument to the function/verb being the name of the data frame and then the other arguments specifying which criteria you'd like the verb to work with.

The `filter` function here works much like the "Filter" option in Microsoft Excel. It allows you to specify criteria about values of a variable in your data set and then chooses only those rows that match that criteria. We begin by focusing only on flights from New York City to Portland, Oregon. The `dest` code (or airport code) for Portland, Oregon is `"PDX"`:

Figure 5.2: Filter diagram from Data Wrangling with dplyr and tidyr cheatsheet

```
portland_flights <- filter(flights, dest == "PDX")
portland_flights
```

```
## # A tibble: 1,354 × 18
##    month   day dep_time sched_dep_time dep_delay arr_time
##    <int> <int>    <int>          <int>     <dbl>    <int>
## 1      1     1     1739           1740        -1     2051
## 2      1     1     1805           1757         8     2117
## 3      1     1     2052           2029        23     2349
## 4      1     2      804            805        -1     1039
## 5      1     2     1552           1550         2     1853
## 6      1     2     1727           1720         7     2042
## 7      1     2     1738           1740        -2     2028
## 8      1     2     2024           2029        -5     2314
## 9      1     3     1755           1745        10     2110
## 10     1     3     1814           1727        47     2108
## # ... with 1,344 more rows, and 12 more variables:
## #   sched_arr_time <int>, arr_delay <dbl>, carrier <chr>, flight <int>,
## #   tailnum <chr>, origin <chr>, dest <chr>, air_time <dbl>,
## #   distance <dbl>, hour <dbl>, minute <dbl>, time_hour <dttm>
```

Note the second equals sign here. You are almost guaranteed to make the mistake at least once of only including one equals sign. Let's see what happens when we make this error:

```
portland_flights <- filter(flights, dest = "PDX")
```

```
Error: filter() takes unnamed arguments. Do you need `==`?
```

We see that there were 1354 flights from New York City to Portland in 2013. Let's combine this with what we saw in the previous subsection to ensure that Portland flights were selected:

```
reordered_flights <- select(flights, dest, everything())
pdx_flights <- filter(reordered_flights, dest == "PDX")
pdx_flights
```

```
## # A tibble: 1,354 × 18
##     dest month   day dep_time sched_dep_time dep_delay arr_time
##    <chr> <int> <int>    <int>          <int>     <dbl>    <int>
## 1    PDX     1     1     1739           1740        -1     2051
## 2    PDX     1     1     1805           1757         8     2117
## 3    PDX     1     1     2052           2029        23     2349
## 4    PDX     1     2      804            805        -1     1039
## 5    PDX     1     2     1552           1550         2     1853
## 6    PDX     1     2     1727           1720         7     2042
## 7    PDX     1     2     1738           1740        -2     2028
## 8    PDX     1     2     2024           2029        -5     2314
## 9    PDX     1     3     1755           1745        10     2110
## 10   PDX     1     3     1814           1727        47     2108
## # ... with 1,344 more rows, and 11 more variables:
## #   sched_arr_time <int>, arr_delay <dbl>, carrier <chr>, flight <int>,
## #   tailnum <chr>, origin <chr>, air_time <dbl>, distance <dbl>,
## #   hour <dbl>, minute <dbl>, time_hour <dttm>
```

We see that Portland flights were selected here. You could also run `View(pdx_flights)` to glance at the data in spreadsheet form.

You can combine multiple criteria together using operators that make comparisons:

- `|` corresponds to "or"
- `&` corresponds to "and"

We can often skip the use of `&` and just separate our conditions with a comma. You'll see this in the example below.

In addition, you can use other mathematical checks (similar to `==`):

- `>` corresponds to "greater than"
- `<` corresponds to "less than"
- `>=` corresponds to "greater than or equal to"
- `<=` corresponds to "less than or equal to"
- `!=` corresponds to "not equal to"

To see many of these in action, let's select all flights that left JFK airport heading to Burlington, Vermont (`"BTV"`) or Seattle, Washington (`"SEA"`) in the months of October, November, or December:

```
btv_sea_flights_fall <- filter(flights,
                               origin == "JFK",
                               (dest == "BTV") | (dest == "SEA"),
                               month >= 10)
```

Another example uses the `!` to pick rows that **DON'T** match a condition. Here we are referring to excluding the Northern Hemisphere summer months of June, July, and August.

```
not_summer_flights <- filter(flights,
                             !between(month, 6, 8))
not_summer_flights
```

```
## # A tibble: 249,781 × 18
##    month   day dep_time sched_dep_time dep_delay arr_time
##    <int> <int>    <int>          <int>     <dbl>    <int>
## 1      1     1      517            515         2      830
## 2      1     1      533            529         4      850
## 3      1     1      542            540         2      923
## 4      1     1      544            545        -1     1004
## 5      1     1      554            600        -6      812
## 6      1     1      554            558        -4      740
## 7      1     1      555            600        -5      913
## 8      1     1      557            600        -3      709
## 9      1     1      557            600        -3      838
## 10     1     1      558            600        -2      753
## # ... with 249,771 more rows, and 12 more variables:
## #   sched_arr_time <int>, arr_delay <dbl>, carrier <chr>, flight <int>,
## #   tailnum <chr>, origin <chr>, dest <chr>, air_time <dbl>,
## #   distance <dbl>, hour <dbl>, minute <dbl>, time_hour <dttm>
```

To check that we are correct here we can use the `count` function in the `dplyr` package on the `month` variable in our `not_summer_flights` data frame to ensure June, July, and August are not selected:

```
count(not_summer_flights, month)
```

```
## # A tibble: 9 × 2
##   month     n
##   <int> <int>
## 1     1 27004
## 2     2 24951
## 3     3 28834
## 4     4 28330
## 5     5 28796
## 6     9 27574
## 7    10 28889
## 8    11 27268
## 9    12 28135
```

The function `between` is a shortcut. We could also have written the following to get the same result:

```
not_summer2 <- filter(flights, month <= 5 | month >= 9)
count(not_summer2, month)
```

```
## # A tibble: 9 × 2
##   month     n
##   <int> <int>
## 1     1 27004
## 2     2 24951
## 3     3 28834
## 4     4 28330
## 5     5 28796
## 6     9 27574
## 7    10 28889
## 8    11 27268
## 9    12 28135
```

Learning check

(LC5.4) What's another way using `!` we could filter only the rows that are not summer months (June, July, or August) in the `flights` data frame?

5.1.3 Summarize variables using `summarize`

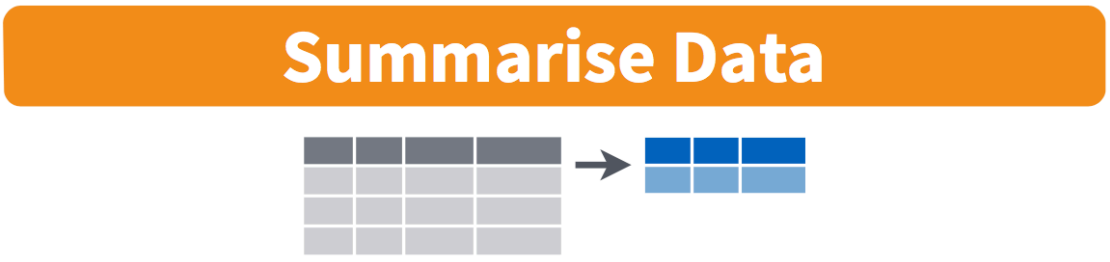


Figure 5.3: Summarize diagram from Data Wrangling with dplyr and tidyr cheatsheet

We saw in Subsection 4.2.1 a way to calculate the standard deviation and mean of the temperature variable `temp` in the `weather` data frame of `nycflights`. We can do so in one step using the `summarize` function in `dplyr`:

Figure 5.4: Another summarize diagram from Data Wrangling with dplyr and tidyr cheatsheet

```
summarize(weather,
          mean = mean(temp),
          std_dev = sd(temp))
```

```
## # A tibble: 1 × 2
##    mean std_dev
##   <dbl>   <dbl>
## 1    NA      NA
```

What happened here? The mean and the standard deviation temperatures are missing? Remember that by default the `mean` and `sd` functions do not ignore missing values. We need to specify `TRUE` for the `na.rm` parameter:

```
summary_temp <- summarize(weather,
          mean = mean(temp, na.rm = TRUE),
          std_dev = sd(temp, na.rm = TRUE)
          )
summary_temp
```

```
## # A tibble: 1 × 2
##       mean  std_dev
##      <dbl>    <dbl>
## 1 55.20351 17.78212
```

We've created a small data frame here called `summary_temp` that includes both the `mean` and the `std_dev` of the `temp` variable in `weather`. If we'd like to access either of these values directly we can use the `$` to specify a column in a data frame:

```
summary_temp$mean
```

```
## [1] 55.20351
```

```
summary_temp$std_dev
```

```
## [1] 17.78212
```

It's often more useful to summarize a variable based on the groupings of another variable. Let's say we were interested in the mean and standard deviation of temperatures for each month. We believe that you will be amazed at just how simple this is:

Figure 5.5: Group by and summarize diagram from Data Wrangling with dplyr and tidyr cheatsheet

```
grouped_weather <- group_by(weather, month)
summary_tempXmonth <- summarize(grouped_weather,
          mean = mean(temp, na.rm = TRUE),
          std_dev = sd(temp, na.rm = TRUE)
          )
summary_tempXmonth
```

```
## # A tibble: 12 × 3
##    month     mean   std_dev
##    <dbl>    <dbl>     <dbl>
## 1      1 35.64127 10.185459
## 2      2 34.15454  6.940228
## 3      3 39.81404  6.224948
## 4      4 51.67094  8.785250
## 5      5 61.59185  9.608687
## 6      6 72.14500  7.603356
## 7      7 80.00967  7.147631
## 8      8 74.40495  5.171365
## 9      9 67.42582  8.475824
## 10    10 60.03305  8.829652
## 11    11 45.10893 10.502249
## 12    12 38.36811  9.940822
```

By simply grouping the `weather` data set by `month` first and then passing this new data frame into `summarize` we get a resulting data frame that shows the mean and standard deviation temperature for each month in New York City.

Another useful function is the `n` function which gives a count of how many entries appeared in the groupings. Suppose we'd like to get a sense for how many flights departed each of the three airports in New York City:

```
grouped_flights <- group_by(flights, origin)
by_origin <- summarize(grouped_flights,
                       count = n())
by_origin
```

```
## # A tibble: 3 × 2
##   origin  count
##    <chr>  <int>
## 1    EWR 120835
## 2    JFK 111279
## 3    LGA 104662
```

We see that Newark (`"EWR"`) had the most flights departing in 2013 followed by `"JFK"` and lastly by LaGuardia (`"LGA"`).

Learning check

(LC5.5) Recall from Chapter 4 when we looked at plots of temperatures by months in NYC. What does the standard deviation column in the `summary_tempXmonth` data frame tell us about temperatures in New York City throughout the year?

(LC5.6) What code would be required to get the mean and standard deviation temperature for each day in 2013 for NYC?

(LC5.7) How could we identify how many flights left each of the three airports in each of the months of 2013?

5.1.4 Create new variables/change old variables using `mutate`

When looking at the `flights` data set, there are some clear additional variables that could be calculated based on the values of variables already in the data set. Passengers are often frustrated when their flights departs late, but change their mood a bit if pilots can make up some time during the flight to get them to their destination close to when they expected to land. This is commonly referred to as "gain" and we will create this variable using the `mutate` function:

Figure 5.6: Mutate diagram from Data Wrangling with dplyr and tidyr cheatsheet

```
flights_plus <- mutate(flights,
         gain = arr_delay - dep_delay)
```

We can now look at summary measures of this `gain` variable and even plot it in the form of a histogram:

```
gain_summary <- summarize(flights_plus,
          min = min(gain, na.rm = TRUE),
          q1 = quantile(gain, 0.25, na.rm = TRUE),
          median = quantile(gain, 0.5, na.rm = TRUE),
          q3 = quantile(gain, 0.75, na.rm = TRUE),
          max = max(gain, na.rm = TRUE),
          mean = mean(gain, na.rm = TRUE),
          sd = sd(gain, na.rm = TRUE),
          missing = sum(is.na(gain))
)
gain_summary
```

```
## # A tibble: 1 × 8
##     min    q1 median    q3   max      mean       sd missing
##   <dbl> <dbl>  <dbl> <dbl> <dbl>     <dbl>    <dbl>   <int>
## 1  -109   -17     -7     3   196 -5.659779 18.04365    9430
```

We've recreated the `summary` function we saw in Chapter 4 here using the `summarize` function in `dplyr`.

```
library(ggplot2)
ggplot(flights_plus, aes(x = gain)) +
  geom_histogram(color = "white", bins = 20)
```

We can also create multiple columns at once and even refer to columns that were just created in a new column. Hadley produces one such example in Chapter 5 of "R for Data Science" (Grolemund and Wickham, 2016):

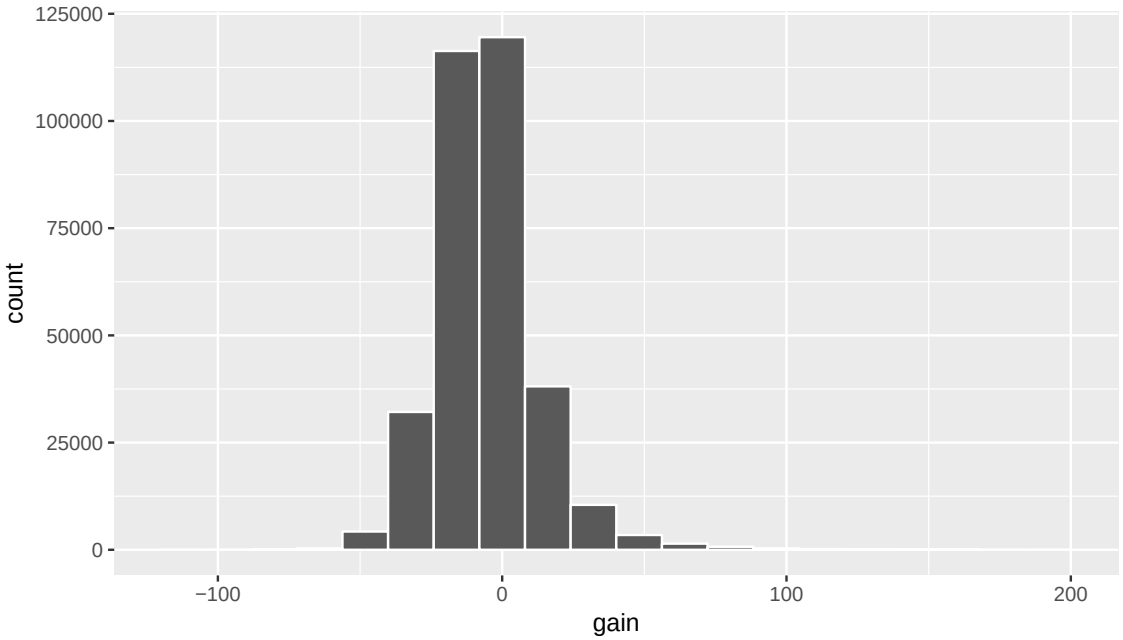


Figure 5.7: Histogram of gain variable

```
flights_plus2 <- mutate(flights,
  gain = arr_delay - dep_delay,
  hours = air_time / 60,
  gain_per_hour = gain / hours
)
```

Learning check

(LC5.8) What do positive values of the `gain` variable in `flights_plus` correspond to? What about negative values? And what about a zero value?

(LC5.9) Could we create the `dep_delay` and `arr_delay` columns by simply subtracting `dep_time` from `sched_dep_time` and similarly for arrivals? Try the code out and explain any differences between the result and what actually appears in `flights`.

(LC5.10) What can we say about the distribution of `gain`? Describe it in a few sentences using the plot and the `gain_summary` data frame values.

5.1.5 Reorder the data frame using `arrange`

As you may have thought about with the data frames we've worked with so far in the book, one of the most common things you'd like to do is sort the data frames by a specific column. Have you ever been asked to calculate a median by hand? This requires you to put the data in order from smallest to highest in value. The `dplyr` package has a function called `arrange` that we will use to sort/reorder our data according to the values of the specified variable. This is most frequently used after we have used the `group_by` and `summarize` functions as we will see.

Let's suppose we were interested in determining the most frequent destination airports from New York City in 2013:

```
by_dest <- group_by(flights, dest)
freq_dest <- summarize(by_dest, num_flights = n())
freq_dest
```

```
## # A tibble: 105 × 2
##     dest num_flights
##    <chr>       <int>
## 1    ABQ         254
## 2    ACK         265
## 3    ALB         439
## 4    ANC           8
## 5    ATL       17215
## 6    AUS        2439
## 7    AVL         275
## 8    BDL         443
## 9    BGR         375
## 10   BHM         297
## # ... with 95 more rows
```

You'll see that by default the values of `dest` are displayed in alphabetical order here. Remember to use `View()` in the R Console to look at all the values of `freq_dest` in spreadsheet format. We are interested in finding those airports that appear most:

```
arrange(freq_dest, num_flights)
```

```
## # A tibble: 105 × 2
##     dest num_flights
##    <chr>       <int>
## 1    LEX           1
## 2    LGA           1
## 3    ANC           8
## 4    SBN          10
## 5    HDN          15
```

```
## 6    MTJ          15
## 7    EYW          17
## 8    PSP          19
## 9    JAC          25
## 10   BZN          36
## # ... with 95 more rows
```

This is actually giving us the opposite of what we are looking for. It tells us the least frequent destination airports first. To switch the ordering to be descending instead of ascending we use the `desc` function:

```
arrange(freq_dest, desc(num_flights))
```

```
## # A tibble: 105 × 2
##     dest num_flights
##    <chr>       <int>
## 1    ORD       17283
## 2    ATL       17215
## 3    LAX       16174
## 4    BOS       15508
## 5    MCO       14082
## 6    CLT       14064
## 7    SFO       13331
## 8    FLL       12055
## 9    MIA       11728
## 10   DCA        9705
## # ... with 95 more rows
```

We can also use the `top_n` function which automatically tells us the most frequent `num_flights`. We specify the top 10 airports here:

```
top_n(freq_dest, n = 10, wt = num_flights)
```

```
## # A tibble: 10 × 2
##     dest num_flights
##    <chr>       <int>
## 1    ATL       17215
## 2    BOS       15508
## 3    CLT       14064
## 4    DCA        9705
## 5    FLL       12055
## 6    LAX       16174
## 7    MCO       14082
## 8    MIA       11728
```

```
## 9    ORD       17283
## 10   SFO       13331
```

We'll still need to arrange this by `num_flights` though:

```
arrange(top_n(freq_dest, n = 10, wt = num_flights), desc(num_flights))
```

```
## # A tibble: 10 × 2
##     dest num_flights
##    <chr>       <int>
## 1    ORD       17283
## 2    ATL       17215
## 3    LAX       16174
## 4    BOS       15508
## 5    MCO       14082
## 6    CLT       14064
## 7    SFO       13331
## 8    FLL       12055
## 9    MIA       11728
## 10   DCA        9705
```

Note: Remember that I didn't pull the `n` and `wt` arguments out of thin air. They can be found by using the `?` function on `top_n`.

Learning check

(LC5.11) Create a new data frame that shows the top 5 airports with the largest arrival delays from NYC in 2013.

5.2 The pipe %>%

Just as the `+` sign was used to add layers to a plot created using `ggplot` we will use the pipe operator (`%>%`) to chain together `dplyr` functions. We'll see that we can even chain together `dplyr` functions and plotting code. (Both `ggplot2` and `dplyr` were created by Hadley after all.)

You may have been a little confused by the last chunk we created above:

```
arrange(top_n(freq_dest, n = 10, wt = num_flights), desc(num_flights))
```

If we don't create temporary variables like we did before with `by_dest`, `grouped_flights`, etc., we start to get into the issue of trying to match parentheses. We could separate this code a bit to help with this:

```
arrange(
  top_n(freq_dest,
        n = 10,
        wt = num_flights),
  desc(num_flights))
```

```
## # A tibble: 10 × 2
##     dest num_flights
##    <chr>       <int>
## 1    ORD       17283
## 2    ATL       17215
## 3    LAX       16174
## 4    BOS       15508
## 5    MCO       14082
## 6    CLT       14064
## 7    SFO       13331
## 8    FLL       12055
## 9    MIA       11728
## 10   DCA        9705
```

Even this make it difficult to understand what is exactly happening though. `desc(num_flights)` is an argument to `arrange` and this isn't easy to see immediately. The best way to fix this problem is the use of the chaining operator called the pipe (`%>%`):

```
freq_dest %>%
  top_n(n = 10, wt = num_flights) %>%
  arrange(desc(num_flights))
```

```
## # A tibble: 10 × 2
##     dest num_flights
##    <chr>       <int>
## 1    ORD       17283
## 2    ATL       17215
## 3    LAX       16174
## 4    BOS       15508
## 5    MCO       14082
## 6    CLT       14064
## 7    SFO       13331
```

```
## 8    FLL       12055
## 9    MIA       11728
## 10   DCA        9705
```

Recall from Chapter 4 that we read the pipe operator as "and then". So here we take the `freq_dest` data frame **AND THEN** we determine the top 10 values of `num_flights` **AND THEN** we arrange these top 10 flights according to descending numbers of flights (from highest to lowest).

We can go one stop further and tie together the `group_by` and `summarize` functions we used to find the most frequent flights:

```
ten_freq_dests <- flights %>%
  group_by(dest) %>%
  summarize(num_flights = n()) %>%
  top_n(n = 10) %>%
  arrange(desc(num_flights))
```

```
## Selecting by num_flights
```

Learning check

(LC5.12) Recreate each of the chunks of code above Subsection 5.1.5 in this chapter using the `%>%` operator. Note that sometimes you can combine multiple subsequent chunks of code together. Do so whenever possible.

(LC5.13) What benefits can you see to using the pipe instead of the other way of doing things as you saw throughout this chapter? Give specific examples.

(LC5.14) Write out exactly how the `ten_freq_dests` data set was created using the "and then" verbiage.

The piping syntax will be our major focus throughout the rest of this book and you'll find that you'll quickly be addicted to the chaining with some practice. If you'd like to see more examples on using `dplyr`, the FMV (in addition to some other `dplyr` verbs), and `%>%` with the `nycflights13` data set, you can check out Chapter 5 of Hadley and Garrett's book (Grolemund and Wickham, 2016).

5.3 Joining/merging data frames

Something you may have thought to yourself as you looked at the most freqent destinations of flights from NYC in 2013 is

- "What cities are these airports in?"
- "Is `"ORD"` Orlando?"
- "Where is `"FLL"`?

The `nycflights13` data package contains multiple data frames. Instead of having to manually look up different values of airport names corresponding to airport codes like `ORD`, we can have R automatically do this "looking up" for us. To do so, we'll need to tell R how to match one data frame to another data frame. Let's first check out the `airports` data frame inside of R:

```
View(airports)
```

The first column `faa` corresponds to the airport codes that we saw in `dest` in our `flights` and subsequent `ten_freq_dests` data sets. Hadley and Garrett (Grolemund and Wickham, 2016) created the following diagram to help us understand how the different data sets are linked:

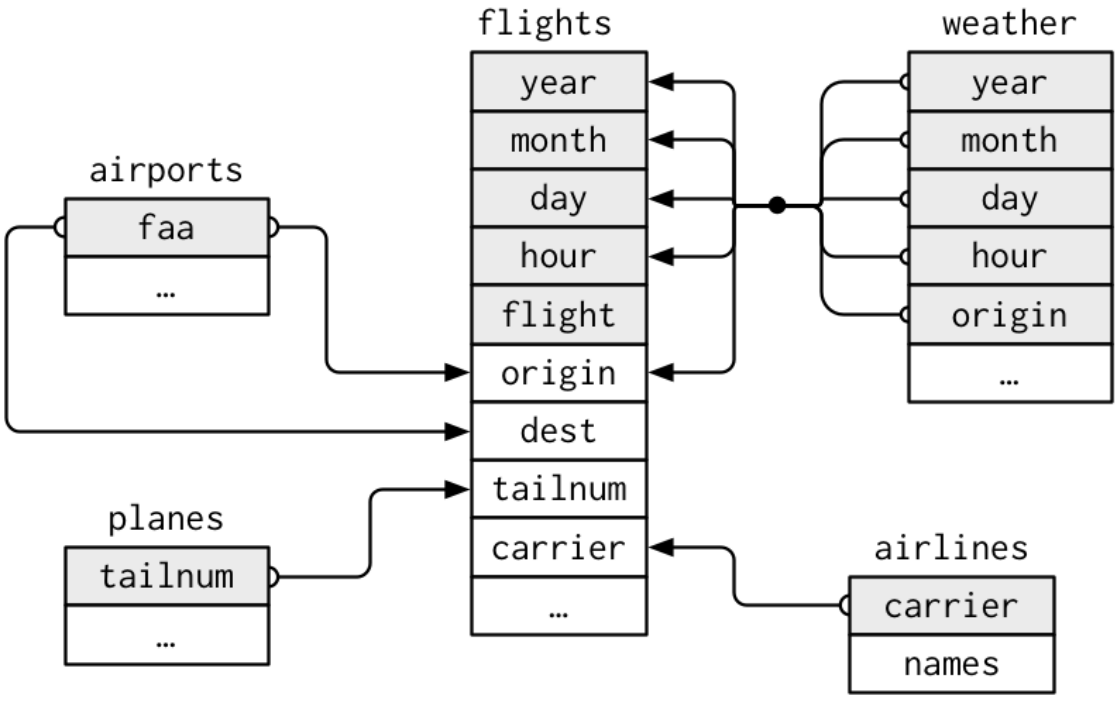


Figure 5.8: Data relationships in nycflights13 from R for Data Science

We see from `View(airports)` that `airports` contains a lot of other information about 1396. We are only really interested here in the `faa` and `name` columns. Let's use the `select` function to only use those variables:

```
airports_small <- airports %>%
  select(faa, name)
```

So if we identify the names of the airports we can use the `inner_join` function to bring two different data frames together. Note that we will also rename the subsequent column `name` as `airport_name`:

```
named_freq_dests <- ten_freq_dests %>%
  inner_join(airports_small, by = c("dest" = "faa")) %>%
  rename(airport_name = name)
named_freq_dests
```

```
## # A tibble: 10 × 3
##     dest num_flights                      airport_name
##    <chr>       <int>                             <chr>
## 1    ORD       17283                 Chicago Ohare Intl
## 2    ATL       17215    Hartsfield Jackson Atlanta Intl
## 3    LAX       16174                   Los Angeles Intl
## 4    BOS       15508 General Edward Lawrence Logan Intl
## 5    MCO       14082                       Orlando Intl
## 6    CLT       14064             Charlotte Douglas Intl
## 7    SFO       13331                 San Francisco Intl
## 8    FLL       12055     Fort Lauderdale Hollywood Intl
## 9    MIA       11728                           Miami Intl
## 10   DCA        9705      Ronald Reagan Washington Natl
```

In case you didn't know, `"ORD"` is the airport code of Chicago O'Hare airport and `"FLL"` is the main airport in Fort Lauderdale, Florida, which we can now see in our `named_freq_dests` data frame.

A visual representation of the `inner_join` is given below (Grolemund and Wickham, 2016):

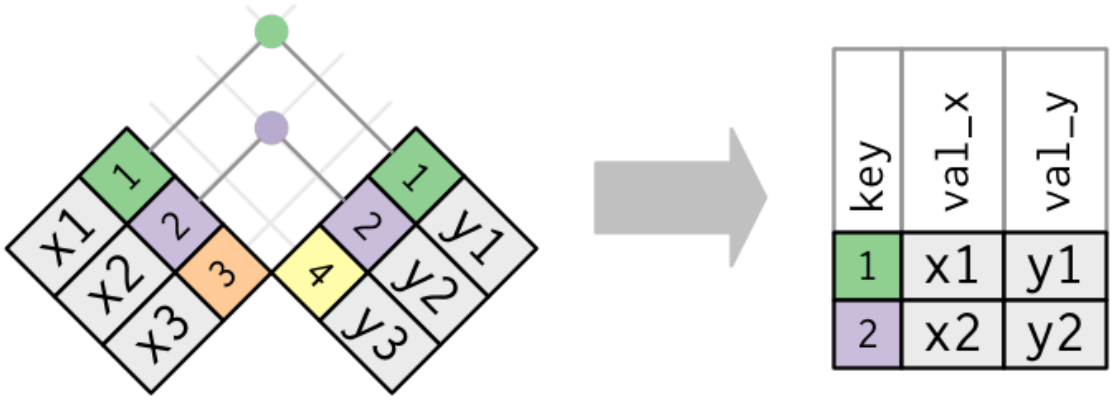


Figure 5.9: Diagram of inner join from R for Data Science

There are more complex joins available, but the `inner_join` will solve nearly all of the problems you'll face in our experience.

Learning check

(LC5.15) What happens when you try to `inner_join` the `ten_freq_dests` data frame with `airports` instead of `airports_small`? How might one use this result to answer further questions about the top 10 destinations?

(LC5.16) What surprises you about the top 10 destinations from NYC in 2013?

5.4 Script of R code

An R script file of all R code used in this chapter is available here.

5.5 What's to come?

This concludes the **Data Exploration** unit of this book. You should be pretty proficient in both plotting variables (or multiple variables together) in various data sets and manipulating data as we've done in this chapter. You are encouraged to step back through the code in earlier chapters and make changes as you see fit based on your updated knowledge.

In Chapter 6, we'll begin to build the pieces needed to understand how this unit of **Data Exploration** can tie into statistical inference in the **Inference** part of the book. Remember that the focus throughout is on data visualization and we'll see that next when we discuss sampling, resampling, and bootstrapping. These ideas will lead us into hypothesis testing and confidence intervals.

Part II

Inference

6

Inference Basics

In this chapter we will introduce new concepts that will serve as the basis for the remainder of the text: **sampling**, **bootstrapping** and **resampling**. We will see that the tools that you learned in the Data Exploration part of this book (tidy data, data manipulation, and data visualization) will also play an important role here. As mentioned before, the concepts all build into a culmination allowing you to create better stories with data.

We begin with some helpful definitions that will help us better understand why statistical inference exists and why it is needed. We will then progress with a famous example from statistics lore and then introduce the second of our main data sets (in addition to the `nycflights13` data you've been working with) about movie ratings from IMDB.com. We will see how we can use samples from this data set to infer more general conclusions about all of the movies (in the population).

6.1 Random sampling

Whenever you hear the phrases "random sampling" or just "sampling" (with regards to statistics), you should think about tasting soup. This likely sounds a little bonkers. Let's dig in to why tasting soup is such an excellent analogy to random sampling.

6.1.1 Tasting soup

Imagine that you have invited a group of friends over to try a new recipe for soup that you've never made before. As in the image above downloaded from here, you'd like to make a bowl of Indian chicken soup with lots of different kinds of vegetables included.

You've carefully followed along with the recipe but you are concerned that you don't have a lot of experience making Indian-style foods. It is coming near the end of the prescribed time to cook given in the recipe. You begin to wonder:

- "Did I add too much curry spice?"
- "Are the carrots cooked enough?"
- "Does this actually taste good?"

Figure 6.1: A bowl of Indian chicken and vegetable soup

How can we answer these questions? Does it matter where we take a bite of soup from? Is there anything we should do to the soup before we taste? Is one taste enough?

Learning check

(LC6.1) Explain in your own words how tasting soup relates to the concepts of sampling covered here.

(LC6.2) Describe a different scenario (not food or drink related) that is analogous to sampling concepts covered here.

6.1.2 Common terms

The process of sampling brings with it many common terms that we define now. As you read over these definitions, think about how they each apply to the tasting soup example above.

Definition: population

The *population* is the (usually) large pool of observational units that we are interested in.

Definition: sample

A *sample* is a smaller collection of observational units that is selected from the population.

Definition: sampling

Sampling refers to the process of selecting observations from a population. There are both random and non-random ways this can be done.

Definition: representative sample

A sample is said be a *representative sample* if the characteristics of observational units selected are a good approximation of the characteristics from the original population.

Definition: bias

Bias corresponds to a favoring of one group in a population over another group.

Definition: generalizability

Generalizability refers to the largest group in which it makes sense to make inferences about from the sample collected. This is directly related to how the sample was selected.

Definition: parameter

A *parameter* is a calculation based on one or more variables measured in the population. Parameters are almost always denoted symbolically using Greek letters such as μ, π, σ, ρ, and β.

Definition: statistic

A *statistic* is a calculated based on one or more variables measured in the sample. Parameters are usually denoted by lower case Arabic letters with other symbols added sometimes. These include $\bar{x}$, $\hat{p}$, s, p, and b.

Let's explore these terms for our tasting soup example:

Population - the entire container of soup that we have cooked.

Sample - any smaller portion of soup collected that isn't the whole container of soup. We could say that each spoonful of soup represents one sample.

Sampling - the process of selecting spoonfuls from the container of soup

Representative sample - A sample we select will only be representative if it tastes like what the soup tastes like in general. If we only select a carrot in our spoonful, we might not have a representative sample.

Bias - As we noted with the carrot selection example above, we may select a sample that is not representative. If you watch chefs cook or if you frequently cook, you'll be sure to stir the soup before you taste it.

Generalizability - If we stir our soup before we taste a spoonful (and if we make sure we don't just pick our favorite item in the soup), results from our sample can be generalized (by and

large) to the larger pot of soup. When we say "Yum! This is good!" after a couple spoonfuls, we can be pretty confident that each bowl of soup for our friends will taste good too.

Parameter - An example here is could be the proportion of curry entered into the entire pot of soup. A measurement of how salty the pot of soup is on average is also a parameter. How crunchy, on average, the carrots are in the pot of soup is one more example.

Statistic - To convert a parameter to a statistic, you need only to think about the same measurement on a spoonful:

- The proportion of curry to non-curry in a spoonful of soup
- How salty the spoonful of soup is that we collected as our sample
- How crunchy the carrots are in our spoonful of soup

Learning check

(LC6.3) Why isn't our population all bowls of soup? All bowls of Indian chicken soup?

(LC6.4) Describe a way in which we could select a sample of flights from `nycflights13` that is not representative.

(LC6.5) If we treat all of the flights in `nycflights13` as the population, give examples of three *parameters* we could calculate.

(LC6.6) If we treat all of the flights in `nycflights13` as the population, give examples of three *statistics* we could calculate.

(LC6.7) What biases might we see if we only select flights to Boston when we are interested in looking at mean flight delays from NYC?

6.2 Simulation

What follows is taken from a book entitled *The Lady Tasting Tea* (Salsburg, 2001):

> It was a summer afternoon in Cambridge, England, in the late 1920s. A group of university dons, their wives, and some guests were sitting around an outdoor table for afternoon tea. One of the women was insisting that tea tasted different depending upon whether the tea was poured into the milk or whether the milk was poured into the tea. The scientific minds among the men scoffed at this as sheer nonsense. What could be the difference? They could not conceive of any difference in the chemistry of the mixtures that could exist. A thin, short man, with thick glasses and a Vandyke beard beginning to turn gray, pounced on the problem. "Let us test the proposition," he said excitedly. He began to outline an experiment in which the lady who insisted there was a difference would be presented with a sequence of cups of tea, in some of

> which the milk had been poured into the tea and in others of which the tea had been poured into the milk…
>
> So it was that sunny summer afternoon in Cambridge. The lady might or might not have been correct about the tea infusion. The fun would be in finding a way to determine if she was right, and, under the direction of the man with the Vandyke beard, they began to discuss how they might make that determination.
>
> Enthusiastically, many of them joined with him in setting up the experiment. Within a few minutes, they were pouring different patterns of infusion in a place where the lady could not see which cup was which. Then, with an air of finality, the man with the Vandyke beard presented her with her first cup. She sipped for a minute and declared that it was one where the milk had been poured into the tea. He noted her response without comment and presented her with the second cup…
>
> The man with the Vandyke beard was Ronald Aylmer Fisher, who was in his late thirties at the time. He would later be knighted Sir Ronald Fisher. In 1935, he wrote a book entitled *The Design of Experiments*, and he described the experiment of the lady tasting tea in the second chapter of that book. In his book, Fisher discusses the lady and her belief as a hypothetical problem. He considers the various ways in which an experiment might be designed to determine if she could tell the difference. The problem in designing the experiment is that, if she is given a single cup of tea, she has a 50 percent chance of guessing correctly which infusion was used, even if she cannot tell the difference. If she is given two cups of tea, she still might guess correctly. In fact, if she knew that the two cups of tea were each made with a different infusion, one guess could be completely right (or completely wrong).
>
> Similarly, even if she could tell the difference, there is some chance that she might have made a mistake, that one of the cups was not mixed as well or that the infusion was made when the tea was not hot enough. She might be presented with a series of ten cups and correctly identify only nine of them, even if she could tell the difference.
>
> In his book, Fisher discusses the various possible outcomes of such an experiment. He describes how to decide how many cups should be presented and in what order and how much to tell the lady about the order of presentations. He works out the probabilities of different outcomes, depending upon whether the lady is or is not correct. Nowhere in this discussion does he indicate that such an experiment was ever run. Nor does he describe the outcome of an actual experiment.

It's amazing that there is no actual evidence that such an event actually took place. This problem is a great introduction into inference though and we can proceed by testing to see how likely it is for a person to guess correctly, say, 9 out of 10 times assuming that that person is just guessing. In other words, is the person just lucky or do we have reason to suspect that they can actually detect whether milk was put in first or not?

We need to think about this problem from the standpoint of hypothesis testing. First, we'll need to identify some important parts of a hypothesis test before we proceed with the analysis.

Learning check

(LC6.8) What does "by chance" mean in this context?

(LC6.9) What is our observed statistic?

(LC6.10) What is this statistic trying to estimate?

(LC6.11) How could we test to see whether the person is just guessing or if they have some special talent of identifying milk before tea or vice-versa?

Let's begin with an experiment. I will flip a coin 10 times. Your job is to try to predict the sequence of my 10 flips. Write down 10 H's and T's corresponding to your predictions. We could compare your guesses with my actual flips and then we will note how many correct guesses you have.

You may be asking yourself how this models a way to test whether the person was just guessing or not. All we are trying to do is see how likely it is to have 9 matches out of 10 if the person was truly guessing. When we say "truly guessing" we are assuming that we have a 50/50 chance of guessing correctly. This can be modeled using a coin flip and then seeing whether we guessed correctly for each of the coin flips. If we guessed correctly, we can think of that as a "success."

We often don't have time to do the physical flipping over and over again and we'd like to be able to do more than just 20 different simulations or so. Luckily, we can use R to simulate this process many times. The `mosaic` package includes a function called `rflip()`, which can be used to flip one coin. Well, not exactly. It uses pseudo-random number generation to "flip" a virtual coin. In order for us all to get the same results here, we can set the seed of the pseudo-random number generator. Let's see an example of this: (Remember to load the `mosaic` package!)

```
library(mosaic)
set.seed(2016)
do(1) * rflip(1)
```

```
##   n heads tails prop
## 1 1     0     1    0
```

This shows us the proportion of "successes" in one flip of a coin. The `do` function in the `mosaic` package will be useful and you can begin to understand what it does with another example.

```
do(13) * rflip(10)
```

```
##     n heads tails prop
## 1  10     4     6  0.4
## 2  10     7     3  0.7
## 3  10     3     7  0.3
## 4  10     3     7  0.3
## 5  10     3     7  0.3
## 6  10     6     4  0.6
## 7  10     2     8  0.2
## 8  10     6     4  0.6
## 9  10     4     6  0.4
## 10 10     4     6  0.4
## 11 10     6     4  0.6
## 12 10     7     3  0.7
## 13 10     2     8  0.2
```

We've now done a simulation of what actually happened when you flipped a coin ten times. We have 13 different simulations of flipping a coin 10 times. Note here that `heads` now corresponds to the number of correct guesses and `tails` corresponds to the number of incorrect guesses. (This can be tricky to understand at first since we've done a switch on what the meaning of "heads" and "tails" are.)

If you look at the output above for our simulation of 13 student guesses, we can begin to get a sense for what an "expected" sample proportion of successes may be. Around five out of 10 seems to be the most likely value. What does this say about our assumed $\hat{p}$ of 9/10? To better answer this question, we can simulate 10,000 student guesses and then look at the distribution of the simulated sample proportion of successes, also known as the **null distribution**.

```
library(dplyr)
library(tibble)
simGuesses <- do(10000) * rflip(10)
simGuesses <- as_tibble(simGuesses)
simGuesses %>%
  group_by(heads) %>%
  summarize(count = n())
```

```
## # A tibble: 11 × 2
##    heads count
##    <dbl> <int>
## 1      0     7
## 2      1    81
## 3      2   424
## 4      3  1084
```

```
## 5       4  2075
## 6       5  2479
## 7       6  2117
## 8       7  1157
## 9       8   461
## 10      9   105
## 11     10    10
```

Note: Here `as_tibble` converts data frames to tibbles. This is also why the `library(tibble)` command is needed. The conversion to `tibble` format is mostly done for allowing for nice printing of large data sets when we mention the name of a data frame object in a chunk by itself. (The data sets in `nycflights13` come as tibbles by default.) You can read more about tibbles in Chapter 10 of Hadley and Garrett's book (Grolemund and Wickham, 2016).

We can see here that we have created a count of how many of each of the 10,000 sets of 10 flips resulted in 0, 1, 2, ..., up to 10 heads. Note the use of the `group_by` and `summarize` functions from Chapter 5 here.

In addition, we can plot the distribution of these simulated `heads` using the ideas from Chapter 4. `heads` is a quantitative variable. Think about which type of plot is most appropriate here before reading further.

We already have an idea as to an appropriate plot by the data summarization that we did in the chunk above. We'd like to see how many heads occurred in the 10,000 sets of 10 flips. In other words, we'd like to see how frequently 9 or more heads occurred in the 10 flips:

```
library(ggplot2)
simGuesses %>% ggplot(aes(x = heads)) +
  geom_bar()
```

This horizontal axis labels are a little confusing here. What does 2.5 or 7.5 heads mean? In `simGuesses`, `heads` is a `numerical` variable. Thus, `ggplot` is expecting the values to be on a continuous scale. We can switch the scale to be discrete by invoking the `factor` function:

```
library(ggplot2)
simGuesses %>% ggplot(aes(x = factor(heads))) +
  geom_bar()
```

You'll frequently need to make this conversion to `factor` when making a barplot with quantitative variables. Remember from "Getting Used to R, RStudio, and R Markdown" (Ismay, 2016), that a `factor` variable is useful when there is a natural ordering to the variable. Our `heads` variable has a natural ordering: 0, 1, 2, ..., 10.

6.2.1 The p-value

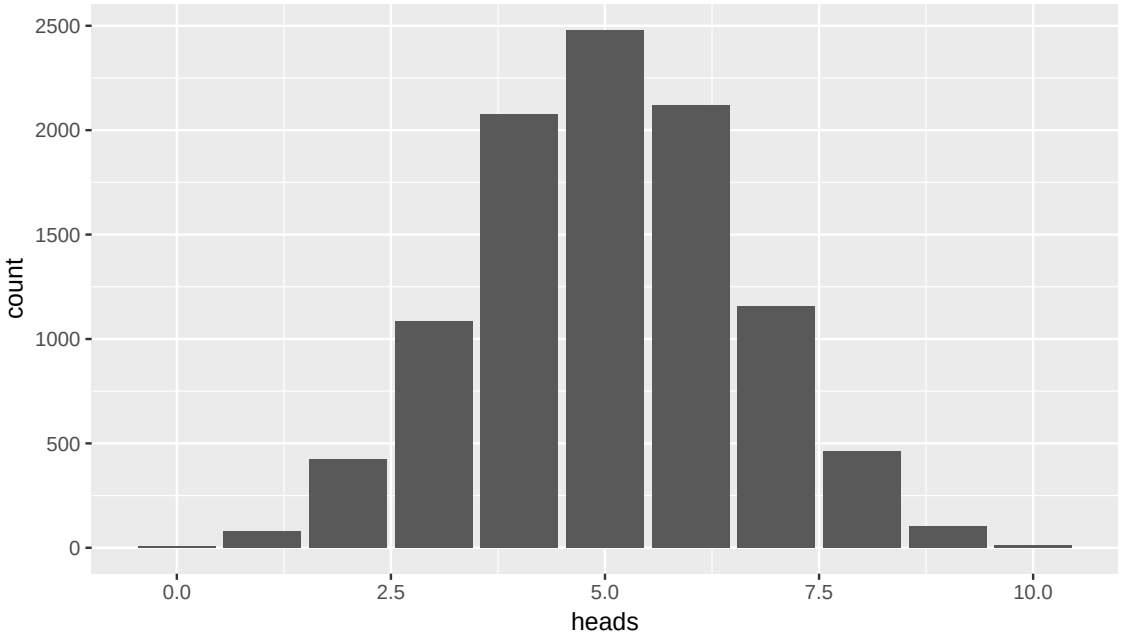


Figure 6.2: Barplot of number of heads in simulation - needs tweaking

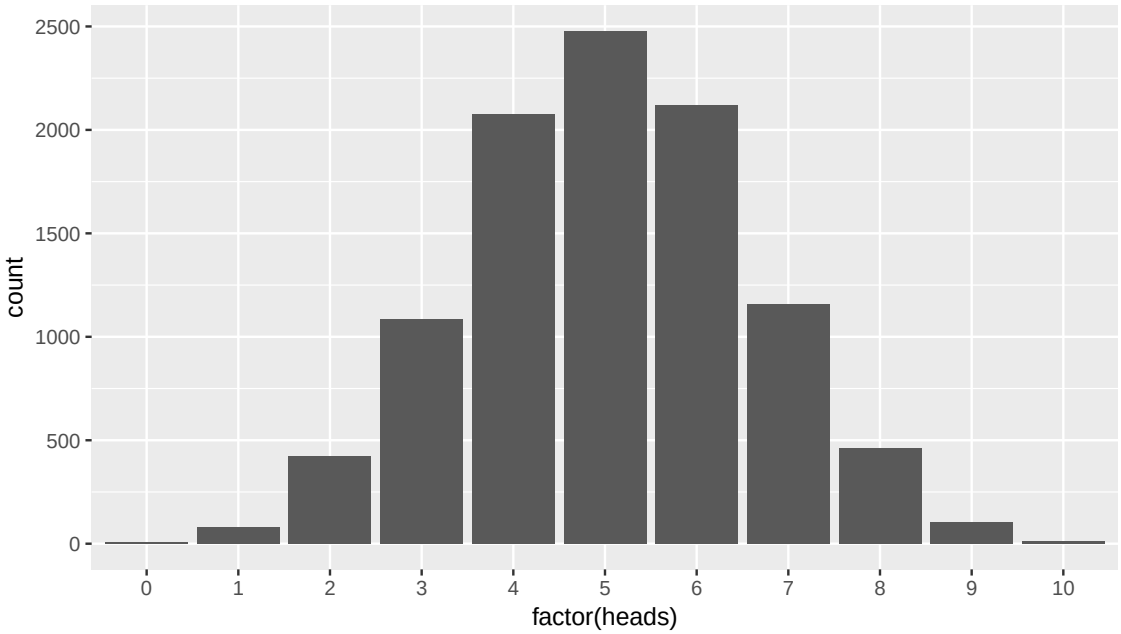


Figure 6.3: Barplot of number of heads in simulation

Definition: ***p*-value**:

The **p-value** is the probability of observing a sample statistic as extreme or more extreme than what was observed, assuming that the null hypothesis of a by chance operation is true.

This definition may be a little intimidating the first time you read it, but it's important to come back to this "The Lady Tasting Tea" problem whenever you encounter p-values as you begin to learn about the concept. Here the p-value corresponds to how many times in our **null distribution** of `heads` 9 or more heads occurred.

We can use another neat feature of R to calculate the p-value for this problem. Note that "more extreme" in this case corresponds to looking at values of 9 or greater since our alternative hypothesis invokes a right-tail test corresponding to a "greater than" hypothesis of $H_a : \pi > 0.5$. In other words, we are looking to see how likely it is for the lady to pick 9 or more correct instead of 9 or less correct. We'd like to go in the right direction.

```
pvalue_tea <- simGuesses %>%
  filter(heads >= 9) %>%
  nrow() / nrow(simGuesses)
```

Let's walk through each step of this calculation:

1. First, `pvalue_tea` will be the name of our calculated p-value and the assignment operator `<-` directs us to this naming.
2. We are working with the `simGuesses` data frame here so that comes immediately before the pipe operator.
3. We would like to only focus on the rows in our `simGuesses` data frame that have `heads` values of 9 or 10. This represents simulated statistics "as extreme or more extreme" than what we observed (9 correct guesses out of 10). Let's get a glimpse of what we have up to this point:

```
simGuesses %>% tbl_df() %>%
  filter(heads >= 9)
```

```
## # A tibble: 115 × 4
##        n heads tails  prop
##    <dbl> <dbl> <dbl> <dbl>
## 1     10     9     1   0.9
## 2     10     9     1   0.9
## 3     10     9     1   0.9
## 4     10     9     1   0.9
## 5     10     9     1   0.9
## 6     10     9     1   0.9
```

```
## 7     10    10     0   1.0
## 8     10     9     1   0.9
## 9     10     9     1   0.9
## 10    10     9     1   0.9
## # ... with 105 more rows
```

4. Now that we have changed the focus to only those rows that have number of heads out of 10 flips corresponding to 9 or more, we count how many of those there are. The function `nrow` gives how many entries are in this filtered data frame and lastly we calculate the proportion that are at least as extreme as our observed value of 9 by dividing by the number of total simulations (10,000).

We can see that the observed statistic of 9 correct guesses is not a likely outcome assuming the null hypothesis is true. Only around 1% of the outcomes in our 10,000 simulations fall at or above 9 successes. We have evidence supporting the conclusion that the person is actually better than just guessing at random at determining whether milk has been added first or not. To better visualize this we can also make use of pink shading on the histogram corresponding to the p-value:

```
library(ggplot2)
simGuesses %>%
  ggplot(aes(x = factor(heads), fill = (heads >= 9))) +
  geom_bar() +
  labs(x = "heads")
```

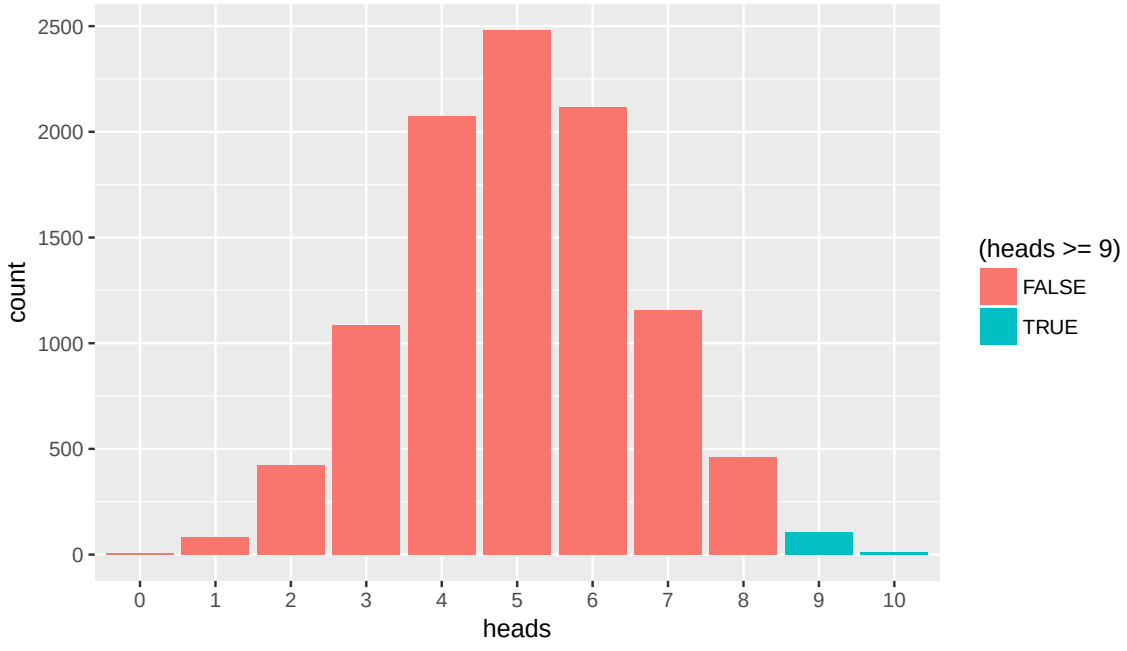


Figure 6.4: Barplot of heads with p-value highlighted

This helps us better see just how few of the values of `heads` are at our observed value or more extreme.

We'll see in Chapters 7 and 8 that this idea of a p-value can be extended to the more traditional methods using normal and t distributions in the traditional way that introductory statistics has been presented. These traditional methods were used because statisticians haven't always been able to do 10,000 simulations on the computer within seconds. We'll elaborate on this more in these later chapters.

Learning check

(LC6.12) What is meant by "pseudo-random number generation?"

(LC6.13) How can simulation be used to help us address the question of whether or not an observed result is statistically significant?

(LC6.14) In Chapter 4, we noted that barplots should be used when creating a plot of categorical variables. Why are we using barplots to make a plot of a numerical variable `heads` in this chapter?

6.3 Bootstrapping

Just as we did in the previous section when making hypotheses about a population proportion with which we would like to test which one is more plausible, we can also use simulation to infer conclusions about a population quantitative statistic such as the mean. In this case, we will focus on constructing confidence intervals to produce plausible values for a population mean. (We can do a similar analysis for a population median or other summary measure as well.)

Traditionally, the way to construct confidence intervals for a mean is to assume a normal distribution for the population or to invoke the Central Limit Theorem and get, what often appears to be magic, results. These methods are often not intuitive, especially for those that lack a strong mathematical background. They also come with their fair share of assumptions and often turn Statistics, a field that is full of tons of useful applications to many different fields and disciplines, into a robotic procedural-based topic. It doesn't have to be that way!

In this section, we will introduce the concept of **bootstrapping**. It will be a useful tool that will allow us to estimate the variability of our statistic from sample to sample. One neat feature of bootstrapping is that it enables us to approximate the sampling distribution and estimate the distribution's standard deviation using ONLY the information in the one selected (original) sample.

It sounds just as plagued with the magical type qualities of traditional theory-based inference on initial glance but we will see that it provides an intuitive and useful way to make inferences, especially when the samples are of medium to large size.

To introduce the concept of bootstrapping, we now introduce the `movies` data set in the `ggplot2movies` data frame. We will load this data frame into R in much the same way as we loaded `flights` and `weather` from the `nycflights13` package. (Remember that to load the package using `library` you need to first make sure you have installed the package using the `install.packages` function.)

```
library(ggplot2movies)
data(movies, package = "ggplot2movies")
```

Let's also glance at this data frame using the `View` function and look at the help documentation for `movies`:

```
View(movies)
?movies
```

We will explore many other features of this data set in the chapters to come, but here we will be focusing on the `rating` variable corresponding to the average IMDB user rating.

You may notice that this data set is quite large: 58,788 movies have data collected about them here. This will correspond to our population of ALL movies. Remember from Chapter 6 that our population is rarely known. We use this data set as our population here to show you the power of bootstrapping in estimating population parameters. We'll see how **confidence intervals** built using the bootstrap distribution do at including our population parameter of interest. Here we can actually calculate these values since our population is known, but remember that in general this isn't the case.

Let's take a look at what the distribution of our population `ratings` looks like. We'll see that we will use the distribution of our sample(s) as an estimate of this population histogram.

```
movies %>% ggplot(aes(x = rating)) +
  geom_histogram(color = "white", bins = 20)
```

Learning check

(LC6.15) Why was a histogram chosen as the plot to make for the `rating` variable above?

(LC6.16) Why does the shape of the `rating` histogram tell us about how IMDB users rate movies? What stands out about the plot?

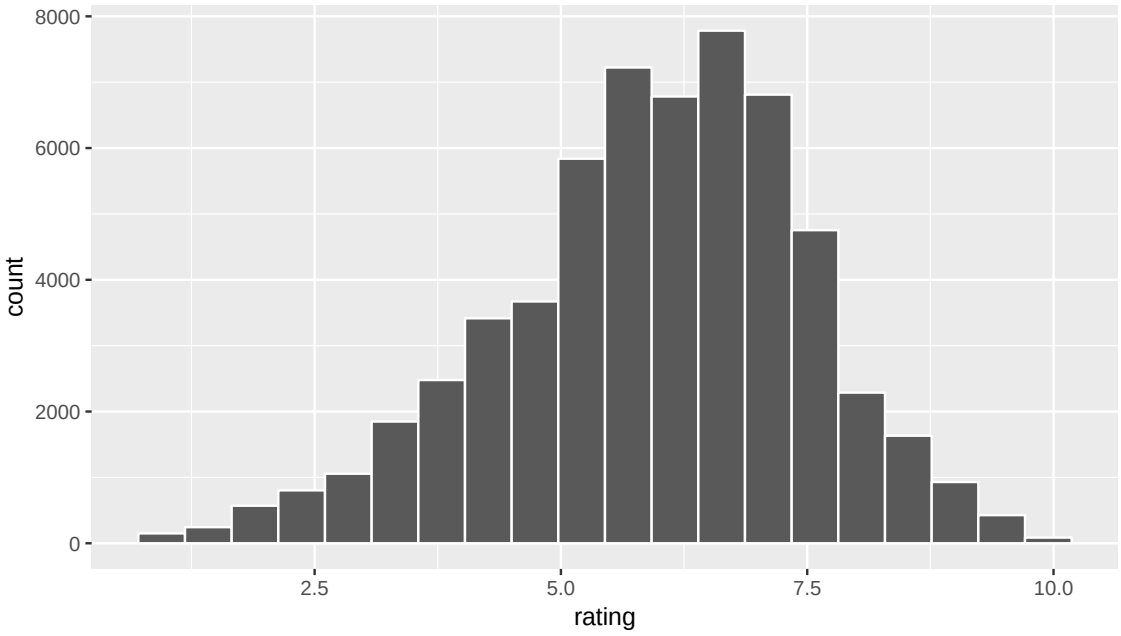


Figure 6.5: Population ratings histogram

It's important to think about what our goal is here. We would like to produce a confidence interval for the population mean `rating`. We will have to pretend for a moment that we don't have all 58,788 movies. Let's say that we only have a random sample of 50 movies from this data set instead. In order to get a random sample, we can use the `sample_n` function from `dplyr`:

```
set.seed(2016)
movies_sample <- movies %>%
  sample_n(50)
```

The `sample_n` function has filtered the data frame `movies` "at random" to choose only 50 rows from the larger `movies` data frame. We store information on these 50 movies in the `movies_sample` data frame.

Let's now explore what the `rating` variable looks like for these 50 movies:

```
movies_sample %>% ggplot(aes(x = rating)) +
  geom_histogram(color = "white", bins = 20)
```

Remember that we can think of this histogram as an estimate of our population distribution histogram that we saw above. We are interested in the population mean rating and trying to find a range of plausible values for that value. A good start in guessing the population mean is to use the mean of our sample `rating` from the `movies_sample` data:

```
(movies_sample_mean <- movies_sample %>% summarize(mean = mean(rating)))
```

```
## # A tibble: 1 × 1
```

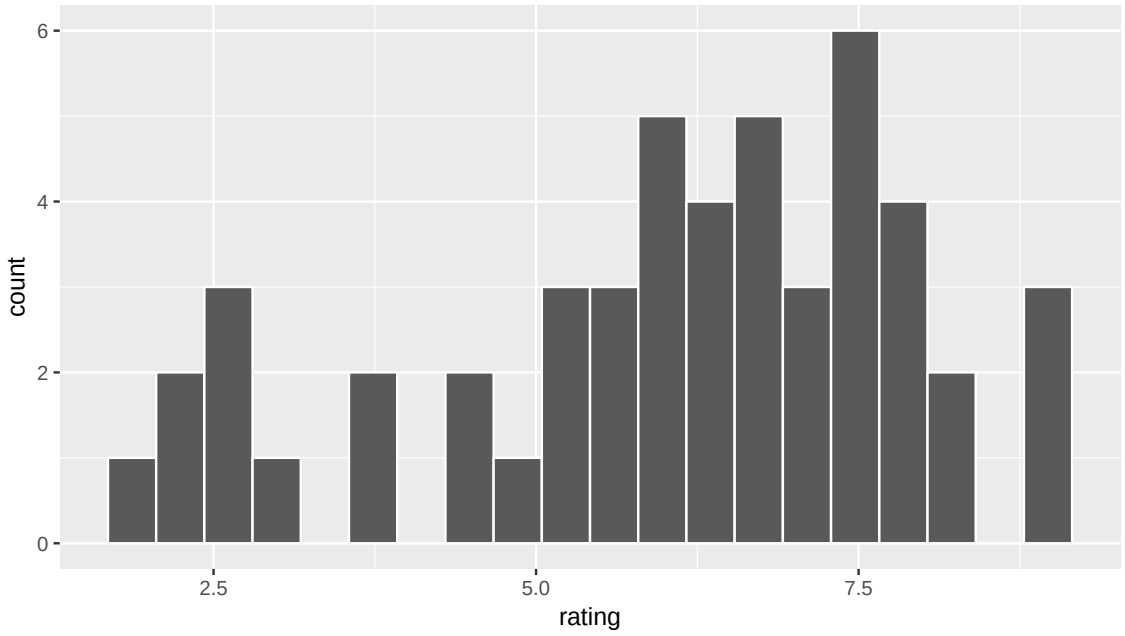


Figure 6.6: Sample ratings histogram

```
##    mean
##   <dbl>
## 1 6.034
```

Note the use of the `( )` at the beginning and the end of this creation of the `movies_sample_mean` object. If you'd like to print out your newly created object, you can enclose it in the parentheses as we have here.

This value of 6.034 is just one guess at the population mean. The idea behind *bootstrapping* is to sample **with replacement** from the original sample to create new **resamples** of the same size as our original sample.

Returning to our example, let's investigate what one such resample of the `movies_sample` data set accomplishes. We can create one resample/bootstrap sample by using the `resample` function in the `mosaic` package.

```
library(mosaic)
library(tibble)
boot1 <- resample(movies_sample, orig.ids = TRUE) %>%
  select(orig.id, everything()) %>%
  arrange(orig.id)
```

Take a look at this resample/bootstrap:

```
View(boot1)
```

The important thing to note here is the original row numbers from the `movies_sample` data

frame in the far left column called `orig.ids`. Since we are sampling with replacement, there is a strong likelihood that some of the 50 observational units are going to be selected again.

You may be asking yourself what does this mean and how to this lead us to creating a distribution for the sample mean. Recall that the original sample mean of our data was calculated using the `summarize` function above.

Learning check

(LC6.17) What happens if we change the seed to our pseudo-random generation? Try it above when we used `sample_n` to describe the resulting `movies_sample`.

(LC6.18) Why is sampling at random important from the `movies` data frame? Why don't we just pick `Action` movies and do bootstrapping with this `Action` movies subset?

(LC6.19) What was the purpose of assuming we didn't have access to the full `movies` data set here?

Before we had a calculated mean in our original sample of 6.034. Let's calculate the mean of `ratings` in our bootstrapped sample:

```
(movies_boot1_mean <- boot1 %>% summarize(mean = mean(rating)))
```

```
## # A tibble: 1 × 1
##    mean
##   <dbl>
## 1 6.144
```

More than likely the calculated bootstrap sample mean is different than the original sample mean. This is what I meant earlier when I said that the sample means have some variability. What we are trying to do is replicate many different samples being taken from a larger population. Our best guess at what the population looks like is multiple copies of the sample we collected. We then can sample from that larger "created" population by generating bootstrap samples.

Similar to what we did in the previous section, we can repeat this process using the `do` function followed by an asterisk. Let's look at 10 different bootstrap means for `ratings` from `movies_sample`. Note the use of the `resample` function here.

```
do(10) * summarize(resample(movies_sample), mean = mean(rating))
```

```
##     mean
## 1  6.020
## 2  6.668
## 3  5.996
## 4  6.056
## 5  6.168
## 6  6.360
## 7  5.702
## 8  6.218
## 9  6.252
## 10 5.904
```

You should see some variability begin to tease its way out here. Many of the simulated means will be close to our original sample mean but many will stray pretty far away. This occurs because outliers may have been selected a couple of times in the resampling or small values were selected more than larger. There are myriad reasons why this might be the case.

So what's the next step now? Just as we repeated the repetitions thousands of times with the "Lady Tasting Tea" example, we can do a similar thing here.

```
trials <- do(10000) * summarize(resample(movies_sample),
                                mean = mean(rating))
trials %>% ggplot(aes(x = mean)) +
  geom_histogram(bins = 30, color = "white")
```

The shape of this resulting distribution may look familiar to you. It resembles the well-known normal (bell-shaped) curve. We will see in Chapters 7 and 8 when we might expect a normal curve to come through as we have here and when we shouldn't. There will be specific assumptions that need to be checked and we will see that the normal distribution doesn't always approximate this bootstrapped distribution well. In those case, we should NOT rely on traditional methods.

At this point, we can easily calculate a confidence interval. In fact, we have a couple different options. We will first use the percentiles of the distribution we just created to isolate the middle 95% of values. This will correspond to our 95% confidence interval for the population mean `rating`, denoted by μ.

```
(ciq_mean_rating <- confint(trials, level = 0.95, method = "quantile"))
```

```
##   name   lower upper level     method estimate
## 1 mean 5.50795  6.54  0.95 percentile    6.034
```

It's always important at this point to interpret the results of this confidence interval calculation. In this context, we can say something like the following:

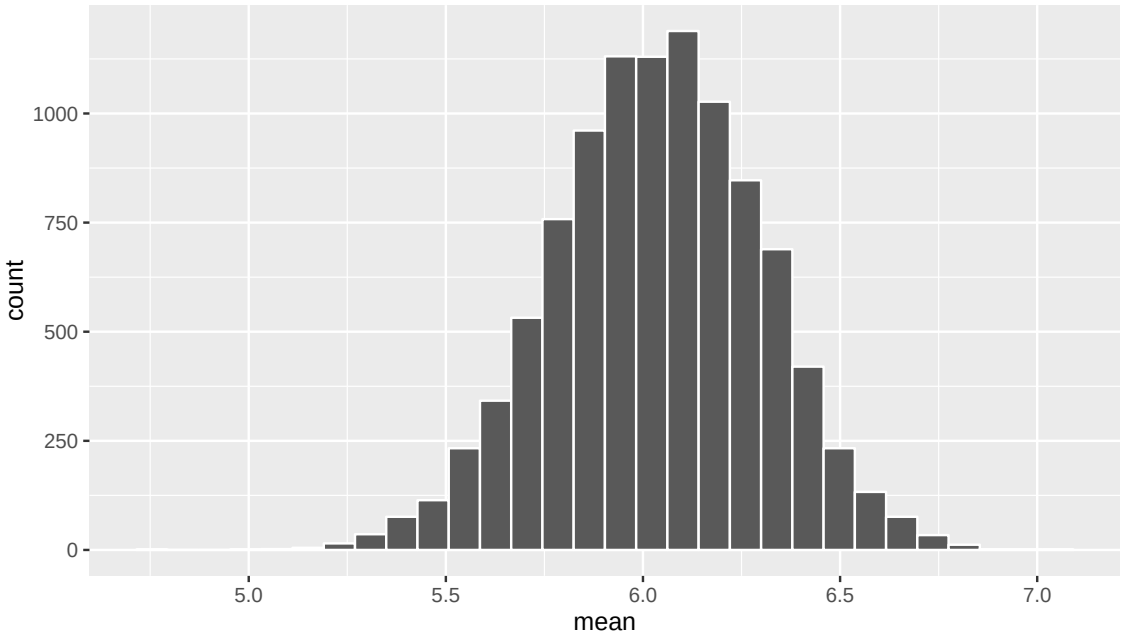


Figure 6.7: Bootstrapped means histogram

Based on the sample data and bootstrapping techniques, we can be 95% confident that the true mean rating of ALL IMDB ratings is between 5.50795 and 6.54.

This statement may seem a little confusing to you. Remember that we are pretending like we don't know what the mean IMDB rating for ALL movies is. Our population here is all of the movies listed in the `movies` data frame from `ggplot2movies`. So does our bootstrapped confidence interval here contain the actual mean value?

```
summarize(movies, mean = mean(rating))
```

```
## # A tibble: 1 × 1
##      mean
##     <dbl>
## 1 5.93285
```

We see here that the population mean does fall in our range of plausible values generated from the bootstrapped samples.

We can also get an idea of how the theory-based inference techniques would have approximated this confidence interval by using the formula

$$\bar{x} \pm (2 * SE),$$

where $\bar{x}$ is our original sample mean and SE stands for **standard error** and corresponds to the standard deviation of the bootstrap distribution. The value of 2 here corresponds to it being a 95% confidence interval. This formula assumes that the bootstrap distribution is symmetric. This is often the case with bootstrap distributions, especially those in which the original distribution of the sample is not highly skewed.

To compute this type of confidence interval, we only need to make a slight modification to the `confint` function seen above. (The expression after the ± sign is known as the **margin of error**.)

```
(cise_mean_rating <- confint(trials, level = 0.95, method = "stderr"))
```

```
##   name    lower    upper level method estimate margin.of.error
## 1 mean 5.516196 6.551379  0.95 stderr    6.034       0.5175914
```

Based on the sample data and bootstrapping techniques, we can be 95% confident that the true mean rating of ALL IMDB ratings is between 5.5161962 and 6.551379.

Learning check

(LC6.20) Reproduce the bootstrapping above using a sample of size 50 instead of 25. What changes do you see?

(LC6.21) Reproduce the bootstrapping above using a sample of size 5 instead of 25. What changes do you see?

(LC6.22) How does the sample size affect the analysis?

(LC6.23) Why must bootstrap samples be the same size as the original sample?

6.3.1 Review of Bootstrapping

We can summarize the process to generate a bootstrap distribution here in a series of steps that clearly identify the terminology we will use (Lock et al., 2012).

- Generate `bootstrap samples` by sampling with replacement from the original sample, using the same sample size.
- Compute the statistic of interest, called a `bootstrap statistic`, for each of the bootstrap samples.
- Collect the statistics for many bootstrap samples to create a `bootstrap distribution`.

Visually, we can represent this process in the following diagram.

6.4 Script of R code

An R script file of all R code used in this chapter is available here.

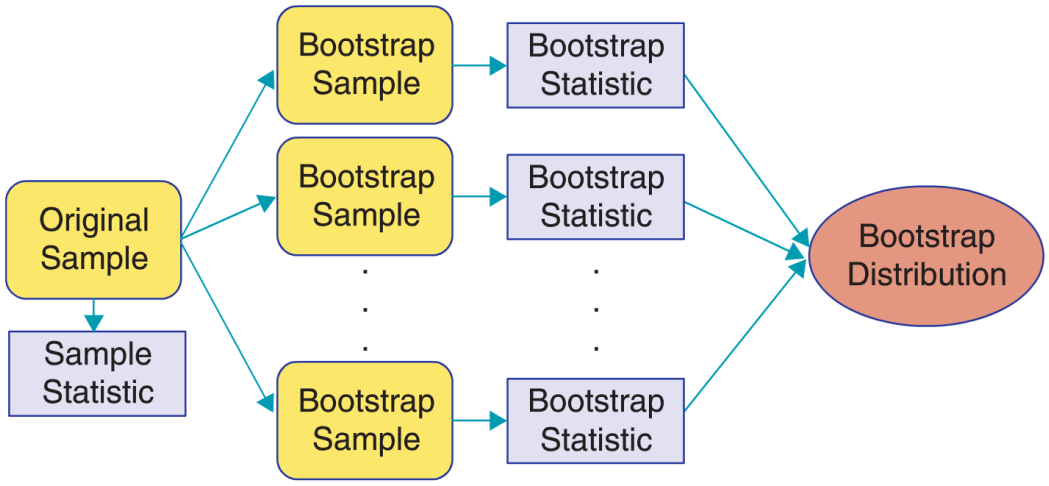


Figure 6.8: Bootstrapping diagram from Lock5 textbook

6.5 What's to come?

This chapter has served as an introduction into inferential techniques that will be discussed in greater detail in Chapter 7 for hypothesis testing and in Chapter 8 for confidence intervals. In these chapters, we will see how we can use a related concept of **resampling** when working with the distributions of two groups.

7

Hypothesis Testing

We saw some of the main concepts of hypothesis testing introduced in Chapter 6. We will expand further on these ideas here and also provide a framework for understanding hypothesis tests in general. Instead of presenting you with lots of different formulas and scenarios, we hope to build a way to think about all hypothesis tests. You can then adapt to different scenarios as needed down the road when you encounter different statistical situations.

In a hypothesis test, we will use data from a sample to help us decide between two competing *hypotheses* about a population. We make these hypotheses more concrete by specifying them in terms of at least one *population parameter* of interest. We refer to the competing claims about the population as the **null hypothesis**, denoted by H_0, and the **alternative (or research) hypothesis**, denoted by H_a. The roles of these two hypotheses are NOT interchangeable.

- The claim for which we seek significant evidence is assigned to the alternative hypothesis. The alternative is usually what the experimenter or researcher wants to establish or find evidence for.
- Usually, the null hypothesis is a claim that there really is "no effect" or "no difference." In many cases, the null hypothesis represents the status quo or that nothing interesting is happening.
- We assess the strength of evidence by assuming the null hypothesis is true and determining how unlikely it would be to see sample results/statistics as extreme (or more extreme) as those in the original sample.

Hypothesis testing brings about many weird and incorrect notions in the scientific community and society at large. One reason for this is that statistics has traditionally been thought of as this magic box of algorithms and procedures to get to results and this has been readily apparent if you do a Google search of "flowchart statistics hypothesis tests". There are so many different complex ways to determine which test is appropriate.

You'll see that we don't need to rely on these complicated series of assumptions and procedures to conduct a hypothesis test any longer. These methods were introduced in a time when computers weren't powerful. Your cellphone (in 2016) has more power than the computers that sent NASA astronauts to the moon after all. We'll see that ALL hypothesis tests can be broken down into the following framework given by Allen Downey here:

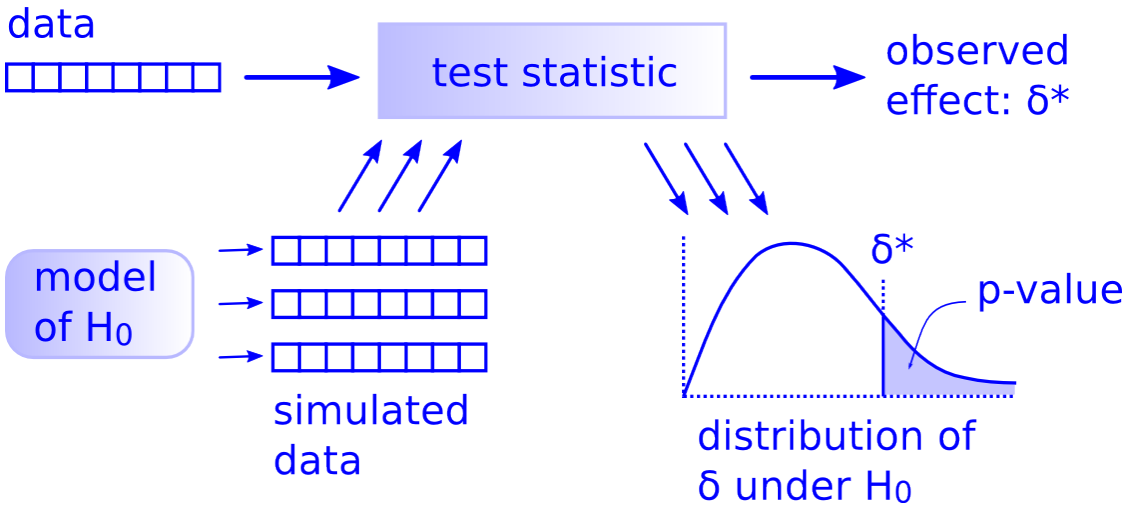


Figure 7.1: Hypothesis Testing Framework

Before we hop into this framework, we will provide another way to think about hypothesis testing that may be useful.

7.1 Criminal trial analogy

We can think of hypothesis testing in the same context as a criminal trial in the United States. A criminal trial in the United States is a familiar situation in which a choice between two contradictory claims must be made.

1. The accuser of the crime must be judged either guilty or not guilty.
2. Under the U.S. system of justice, the individual on trial is initially presumed not guilty.
3. Only STRONG EVIDENCE to the contrary causes the not guilty claim to be rejected in favor of a guilty verdict.
4. The phrase "beyond a reasonable doubt" is often used to set the cutoff value for when enough evidence has been given to convict.

Theoretically, we should never say "The person is innocent." but instead "There is not sufficient evidence to show that the person is guilty."

Now let's compare that to how we look at a hypothesis test.

1. The decision about the population parameter(s) must be judged to follow one of two hypotheses.
2. We initially assume that H_0 is true.
3. The null hypothesis H_0 will be rejected (in favor of H_a) only if the sample evidence strongly suggests that H_0 is false. If the sample does not provide such evidence, H_0 will not be rejected.

4. The analogy to "beyond a reasonable doubt" in hypothesis testing is what is known as the **significance level**. This will be set before conducting the hypothesis test and is denoted as α. Common values for α are 0.1, 0.01, and 0.05.

7.1.1 Two possible conclusions

Therefore, we have two possible conclusions with hypothesis testing:

- Reject H_0
- Fail to reject H_0

Gut instinct says that "Fail to reject H_0" should say "Accept H_0" but this technically is not correct. Accepting H_0 is the same as saying that a person is innocent. We cannot show that a person is innocent; we can only say that there was not enough substantial evidence to find the person guilty.

When you run a hypothesis test, you are the jury of the trial. You decide whether there is enough evidence to convince yourself that H_a is true ("the person is guilty") or that there was not enough evidence to convince yourself H_a is true ("the person is not guilty"). You must convince yourself (using statistical arguments) which hypothesis is the correct one given the sample information.

Important note: Therefore, DO NOT WRITE "Accept H_0" any time you conduct a hypothesis test. Instead write "Fail to reject H_0."

7.1.2 Basic Logic of Hypothesis Testing

- Take a random sample (or samples) from a population (or two populations)
- If the sample data are consistent with the null hypothesis, do not reject the null hypothesis.
- If the sample data are inconsistent with the null hypothesis (in the direction of the alternative hypothesis), reject the null hypothesis and conclude that there is evidence the alternative hypothesis is true (based on the particular sample collected).

7.1.3 Statistical Significance

The idea that sample results are more extreme than we would reasonably expect to see by random chance if the null hypothesis were true is the fundamental idea behind statistical hypothesis tests. If data as extreme would be very unlikely if the null hypothesis were true, we say the data are **statistically significant**. Statistically significant data provide convincing evidence against the null hypothesis in favor of the alternative, and allow us to generalize our sample results to the claim about the population.

Definition: Statistical Significance

When results as extreme as the observed sample statistic are unlikely to occur by random chance alone (assuming the null hypothesis is true), we say the sample results/statistics are *statistically significant*. If our sample is statistically significant, we have convincing evidence against H_0 and in favor of H_a.

7.2 Randomization

We will now focus on building hypotheses looking at the difference between two population means in an example. We will denote population means using the Greek symbol μ (pronounced "mu"). Thus, we will be looking to see if one group "out-performs" another group. This is quite possibly the most common type of statistical inference and serves as a basis for many other types of analyses when comparing two groups.

Our null hypothesis will be of the form $H_0 : \mu_1 = \mu_2$, which can also be written as $H_0 : \mu_1 - \mu_2 = 0$. Our alternative hypothesis will be of the form $H_0 : \mu_1 \star \mu_2$ (or $H_a : \mu_1 - \mu_2 \star 0$) where $\star = <, \neq$, or $>$ depending on the context of the problem. You needn't focus on these new symbols too much at this point. It will just be a shortcut way for us to describe our hypotheses.

As we saw in Chapter 6, simulation and bootstrapping are valuable tools when conducting inferences based on one population variable. We will see that the process of **randomization**, which is a resampling procedure similar to bootstrapping in some ways, will be valuable in conducting tests comparing quantitative values from two groups.

Learning check

(LC7.1) What is wrong about saying "The defendant is innocent." based on the US system of criminal trials?

(LC7.2) What is the purpose of hypothesis testing?

(LC7.3) What are some flaws with hypothesis testing? How could we alleviate them?

7.2.1 Comparing Action and Romance Movies

The `movies` data set in the `ggplot2movies` package contains information on a large number of movies that have been rated by users of IMDB.com. We are interested in the question here of whether `Action` movies are rated higher on IMDB than `Romance` movies. We will first need to

do a little bit of data manipulation using the ideas from Chapter 5 to get the data in the form that we would like:

```
library(dplyr)
library(ggplot2movies)
(movies_trimmed <- movies %>% select(title, year, rating, Action, Romance))
```

```
## # A tibble: 58,788 × 5
##                        title  year rating Action Romance
##                        <chr> <int>  <dbl>  <int>   <int>
## 1                          $  1971    6.4      0       0
## 2          $1000 a Touchdown  1939    6.0      0       0
## 3    $21 a Day Once a Month  1941    8.2      0       0
## 4                   $40,000  1996    8.2      0       0
## 5  $50,000 Climax Show, The  1975    3.4      0       0
## 6                     $pent  2000    4.3      0       0
## 7                   $windle  2002    5.3      1       0
## 8                      '15'  2002    6.7      0       0
## 9                       '38  1987    6.6      0       0
## 10                  '49-'17  1917    6.0      0       0
## # ... with 58,778 more rows
```

Note that `Action` and `Romance` are binary variables here. To remove any overlap of movies (and potential confusion) that are both `Action` and `Romance`, we will remove them from our *population*:

```
movies_trimmed <- movies_trimmed %>%
  filter(!(Action == 1 & Romance == 1))
```

We will now create a new variable called `genre` that specifies whether a movie in our `movies_trimmed` data frame is an `"Action"` movie, a `"Romance"` movie, or `"Neither"`. We aren't really interested in the `"Neither"` category here so we will exclude those rows as well. Lastly, the `Action` and `Romance` columns are not needed anymore since they are encoded in the `genre` column.

```
movies_trimmed <- movies_trimmed %>%
  mutate(genre = ifelse(Action == 1, "Action",
                        ifelse(Romance == 1, "Romance",
                               "Neither"))) %>%
  filter(genre != "Neither") %>%
  select(-Action, -Romance)
```

We are left with 8878 movies in our *population* data set that focuses on only `"Action"` and `"Romance"` movies.

Learning check

(LC7.4) Why are the different genre variables stored as binary variables (1s and 0s) instead of just listing the `genre` as a column of values like "Action", "Comedy", etc.?

(LC7.5) What complications could come above with us excluding action romance movies? Should we question the results of our hypothesis test? Explain.

Let's now visualize the distributions of `rating` across both levels of `genre`. Think about what type(s) of plot is/are appropriate here before you proceed:

```
library(ggplot2)
movies_trimmed %>% ggplot(aes(x = genre, y = rating)) +
  geom_boxplot()
```

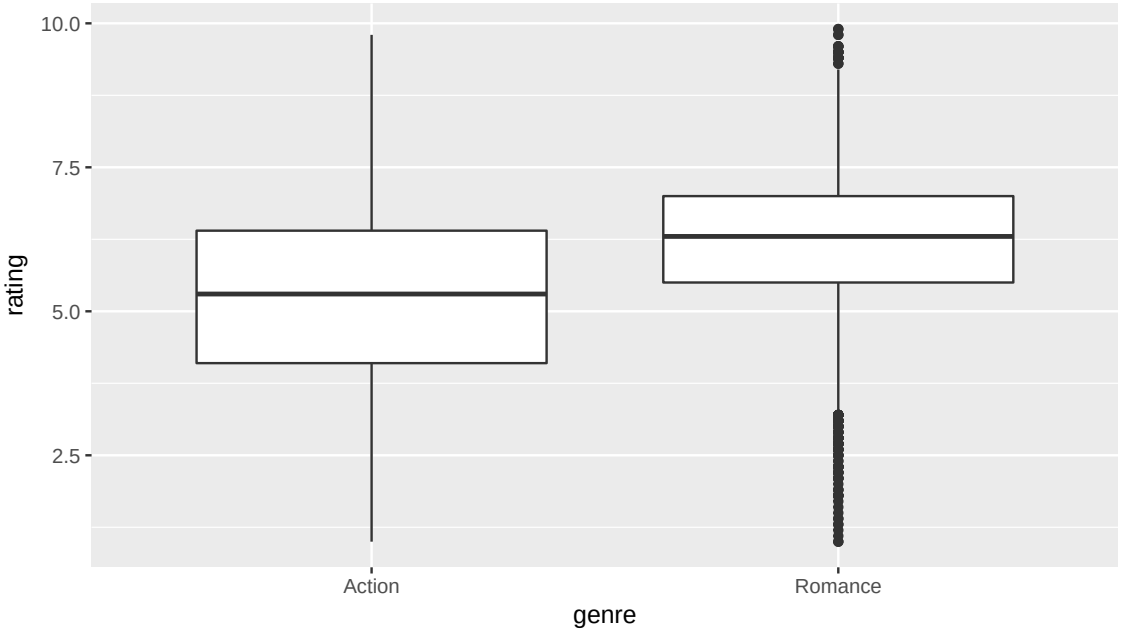


Figure 7.2: Rating vs genre in the population

We can see that the middle 50% of ratings for `"Action"` movies is more spread out than that of `"Romance"` movies in the population. `"Romance"` has outliers at both the top and bottoms of the scale though. We are initially interested in comparing the mean `rating` across these two groups so a faceted histogram may also be useful:

```
movies_trimmed %>% ggplot(mapping = aes(x = rating)) +
  geom_histogram(binwidth = 1, color = "white", fill = "dodgerblue") +
  facet_grid(genre ~ .)
```

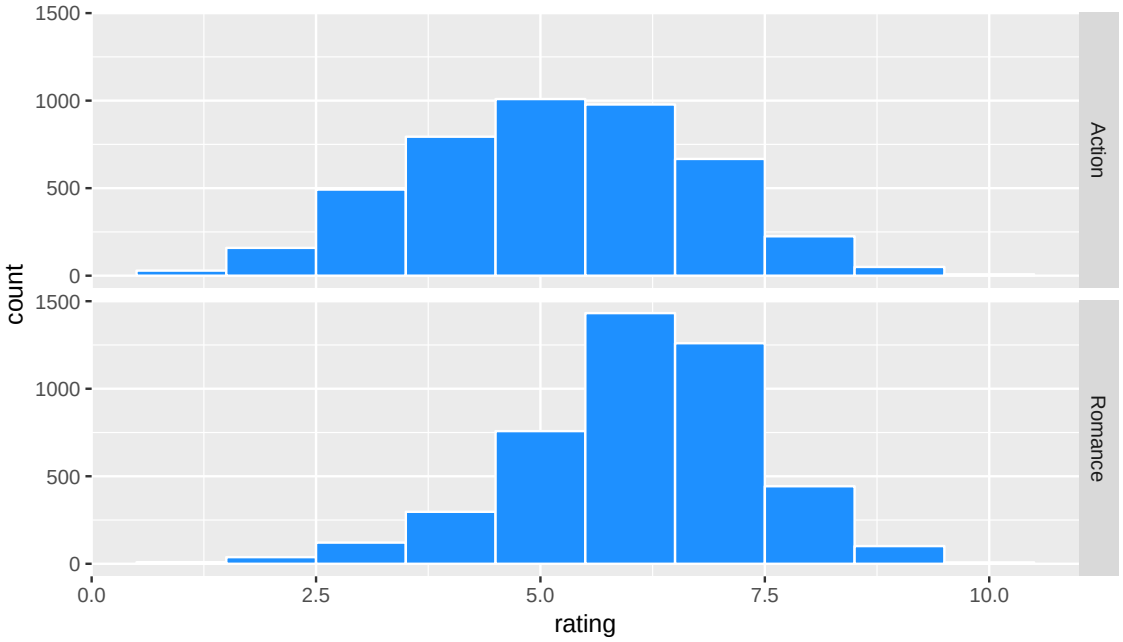


Figure 7.3: Faceted histogram of genre vs rating

Important note: Remember that we hardly ever have access to the population values as we do here. This example and the `nycflights13` data set were used to create a common flow from chapter to chapter. In nearly all circumstances, we'll be needing to use only a sample of the population to try to infer conclusions about the unknown population parameter values. These examples do show a nice relationship between statistics (where data is usually small and more focused on experimental settings) and data science (where data is frequently large and collected without experimental conditions).

7.2.2 Sampling → Randomization

We can use hypothesis testing to investigate ways to determine, for example, whether a **treatment** has an effect over a **control** and other ways to statistically analyze if one group performs better than, worse than, or different than another. We will also use confidence intervals to determine the size of the effect if it exists. You'll see more on this in Chapter 8.

We are interested here in seeing how we can use a random sample of action movies and a random sample of romance movies from `movies` to determine if a statistical difference exists in the mean ratings of each group.

Learning check

(LC7.6) Define the relevant parameters here in terms of the populations of movies.

Let's select a random sample of 34 action movies and a random sample of 34 romance movies. (The number 34 was chosen somewhat arbitrarily here.)

```
library(dplyr)
library(mosaic)
set.seed(2016)
movies_genre_sample <- movies_trimmed %>%
  group_by(genre) %>%
  sample_n(34)
```

We can now observe the distributions of our two sample ratings for both groups. Remember that these plots should be rough approximations of our population distributions of movie ratings for `"Action"` and `"Romance"` in our population of all movies in the `movies` data frame.

```
movies_genre_sample %>% ggplot(aes(x = genre, y = rating)) +
  geom_boxplot()
```

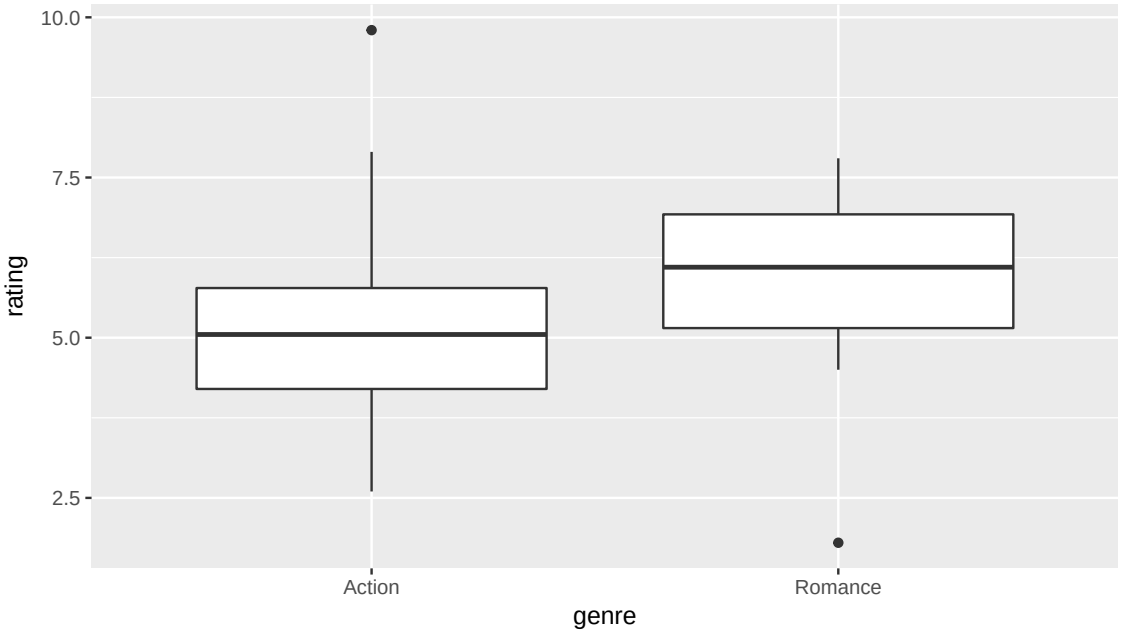


Figure 7.4: Genre vs rating for our sample

```
movies_genre_sample %>% ggplot(mapping = aes(x = rating)) +
  geom_histogram(binwidth = 1, color = "white", fill = "dodgerblue") +
  facet_grid(genre ~ .)
```

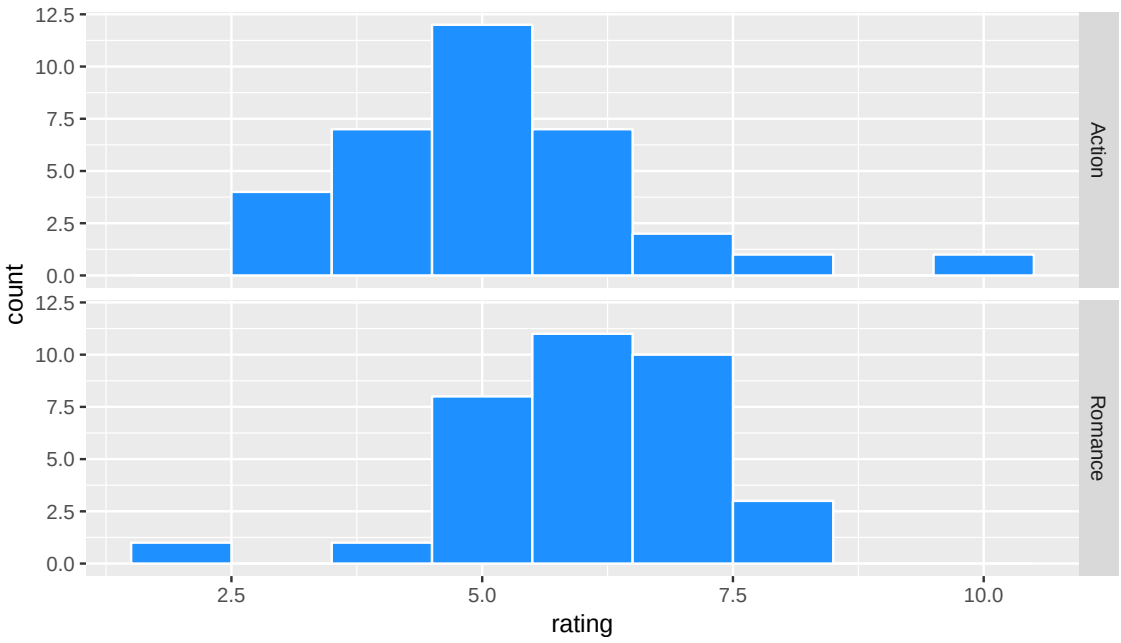


Figure 7.5: Genre vs rating for our sample as faceted histogram

---

Learning check

(LC7.7) What single value could we change to improve the approximation using the sample distribution on the population distribution?

Do we have reason to believe, based on the sample distributions of `rating` over the two groups of `genre`, that there is a significant difference between the mean `rating` for action movies compared to romance movies? It's hard to say just based on the plots. The boxplot does show that the median sample rating is higher for romance movies, but the histogram isn't as clear. The two groups have somewhat differently shaped distributions but they are both over similar values of `rating`. It's often useful to calculate the mean and standard deviation as well, conditioned on the two levels.

```
summary_ratings <- movies_genre_sample %>%
  group_by(genre) %>%
  summarize(mean = mean(rating),
            std_dev = sd(rating))
summary_ratings
```

```
## # A tibble: 2 × 3
##     genre     mean  std_dev
##     <chr>    <dbl>    <dbl>
## 1  Action 5.197059 1.464837
## 2 Romance 6.026471 1.202096
```

Learning check

(LC7.8) Why did we not specify `na.rm = TRUE` here as we did in Chapter 5?

We see that the sample mean rating for romance movies, $\bar{x}_r$, is greater than the similar measure for action movies, $\bar{x}_a$. But is it statistically significantly greater (thus, leading us to conclude that the means are statistically different)? The standard deviation can provide some insight here but with these standard deviations being so similar it's still hard to say for sure.

Learning check

(LC7.9) Why might the standard deviation provide some insight about the means being statistically different or not?

The hypotheses we specified can also be written in another form to better give us an idea of what we will be simulating to create our null distribution.

- $H_0 : \mu_r - \mu_a = 0$
- $H_a : \mu_r - \mu_a \neq 0$

We are, therefore, interested in seeing whether the difference in the sample means, $\bar{x}_r - \bar{x}_a$, is statistically different than 0. R has a built-in command that can calculate the difference in these two sample means.

```
mean_ratings <- movies_genre_sample %>% group_by(genre) %>%
  summarize(mean = mean(rating))
obs_diff <- diff(mean_ratings$mean)
```

We see here that the `diff` function calculates $\bar{x}_r - \bar{x}_a = 6.0264706 - 5.1970588 = 0.8294118$. We will now proceed similarly to how we conducted hypothesis tests in Chapter 6 using simulation. Our goal is figure out a random process with which to simulate the null hypothesis being true. In Chapter 6, we used flipping of a fair coin as the random process we were simulating with the null hypothesis being true ($H_0 : \pi = 0.5$).

Here, with us assuming the two population means are equal ($H_0 : \mu_r - \mu_a = 0$), we can look at this from a tactile point of view by using index cards. There are $n_r = 34$ data elements corresponding to romance movies and $n_a = 34$ for action movies. We can write the 34 ratings from our sample for romance movies on one set of 34 index cards and the 34 ratings for action movies on another set of 34 index cards. (Note that the sample sizes need not be the same.)

The next step is to put the two stacks of index cards together, creating a new set of 68 cards. If we assume that the two population means are equal, we are saying that there is no association between ratings and genre (romance vs action). We can use the index cards to create two **new** stacks for romance and action movies. First, we must shuffle all the cards thoroughly. After doing so, in this case with equal values of sample sizes, we split the deck in half. (You should be thinking about how this process is similar to what was done with **bootstrapping** in Chapter 6.)

We then calculate the new sample mean rating of the romance deck, and also the new sample mean rating of the action deck. This creates one simulation of the samples that were collected originally. We next want to calculate a statistic from these two samples. Instead of actually doing the calculation using index cards, we can use R as we have before to simulate this process.

Learning check

(LC7.10) How would the tactile shuffling of index cards change if we had different samples of say 20 action movies and 60 romance movies? Describe each step that would change.

(LC7.11) Why are we taking the difference in the means of the cards in the new shuffled decks?

```
library(mosaic)
shuffled_ratings <- movies_trimmed %>%
     mutate(rating = shuffle(rating)) %>%
     group_by(genre) %>%
     summarize(mean = mean(rating))
diff(shuffled_ratings$mean)
```

```
## [1] -0.02287811
```

The only new command here is `shuffle` from the `mosaic` package, which does what we would expect it to do. It simulates a shuffling of the ratings between the two levels of `genre` just as we could have done with index cards. We can now proceed in a similar way to what we have done previously in Chapter 6 by repeating this process many times to create a *null distribution* of simulated differences in sample means.

```
set.seed(2016)
many_shuffles <- do(10000) *
  (movies_trimmed %>%
     mutate(rating = shuffle(rating)) %>%
     group_by(genre) %>%
     summarize(mean = mean(rating))
   )
```

It is a good idea here to `View` the `many_shuffles` data frame via `View(many_shuffles)`. We need to figure out a way to subtract the first value of `mean` from the second value of `mean` for each of the 10,000 simulations. This is a little tricky but the `group_by` function comes to our rescue here:

```
rand_distn <- many_shuffles %>%
  group_by(.index) %>%
  summarize(diffmean = diff(mean))
```

We can now plot the distribution of these simulated differences in means:

```
rand_distn %>% ggplot(aes(x = diffmean)) +
  geom_histogram(color = "white", bins = 20)
```

Remember that we are interested in seeing where our observed sample mean difference of 0.8294118 falls on this null/randomization distribution. We are interested in simply a difference here so "more extreme" corresponds to values in both tails on the distribution. Let's shade our null distribution to show a visual representation of our p-value:

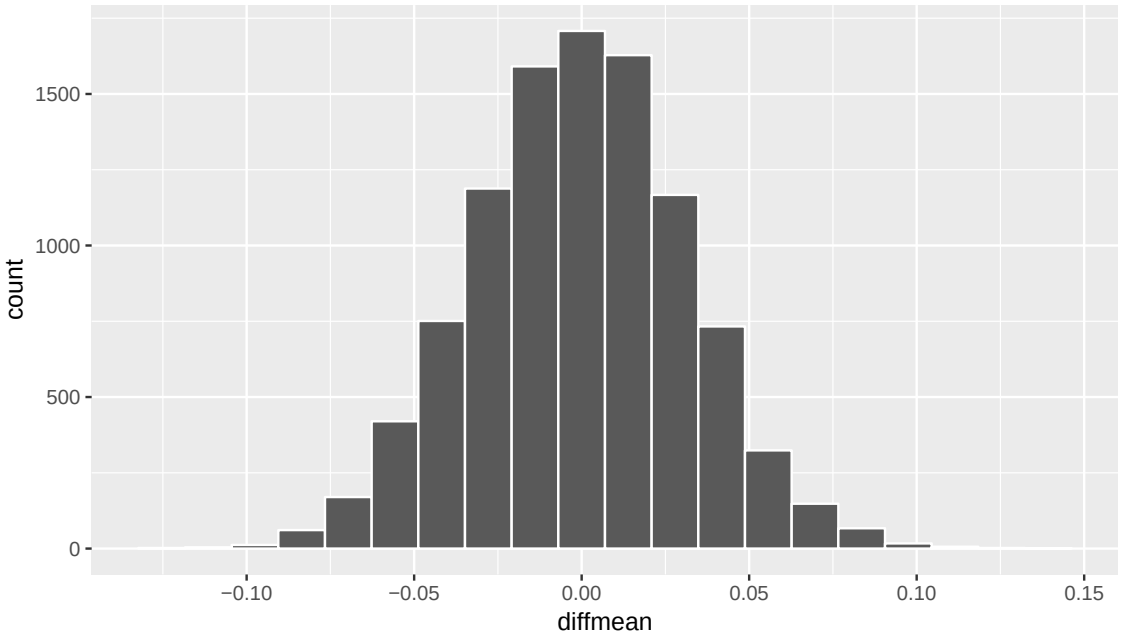


Figure 7.6: Simulated differences in means histogram

```
rand_distn %>% ggplot(aes(x = diffmean, fill = (abs(diffmean) >= obs_diff))) +
  geom_histogram(color = "white", bins = 20)
```

You may initially think there is an error here, but remember that the observed difference in means was 0.8294118. It falls far outside the range of simulated differences. We can add a vertical line to represent both it and its negative (since this is a two-tailed test) instead:

```
rand_distn %>% ggplot(aes(x = diffmean)) +
  geom_histogram(color = "white", bins = 100) +
  geom_vline(xintercept = obs_diff, color = "red") +
  geom_vline(xintercept = -obs_diff, color = "red")
```

Based on this plot, we have evidence supporting the conclusion that the mean rating for romance movies is different from that of action movies. (It doesn't really matter what significance level was chosen in this case. Think about why.) The next important idea is to better understand just how much higher of a mean rating can we expect the romance movies to have compared to that of action movies. This can be addressed by creating a 95% confidence interval as we will explore in Chapter 8.

Learning check

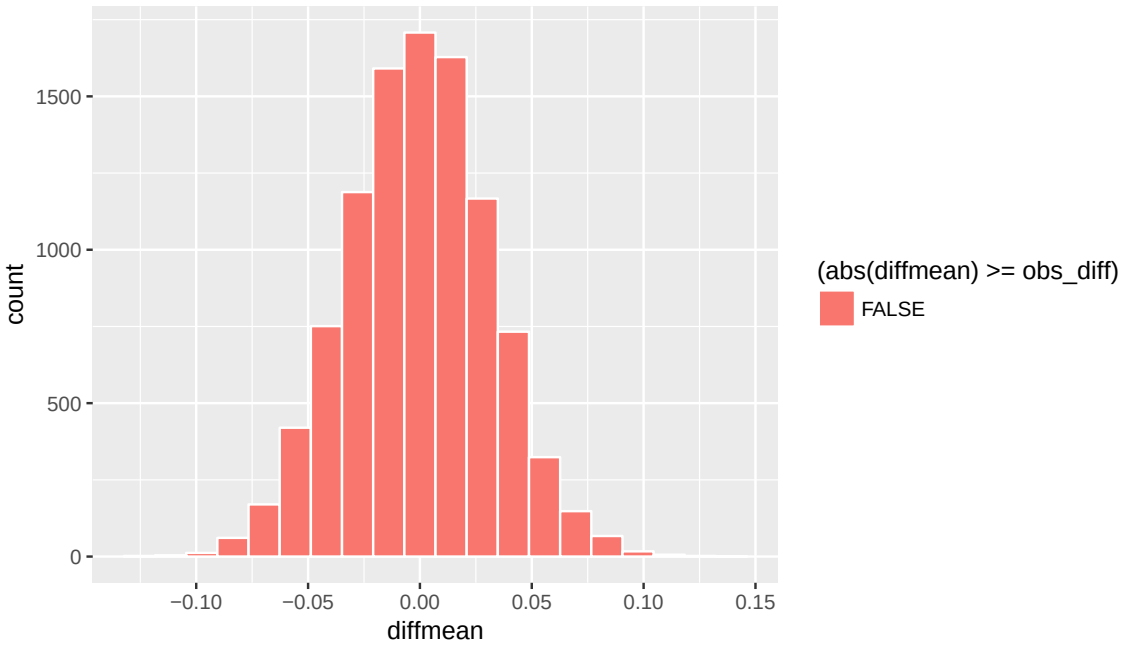


Figure 7.7: Shaded histogram to show p-value

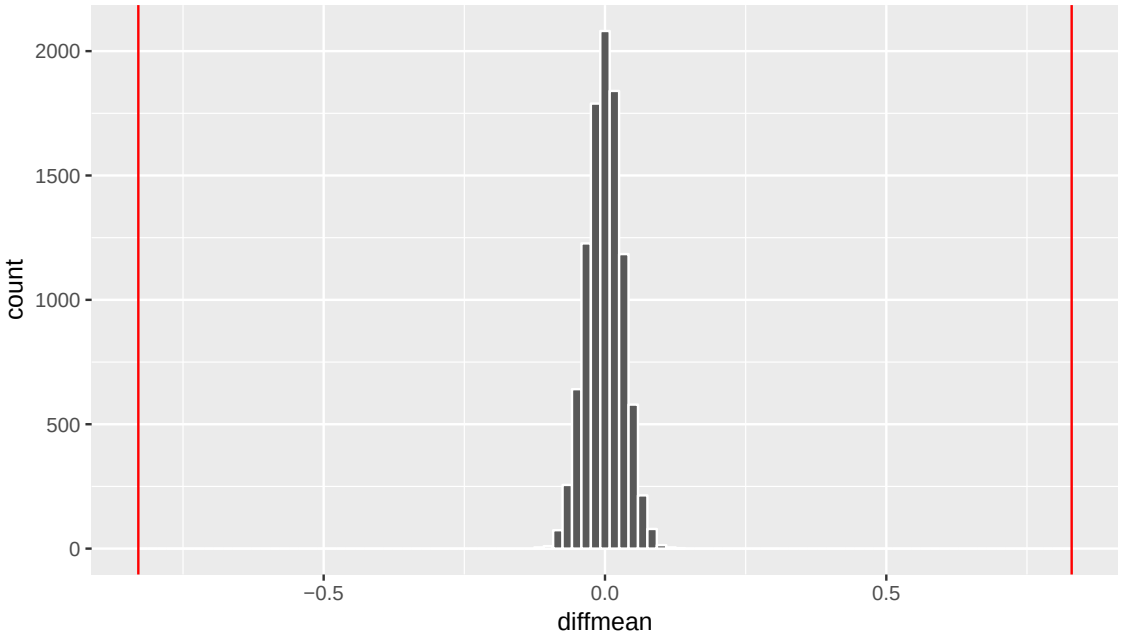


Figure 7.8: Histogram with vertical lines corresponding to observed statistic

(LC7.12) Conduct the same analysis comparing action movies versus romantic movies using the median rating instead of the mean rating? Make sure to use the `%>%` as much as possible. What was different and what was the same?

(LC7.13) What conclusions can you make from viewing the faceted histogram looking at `rating` versus `genre` that you couldn't see when looking at the boxplot?

(LC7.14) Describe in a paragraph how we used Allen Downey's diagram to conclude if a statistical difference existed between mean movie ratings for action and romance movies.

(LC7.15) Why are we relatively confident that the distributions of the sample ratings will be good approximations of the population distributions of ratings for the two genres?

(LC7.16) Using the definition of "p-value" in Chapter 6, write in words what the p-value represents for the hypothesis test above comparing the mean rating of romance to action movies.

(LC7.17) What is the value of the p-value for the hypothesis test comparing the mean rating of romance to action movies?

(LC7.18) Do the results of the hypothesis test match up with the original plots we made looking at the population of movies? Why or why not?

7.2.3 Summary

To review, these are the steps one would take whenever you'd like to do a hypothesis test comparing values from the distributions of two groups:

- Simulate many samples using a random process that matches the way the original data were collected and that *assumes the null hypothesis is true*.
- Collect the values of a sample statistic for each sample created using this random process to build a *randomization distribution*.
- Assess the significance of the *original* sample by determining where its sample statistic lies in the randomization distribution.
- If the proportion of values as extreme or more extreme than the observed statistic in the randomization distribution is smaller than the pre-determined significance level α, we reject H_0. Otherwise, we fail to reject H_0. (If no significance level is given, one can assume $\alpha = 0.05$.)

7.3 Script of R code

An R script file of all R code used in this chapter is available here.

7.4 What's to come?

This chapter examined how to conclude whether two sample statistics are statistically different using hypothesis testing. This is the same thing as trying to conclude if the difference in sample statistics is statistically different from zero. We will see that this value of zero plays an important role in confidence intervals as well. We'll also see in Chapter 8 the relationship between confidence intervals and two-sided hypothesis tests as we worked with in this chapter.

8

Confidence Intervals

Definition: Confidence Interval

A *confidence interval* gives a range of plausible values for a parameter. It depends on a specified *confidence level* with higher confidence levels corresponding to wider confidence intervals and lower confidence levels corresponding to narrower confidence intervals. Common confidence levels include 90%, 95%, and 99%.

8.1 Relation to hypothesis testing

Recall that we found a statistically significant difference in the sample mean of romance movie ratings compared to the sample mean of action movie ratings. We concluded Chapter 7 by attempted to understand just how much greater we could expect the *population* mean romance movie rating to be as compared to the *population* mean action movie rating. In order to do so, we will calculate a confidence interval for the difference $\mu_r - \mu_a$. We'll then go back to our population parameter values and see if our confidence interval contains our parameter value.

We could use bootstrapping in a way similar to that done in the Chapter 6, except now on a difference in sample means, to create a distribution and then use the `confint` function with the option of `quantile` to determine a confidence interval for the plausible values of the difference in population means. This is an excellent programming activity and the reader is urged to try to do so.

Recall what the randomization/null distribution looked like for our simulated shuffled sample means:

```
library(ggplot2)
library(dplyr)
rand_distn %>% ggplot(aes(x = diffmean)) +
  geom_histogram(color = "white", bins = 20)
```

With this null distribution being quite symmetric, the standard error method introduced in Chapter 6 likely provides a good estimate of a range of plausible values for $\mu_r - \mu_a$. Another

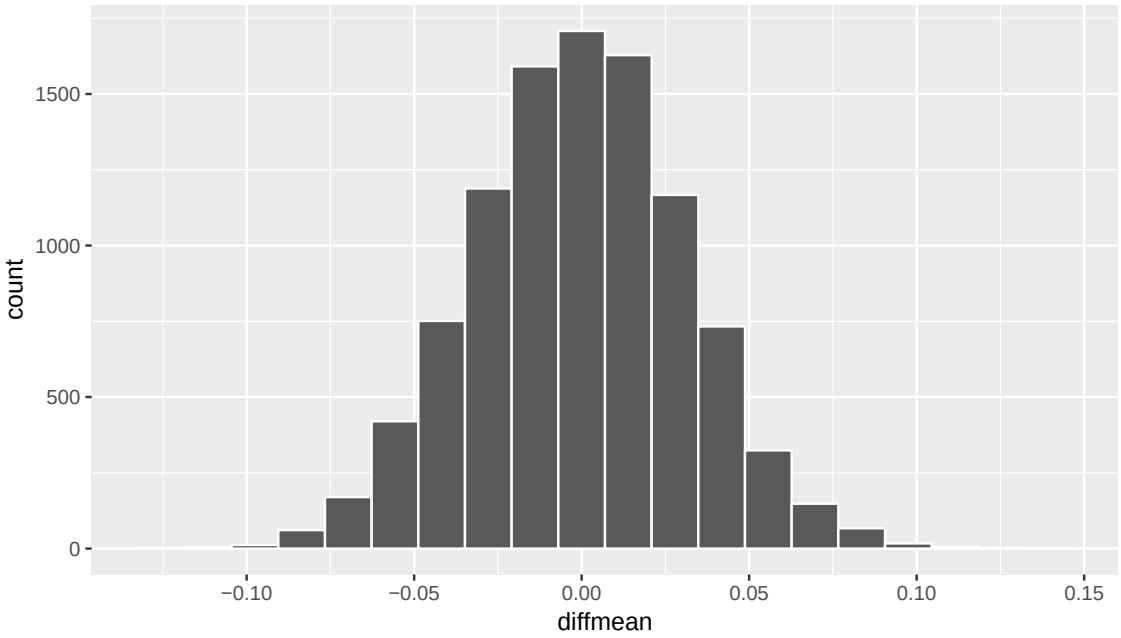


Figure 8.1: Simulated shuffled sample means histogram

nice option here is that we can use the standard deviation of the null/randomization distribution we just found with our hypothesis test.

```
(std_err <- rand_distn %>% summarize(se = sd(diffmean)))
```

```
## # A tibble: 1 × 1
##           se
##        <dbl>
## 1 0.03182225
```

Remembering that we can use the general formula of $statistic \pm (2 * SE)$ we get the following result for plausible values of the difference in population means at the 95% level.

```
(lower <- obs_diff - (2 * std_err))
```

```
##          se
## 1 0.7657673
```

```
(upper <- obs_diff + (2 * std_err))
```

```
##          se
## 1 0.8930563
```

We can, therefore, say that we are 95% confident that the population mean rating for romance movies is between 0.766 and 0.893 points higher than for that of action movies.

The important thing to check here is whether 0 is contained in the confidence interval. If it is, it is plausible that the difference in the two population means between the two groups is 0. This means that the null hypothesis is plausible. The results of the hypothesis test and the confidence interval should match as they do here. We rejected the null hypothesis with hypothesis testing and we have evidence here than the mean rating for romance movies is higher than for action movies.

8.2 Effect size

The phrase **effect size** has been thrown around recently as an alternative to p-values. In combination with the confidence interval, it can be often more valuable than just looking at the results of a hypothesis test. It depends on the scientific discipline exactly what is meant by "effect size" but, in general, it refers to *the magnitude of the difference between group measurements*. For our two sample problem involving movies, it is the observed difference in sample means `obs_diff`.

It's worthy of mention here that confidence intervals are always centered at the observed statistic. In other words, if you are looking at a confidence interval and someone asks you what the "effect size" is you can simply find the midpoint of the stated confidence interval.

Learning check

(LC8.1) Check to see whether the difference in population mean ratings for the two genres falls in the confidence interval we found here. Are we guaranteed that it will fall in the range of plausible values?

(LC8.2) Why do you think many scientific fields are shifting to preferring inclusion of confidence intervals in articles over just p-values and hypothesis tests?

(LC8.3) Why is 95% related to a value of 2 in the margin of error? What would approximate values be for 90% and for 99%?

(LC8.4) Why is a 95% confidence interval wider than a 90% confidence interval? Explain by using a concrete example from everyday life about what is meant by "confidence."

(LC8.5) How would confidence intervals correspond to one-sided hypothesis tests?

(LC8.6) There is a relationship between the significance level and the confidence level. What do you think it is?

8.3 Script of R code

An R script file of all R code used in this chapter is available here.

Part III

Conclusion

9

Concluding Remarks

If you've come to this point in the book, I'd suspect that you know a thing or two about how to work with data in R. You've also gained a lot of knowledge about how to use simulation techniques to determine statistical significance. The hope is that you've come to appreciate data manipulation, tidy data sets, and the power of statistical visualization. Actually, the data visualization part may be the most important thing here. If you can create truly beautiful graphics that display information in ways that the reader can clearly decipher, you've picked up a great skill. Let's hope that that skill keeps you creating great stories with data into the near and far distant future. Thanks for coming along for the ride as we dove into modern data analysis using R!

A

Intermediate R

A.1 Sorted barplots

Building upon the example in Section 4.4:

```
library(nycflights13)
library(ggplot2)
flights_table <- table(flights$carrier)
flights_table
```

```
##
##    9E    AA    AS    B6    DL    EV    F9    FL    HA    MQ    OO    UA
## 18460 32729   714 54635 48110 54173   685  3260   342 26397    32 58665
##    US    VX    WN    YV
## 20536  5162 12275   601
```

We can sort this table from highest to lowest counts by using the `sort` function:

```
sorted_flights <- sort(flights_table, decreasing = TRUE)
names(sorted_flights)
```

```
##  [1] "UA" "B6" "EV" "DL" "AA" "MQ" "US" "9E" "WN" "VX" "FL" "AS" "F9"
## [14] "YV" "HA" "OO"
```

It is often preferred for barplots to be ordered corresponding to the heights of the bars. This allows the reader to more easily compare the ordering of different airlines in terms of departed flights (Robbins, 2013). We can also much more easily answer questions like "How many airlines have more departing flights than Southwest Airlines?".

We can use the sorted table giving the number of flights defined as `sorted_flights` to **reorder** the `carrier`.

```
ggplot(data = flights, mapping = aes(x = carrier)) +
  geom_bar() +
  scale_x_discrete(limits = names(sorted_flights))
```

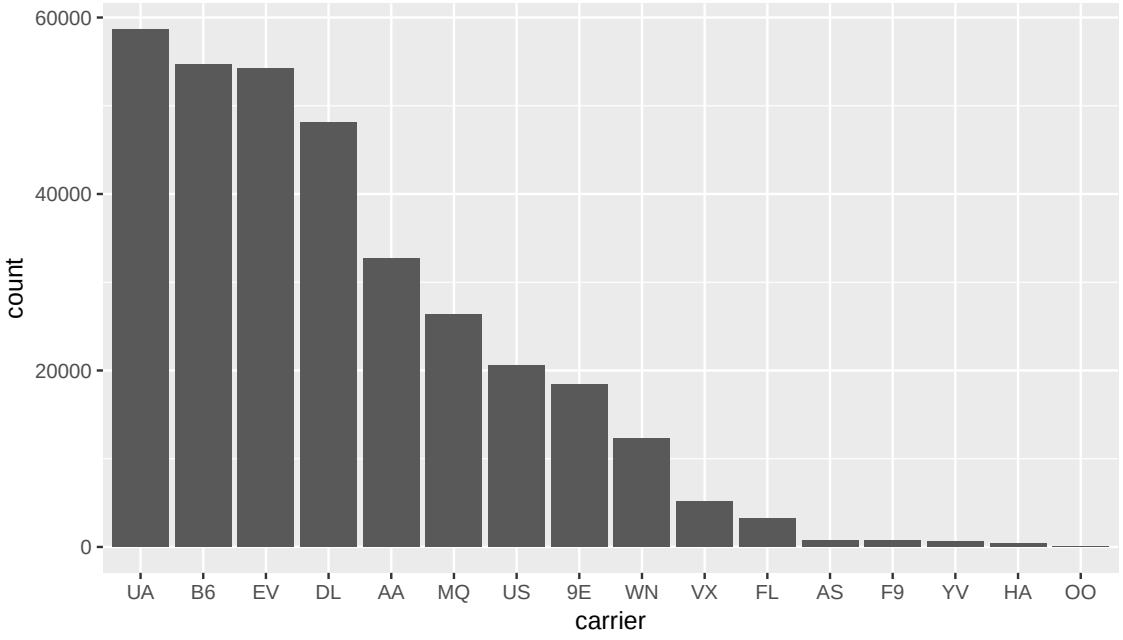


Figure A.1: Number of flights departing NYC in 2013 by airline - Descending numbers

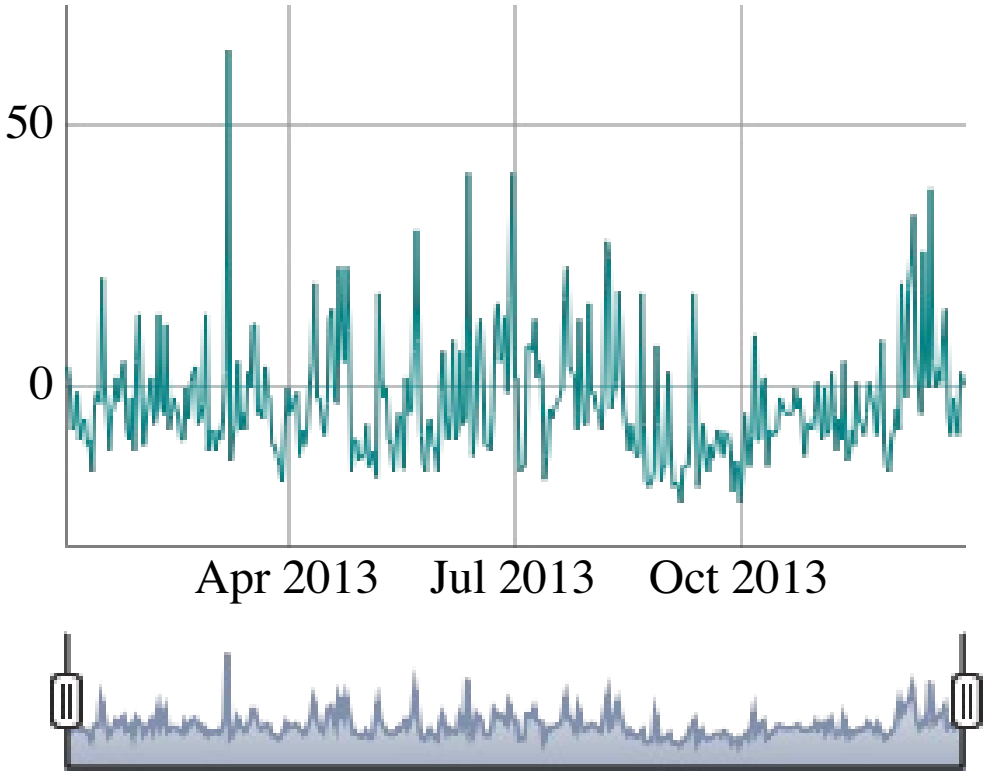
The last addition here specifies the values of the horizontal `x` axis on a discrete scale to correspond to those given by the entries of `sorted_flights`.

A.2 Interactive graphics

A.2.1 Interactive line-graphs

Another useful tool for viewing line-graphs such as this is the `dygraph` function in the `dygraphs` package in combination with the `dyRangeSelector` function. This allows us to zoom in on a selected range and get an interactive plot for us to work with:

```
library(dygraphs)
rownames(flights_summarized) <- flights_summarized$date
flights_summarized <- select(flights_summarized, -date)
dyRangeSelector(dygraph(flights_summarized))
```



The syntax here is a little different than what we have covered so far. The `dygraph` function is expecting for the dates to be given as the `rownames` of the object. We then remove the `date` variable from the `flights_summarized` dataframe since it is accounted for in the `rownames`. Lastly, we run the `dygraph` function on the new dataframe that only contains the median arrival delay as a column and then provide the ability to have a selector to zoom in on the interactive plot via `dyRangeSelector`. (Note that this plot will only be interactive in the HTML version of this book.)

B
Statistical Basics

B.1 Basic statistical terms

B.1.1 Mean

The mean is the most commonly reported measure of center. It is commonly called the "average" though this term can be a little ambiguous. The mean is the sum of all of the data elements divided by how many elements there are. If we have n data points, the mean is given by:

$$Mean = \frac{x_1 + x_2 + \cdots + x_n}{n}$$

B.1.2 Median

The median is calculated by first sorting a variable's data from smallest to largest. After sorting the data, the middle element in the list is the **median**. If the middle falls between two values, then the median is the mean of those two values.

B.1.3 Standard deviation

We will next discuss the **standard deviation** of a sample data set pertaining to one variable. The formula can be a little intimidating at first but it is important to remember that it is essentially a measure of how far to expect a given data value is from its mean:

$$Standard\,deviation = \sqrt{\frac{(x_1 - Mean)^2 + (x_2 - Mean)^2 + \cdots + (x_n - Mean)^2}{n-1}}$$

B.1.4 Five-number summary

The **five-number summary** consists of five values: minimum, first quantile (25^{th} percentile), median (50^{th} percentile), third quantile (75^{th}) quantile, and maximum. The quantiles are calculated as

- first quantile (Q_1): the median of the first half of the sorted data
- third quantile (Q_3): the median of the second half of the sorted data

The *interquartile range* is defined as $Q_3 - Q_1$ and is a measure of how spread out the middle 50% of values is. The five-number summary is not influenced by the presence of outliers in the ways that the mean and standard deviation are. It is, thus, recommended for skewed data sets.

B.1.5 Distribution

The **distribution** of a variable/data set corresponds to generalizing patterns in the data set. It often shows how frequently elements in the data set appear. It shows how the data varies and gives some information about where a typical element in the data might fall. Distributions are most easily seen through data visualization.

B.1.6 Outliers

Outliers correspond to values in the data set that fall far outside the range of "ordinary" values. In regards to a boxplot (by default), they correspond to values below $Q_1 - (1.5 * IQR)$ or above $Q_3 + (1.5 * IQR)$.

Note that these terms (aside from **Distribution**) only apply to quantitative variables.

References

Chihara, L. M. and Hesterberg, T. C. (2011). *Mathematical Statistics with Resampling and R*. John Wiley and Sons, Hoboken, NJ.

Diez, D. M., Barr, C. D., and Çetinkaya Rundel, M. (2014). *Introductory Statistics with Randomization and Simulation*. First edition edition.

Grolemund, G. and Wickham, H. (2016). *R for Data Science*.

Ismay, C. (2016). *Getting used to R, RStudio, and R Markdown*.

Lock, R., Lock, P. F., Morgan, K. L., Lock, E. F., and Lock, D. F. (2012). *Statistics: Un-LOCKing the Power of Data*. Wiley.

Robbins, N. (2013). *Creating More Effective Graphs*. Chart House.

Salsburg, D. (2001). *The Lady Tasting Tea: How Statistics Revolutionized Science in the Twentieth Century*. W.H. Freeman, New York, NY, first edition edition.

Wickham, H. (2014). Tidy data. *Journal of Statistical Software*, Volume 59(Issue 10).

Wickham, H. (2016). *nycflights13: Flights that Departed NYC in 2013*. R package version 0.2.0.

Wickham, H. and Chang, W. (2016). *ggplot2: Create Elegant Data Visualisations Using the Grammar of Graphics*. http://ggplot2.tidyverse.org, https://github.com/tidyverse/ggplot2.

Wickham, H. and Francois, R. (2016). *dplyr: A Grammar of Data Manipulation*. R package version 0.5.0.

Wilkinson, L. (2005). *The Grammar of Graphics (Statistics and Computing)*. Springer-Verlag New York, Inc., Secaucus, NJ, USA.