Intermediate Statistics with R

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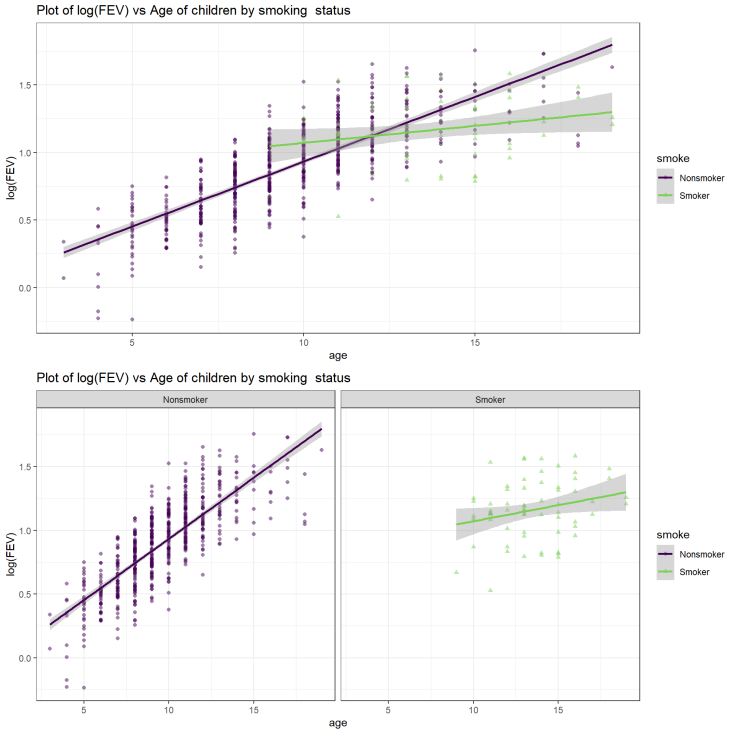

Contents

Acknowledgments

I would like to thank all the students and instructors who have provided input in the development of the current version of STAT 217 and that have impacted the choice of topics and how we try to teach them that show up in this book. Dr. Jim Robison-Cox initially developed this course using R and much of this work retains his initial ideas. The first three editions of the book were co-authored with Dr. Katharine Banner, who had a major impact on all aspects of the book as it exists today. I would also like to thank Jacob Rich, who introduced me to pirate-plots that are incorporated in the newest version. Many years of teaching these topics and helping researchers use these topics has helped to refine how they are presented here. Observing students years after the course has also impacted what we try to teach in the course, trying to prepare these students for the next levels of statistics courses that they might encounter, the next class where they might need or want to use statistics, and for potentially using statistics in the rest of their lives.

I have intentionally taken a first person perspective at times to be able to include stories from some of those interactions to try to help you avoid some of their pitfalls in your current or future usage of statistics. When I take the perspective of "we", I am referring to the team of instructors that help to deliver this material to the students. I would also like to thank my wife, Teresa Greenwood, for allowing me the time and providing support as I repeatedly work on this. Buster Greenwood (our dog) played a role in approving everything that I wrote. I would like to acknowledge Dr. Gordon Bril (Luther College) who introduced me to statistics while I was an undergraduate and Dr. Snehalata Huzurbazar when I was at the University of Wyoming that guided me to completing my Master's and Ph.D. in Statistics and continues to be a valued mentor and friend to me.

The development of this text was initially supported with funding from Montana State University's Instructional Innovation Grant Program with the grant *Towards more active learning in STAT 217* and versions 2.1 and 2.2 were supported by an Open Educational Research Award from the Montana State University Library, and Version 3.0 was developed with their continuing support. This book was born with the goal of having a targeted presentation of topics that we cover (and few that we don't) that minimizes cost to students and incorporates the statistical software R (and the interface RStudio) from day one and every day after that. The software is a free, open-source platform and so is dynamically changing over time. This has necessitated frequent revisions of the text.

This is Version 3.0 of the book with this title but the eighth version of most of the content. Version 3.0 changes to using the "tidyverse" for data wrangling and `ggplot` for many of the data visualizations. This modernizes the way data are modified and prepared for analyses as well as allowing much more customization for the user for data visualizations. There are places where the code is more involved but the benefits of learning to data wrangle and plot using these tools is to create a more understandable flow of both (often done together) and the ability to layer multiple commands and plots together to attain a final destination of analysis and plots.

This text has been created by Greta Linse of Great Lines Writing and Consulting Services (https://www.greatlineswriting.com/) who ported the book into RStudio's bookdown format and tried to edit and improve the writing in the text. Any remaining errors are the responsibility of Mark Greenwood. The book was initially developed during Fall 2013 and the text has continually evolved since its creation. The frequent updates are primarily motivated by changes in the R software that impact the methods and results that are provided here and hopefully the code will work when you try it.

We have made every attempt to keep costs for the book as low as possible by making it possible for most pages to be printed in black and white and be color-blind friendly. The printed text is available from the Montana State University Bookstore. The text (in full color and with dynamic links) is also available as a free digital download from Montana State University's ScholarWorks repository at https://scholarworks.montana.edu/xmlui/handle/1/2999.

Enjoy your journey from introductory to intermediate statistics!

Chapter 1

Preface

This book is designed primarily for use in a second semester statistics course although it can also be useful for researchers needing a quick review or ideas for using R for the methods discussed in the text. As a text primarily designed for a second statistics course, it presumes that you have had an introductory statistics course. There are now many different varieties of introductory statistics from traditional, formula-based courses (called "consensus" curriculum courses) to more modern, computational-intensive courses that use randomization ideas to try to enhance learning of basic statistical methods. We are not going to presume that you have had a particular "flavor" of introductory statistics or that you had your introductory statistics out of a particular text, just that you have had a course that tried to introduce you to the basic terminology and ideas underpinning statistical reasoning. We would expect that you are familiar with the logic (or sometimes illogic) of hypothesis testing including null and alternative hypothesis and confidence interval construction and interpretation and that you have seen all of this in a couple of basic situations. We start with a review of these ideas in one and two group situations with a quantitative response, something that you should have seen before.

This text covers a wide array of statistical tools that are connected through situation, methods used, or both. As we explore various techniques, look for the identifying characteristics of each method – what type of research questions are being addressed (relationships or group differences, for example) and what type of variables are being analyzed (quantitative or categorical). ***Quantitative variables*** are made up of numerical measurements that have meaningful units attached to them. ***Categorical variables*** take on values that are categories or labels. Additionally, you will need to carefully identify the ***response*** and ***explanatory*** variables, where the study and variable characteristics should suggest which variables should be used as the explanatory variables that may explain variation in the response variable. Because this is an intermediate statistics course, we will start to handle more complex situations (many explanatory variables) and will provide some tools for graphical explorations to complement the more sophisticated statistical models required to handle these situations.

1.1 Overview of methods

After you are introduced to basic statistical ideas, a wide array of statistical methods become available. The methods explored here focus on assessing (estimating and testing for) relationships between variables, sometimes when controlling for or modifying relationships based on levels of another variable – which is where statistics gets interesting and really useful. Early statistical analyses (approximately 100 years ago) were focused on describing a single variable. Your introductory statistics course should have heavily explored methods for summarizing and doing inference in situations with one group or where you were comparing results for two groups of observations. Now, we get to consider more complicated situations – culminating in a set of tools for working with multiple explanatory variables, some of which might be categorical and related to having different groups of subjects that are being compared. Throughout the methods we will cover, it will

be important to retain a focus on how the appropriate statistical analysis depends on the research question and data collection process as well as the types of variables measured.

Figure 1.1 frames the topics we will discuss. Taking a broad view of the methods we will consider, there are basically two scenarios – one when the response is quantitative and one when the response is categorical. Examples of quantitative responses we will see later involve *passing distance of cars for a bicycle rider* (in centimeters (cm)) and *body fat* (percentage). Examples of categorical variables include *improvement* (none, some, or marked) in a clinical trial related to arthritis symptoms or whether a student has turned in copied work (never, done this on an exam or paper, or both). There are going to be some more nuanced aspects to all these analyses as the complexity of both sides of Figure 1.1 suggest, but note that near the bottom, each tree converges on a single procedure, using a ***linear model*** for a quantitative response variable or using a ***Chi-square test*** for a categorical response. After selecting the appropriate procedure and completing the necessary technical steps to get results for a given data set, the final step involves assessing the scope of inference and types of conclusions that are appropriate based on the design of the study.

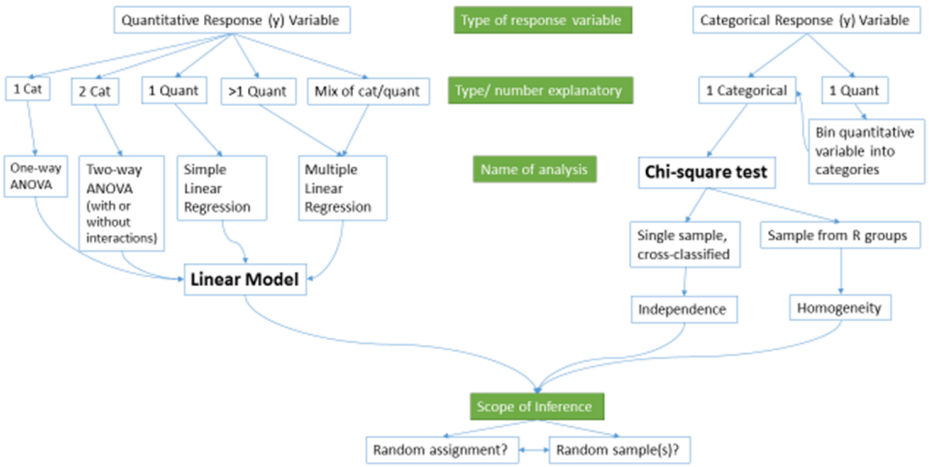

Figure 1.1: Flow chart of methods.

We will be spending most of the semester working on methods for quantitative response variables (the left side of Figure 1.1 is covered in Chapters 2, **??**, **??**, **??**, **??**, and **??**), stepping over to handle the situation with a categorical response variable in Chapter **??** (right side of Figure 1.1). Chapter **??** contains case studies illustrating all the methods discussed previously, providing a final opportunity to explore additional examples that illustrate how finding a path through Figure 1.1 can lead to the appropriate analysis.

The first topics (Chapters 1, and 2) will be more familiar as we start with single and two group situations with a quantitative response. In your previous statistics course, you should have seen methods for estimating and quantifying uncertainty for the mean of a single group and for differences in the means of two groups. Once we have briefly reviewed these methods and introduced the statistical software that we will use throughout the course, we will consider the first new statistical material in Chapter **??**. It involves the situation with a quantitative response variable where there are more than 2 groups to compare – this is what we call the ***One-Way ANOVA*** situation. It generalizes the 2-independent sample hypothesis test to handle situations where more than 2 groups are being studied. When we learn this method, we will begin discussing model assumptions and methods for assessing those assumptions that will be present in every analysis involving a quantitative response. The ***Two-Way ANOVA*** (Chapter **??**) considers situations with two categorical explanatory variables and a quantitative response. To make this somewhat concrete, suppose we are interested in assessing differences in, say, the *yield* of wheat from a field based on the amount of *fertilizer* applied (none, low, or high) and *variety* of wheat (two types). Here, *yield* is a quantitative response variable that might be measured in bushels per acre and there are two categorical explanatory variables, *fertilizer*, with three levels, and *variety*, with two levels. In this material, we introduce the idea of an ***interaction*** between the

two explanatory variables: the relationship between one categorical variable and the mean of the response changes depending on the levels of the other categorical variable. For example, extra fertilizer might enhance the growth of one variety and hinder the growth of another so we would say that *fertilizer* has different impacts based on the level of *variety*. Given this interaction may or may not actually be present, we will consider two versions of the model in Two-Way ANOVAs, what are called the ***additive*** (no interaction) and the ***interaction*** models.

Following the methods for two categorical variables and a quantitative response, we explore a method for analyzing data where the response is categorical, called the ***Chi-square test*** in Chapter **??**. This most closely matches the One-Way ANOVA situation with a single categorical explanatory variable, except now the response variable is categorical. For example, we will assess whether taking a drug (vs taking a ***placebo***[1]) has an ***effect***[2] on the type of improvement the subjects demonstrate. There are two different scenarios for study design that impact the analysis technique and hypotheses tested in Chapter **??**. If the explanatory variable reflects the group that subjects were obtained from, either through randomization of the treatment level to the subjects or by taking samples from separate populations, this is called a ***Chi-square Homogeneity Test***. It is also possible to obtain a single sample from a population and then obtain information on the levels of the explanatory variable for each subject. We will analyze these results using what is called a ***Chi-square Independence Test***. They both use the same test statistic but we use slightly different graphics and are testing different hypotheses in these two related situations. Figure 1.1 also shows that if we had a quantitative explanatory variable and a categorical response that we would need to "bin" or create categories of responses from the quantitative variable to use the Chi-square testing methods.

If the predictor and response variables are both quantitative, we start with scatterplots, correlation, and ***simple linear regression*** models (Chapters **??** and **??**) – things you should have seen, at least to some degree, previously. The biggest differences here will be the depth of exploration of diagnostics and inferences for this model and discussions of transformations of variables. If there is more than one explanatory variable, then we say that we are doing ***multiple linear regression*** (Chapter **??**) – the "multiple" part of the name reflects that there will be more than one explanatory variable. We use the same name if we have a mix of categorical and quantitative predictor variables but there are some new issues in setting up the models and interpreting the coefficients that we need to consider. In the situation with one categorical predictor and one quantitative predictor, we revisit the idea of an interaction. It allows us to consider situations where the estimated relationship between a quantitative predictor and the mean response varies among different levels of the categorical variable. In Chapter **??**, connections among all the methods used for quantitative responses are discussed, showing that they are all just linear models . We also show how the methods discussed can be applied to a suite of new problems with a set of case studies and how that relates to further extensions of the methods.

By the end of Chapter **??** you should be able to identify, perform using the statistical software R [R Core Team, 2021], and interpret the results from each of these methods. There is a lot to learn, but many of the tools for using R and interpreting results of the analyses accumulate and repeat throughout the textbook. If you work hard to understand the initial methods, it will help you when the methods get more complicated. You will likely feel like you are just starting to learn how to use R at the end of the semester and for learning a new language that is actually an accomplishment. We will just be taking you on the first steps of a potentially long journey and it is up to you to decide how much further you want to go with learning the software.

All the methods you will learn require you to carefully consider how the data were collected, how that pertains to the population of interest, and how that impacts the inferences that can be made. The ***scope of inference*** from the bottom of Figure 1.1 is our shorthand term for remembering to think about two aspects of the study – ***random assignment*** and ***random sampling***. In a given situation, you need to use the description of the study to decide if the explanatory variable was randomly assigned to study units (this allows for ***causal inferences*** if differences are detected) or not (so no causal statements are possible). As

[1] A ***placebo*** is a treatment level designed to mimic the potentially efficacious level(s) but that can have no actual effect. The ***placebo effect*** is the effect that thinking that an effective treatment was received has on subjects. There are other related issues in performing experiments like the ***Hawthorne*** or ***observer effect*** where subjects modify behavior because they are being observed.

[2] We will reserve the term "effect" for situations where we could potentially infer causal impacts on the response of the explanatory variable which occurs in situations where the levels of the explanatory variable are randomly assigned to the subjects.

an example, think about two studies, one where students are randomly assigned to either get tutoring with their statistics course or not and another where the students are asked at the end of the semester whether they sought out tutoring or not. Suppose we compare the final grades in the course for the two groups (tutoring/not) and find a big difference. In the first study with random assignment, we can say the tutoring caused the differences we observed. In the second, we could only say that the tutoring was associated with differences but because students self-selected the group they ended up in, we can't say that the tutoring caused the differences. The other aspect of scope of inference concerns random sampling: If the data were obtained using a random sampling mechanism, then our inferences can be safely extended to the population that the sample was taken from. However, if we have a non-random sample, our inference can only apply to the sample collected. In the previous example, the difference would be studying a random sample of students from the population of, say, Introductory Statistics students at a university versus studying a sample of students that volunteered for the research project, maybe for extra credit in the class. We could still randomly assign them to tutoring/not but the non-random sample would only lead to conclusions about those students that volunteered. The most powerful scope of inference is when there are randomly assigned levels of explanatory variables with a random sample from a population – conclusions would be about causal impacts that would happen in the population.

By the end of this material, you should have some basic R skills and abilities to create basic ANOVA and regression models, as well as to handle Chi-square testing situations. Together, this should prepare you for future statistics courses or for other situations where you are expected to be able to identify an appropriate analysis, do the calculations and required graphics using the data set, and then effectively communicate interpretations for the methods discussed here.

1.2 Getting started in R

You will need to download the statistical software package called R and an enhanced interface to R called RStudio [RStudio Team, 2018]. They are open source and free to download and use (and will always be that way). This means that the skills you learn now can follow you the rest of your life. R is becoming the primary language of statistics and is being adopted across academia, government, and businesses to help manage and learn from the growing volume of data being obtained. Hopefully you will get a sense of some of the power of R in this book.

The next pages will walk you through the process of getting the software downloaded and provide you with an initial experience using RStudio to do things that should look familiar even though the interface will be a new experience. Do not expect to master R quickly – it takes years (sorry!) even if you know the statistical methods being used. We will try to keep all your interactions with R code in a similar code format and that should help you in learning how to use R as we move through various methods. We will also often provide you with example code. Everyone that learns R starts with copying other people's code and then making changes for specific applications – so expect to go back to examples from the text and focus on learning how to modify that code to work for your particular data set. Only really experienced R users "know" functions without having to check other resources. After we complete this basic introduction, Chapter 2 begins doing more sophisticated things with R, allowing us to compare quantitative responses from two groups, make some graphical displays, do hypothesis testing and create confidence intervals in a couple of different ways.

You will have two[3] downloading activities to complete before you can do anything more than read this book[4]. First, you need to download R. It is the engine that will do all the computing for us, but you will only interact with it once. Go to http://cran.rstudio.com and click on the "**Download R for...**" button that corresponds to your operating system. On the next page, click on "**base**" and then it will take you to a

[3]There is a cloud version of R Studio available at https://rstudio.cloud/ that is free for limited usage and some institutions have locally hosted versions that you can use with a web-browser (check with your instructor for those options). We recommend following the steps to be able to work locally but try this option if you have issues with the installation process and need to complete an assignment or two until you get the installation sorted out.

[4]I created this interactive website (https://greenwood-stat.shinyapps.io/InstallDemo/) that contains discussions and activities related to installing and using R and RStudio.

screen to download the most current version of R that is compiled for your operating system, something like "**Download R 4.1.0 for Windows**". Click on that link and then open the file you downloaded. You will need to select your preferred language (choose English so your instructor can help you), then hit "**Next**" until it starts to unpack and install the program (all the base settings will be fine). After you hit "**Finish**" you will not do anything further with R directly.

Second, you need to download RStudio. It is an enhanced interface that will make interacting with R less frustrating and allow you to directly create reports that include the code and output. To download RStudio, go near the bottom of https://www.rstudio.com/products/rstudio/download/ and select the correct version under "Installers for Supported Platforms" for your operating system. Download and then install RStudio using the installer. From this point forward, you should only open RStudio; it provides your interface with R. Note that both R and RStudio are updated frequently (up to four times a year) and if you downloaded either more than a few months previously, you should download the up-to-date versions, especially if something you are trying to do is not working. Sometimes code will not work in older versions of R and sometimes old code won't work in new versions of R.[5]

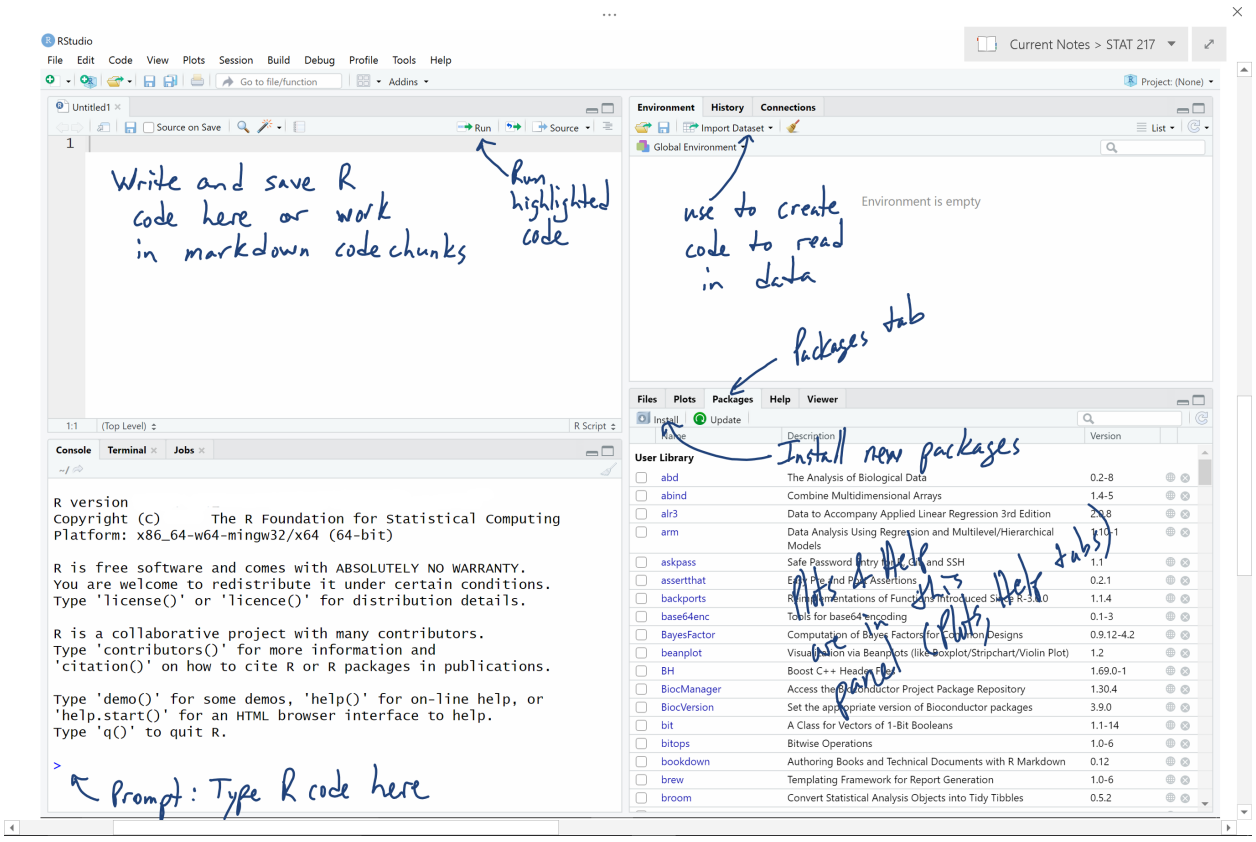

Figure 1.2: Initial RStudio layout.

[5]The need to keep the code up-to-date as R continues to evolve is one reason that this book is locally published and that this is the 8th time it has been revised in eight years...

To get started, we can complete some basic tasks in R using the RStudio interface. When you open RStudio, you will see a screen like Figure 1.2. The added annotation in this and the following screen-grabs is there to help you get initially oriented to the software interface. R is command-line software – meaning that in some way or another you have to create code and get it evaluated, either by entering and execute it at a command prompt or by using the RStudio interface to run the code that is stored in a file. RStudio makes the management and execution of that code more efficient than the basic version of R. In RStudio, the lower left panel is called the "console" window and is where you can type R code directly into R or where you will see the code you run and (most importantly!) where the results of your executed commands will show up. The most basic interaction with R is available once you get the cursor active at the command prompt ">" by clicking in that panel (look for a blinking vertical line). The upper left panel is for writing, saving, and running your R code either in .R script files or .Rmd (markdown) files, discussed below. Once you have code available in this window, the "Run" button will execute the code for the line that your cursor is on or for any text that you have highlighted with your mouse. The "data management" or environment panel is in the upper right, providing information on what data sets have been loaded. It also contains the "Import Dataset" button that provides the easiest way for you to read a data set into R so you can analyze it. The lower right panel contains information on the "Packages" (additional code we will download and install to add functionality to R) that are available and is where you will see plots that you make and requests for "Help" on specific functions.

As a first interaction with R we can use it as a calculator. To do this, click near the command prompt (`>`) in the lower left "console" panel, type 3+4, and then hit enter. It should look like this:

```
> 3+4
[1] 7
```

You can do more interesting calculations, like finding the mean of the numbers -3, 5, 7, and 8 by adding them up and dividing by 4:

```
> (-3+5+7+8)/4
[1] 4.25
```

Note that the parentheses help R to figure out your desired order of operations. If you drop that grouping, you get a very different (and wrong!) result:

```
> -3+5+7+8/4
[1] 11
```

We could estimate the standard deviation similarly using the formula you might remember from introductory statistics, but that will only work in very limited situations. To use the real power of R this semester, we need to work with data sets that store the observations for our subjects in *variables*. Basically, we need to store observations in named vectors (one dimensional arrays) that contain a list of the observations. To create a vector containing the four numbers and assign it to a variable named *variable1*, we need to create a vector using the concatenate function `c` which means "combine the items" that follow, if they are inside parentheses and have commas separating the values, as follows:

```
> c(-3, 5, 7, 8)
[1] -3 5 7 8
```

To get this vector stored in a variable called *variable1* we need to use the assignment operator, `<-` (read as "is defined to contain") that assigns the information on the right into the variable that you are creating on the left.

```
> variable1 <- c(-3, 5, 7, 8)
```

In R, the assignment operator, `<-`, is created by typing a "less than" symbol `<` followed by a "minus" sign (`-`) **without a space between them**. If you ever want to see what numbers are residing in an object in R, just type its name and hit *enter*. You can see how that variable contains the same information that was initially generated by `c(-3, 5, 7, 8)` but is easier to access since we just need the text for the variable name representing that vector.

```
> variable1
[1] -3 5 7 8
```

With the data stored in a variable, we can use functions such as `mean` and `sd` to find the mean and standard deviation of the observations contained in `variable1`:

```
> mean(variable1)
[1] 4.25
> sd(variable1)
[1] 4.99166
```

When dealing with real data, we will often have information about more than one variable. We could enter all observations by hand for each variable but this is prone to error and onerous for all but the smallest data sets. If you are to ever utilize the power of statistics in the evolving data-centered world, data management has to be accomplished in a more sophisticated way. While you can manage data sets quite effectively in R, it is often easiest to start with your data set in something like Microsoft Excel or OpenOffice's Calc. You want to make sure that observations are in the rows and the names of variables are in first row of the columns and that there is no "extra stuff" in the spreadsheet. If you have missing observations, they should be represented with blank cells. The file should be saved as a ".csv" file (stands for comma-separated values although Excel calls it "CSV (Comma Delimited)"), which basically strips off some of the junk that Excel adds to the necessary information in the file. Excel will tell you that this is a bad idea, but it actually creates a more stable archival format and one that R can use directly.[6]

The following code to read in the data set relies on an R package called `readr` [Wickham and Hester, 2020]. Packages in R provide additional functions and data sets that are not available in the initial download of R or RStudio. To get access to the packages, first "install" (basically download) and then "load" the package. To install an R package, go to the **Packages** tab in the lower right panel of RStudio. Click on the **Install** button and then type in the name of the package in the box (here type in `readr`). RStudio will try to auto-complete the package name you are typing which should help you make sure you got it typed correctly. If you are working in a .Rmd file, a highlighted message may show up on the top of the file to suggest packages to install that are not present – look for this to help make sure you have the needed packages installed. This will be the first of *many* times that we will mention that R is case sensitive – in other words, `Readr` is different from `readr` in R syntax and this sort of thing applies to everything you do in R. You should only need to install each R package once on a given computer. If you ever see a message that R can't find a package, make sure it appears in the list in the **Packages** tab. If it doesn't, repeat the previous steps to install it.

Important: R is case sensitive! `Readr` is not the same as `readr`!

[6] There are ways to read ".xls" and ".xlsx" files directly into R that we will explore later so you can also use that format if you prefer.

After installing the package, we need to load it to make it active in a given work session. Go to the command prompt and type (or copy and paste) `library(readr)` or `require(readr)`:

```
> library(readr)
```

With a data set converted to a CSV file and `readr` installed and loaded, we need to read the data set into the active workspace. There are two ways to do this, either using the point-and-click GUI in RStudio (click the "Import Dataset" button in the upper right "Environment" panel as indicated in Figure 1.2) or modifying the `read_csv` function to find the file of interest. To practice this, you can download an Excel (.xls) file from http://www.math.montana.edu/courses/s217/documents/treadmill.xls that contains observations on 31 males that volunteered for a study on methods for measuring fitness [Westfall and Young, 1993]. In the spreadsheet, you will find a data set that starts and ends with the following information (only results for Subjects 1, 2, 30, and 31 shown here):

Subject	TreadMillOx	TreadMillMaxPulse	RunTime	RunPulse	Rest Pulse	BodyWeight	Age
1	60.05	186	8.63	170	48	81.87	38
2	59.57	172	8.17	166	40	68.15	42
...	...	...	...	...	...	...	...
30	39.2	172	12.88	168	44	91.63	54
31	37.39	192	14.03	186	56	87.66	45

The variables contain information on the subject number (*Subject*), subjects' maximum treadmill oxygen consumption (*TreadMillOx*, in ml per kg per minute, also called maximum VO2) and maximum pulse rate (*TreadMillMaxPulse*, in beats per minute), time to run 1.5 miles (*Run Time*, in minutes), maximum pulse during 1.5 mile run (*RunPulse*, in beats per minute), resting pulse rate (*RestPulse*, beats per minute), Body Weight (*BodyWeight*, in kg), and *Age* (in years). Open the file in Excel or equivalent software and then save it as a .csv file in a location you can find on your computer. Then go to RStudio and click on **File**, then **Import Dataset**, then **From Text (readr)...**[7] Click "**Import**" and find your file. R will store the data set as an object with the same name as the .csv file. You could use another name as well, but it is often easiest just to keep the data set name in R related to the original file name. You should see some text appear in the console (lower left panel) like in Figure 1.3. The text that is created will look something like the following – if you had stored the file in a drive labeled D:, it would be:

```
treadmill <- read_csv("D:/treadmill.csv")
```

What is put inside the `" "` will depend on the location and name of your saved .csv file. A version of the data set in what looks like a spreadsheet will appear in the upper left window due to the second line of code (`View(treadmill)`).

Just directly typing (or using) a line of code like this is actually the other way that we can read in files. If you choose to use the text-only interface, then you need to tell R where to look in your computer to find the data file. `read_csv` is a function that takes a path as an argument. To use it, specify the path to your data file, put quotes around it, and put it as the input to `read_csv(...)`. For some examples later in the book, you will be able to copy a command like this from the text and read data sets and other code directly from the website, assuming you are connected to the internet.

To verify that you read the data set in correctly, it is always good to check its contents. We can view the first and last rows in the data set using the `head` and `tail` functions on the data set, which show the following results for the `treadmill` data. Note that you will sometimes need to resize the console window in RStudio to get all the columns to display in a single row which can be performed by dragging the gray bars that separate the panels.

[7] If you are having trouble getting the file converted and read into R, copy and run the following code: `treadmill <- read_csv("http://www.math.montana.edu/courses/s217/documents/treadmill.csv")`.

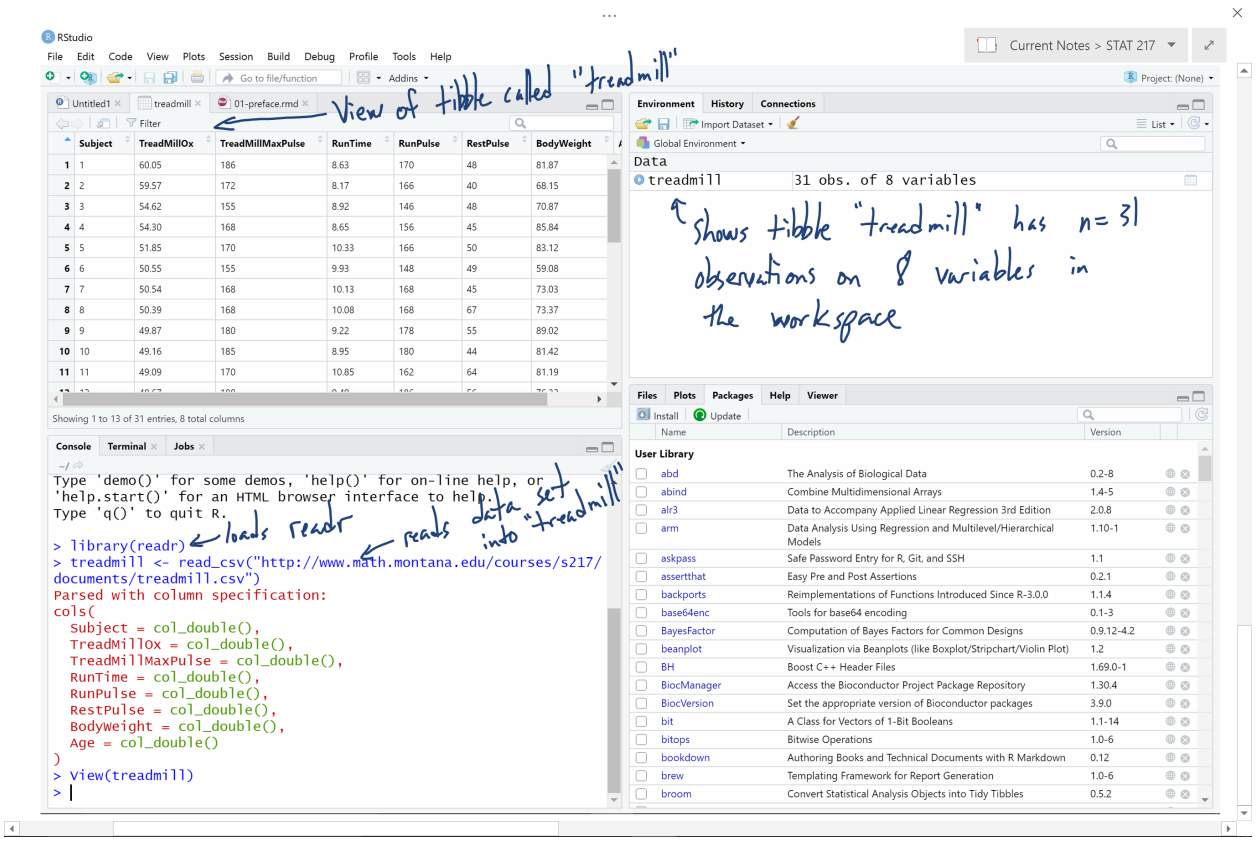

Figure 1.3: RStudio with initial data set loaded.

```
> head(treadmill)
# A tibble: 6 x 8
  Subject TreadMillOx TreadMillMaxPulse RunTime RunPulse RestPulse BodyWeight   Age
    <int>       <dbl>             <int>   <dbl>     <int>      <int>      <dbl> <int>
1       1       60.05               186    8.63       170         48       81.87    38
2       2       59.57               172    8.17       166         40       68.15    42
3       3       54.62               155    8.92       146         48       70.87    50
4       4       54.30               168    8.65       156         45       85.84    44
5       5       51.85               170   10.33       166         50       83.12    54
6       6       50.55               155    9.93       148         49       59.08    57

> tail(treadmill)
# A tibble: 6 x 8
  Subject TreadMillOx TreadMillMaxPulse RunTime RunPulse RestPulse BodyWeight   Age
    <int>       <dbl>             <int>   <dbl>     <int>      <int>      <dbl> <int>
1      26       44.61               182   11.37       178         62       89.47    44
2      27       40.84               172   10.95       168         57       69.63    51
3      28       39.44               176   13.08       174         63       81.42    44
4      29       39.41               176   12.63       174         58       73.37    57
5      30       39.20               172   12.88       168         44       91.63    54
6      31       37.39               192   14.03       186         56       87.66    45
```

When you load an installed package with `library`, you may see a warning message about versions of the package and versions of R – this is *usually* something you can ignore. Other warning messages could be more ominous for proceeding but before getting too concerned, there are couple of basic things to check. First, double check that the package is installed (see previous steps). Second, check for typographical errors in your code – especially for mis-spellings or unintended capitalization. If you are still having issues, try repeating the installation process. Then click on the "**Update**" button to check for potentially newer versions of packages. If all that fails, try the cloud version of RStudio discussed before and repeat the steps there.

To help you go from basic to intermediate R usage and especially to help with more complicated problems, you will want to learn how to manage and save your R code. The best way to do this is using the upper left panel in RStudio. If you just want to manage code, then you can use what are called R Scripts, which are files that have a file extension of ".R". To start a new ".R" file to store your code, click on **File**, then **New File**, then **R Script**. This will create a blank page to enter and edit code – then save the file as something like "MyFileName.R" in your preferred location. Saving your code will mean that you can return to where you were working last by simply re-running the saved script file. With code in the script window, you can place the cursor on a line of code or highlight a chunk of code and hit the "Run" button[8] on the upper part of the panel. It will appear in the console with results just like what you would obtain if you typed it after the command prompt and hit enter for each line. Figure 1.4 shows the screen with the code used in this section in the upper left panel, saved in a file called "Ch1.R", with the results of highlighting and executing the first section of code using the "Run" button.

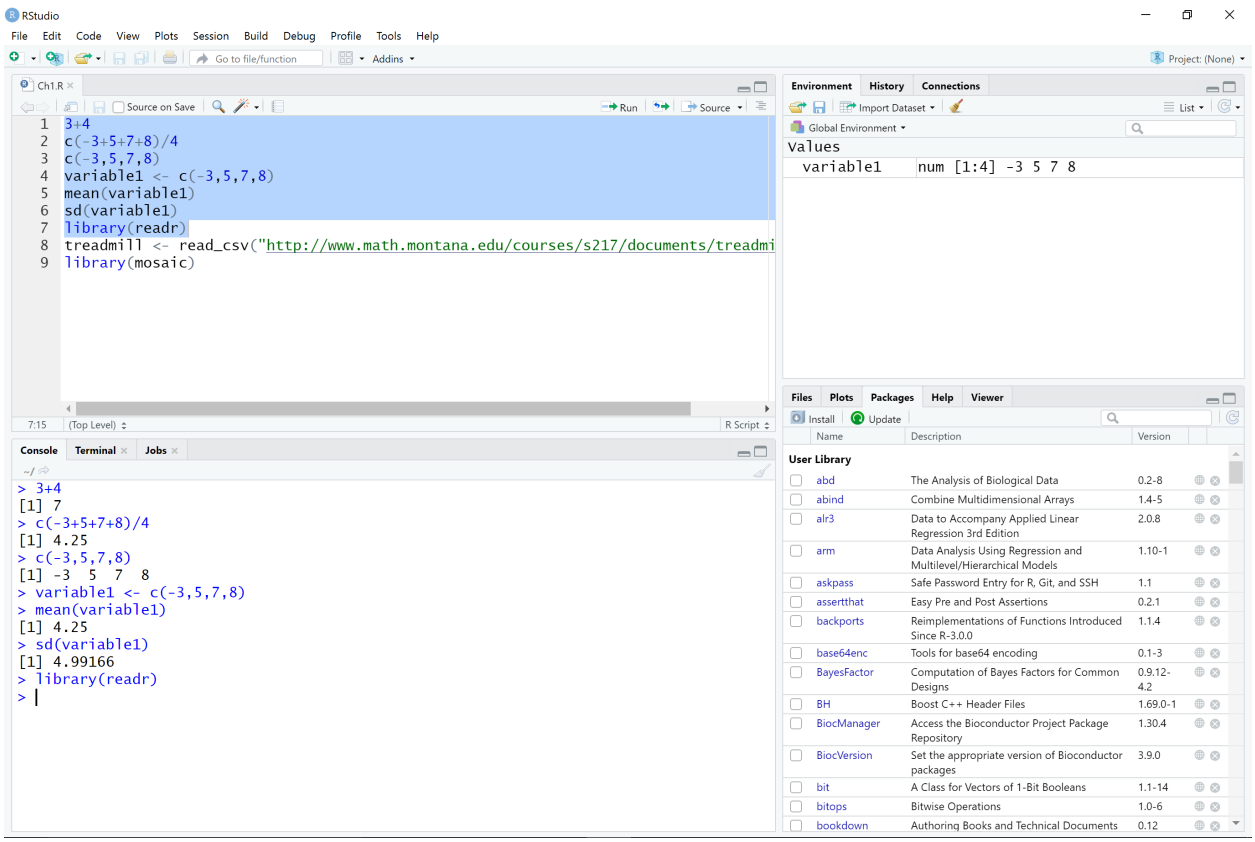

Figure 1.4: RStudio with highlighted code run.

[8] You can also use Ctrl+Enter if you like hot keys.

1.3 Basic summary statistics, histograms, and boxplots using R

For the following material, you will need to install and load the `mosaic` package [Pruim et al., 2021b].

```
> library(mosaic)
```

It provides a suite of enhanced functions to aid our initial explorations. With RStudio running, the `mosaic` package loaded, a place to write and save code, and the `treadmill` data set loaded, we can (finally!) start to summarize the results of the study. The `treadmill` object is what R calls a ***tibble***[9] and contains columns corresponding to each variable in the spreadsheet. Every function in R will involve specifying the variable(s) of interest and how you want to use them. To access a particular variable (column) in a tibble, you can use a $ between the name of the tibble and the name of the variable of interest, generically as `tibblename$variablename`. You can think of this as *tibblename's variablename* where the *'s* is replaced by the dollar sign. To identify the `RunTime` variable here it would be `treadmill$RunTime`. In the command line it would look like:

```
> treadmill$RunTime
 [1]  8.63  8.17  8.92  8.65 10.33  9.93 10.13 10.08  9.22  8.95 10.85  9.40 11.50 10.50
[15] 10.60 10.25 10.00 11.17 10.47 11.95  9.63 10.07 11.08 11.63 11.12 11.37 10.95 13.08
[29] 12.63 12.88 14.03
```

Just as in the previous section, we can generate summary statistics using functions like `mean` and `sd` by running them on a specific variable:

```
> mean(treadmill$RunTime)
[1] 10.58613
> sd(treadmill$RunTime)
[1] 1.387414
```

And now we know that the average running time for 1.5 miles for the subjects in the study was 10.6 minutes with a standard deviation (SD) of 1.39 minutes. But you should remember that the mean and SD are only appropriate summaries if the distribution is roughly ***symmetric*** (both sides of the distribution are approximately the same shape and length). The `mosaic` package provides a useful function called `favstats` that provides the mean and SD as well as the ***5 number summary***: the minimum (`min`), the first quartile (`Q1`, the 25th percentile), the median (50th percentile), the third quartile (`Q3`, the 75th percentile), and the maximum (`max`). It also provides the number of observations (`n`) which was 31, as noted above, and a count of whether any missing values were encountered (`missing`), which was 0 here since all subjects had measurements available on this variable.

```
> favstats(treadmill$RunTime)
  min   Q1 median    Q3   max     mean       sd  n missing
 8.17 9.78  10.47 11.27 14.03 10.58613 1.387414 31       0
```

We are starting to get somewhere with understanding that the runners were somewhat fit with the worst runner covering 1.5 miles in 14 minutes (the equivalent of a 9.3 minute mile) and the best running at a 5.4 minute mile pace. The limited variation in the results suggests that the sample was obtained from a restricted group with somewhat common characteristics. When you explore the ages and weights of the subjects in the Practice Problems in Section 1.6, you will get even more information about how similar all the subjects in this study were. Researchers often publish numerical summaries of this sort of demographic information to help readers understand the subjects that they studied and that their results might apply to.

[9] Tibbles are R objects that can contain both categorical and quantitative variables on your n subjects with a name for each variable that is also the name of each column in a matrix. Each subject is a row of the data set. The name (supposedly) is due to the way *table* sounds in the accent of a particularly influential developer at RStudio who is from New Zealand.

A graphical display of these results will help us to assess the shape of the distribution of run times – including considering the potential for the presence of a ***skew*** (whether the right or left tail of the distribution is noticeably more spread out, with left skew meaning that the left tail is more spread out than the right tail) and ***outliers*** (unusual observations). A ***histogram*** is a good place to start. Histograms display connected bars with counts of observations defining the height of bars based on a set of bins of values of the quantitative variable. We will apply the `hist` function to the `RunTime` variable, which produces Figure 1.5.

```
> hist(treadmill$RunTime)
```

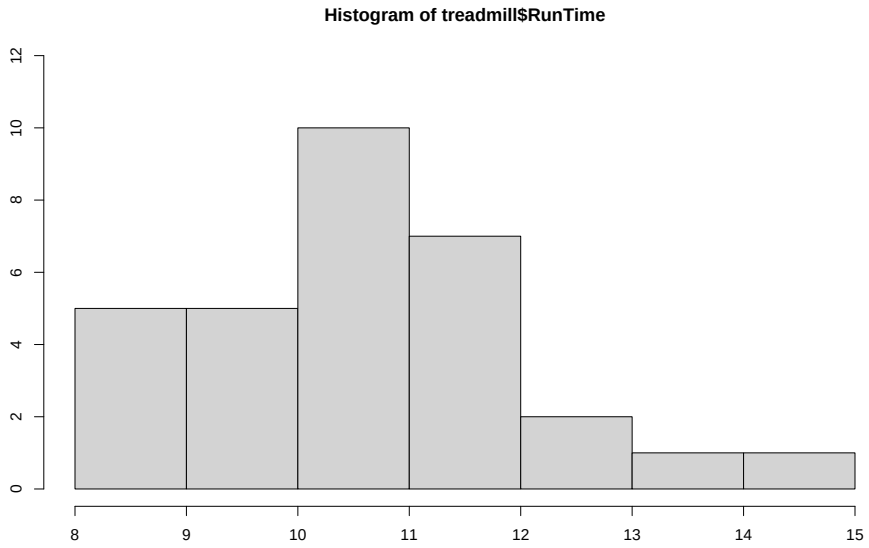

Figure 1.5: Histogram of Run Times (minutes) of n=31 subjects in Treadmill study, bar heights are counts.

You can save this plot by clicking on the **Export** button found above the plot, followed by **Copy to Clipboard** and clicking on the **Copy Plot** button. Then if you open your favorite word-processing program, you should be able to paste it into a document for writing reports that include the figures. You can see the first parts of this process in the screen grab in Figure 1.6. You can also directly save the figures as separate files using **Save as Image** or **Save as PDF** and then insert them into your word processing documents.

The function `hist` defaults into providing a histogram on the ***frequency*** (count) scale. In most R functions, there are the default options that will occur if we don't make any specific choices but we can override the default options if we desire. One option we can modify here is to add labels to the bars to be able to see exactly how many observations fell into each bar. Specifically, we can turn the `labels` option "on" by making it true ("T") by adding `labels=T` to the previous call to the `hist` function, separated by a comma. Note that we will use the `=` sign only for changing options within functions.

```
> hist(treadmill$RunTime, labels=T)
```

Based on this histogram (Figure 1.8), it does not appear that there any outliers in the responses since there are no bars that are separated from the other observations. However, the distribution does not look symmetric and there might be a skew to the distribution. Specifically, it appears to be ***skewed right*** (the right tail is longer than the left). But histograms can sometimes mask features of the data set by binning observations and it is hard to find the percentiles accurately from the plot.

When assessing outliers and skew, the ***boxplot*** (or *Box and Whiskers* plot) can also be helpful (Figure 1.8) to describe the shape of the distribution as it displays the 5-number summary and will also indicate observations that are "far" above the middle of the observations. R's `boxplot` function uses the standard rule to indicate an observation as a ***potential outlier*** if it falls more than 1.5 times the ***IQR*** (Inter-Quartile

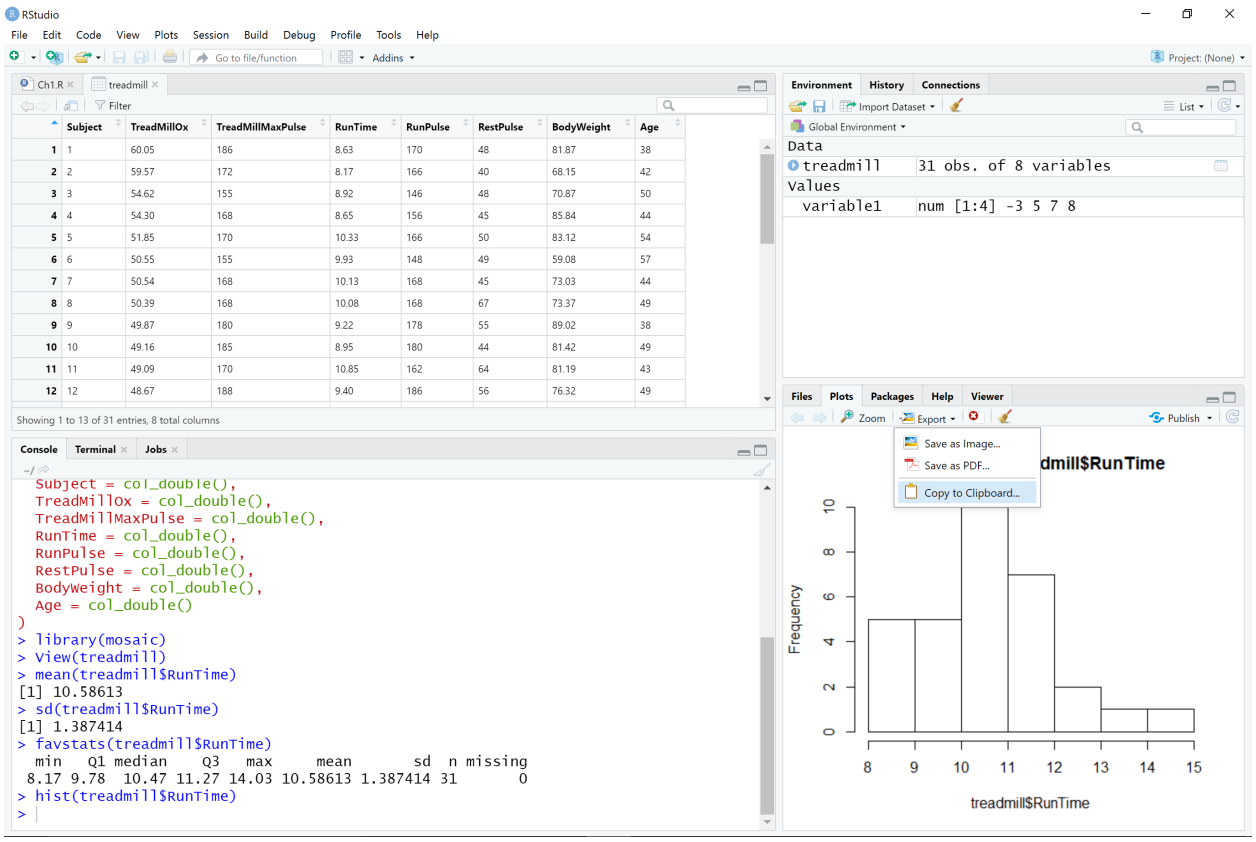

Figure 1.6: RStudio while in the process of copying the histogram.

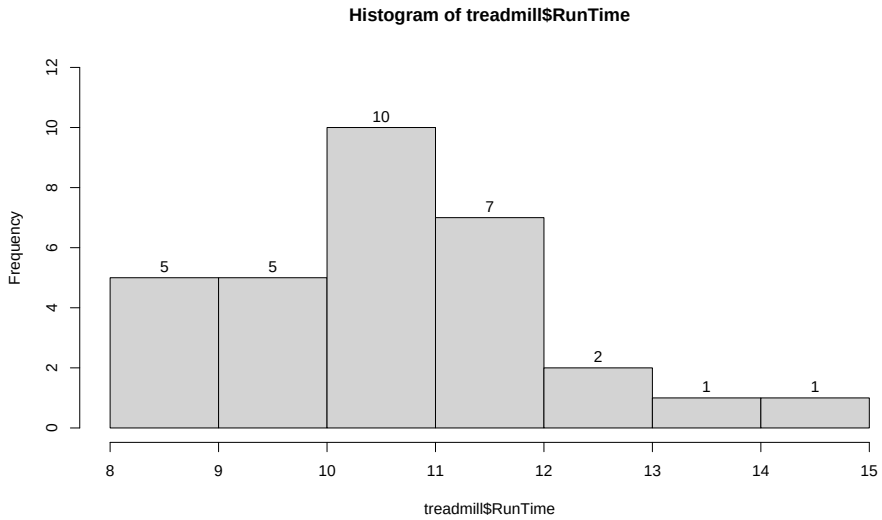

Figure 1.7: Histogram of Run Times with counts in bars labeled.

Range, calculated as Q3 – Q1) below Q1 or above Q3. The potential outliers are plotted with circles and the *Whiskers* (lines that extend from Q1 and Q3 typically to the minimum and maximum) are shortened to only go as far as observations that are within 1.5∗IQR of the upper and lower quartiles. The *box* part of the

boxplot is a box that goes from Q1 to Q3 and the median is displayed as a line somewhere inside the box.[10] Looking back at the summary statistics above, Q1=9.78 and Q3=11.27, providing an IQR of:

```
> IQR <- 11.27 - 9.78
> IQR
[1] 1.49
```

One observation (the maximum value of 14.03) is indicated as a potential outlier based on this result by being larger than Q3 +1.5∗IQR, which was 13.505:

```
> 11.27 + 1.5*IQR
[1] 13.505
```

The boxplot also shows a slight indication of a right skew (skew towards larger values) with the distance from the minimum to the median being smaller than the distance from the median to the maximum. Additionally, the distance from Q1 to the median is smaller than the distance from the median to Q3. It is modest skew, but worth noting.

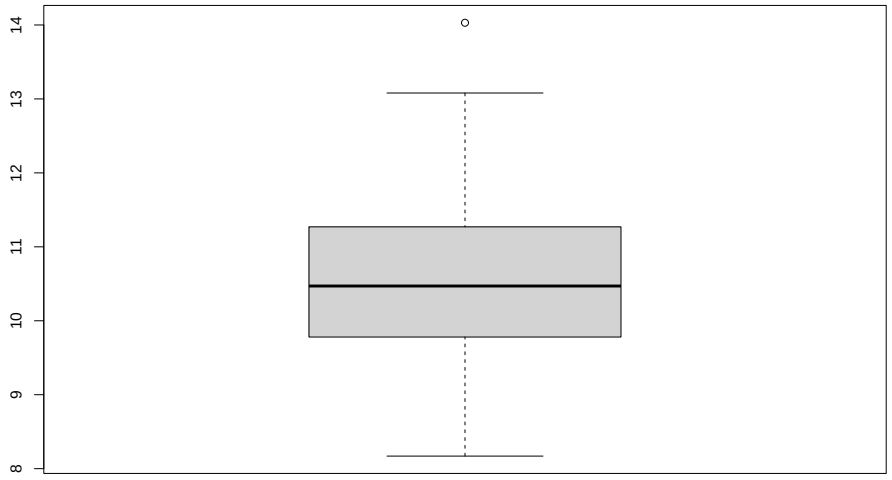

Figure 1.8: Boxplot of 1.5 mile Run Times.

```
> boxplot(treadmill$RunTime)
```

While the default boxplot is fine, it fails to provide good graphical labels, especially on the y-axis. Additionally, there is no title on the plot. The following code provides some enhancements to the plot by using the `ylab` and `main` options in the call to `boxplot`, with the results displayed in Figure 1.9. When we add text to plots, it will be contained within quotes and be assigned into the options `ylab` (for y-axis) or `main` (for the title) here to put it into those locations.

```
> boxplot(treadmill$RunTime, ylab="1.5 Mile Run Time (minutes)",
          main="Boxplot of the Run Times of n=31 participants")
```

Throughout the book, we will often use extra options to make figures that are easier for you to understand.

[10]The median, quartiles and whiskers sometimes occur at the same values when there are many tied observations. If you can't see all the components of the boxplot, produce the numerical summary to help you understand what happened.

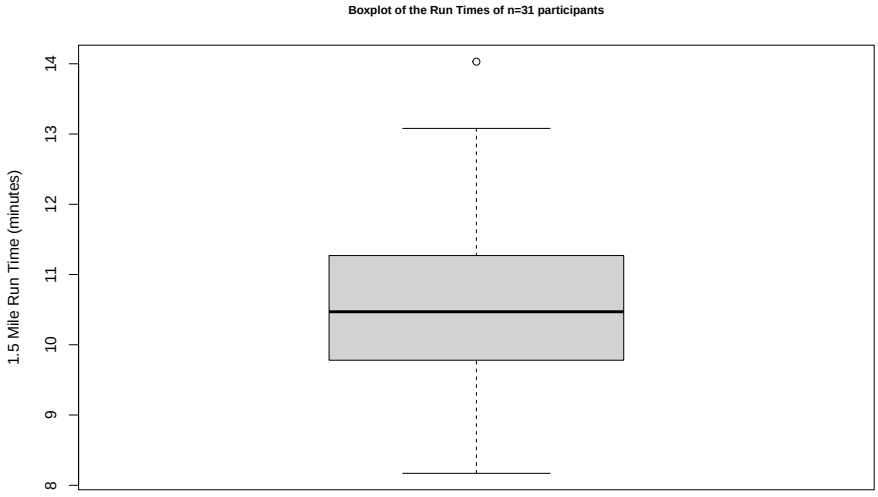

Figure 1.9: Boxplot of Run Times with improved labels.

There are often simpler versions of the functions that will suffice but the extra work to get better labeled figures is often worth it. I guess the point is that "a picture is worth a thousand words" but in data visualization, that is only true if the reader can understand what is being displayed. It is also important to think about the quality of the information that is being displayed, regardless of how pretty the graphic might be. So maybe it is better to say "a picture can be worth a thousand words" if it is well-labeled?

1.4 R Markdown

The previous results were created by running the R code and then copying the results from either the console or by copying the figure and then pasting the results into the typesetting program. There is another way to use RStudio where you can have it compile the results (both output and figures) directly into a document together with other writing and the code that generated it, using what is called R Markdown (http://shiny.rstudio.com/articles/rmarkdown.html). It is basically what we used to prepare this book and what you should learn to use to do your work. From here forward, you will see a change in formatting of the R code and output as you will no longer see the command prompt (">") with the code. The output will be flagged by having two "##"'s before it. For example, the summary statistics for the *RunTime* variable from `favstats` function would look like when run using R Markdown:

```
favstats(treadmill$RunTime)
```

```
##   min   Q1 median    Q3   max     mean       sd  n missing
##  8.17 9.78  10.47 11.27 14.03 10.58613 1.387414 31       0
```

Statisticians (and other scientists) are starting to use R Markdown and similar methods because they provide what is called "Reproducible research" [Gandrud, 2015] where all the code and output it produced are available in a single place. This allows different researchers to run and verify results (so "reproducible results") or the original researchers to revisit their earlier work at a later date and recreate all their results exactly[11]. Scientific publications are currently encouraging researchers to work in this way and may someday require it. The term ***reproducible*** can also be related to whether repeated studies (with new, independent data collection stages and analyses) get the same result (also called ***replication***) – further discussion of these terms and the implications for scientific research are discussed in Chapter 2.

In order to get some practice using R Markdown, create a sample document in this format using File -> New File -> R Markdown... Choose a title for your file and select the "Word" option. This will create a new file in the upper left window where we stored our .R script. Save that file to your computer. Then you can use the "Knit" button to have RStudio run the code and create a word document with the results. R Markdown documents contain basically two components, "code chunks" that contain your code and the rest of the document where you can write descriptions and interpretations of the results that code generates. The code chunks can be inserted using the "Insert" button by selecting the "R" option. Then write your code in between the ```` ```{r} ```` and ```` ``` ```` lines (it should have grey highlights for those lines and white for the rest of the portions of the .Rmd document). Once you write some code inside a code chunk, you can test your code using the triangle on the upper right side of it to run all the code that resides in that chunk. Keep your write up outside of these code chunks to avoid code errors and failures to compile. Once you think your code and writing is done, you can use the "Knit" button to try to compile the file. As you are learning, you may find this challenging, so start with trying to review the sample document and knit each time you get a line of code written so you know which line was responsible for preventing the knitting from being successful. Also look around for posted examples of .Rmd files to learn how others have incorporated code with write-ups. You might even be given a template of homework or projects as .Rmd files from your instructor. After you do this a couple of times, you will find that the challenge of working with markdown files is more than matched by the simplicity of the final product and, at least to researchers, the reproducibility and documentation of work that this way of working provides.

1.5 Grammar of Graphics

The previous plots were made using what is called "base R" graphics. It is possible to make versions of all the graphics we need in this material using single function calls like `boxplot` - and there are some places we will utilize these simple versions because they get us exactly what we want to see. But to make more

[11] I recently had to revisit some work from almost a decade ago (before I switched to using R Markdown) as we were working on a journal article submission that re-used some of that work and it was unclear where some results came from, so I had to do some new work that could have been avoided if I had worked in a reproducible fashion.

complex displays and have complete control of the way the graphs look, we will utilize the `ggplot2` package [Wickham et al., 2021] which was built to implement a type of grammar for making and layering graphical displays of data, adding each layer step by step. While it takes a little bit of work to get started, the power of these displays will ultimately make the investment worthwhile[12].

As opposed to base graphics, the ggplots will contain multiple components that are patched together with a `+`, with the general format of `ggplot(data = <DATA>, mapping = aes(<VARIABLE MAPPINGS>)) + <GEOM_FUNCTION>()`. Breaking this down, the `data = ...` tells the `ggplot` function where to look, the information inside the `aes` (or aesthetic) defines which variables in the data set to use and how to use them (often with `x = variable1`, `y = variable2`, etc., with `x = ...` for the variable on the x (horizontal) axis and `y = ...` for the variable on the y (vertical) axis), and the `+ <GEOM_FUNCTION>()` defines which type of graph to make (there are `geom_histogram` and `geom_boxplot` to make the graphs discussed previously and many, many more). Because we often have many "+"'s to include, the common practice is to hit return after the "+" and start the next layer or option on the following line for better readability. Figure 1.10 shows a histogram of the `RunTime` variable made using the `+ geom_histogram()`.

```
library(ggplot2)
ggplot(data = treadmill, mapping = aes(x = RunTime)) + geom_histogram()
```

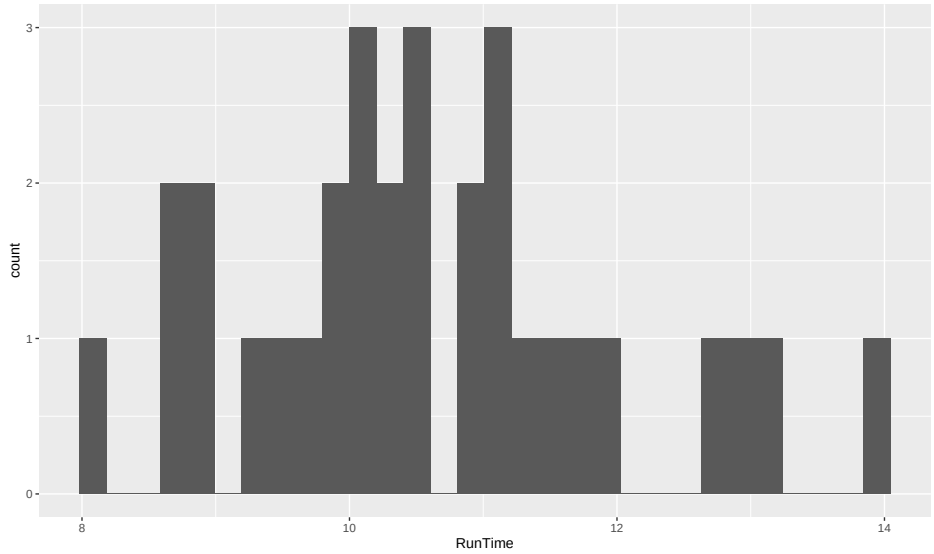

Figure 1.10: Default histogram of Run Times using `ggplot`.

The warning message reflects a challenge in making histograms that involves how many bins to use. In `geom_histogram`, it always uses 30 bins and expects you to make your own choice, compared to `hist` that used a different method to try to make a better automatic choice, but there is no single right answer. So maybe we should try out other values to get a "smoother" result here, which we can do by adding the `bins = ...` to the `+ geom_histogram()`, such as `+ geom_histogram(bins = 8)` to get an 8 bin histogram in Figure 1.11.

```
ggplot(data = treadmill, mapping = aes(x = RunTime)) +
  geom_histogram(bins = 8)
```

The following chapters will explore further modifications for these plots, but there are a couple of additions to highlight. The first is that we can often layer multiple geoms on the same plot and the order of the additions

[12]This discussion is based on materials developed for a data visualization workshop originally developed by Dr. Allison Theobold and related to the https://datacarpentry.org/ workshops.

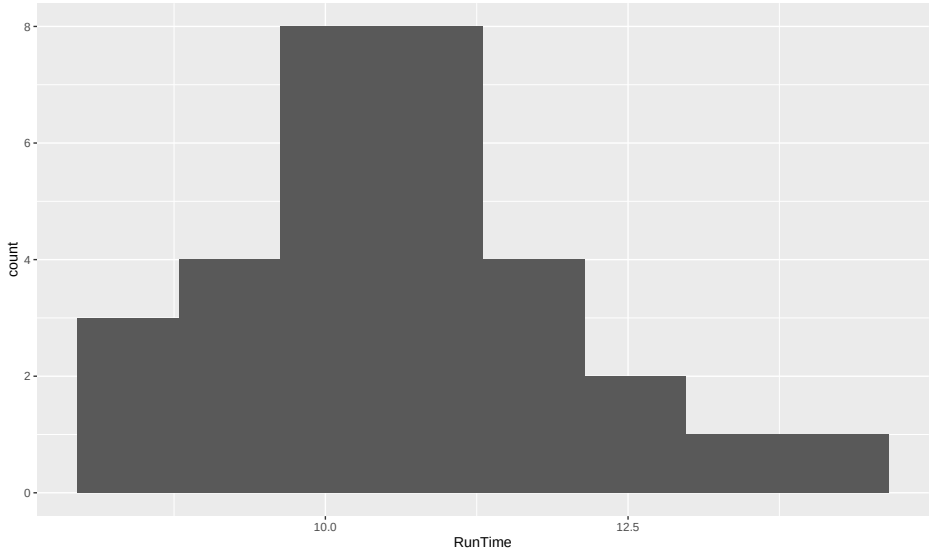

Figure 1.11: Histogram of Run Times using `ggplot` with 8 bins.

defines which layer is "on top", with the plot built up sequentially. So we can add a boxplot on top of a histogram by putting it after the histogram layer. Also in Figure 1.12, the `geom_rug` is also added, which puts a tick mark for each observation on the lower part of the x-axis. Rug plots use a graphical technique called ***jittering*** to add a little noise[13] to each observation so that multiple similar or tied observations do not plot as a single line. There are options to control the color of individual components when we add them (the histogram is filled with grey (`fill = "grey"`), the boxplot is in "tomato" (`color = "tomato"`), and the rug plot is in "skyblue"). Finally, the last change here is to the "theme" for the plot[14] which we can include one of a suite of different layouts with themes such as `+ theme_bw()` or `+ theme_light()`. If you add the `ggthemes` package[Arnold, 2021], you can access a long list of alternative looks for your plot (see https://jrnold.github.io/ggthemes/reference/index.html for options there).

```
ggplot(data = treadmill, mapping = aes(x = RunTime)) +
  geom_histogram(fill = "grey", bins = 8) +
  geom_boxplot(color = "tomato") +
  geom_rug(color = "skyblue") +
  theme_light()
```

1.6 Exiting RStudio

Finally, when you are done with your work and attempt to exit out of RStudio, it will ask you to save your workspace. ***DO NOT DO THIS!*** It will just create a cluttered workspace and could even cause you to get incorrect results.

In fact, you should go into the Tools -> Global Options and then make sure that "Save workspace to .RData on exit" option on the first screen you will see is set to ***Never***. If you save your R code either as a .R or (better) an R Markdown (.Rmd) file, you can re-create any results by simply re-running that code or re-knitting the file. If you find that you have lots of "stuff" in your workspace because you accidentally saved

[13] Jittering typically involves adding random variability to each observation that is uniformly distributed in a range determined based on the spacing of the observation. The idea is to jitter just enough to see all the points but not too much. This means that if you re-run the `jitter` function, the results will change if you do not set the random number seed using `set.seed` that is discussed more below. For more details, type `help(jitter)` in the console in RStudio.

[14] This certainly could have waited until later, but I have now seen enough base ggplot graphs that I really like to change their overall look.

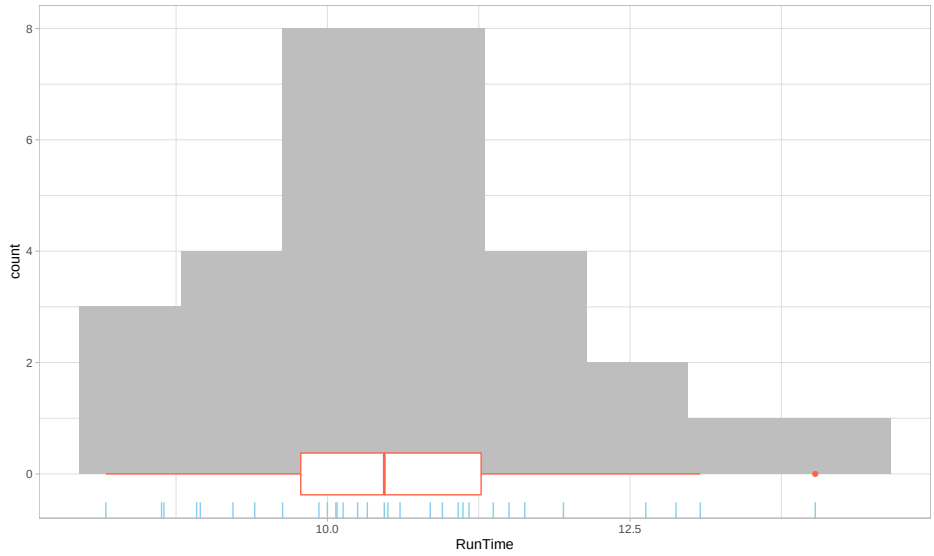

Figure 1.12: Histogram with boxplot and rug of Run Times using `ggplot` with modified colors and theme.

your workspace, just run `rm(list = ls())`. It will delete all the data sets from your workspace.

1.7 Chapter summary

This chapter covered getting R and RStudio downloaded and some basics of working with R via RStudio. You should be able to read a data set into R and run some basic functions, all done using the RStudio interface. If you are struggling with this, you should seek additional help with these technical issues so that you are ready for more complicated statistical methods that are going to be encountered in the following chapters. The way everyone learns R is by starting with some example code that does most of what you want to do and then you modify it. If you can complete the Practice Problems that follow, you are well on your way to learning to use R.

The statistical methods in this chapter were minimal and all should have been review. They involved a quick reminder of summarizing the center, spread, and shape of distributions using numerical summaries of the mean and SD and/or the min, Q1, median, Q3, and max and the histogram and boxplot as graphical summaries. We revisited the ideas of symmetry and skew. But the main point was really to get a start on using R via RStudio to provide results you should be familiar with from your previous statistics experience(s) and to introduce some of the code we will be building on in the next chapters.

1.8 Summary of important R code

To help you learn and use R, there is a section highlighting the most important R code used near the end of each chapter. The bold text will never change but the lighter and/or ALL CAPS text (red in the online or digital version) will need to be customized to your particular application. The sub-bullet for each function will discuss the use of the function and pertinent options or packages required. You can use this as a guide to finding the function names and some hints about options that will help you to get the code to work. You can also revisit the worked examples using each of the functions.

- FILENAME **<- read_csv(**"path to csv file/FILENAME.csv"**)**
  - Can be generated using "Import Dataset" button or by modifying this text.
  - Requires the `readr` package to be loaded (`library(readr)`) when using the code directly.
  - Imports a text file saved in the CSV format.
- DATASETNAME**$**VARIABLENAME
  - To access a particular variable in a tibble called DATASETNAME, use a $ and then the VARIABLENAME.
- **head(**DATASETNAME**)**
  - Provides a list of the first few rows of the data set for all the variables in it.
- **tail(**DATASETNAME**)**
  - Provides a list of the last few rows of the data set for all the variables in it.
- **mean(**DATASETNAME**$**VARIABLENAME**)**
  - Calculates the mean of the observations in a variable.
- **sd(**DATASETNAME**$**VARIABLENAME**)**
  - Calculates the standard deviation of the observations in a variable.
- **favstats(**DATASETNAME$VARIABLENAME**)**
  - Requires the `mosaic` package to be loaded (`library(mosaic)`) after installing the package).
  - Provides a suite of numerical summaries of the observations in a variable.
- **hist(**DATASETNAME**$**VARIABLENAME**)**
  - Makes a histogram.
- **boxplot(**DATASETNAME**$**VARIABLENAME**)**
  - Makes a boxplot.
- **ggplot(data =** DATASETNAME**, mapping = aes(**VARIABLENAME**)) + geom_histogram(bins =** 10**)**
  - Makes a histogram with 10 bins using `ggplot`, requires the `ggplot2` library is installed and loaded.

1.9 Practice problems

In each chapter, the last section contains some questions for you to complete to make sure you understood the material. You can download the code to answer questions 1.1 to 1.5 below at http://www.math.montana.edu/courses/s217/documents/Ch1.Rmd. But to practice learning R, it would be most useful for you to try to accomplish the requested tasks yourself and then only refer to the provided R code if/when you struggle. These questions provide a great venue to check your learning, often to see the methods applied to another data set, and for something to discuss in study groups, with your instructor, and at the Math Learning Center.

1.1. Open RStudio and go to File -> New File -> R Markdown... to create a .Rmd. Click on the "Knit" button and see what happens. Try to complete the following questions in that document, clicking on the Knit button after you add a code chunk with code to complete each question. Part of the assignment on this question is to not get frustrated the first time you are trying this and seek out help to answer questions you have when practicing.

1.2. Read in the treadmill data set discussed previously and find the mean and SD of the Ages (`Age` variable) and Body Weights (`BodyWeight` variable). In studies involving human subjects, it is common to report a summary of characteristics of the subjects. Why does this matter? Think about how your interpretation of any study of the fitness of subjects would change if the mean age (same spread) had been 20 years older or 35 years younger.

1.3. How does knowing about the distribution of results for *Age* and *BodyWeight* help you understand the results for the Run Times discussed previously?

1.4. The mean and SD are most useful as summary statistics only if the distribution is relatively symmetric. Make a histogram of *Age* responses and discuss the shape of the distribution (is it skewed right, skewed left, approximately symmetric?; are there outliers?). Approximately what range of ages does this study pertain to?

1.5. The weight responses are in kilograms and you might prefer to see them in pounds. The conversion is `lbs=2.205*kgs`. Create a new variable in the `treadmill` tibble called *BWlb* using this code:

```
treadmill$BWlb <- 2.205*treadmill$BodyWeight
```

and find the mean and SD of the new variable (*BWlb*).

1.6. Make histograms and boxplots of the original *BodyWeight* and new *BWlb* variables, both using base R plots and using `ggplot2`. Discuss aspects of the distributions that changed and those that remained the same with the transformation from kilograms to pounds. What does this tell you about changing the units of a variable in terms of its distribution?

Chapter 2

(R)e-Introduction to statistics

The previous material served to get us started in R and to get a quick review of same basic graphical and descriptive statistics. Now we will begin to engage some new material and exploit the power of R to do statistical inference. Because inference is one of the hardest topics to master in statistics, we will also review some basic terminology that is required to move forward in learning more sophisticated statistical methods. To keep this "review" as short as possible, we will not consider every situation you learned in introductory statistics and instead focus exclusively on the situation where we have a quantitative response variable measured on two groups, adding a new graphic called a "pirate-plot" to help us see the differences in the observations in the groups.

2.1 Data wrangling and density curves

Part of learning statistics is learning to correctly use the terminology, some of which is used colloquially differently than it is used in formal statistical settings. The most commonly "misused" statistical term is ***data***. In statistical parlance, we want to note the plurality of data. Specifically, ***datum*** is a single measurement, possibly on multiple random variables, and so it is appropriate to say that "**a datum is...**". Once we move to discussing data, we are now referring to more than one observation, again on one, or possibly more than one, random variable, and so we need to use "**data are...**" when talking about our observations. We want to distinguish our use of the term "data" from its more colloquial[1] usage that often involves treating it as singular. In a statistical setting "data" refers to measurements of our cases or units. When we summarize the results of a study (say providing the mean and SD), that information is not "data". We used our data to generate that information. Sometimes we also use the term "data set" to refer to all our observations and this is a singular term to refer to the group of observations and this makes it really easy to make mistakes on the usage of "data"[2].

It is also really important to note that ***variables*** have to vary – if you measure the level of education of your subjects but all are high school graduates, then you do not have a "variable". You may not know if you have real variability in a "variable" until you explore the results you obtained.

The last, but probably most important, aspect of data is the context of the measurement. The "who, what, when, and where" of the collection of the observations is critical to the sort of conclusions we can make based on the results. The information on the study design provides information required to assess the ***scope of inference*** (SOI) of the study (see Table 2.1 for more on SOI). Generally, remember to think about the

[1] You will more typically hear "data is" but that more often refers to information, sometimes even statistical summaries of data sets, than to observations made on subjects collected as part of a study, suggesting the confusion of this term in the general public. We will explore a data set in Chapter **??** related to perceptions of this issue collected by researchers at http://fivethirtyeight.com/.

[2] Either try to remember "data is a plural word" or replace "data" with "things" or, as one former student suggested that helped her with this, replace "data" with "puppies" or "penguins" in your sentence and consider whether it sounds right.

research questions the researchers were trying to answer and whether their study actually would answer those questions. There are no formulas to help us sort some of these things out, just critical thinking about the context of the measurements.

To make this concrete, consider the data collected from a study [Walker et al., 2014] to investigate whether clothing worn by a bicyclist might impact the passing distance of cars. One of the authors wore seven different outfits (outfit for the day was chosen randomly by shuffling seven playing cards) on his regular 26 km commute near London in the United Kingdom. Using a specially instrumented bicycle, they measured how close the vehicles passed to the widest point on the handlebars. The seven outfits ("conditions") that you can view at https://www.sciencedirect.com/science/article/pii/S0001457513004636 were:

- COMMUTE: Plain cycling jersey and pants, reflective cycle clips, commuting helmet, and bike gloves.
- CASUAL: Rugby shirt with pants tucked into socks, wool hat or baseball cap, plain gloves, and small backpack.
- HIVIZ: Bright yellow reflective cycle commuting jacket, plain pants, reflective cycle clips, commuting helmet, and bike gloves.
- RACER: Colorful, skin-tight, Tour de France cycle jersey with sponsor logos, Lycra bike shorts or tights, race helmet, and bike gloves.
- NOVICE: Yellow reflective vest with "Novice Cyclist, Pass Slowly" and plain pants, reflective cycle clips, commuting helmet, and bike gloves.
- POLICE: Yellow reflective vest with "POLICEwitness.com – Move Over – Camera Cyclist" and plain pants, reflective cycle clips, commuting helmet, and bike gloves.
- POLITE: Yellow reflective vest with blue and white checked banding and the words "POLITE notice, Pass Slowly" looking similar to a police jacket and plain pants, reflective cycle clips, commuting helmet, and bike gloves.

They collected data (distance to the vehicle in cm for each car "overtake") on between 8 and 11 rides in each outfit and between 737 and 868 "overtakings" across these rides. The outfit is a categorical *predictor* or *explanatory* variable) that has seven different levels here. The distance is the *response* variable and is a quantitative variable here[3]. Note that we do not have the information on which overtake came from which ride in the data provided or the conditions related to individual overtake observations other than the distance to the vehicle (they only included overtakings that had consistent conditions for the road and riding).

The data are posted on my website[4] at http://www.math.montana.edu/courses/s217/documents/Walker 2014_mod.csv if you want to download the file to a local directory and then import the data into R using "Import Dataset". Or you can use the code in the following code chunk to directly read the data set into R using the URL.

```
suppressMessages(library(readr))
dd <- read_csv("http://www.math.montana.edu/courses/s217/documents/Walker2014_mod.csv")
```

It is always good to review the data you have read by running the code and printing the tibble by typing the tibble name (here `> dd`) at the command prompt in the console, using the `View` function, (here `View(dd)`), to open a spreadsheet-like view, or using the `head` and `tail` functions have been show the first and last ten observations:

[3]Of particular interest to the bicycle rider might be the "close" passes and we will revisit this as a categorical response with "close" and "not close" as its two categories later.

[4]Thanks to Ian Walker for allowing me to use and post these data.

```
head(dd)
```

```
## # A tibble: 6 x 8
##   Condition Distance Shirt Helmet Pants Gloves ReflectClips Backpack
##   <chr>        <dbl> <chr> <chr>  <chr> <chr>  <chr>        <chr>
## 1 casual         132 Rugby hat    plain plain  no           yes
## 2 casual         137 Rugby hat    plain plain  no           yes
## 3 casual         174 Rugby hat    plain plain  no           yes
## 4 casual          82 Rugby hat    plain plain  no           yes
## 5 casual         106 Rugby hat    plain plain  no           yes
## 6 casual          48 Rugby hat    plain plain  no           yes
```

```
tail(dd)
```

```
## # A tibble: 6 x 8
##   Condition Distance Shirt      Helmet Pants Gloves ReflectClips Backpack
##   <chr>        <dbl> <chr>      <chr>  <chr> <chr>  <chr>        <chr>
## 1 racer          122 TourJersey race   lycra bike   yes          no
## 2 racer          204 TourJersey race   lycra bike   yes          no
## 3 racer          116 TourJersey race   lycra bike   yes          no
## 4 racer          132 TourJersey race   lycra bike   yes          no
## 5 racer          224 TourJersey race   lycra bike   yes          no
## 6 racer           72 TourJersey race   lycra bike   yes          no
```

Another option is to directly access specific rows and/or columns of the tibble, especially for larger data sets. In objects containing data, we can select certain rows and columns using the ***brackets***, `[..., ...]`, to specify the row (first element) and column (second element). For example, we can extract the datum in the fourth row and second column using `dd[4,2]`:

```
dd[4,2]
```

```
## # A tibble: 1 x 1
##   Distance
##      <dbl>
## 1       82
```

This provides the distance (in cm) of a pass at 82 cm. To get all of either the rows or columns, a space is used instead of specifying a particular number. For example, the information in all the columns on the fourth observation can be obtained using `dd[4, ]`:

```
dd[4,]
```

```
## # A tibble: 1 x 8
##   Condition Distance Shirt Helmet Pants Gloves ReflectClips Backpack
##   <chr>        <dbl> <chr> <chr>  <chr> <chr>  <chr>        <chr>
## 1 casual          82 Rugby hat    plain plain  no           yes
```

So this was an observation from the `casual` condition that had a passing distance of 82 cm. The other columns describe some other specific aspects of the condition. To get a more complete sense of the data set, we can extract a suite of observations from each condition using their row numbers concatenated, `c()`, together, extracting all columns for two observations from each of the conditions based on their rows.

```
dd[c(1, 2, 780, 781, 1637, 1638, 2374, 2375, 3181, 3182, 3971, 3972, 4839, 4840),]
```

```
## # A tibble: 14 x 8
##    Condition Distance Shirt       Helmet   Pants Gloves ReflectClips Backpack
##    <chr>        <dbl> <chr>       <chr>    <chr> <chr>  <chr>        <chr>
##  1 casual         132 Rugby       hat      plain plain  no           yes
##  2 casual         137 Rugby       hat      plain plain  no           yes
##  3 commute         70 PlainJersey commuter plain bike   yes          no
##  4 commute        151 PlainJersey commuter plain bike   yes          no
##  5 hiviz           94 Jacket      commuter plain bike   yes          no
##  6 hiviz          145 Jacket      commuter plain bike   yes          no
##  7 novice          12 Vest_Novice commuter plain bike   yes          no
##  8 novice         122 Vest_Novice commuter plain bike   yes          no
##  9 police         113 Vest_Police commuter plain bike   yes          no
## 10 police         174 Vest_Police commuter plain bike   yes          no
## 11 polite         156 Vest_Polite commuter plain bike   yes          no
## 12 polite          14 Vest_Polite commuter plain bike   yes          no
## 13 racer          104 TourJersey  race     lycra bike   yes          no
## 14 racer          141 TourJersey  race     lycra bike   yes          no
```

Now we can see the `Condition` variable seems to have seven different levels, the `Distance` variable contains the overtake distance, and then a suite of columns that describe aspects of each outfit, such as the type of shirt or whether reflective cycling clips were used or not. We will only use the "Distance" and "Condition" variables to start with.

When working with data, we should always start with summarizing the sample size. We will use $\boldsymbol{n}$ for the number of subjects in the sample and denote the population size (if available) with $\boldsymbol{N}$. Here, the sample size is $\boldsymbol{n=5690}$. In this situation, we do not have a random sample from a population (these were all of the overtakes that met the criteria during the rides) so we cannot make inferences from our sample to a larger group (other rides or for other situations like different places, times, or riders). But we can assess whether there is a ***causal effect***[5]: if sufficient evidence is found to conclude that there is some difference in the responses across the conditions, we can attribute those differences to the treatments applied, since the overtake events should be same otherwise due to the outfit being randomly assigned to the rides. The story of the data set – that it was collected on a particular route for a particular rider in the UK – becomes pretty important in thinking about the ramifications of any results. Are drivers and roads in Montana or South Dakota different from drivers and roads near London? Are the road and traffic conditions likely to be different? If so, then we should not assume that the detected differences, if detected, would also exist in some other location for a different rider. The lack of a random sample here from all the overtakes in the area (or more generally all that happen around the world) makes it impossible to assume that this set of overtakes might be like others. So there are definite limitations to the inferences in the following results. But it is still interesting to see if the outfits worn caused a difference in the mean overtake distances, even though the inferences are limited to the conditions in this individual's commute. If this had been an observational study (suppose that the researcher could select their outfit), then we would have to avoid any of the "causal" language that we can consider here because the outfits were not randomly assigned to the rides. Without random assignment, the explanatory variable of outfit choice could be ***confounded*** with another characteristic of rides that might be related to the passing distances, such as wearing a particular outfit because of an expectation of heavy traffic or poor light conditions. Confounding is not the only reason to avoid causal statements with non-random assignment but the inability to separate the effect of other variables (measured or unmeasured) from the differences we are observing means that our inferences in these situations need to be carefully stated to avoid implying causal effects.

In order to get some summary statistics, we will rely on the R package called `mosaic` [Pruim et al., 2021b]

[5] As noted previously, we reserve the term "effect" for situations where random assignment allows us to consider causality as the reason for the differences in the response variable among levels of the explanatory variable.

as introduced previously. First (but only once), you need to install the package, which can be done either using the Packages tab in the lower right panel of RStudio or using the `install.packages` function with quotes around the package name:

```
> install.packages("mosaic")
```

If you open a .Rmd file that contains code that incorporates packages and they are not installed, the bar at the top of the R Markdown document will prompt you to install those missing packages. This is the easiest way to get packages you might need installed. After making sure that any required packages are installed, use the `library` function around the package name (no quotes now!) to load the package, something that you need to do any time you want to use features of a package.

```
library(mosaic)
```

When you are loading a package, R might mention a need to install other packages. If the output says that it needs a package that is unavailable, then follow the same process noted above to install that package and then repeat trying to load the package you wanted. These are called package "dependencies" and are due to one package developer relying on functions that already exist in another package.

With tibbles, you have to declare categorical variables as "factors" to have R correctly handle the variables using the `factor` function, either creating a new variable or replacing the "character" version of the variable that is used to read in the data initially. The following code replaces the `Condition` character variable with a `factor` version of the same variable with the same name.

```
dd$Condition <- factor(dd$Condition)
```

We use this sort of explicit declaration for either character coded (non-numeric) variables or for numerically coded variables where the numbers represent categories to force R to correctly work with the information on those variables. For quantitative variables, we do not need to declare their type and they are stored as numeric variables as long as there is no text in that column of the spreadsheet other than the variable name.

The one-at-a-time declaration of the variables as factors when there are many (here there are six more) creates repetitive and cumbersome code. There is another way of managing this and other similar related "data wrangling"[6]. To do this, we will combine using the pipe operator (`%>%` from the `magrittr` package or `|>` in base R) and using the `mutate` function from `dplyr`, both `%>%` and `mutate` are part of the `tidyverse` and start to help us write code that flows from left to right to accomplish multiple tasks. \index{`mutate()` The pipe operator (`%>%` or `|>`) allows us to pass a data set to a function (sometimes more than one if you have multiple data wrangling tasks to complete - see work below) and there is a keyboard short-cut to get the combination of characters for it by using Ctrl+Shift+M on a PC or Cmd+Shift+M on a Mac. The `mutate` function allows us to create new columns or replace existing ones by using information from other columns, separating each additional operation by a comma (and a "return" for proper style). You will gradually see more reasons why we want to learn these functions, but for now this allows us to convert the character variables into `factor` variables within `mutate` and when we are all done to assign our final data set back in the same `dd` tibble that we started with.

```
dd <- dd %>% mutate(Shirt = factor(Shirt),
                    Helmet = factor(Helmet),
                    Pants = factor(Pants),
                    Gloves = factor(Gloves),
                    ReflectClips = factor(ReflectClips),
```

[6]Some might call this data manipulation or transformation, but those terms can have other meanings and we want a term to capture organizing, preparing, and possibly modifying the data to prepare for analysis and doing it reproducibly in what we like to call "data wrangling".

```
              Backpack = factor(Backpack)
              )
```

The first part of the codechunk (`dd <-`) is to save our work that follows into the `dd` tibble. The `dd %>% mutate` is translated as "take the tibble `dd` and apply the `mutate` function. Inside the `mutate` function, each line has a `variablename = factor(variablename)` that declares each variable as a factor variable with the same name as in the original tibble.

With many variables in a data set and with some preliminary data wrangling completed, it is often useful to get some quick information about all of the variables; the `summary` function provides useful information whether the variables are categorical or quantitative and notes if any values were missing.

```
summary(dd)
```

```
##    Condition      Distance            Shirt          Helmet       Pants        Gloves     ReflectClips Backpack
##  casual :779   Min.   :  2.0   Jacket     :737   commuter:4059   lycra: 852   bike :4911   no : 779     no :4911
##  commute:857   1st Qu.: 99.0   PlainJersey:857   hat     : 779   plain:4838   plain: 779   yes:4911     yes: 779
##  hiviz  :737   Median :117.0   Rugby      :779   race    : 852
##  novice :807   Mean   :117.1   TourJersey :852
##  police :790   3rd Qu.:134.0   Vest_Novice:807
##  polite :868   Max.   :274.0   Vest_Police:790
##  racer  :852                   Vest_Polite:868
```

The output is organized by variable, providing summary information based on the type of variable, either counts by category for categorical variables or the 5-number summary plus the mean for the quantitative variable `Distance`. If present, you would also get a count of missing values that are called "NAs" in R. For the first variable, called `Condition` and that we might more explicitly name *Outfit*, we find counts of the number of overtakes for each outfit: 779 out of 5,690 were when wearing the casual outfit, 857 for "commute", and the other observations from the other five outfits, with the most observations when wearing the "polite" vest. We can also see that overtake distances (variable `Distance`) ranged from 2 cm to 274 cm with a median of 117 cm.

To accompany the numerical summaries, histograms and boxplots can provide some initial information on the shape of the distribution of the responses for the different *Outfits*. Figure 2.1 contains the histogram with a boxplot and a rug of *Distance*, all ignoring any information on which outfit was being worn. There are some additional layers and modifications in this version of the `ggplot`. The code uses our new pipe operator to pass our tibble into the `ggplot`, skipping the `data = ...` within `ggplot()`. There are some additional options modifying the title and the x- and y-axis labels inside the `labs()` part of the code, which will be useful for improving the labels in your plots and work across most plots made in the framework.

```
dd %>% ggplot(mapping = aes(x = Distance)) +
  geom_histogram(bins=20, fill = "grey") +
  geom_rug() +
  geom_boxplot(color = "tomato", width=30) +
      #width used to scale boxplot to make it more visible
  theme_bw() +
  labs(title = "Plot of Passing Distances",
       x = "Distance (cm)",
       y = "Count")
```

Based on Figure 2.1, the distribution appears to be relatively symmetric with many observations in both tails flagged as potential outliers. Despite being flagged as potential outliers, they seem to be part of a common distribution. In real data sets, outliers are commonly encountered and the first step is to verify that they were not errors in recording (if so, fixing or removing them is easily justified). If they cannot be easily dismissed or fixed, the next step is to study their impact on the statistical analyses performed, potentially

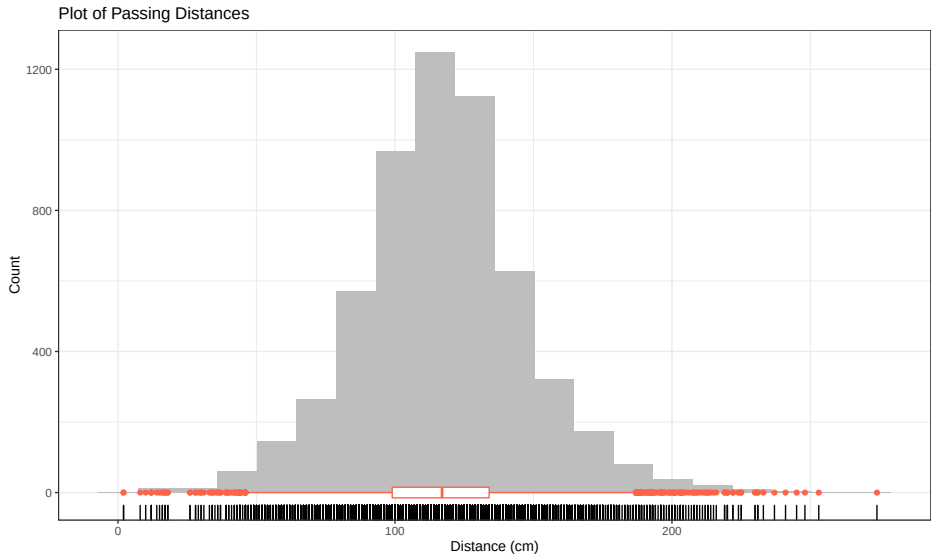

Figure 2.1: Histogram (with 20 bins), boxplot, and rug of passing distances (in cm).

considering reporting results with and without the influential observation(s) in the results (if there are just handful). If the analysis is unaffected by the "unusual" observations, then it matters little whether they are dropped or not. If they do affect the results, then reporting both versions of results allows the reader to judge the impacts for themselves. It is important to remember that sometimes the outliers are the most interesting part of the data set. For example, those observations that were the closest would be of great interest, whether they are outliers or not.

Often when statisticians think of distributions of data, we think of the smooth underlying shape that led to the data set that is being displayed in the histogram. Instead of binning up observations and making bars in the histogram, we can estimate what is called a ***density curve*** as a smooth curve that represents the observed distribution of the responses. Density curves can sometimes help us see features of the data sets more clearly.

To understand the density curve, it is useful to initially see the histogram and density curve together. The height of the density curve is scaled so that the total area under the curve[7] is 1. To make a comparable histogram, the y-axis needs to be scaled so that the histogram is also on the "density" scale which makes the bar heights adjust so that the proportion of the total data set in each bar is represented by the area in each bar (remember that area is height times width). So the height depends on the width of the bars and the total area across all the bars has to be 1. In the `geom_histogram`, its aesthetic is modified using the (criptic[8]) code of `(y = ..density..)`. The density curve is added to the histogram using the `geom_density`, producing the result in Figure 2.2 with added modifications for filling the density curve but using `alpha = 0.1` to make the density curve fill transparent (alpha values range between 0 and 1 with lower values providing more transparency) and in purple (`fill = purple`). You can see how the density curve somewhat matches the histogram bars but deals with the bumps up and down and edges a little differently. We can pick out the relatively symmetric distribution using either display and will rarely make both together.

```
set.seed(555)
dd %>% ggplot(mapping = aes(x = Distance)) +
```

[7] If you've taken calculus, you will know that the curve is being constructed so that the integral from $-\infty$ to ∞ is 1. If you don't know calculus, think of a rectangle with area of 1 based on its height and width. These cover the same area but the top of the region wiggles.

[8] I admit that there are parts of the logic of using `ggplot` that are confusing to me and this is one of them - but I learned to plot in R before `ggplot2` and have been growing fonder and fonder of this way of working. Now instead of searching the internet, I will just get to search my book for the code to make this version of the plot.

```
  geom_histogram(bins=20, fill = "grey", aes(y =..density..)) +
  geom_density(fill = "purple", alpha=0.1) +
  geom_rug() +
  theme_bw() +
  labs(title = "Plot of Passing Distances",
       x = "Distance (cm)",
       y = "Density")
```

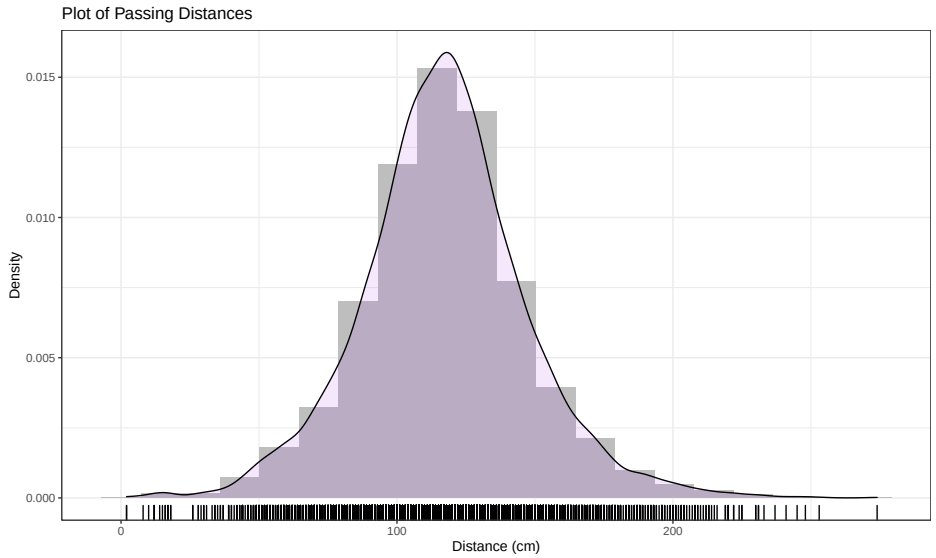

Figure 2.2: Histogram (density scaled), density curve, and rug plot of Distance responses.

```
dd %>% ggplot(mapping = aes(x = Distance)) +
  geom_histogram(bins=15, fill = "grey", aes(y =..density..)) +
  geom_density(fill = "purple", alpha=0.1) +
  geom_rug() +
  theme_bw() +
  labs(title = "Plot of Passing Distances",
       x = "Distance (cm)",
       y = "Density")
```

Histograms can be sensitive to the choice of the number of bars and even the cut-offs used to define the bins for a given number of bars. Small changes in the definition of cut-offs for the bins can have noticeable impacts on the shapes observed but this does not impact density curves. We have engaged the arbitrary choice of the number of bins, but we can add information on the original observations being included in each bar to better understand the choices that `geom_hist` is making. We can (barely) see how there are 2 observations at 2 cm (the noise added generates a wider line than for an individual observation so it is possible to see that it is more than one observation there but I had to check the data set to confirm this). A limitation of the histogram arises at the center of the distribution where the bar that goes from approximately 110 to 120 cm suggests that the mode (peak) is in this range (but it is unclear where) but the density curve suggests that the peak is closer to 120 than 110. Both density curves and histograms can react to individual points in the tails of distributions, but sometimes in different ways.

The graphical tools we've just discussed are going to help us move to comparing the distribution of responses across more than one group. We will have two displays that will help us make these comparisons. The simplest is the ***side-by-side boxplot***, where a boxplot is displayed for each group of interest using

the same y-axis scaling. In the base R `boxplot` function, we can use its ***formula*** notation to see if the response (`Distance`) differs based on the group (`Condition`) by using something like `Y~X` or, here, `Distance ~ Condition`. We also need to tell R where to find the variables – use the last option in the command, `data = DATASETNAME` , to inform R of the tibble to look in to find the variables. In this example, `data = dd`. We will use the formula and `data = ...` options in almost every function we use from here forward, except in `ggplot` which has too many options for formulas to be useful.

Figure 2.3 contains the side-by-side boxplots showing similar distributions for all the groups, with a slightly higher median in the "police" group and some potential outliers identified in both tails of the distributions in all groups.

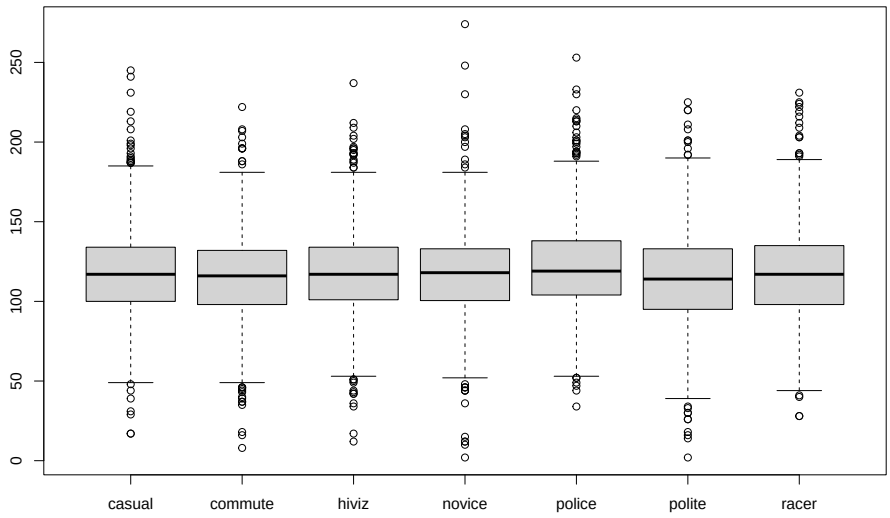

Figure 2.3: Side-by-side boxplot of distances based on outfits.

```
boxplot(Distance ~ Condition, data = dd)
```

The "~" (which is read as the *tilde* symbol[9], which you can find in the upper left corner of your keyboard) notation will be used in two ways in this material. The formula use in R employed previously declares that the response variable here is *Distance* and the explanatory variable is *Condition*. The other use for "~" is as shorthand for "is distributed as" and is used in the context of $Y \sim N(0, 1)$, which translates (in statistics) to defining the random variable Y as following a Normal distribution[10] with mean 0 and variance of 1 (which also means that the standard deviation is 1). In the current situation, we could ask whether the `Distance` variable seems like it may follow a normal distribution in each group, in other words, is Distance $\sim N(\mu, \sigma^2)$? Since the responses are relatively symmetric, it is not clear that we have a violation of the assumption of the normality assumption for the *Distance* variable for any of the seven groups (more later on how we can assess this and the issues that occur when we have a violation of this assumption). Remember that μ and σ are parameters where μ ("mu") is our standard symbol for the ***population mean*** and that σ ("sigma") is the symbol of the ***population standard deviation*** and σ^2 is the symbol of the ***population variance***.

[9] If you want to type this character in R Markdown, try `$\sim$` outside of code chunks.

[10] Remember the bell-shaped curve you encountered in introductory statistics? If not, you can see some at https://en.wikipedia.org/wiki/Normal_distribution.

2.2 Pirate-plots

An alternative graphical display for comparing multiple groups that we will use is a display called a ***pirate-plot*** [Phillips, 2017] from the `yarrr` package[11]. Figure 2.4 shows an example of a pirate-plot that provides a side-by-side display that contains the density curves, the original observations that generated the density curve as jittered points (jittered both vertically and horizontally a little), the sample mean of each group (wide bar), and vertical lines to horizontal bars that represents the confidence interval for the true mean of that group. For each group, the density curves are mirrored to aid in visual assessment of the shape of the distribution. This mirroring also creates a shape that resembles the outline of a violin with skewed distributions so versions of this display have also been called a "violin plot" or a "bean plot" (I call these "enhanced violin plots" when I use them in journal articles instead of "pirate plots"). All together this plot shows us information on the original observations, center (mean) and its confidence interval, spread, and shape of the distributions of the responses. Our inferences typically focus on the means of the groups and this plot allows us to compare those across the groups while gaining information on the shapes of the distributions of responses in each group.

To use the `pirateplot` function we need to install and then load the `yarrr` package. The function works like the boxplot used previously except that options for the type of confidence interval needs to be specified with `inf.method = "ci"` - otherwise you will get a different kind of interval than you learned in introductory statistics and we don't want to get caught up in trying to understand the kind of interval it makes by default. And it seems useful to add `inf.disp = "line"` as an additional option to add bars for the confidence interval[12]. There are many other options in the function that might be useful in certain situations, but these are the only ones that are really needed to get started with pirate-plots. While we could build this plot using `ggplot`, the simplicity of this function keeps it a favorite way to display a quantitative variable across groups even though we lose the grammar of graphics way of modifying the plot.

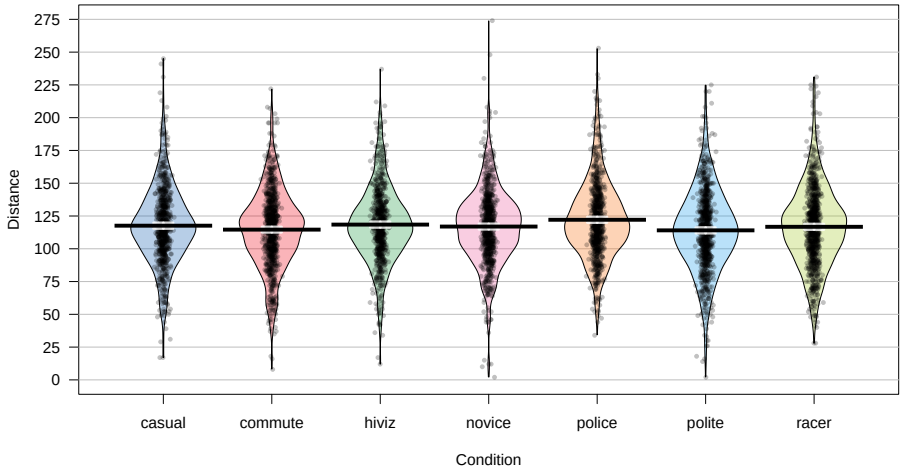

Figure 2.4: Pirate-plot of distances by outfit group. Bold horizontal lines correspond to sample mean of each group, boxes around lines (here they are very tight to the lines for the means) are the 95% confidence intervals.

```
library(yarrr)
```

[11] The package and function are intentionally amusingly titled but are based on ideas in the beanplot in Kampstra [2008] and provide what they call an ***RDI graphic*** - ***R***aw data, ***D***escriptive, and ***I***nferential statistic in the same display.

[12] The default version seems to get mis-interpreted as the box from a boxplot too easily. This display choice also matches the display style for later plots for confidence intervals in term-plots.

```
pirateplot(Distance ~ Condition, data = dd, inf.method = "ci", inf.disp = "line")
```

Figure 2.4 suggests that the distributions are relatively symmetric which would suggest that the means and medians are similar even though only the means are displayed in these plots. In this display, none of the observations are flagged as outliers (it is not a part of this display). It is up to the consumer of the graphic to decide if observations look to be outside of the overall pattern of the rest of the observations. By plotting the observations by groups, we can also explore the narrowest (and likely most scary) overtakes in the data set. The *police* and *racer* conditions seem to have all observations over 25 cm and the most close passes were in the *novice* and *polite* outfits, including the two 2 cm passes. By displaying the original observations, we are able to explore and identify features that aggregation and summarization in plots can sometimes obfuscate. But the pirate-plots also allow you to compare the shape of the distributions (relatively symmetric and somewhat bell-shaped), variability (they look to have relatively similar variability), and the means of the groups. Our inferences are going to focus on the means but those inferences are only valid if the distributions are either approximately normal or at least have similar shapes and spreads (more on this soon).

It appears that the mean for *police* is higher than the other groups but that the others are not too different. But is this difference real? We will never know the answer to that question, but we can assess how likely we are to have seen a result as extreme or more extreme than our result, assuming that there is no difference in the means of the groups. And if the observed result is (extremely) unlikely to occur, then we have (extremely) strong evidence against the hypothesis that the groups have the same mean and can then conclude that there is likely a real difference. If we discover that our result was not very unlikely, given the assumption of no difference in the mean of the groups, then we can't conclude that there is a difference but also can't conclude that they are equal, just that we failed to find enough evidence against the equal means assumption to discard it as a possibility. Whether the result is unusual or not, we will want to carefully explore how big the estimated differences in the means are – is the difference in means large enough to matter to you? We would be more interested in the implications of the difference in the means when there is strong evidence against the null hypothesis that the means are equal but the size of the estimated differences should always be of some interest. To accompany the pirate-plot that displays estimated means, we need to have numerical values to compare. We can get means and standard deviations by groups easily using the same formula notation as for the plots with the `mean` and `sd` functions, if the `mosaic` package is loaded.

```
library(mosaic)
mean(Distance ~ Condition, data = dd)
```

```
##   casual  commute    hiviz   novice   police   polite    racer
## 117.6110 114.6079 118.4383 116.9405 122.1215 114.0518 116.7559
```

```
sd(Distance ~ Condition, data = dd)
```

```
##   casual  commute    hiviz   novice   police   polite    racer
## 29.86954 29.63166 29.03384 29.03812 29.73662 31.23684 30.60059
```

We can also use the `favstats` function to get those summaries and others by groups.

```
favstats(Distance ~ Condition, data = dd)
```

```
##   Condition min    Q1 median  Q3 max     mean       sd   n missing
## 1    casual  17 100.0    117 134 245 117.6110 29.86954 779       0
## 2   commute   8  98.0    116 132 222 114.6079 29.63166 857       0
## 3     hiviz  12 101.0    117 134 237 118.4383 29.03384 737       0
## 4    novice   2 100.5    118 133 274 116.9405 29.03812 807       0
## 5    police  34 104.0    119 138 253 122.1215 29.73662 790       0
## 6    polite   2  95.0    114 133 225 114.0518 31.23684 868       0
```

```
## 7     racer  28  98.0    117 135 231 116.7559 30.60059 852       0
```

Based on these results, we can see that there is an estimated difference of over 8 cm between the smallest mean (*polite* at 114.05 cm) and the largest mean (*police* at 122.12 cm). The differences among some of the other groups are much smaller, such as between *casual* and *commute* with sample means of 117.611 and 114.608 cm, respectively. Because there are seven groups being compared in this study, we will have to wait until Chapter 3 and the One-Way ANOVA test to fully assess evidence related to some difference among the seven groups. For now, we are going to focus on comparing the mean *Distance* between *casual* and *commute* groups – which is a ***two independent sample mean*** situation and something you should have seen before. Remember that the "independent" sample part of this refers to observations that are independently observed for the two groups as opposed to the paired sample situation that you may have explored where one observation from the first group is related to an observation in the second group (the same person with one measurement in each group (we generically call this "repeated measures") or the famous "twin" studies with one twin assigned to each group). This study has some potential violations of the "independent" sample situation (for example, repeated measurements made during a single ride), but those do not clearly fit into the matched pairs situation, so we will note this potential issue and proceed with exploring the method that assumes that we have independent samples, even though this is not true here. In Chapter 9, methods for more complex study designs like this one will be discussed briefly, but mostly this is beyond the scope of this material.

Here we are going to use the "simple" two independent group scenario to review some basic statistical concepts and connect two different frameworks for conducting statistical inference: randomization and parametric inference techniques. ***Parametric*** statistical methods involve making assumptions about the distribution of the responses and obtaining confidence intervals and/or p-values using a *named* distribution (like the z or t-distributions). Typically these results are generated using formulas and looking up areas under curves or cutoffs using a table or a computer. ***Randomization***-based statistical methods use a computer to shuffle, sample, or simulate observations in ways that allow you to obtain distributions of possible results to find areas and cutoffs without resorting to using tables and named distributions. Randomization methods are what are called ***nonparametric*** methods that often make fewer assumptions (they are ***not free of assumptions***!) and so can handle a larger set of problems more easily than parametric methods. When the assumptions involved in the parametric procedures are met by a data set, the randomization methods often provide very similar results to those provided by the parametric techniques. To be a more sophisticated statistical consumer, it is useful to have some knowledge of both of these techniques for performing statistical inference and the fact that they can provide similar results might deepen your understanding of both approaches.

To be able to work just with the observations from two of the conditions (*casual* and *commute*) we could remove all the other observations in a spreadsheet program and read that new data set back into R, but it is actually pretty easy to use R to do data management once the data set is loaded. It is also a better scientific process to do as much of your data management within R as possible so that your steps in managing the data are fully documented and reproducible. Highlighting and clicking in spreadsheet programs is a dangerous way to work and can be impossible to recreate steps that were taken from initial data set to the version that was analyzed. In R, we could identify the rows that contain the observations we want to retain and just extract those rows, but this is hard with over five thousand observations. The `filter` function from the `dplyr` package (part of the `tidyverse` suite of packages) is the best way to be able to focus on observations that meet a particular condition; we can "filter" the data set to retain just those rows. The `filter` function takes the data set via the pipe operate and then we need to define the condition we want to meet to retain those rows. Here we need to define the variable we want to work with, `Condition`, and then request rows that meet a condition (are `%in%`) and the aspects that meet that condition (here by concatenating the two levels of "casual" and "commute"), leading to code of:

```
dd %>% filter(Condition %in% c("casual", "commute"))
```

We want to save that new filtered data set into a new tibble for future work, so we can use the assignment operator (`<-`) to save the reduced data set into `ddsub`:

```
ddsub <- dd %>% filter(Condition %in% c("casual", "commute"))
```

There is also the `select` function that we could also use with an additional pipe operator to just focus on certain columns in the data set, here to just retain the `Condition` and `Distance` variables using:

```
ddsub <- dd %>%
  filter(Condition %in% c("casual","commute")) %>%
  select(Distance, Condition)
```

The `select` function shows up in multiple packages so in later chapters you will see (and might need to use yourself) `dplyr::select()` which tells R to use the version of `select` that is in `dplyr`. When you are working to filter or subset your data set you should always check that the correct observations were dropped either using `View(ddsub)` or by doing a quick summary of the `Condition` variable in the new tibble.

```
summary(ddsub$Condition)
```

```
##  casual commute   hiviz  novice  police  polite   racer
##     779     857       0       0       0       0       0
```

It ends up that R remembers the categories for observations that we removed even though there are 0 observations in them now and that can cause us some problems. When we remove a group of observations, we sometimes need to clean up categorical variables to just reflect the categories that are present. The `factor` function creates categorical variables based on the levels of the variables that are observed and is useful to run here to clean up `Condition` to just reflect the categories that are now present.

```
ddsub <- ddsub %>% mutate(Condition = factor(Condition))
summary(ddsub$Condition)
```

```
##  casual commute
##     779     857
```

The two categories of interest now were selected because neither looks particularly "racey" or has high visibility but could present a common choice between getting fully "geared up" for the commute or just jumping on a bike to go to work. Now if we remake the boxplots and pirate-plots, they only contain results for the two groups of interest here as seen in Figure 2.5. Note that these are available in the previous version of the plots, but now we will just focus on these two groups.

```
boxplot(Distance ~ Condition, data = ddsub)
pirateplot(Distance ~ Condition, data = ddsub, inf.method = "ci", inf.disp = "line")
```

The two-sample mean techniques you learned in your previous course all start with comparing the means the two groups. We can obtain the two means using the `mean` function or directly obtain the difference in the means using the `diffmean` function (both require the `mosaic` package). The `diffmean` function provides $\bar{x}_{\text{commute}} - \bar{x}_{\text{casual}}$ where $\bar{x}$ (read as "x-bar") is the sample mean of observations in the subscripted group. Note that there are two directions that you could compare the means and this function chooses to take the mean from the second group name *alphabetically* and subtract the mean from the first alphabetical group name. It is always good to check the direction of this calculation as having a difference of -3.003 cm versus 3.003 cm could be important.

```
mean(Distance ~ Condition, data = ddsub)
```

```
##   casual  commute
```

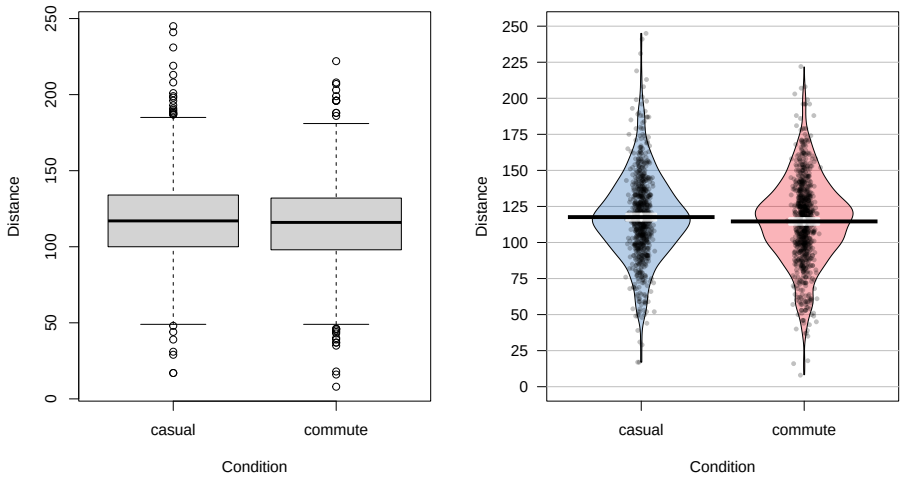

Figure 2.5: Boxplot and pirate-plot of the *Distance* responses on the reduced `ddsub` data set.

```
## 117.6110 114.6079
```

```
diffmean(Distance ~ Condition, data = ddsub)
```

```
##  diffmean
## -3.003105
```

2.3 Models, hypotheses, and permutations for the two sample mean situation

There appears to be some evidence that the *casual* clothing group is getting higher average overtake distances than the *commute* group of observations, but we want to try to make sure that the difference is real – to assess evidence against the assumption that the means are the same "in the population" and possibly decide that this is not a reasonable assumption. First, a ***null hypothesis***[13] which defines a ***null model***[14] needs to be determined in terms of ***parameters*** (the true values in the population). The research question should help you determine the form of the hypotheses for the assumed population. In the two independent sample mean problem, the interest is in testing a null hypothesis of $H_0 : \mu_1 = \mu_2$ versus the alternative hypothesis of $H_A : \mu_1 \neq \mu_2$, where μ_1 is the parameter for the true mean of the first group and μ_2 is the parameter for the true mean of the second group. The alternative hypothesis involves assuming a statistical model for the i^{th} $(i = 1, \ldots, n_j)$ response from the j^{th} $(j = 1, 2)$ group, $\boldsymbol{y}_{ij}$, that involves modeling it as $y_{ij} = \mu_j + \varepsilon_{ij}$, where we assume that $\varepsilon_{ij} \sim N(0, \sigma^2)$. For the moment, focus on the models that either assume the means are the same (null) or different (alternative), which imply:

- Null Model: $y_{ij} = \mu + \varepsilon_{ij}$ There is **no** difference in **true** means for the two groups.
- Alternative Model: $y_{ij} = \mu_j + \varepsilon_{ij}$ There is **a** difference in **true** means for the two groups.

Suppose we are considering the alternative model for the 4^{th} observation $(i = 4)$ from the second group $(j = 2)$, then the model for this observation is $y_{42} = \mu_2 + \varepsilon_{42}$, that defines the response as coming from

[13]The hypothesis of no difference that is typically generated in the hopes of being rejected in favor of the alternative hypothesis, which contains the sort of difference that is of interest in the application.

[14]The null model is the statistical model that is implied by the chosen null hypothesis. Here, a null hypothesis of no difference translates to having a model with the same mean for both groups.

the true mean for the second group plus a random error term for that observation, ε_{42}. For, say, the 5^{th} observation from the first group ($j = 1$), the model is $y_{51} = \mu_1 + \varepsilon_{51}$. If we were working with the null model, the mean is always the same (μ) – the group specified does not change the mean we use for that observation, so the model for y_{42} would be $\mu + \varepsilon_{42}$.

It can be helpful to think about the null and alternative models graphically. By assuming the null hypothesis is true (means are equal) and that the random errors around the mean follow a normal distribution, we assume that the truth is as displayed in the left panel of Figure 2.6 – two normal distributions with the same mean and variability. The alternative model allows the two groups to potentially have different means, such as those displayed in the right panel of Figure 2.6 where the second group has a larger mean. Note that in this scenario, we assume that the observations all came from the same distribution except that they had different means. Depending on the statistical procedure we are using, we basically are going to assume that the observations (y_{ij}) either were generated as samples from the null or alternative model. You can imagine drawing observations at random from the pictured distributions. For hypothesis testing, the null model is assumed to be true and then the unusualness of the actual result is assessed relative to that assumption. In hypothesis testing, we have to decide if we have enough evidence to reject the assumption that the null model (or hypothesis) is true. If we think that we have sufficient evidence to conclude that the null hypothesis is wrong, then we would conclude that the other model considered (the alternative model) is more reasonable. The researchers obviously would have hoped to encounter some sort of noticeable difference in the distances for the different outfits and have been able to find enough evidence to against the null model where the groups "look the same" to be able to conclude that they differ.

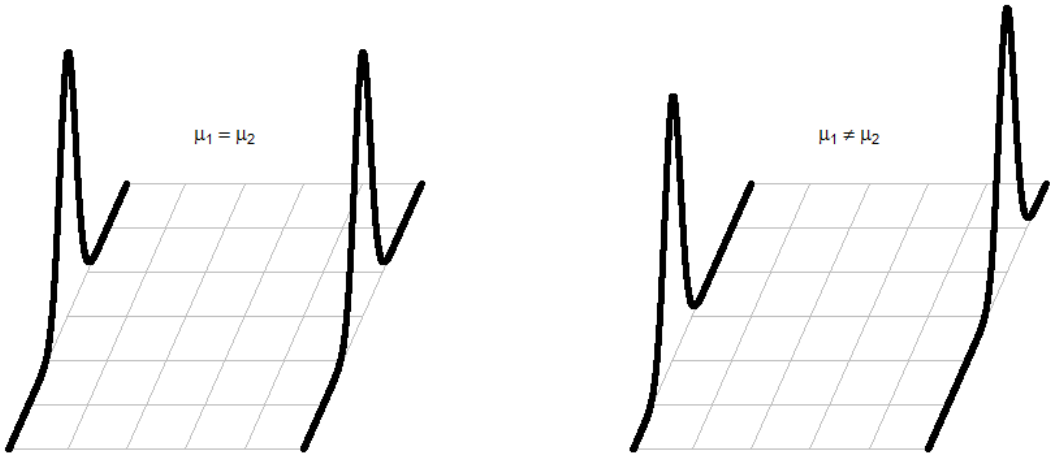

Figure 2.6: Illustration of the assumed situations under the null (left) and a single possibility that could occur if the alternative were true (right) and the true means were different. There are an infinite number of ways to make a plot like the right panel that satisfies the alternative hypothesis.

In statistical inference, null hypotheses (and their implied models) are set up as "straw men" with every interest in rejecting them even though we assume they are true to be able to assess the evidence against them. Consider the original study design here, the outfits were randomly assigned to the rides. If the null hypothesis were true, then we would have no difference in the population means of the groups. And this would apply if we had done a different random assignment of the outfits. So let's try this: assume that the null hypothesis is true and randomly re-assign the treatments (outfits) to the observations that were obtained. In other words, keep the *Distance* results the same and shuffle the group labels randomly. The technical term for this is doing

a ***permutation*** (a random shuffling of a grouping[15] variable relative to the observed responses). If the null is true and the means in the two groups are the same, then we should be able to re-shuffle the groups to the observed *Distance* values and get results similar to those we actually observed. If the null is false and the means are really different in the two groups, then what we observed should differ from what we get under other random permutations and the differences between the two groups should be more noticeable in the observed data set than in (most) of the shuffled data sets. It helps to see an example of a permutation of the labels to understand what this means here.

The data set we are working with is a little on the large size, especially to explore individual observations. So for the moment we are going to work with a random sample of 30 of the $n = 1,636$ observations in `ddsub`, fifteen from each group, that are generated using the `sample` function. To do this[16], we will use the `sample` function twice - once to sample from the subsetted *commute* observations (creating the `s1` data set) and once to sample from the *casual* ones (creating `s2`). A new function for us, called `rbind`, is used to bind the rows together — much like pasting a chunk of rows below another chunk in a spreadsheet program. This operation only works if the columns all have the same names and meanings both for `rbind` and in a spreadsheet. Together this code creates the `dsample` data set that we will analyze below and compare to results from the full data set. The sample means are now 135.8 and 109.87 cm for *casual* and *commute* groups, respectively, and so the difference in the sample means has increased in magnitude to -25.93 cm (commute - casual). This difference would vary based on the different random samples from the larger data set, but for the moment, pretend this was the entire data set that the researchers had collected and that we want to try to assess how unusual our sample difference was from what we might expect, if the null hypothesis that the true means are the same in these two groups was true.

```
set.seed(9432)
s1 <- sample(ddsub %>% filter(Condition %in% "commute"), size=15)
s2 <- sample(ddsub %>% filter(Condition %in% "casual"), size=15)
dsample <- rbind(s1, s2)
mean(Distance ~ Condition, data = dsample)
```

```
##   casual  commute
## 135.8000 109.8667
```

In order to assess evidence against the null hypothesis of no difference, we want to permute the group labels versus the observations. In the `mosaic` package, the `shuffle` function allows us to easily perform a permutation[17]. One permutation of the treatment labels is provided in the `PermutedCondition` variable below. Note that the `Distances` are held in the same place while the group labels are shuffled.

```
Perm1 <- dsample %>% select(Distance, Condition) %>% mutate(PermutedCondition = shuffle(Condition))
#To force the tibble to print out all rows in data set - not used often
data.frame(Perm1)
```

```
##    Distance Condition PermutedCondition
## 1       168   commute           commute
## 2       137   commute           commute
## 3        80   commute            casual
## 4       107   commute           commute
## 5       104   commute            casual
## 6        60   commute            casual
## 7        88   commute           commute
## 8       126   commute           commute
```

[15] Later we will shuffle other types of explanatory variables.

[16] While not required, we often set our random number seed using the `set.seed` function so that when we re-run code with randomization in it we get the same results.

[17] We'll see the `shuffle` function in a more common usage below; here we are creating a new variable using `mutate` to show the permuted results that are stored in `Perm1`.

```
## 9       115   commute            casual
## 10      120   commute            casual
## 11      146   commute           commute
## 12      113   commute            casual
## 13       89   commute           commute
## 14       77   commute           commute
## 15      118   commute            casual
## 16      148    casual            casual
## 17      114    casual            casual
## 18      124    casual           commute
## 19      115    casual            casual
## 20      102    casual            casual
## 21       77    casual            casual
## 22       72    casual           commute
## 23      193    casual           commute
## 24      111    casual           commute
## 25      161    casual            casual
## 26      208    casual           commute
## 27      179    casual            casual
## 28      143    casual           commute
## 29      144    casual           commute
## 30      146    casual            casual
```

If you count up the number of subjects in each group by counting the number of times each label (commute, casual) occurs, it is the same in both the `Condition` and `PermutedCondition` columns (15 each). Permutations involve randomly re-ordering the values of a variable – here the `Condition` group labels – without changing the content of the variable. This result can also be generated using what is called ***sampling without replacement***: sequentially select n labels from the original variable (*Condition*), removing each observed label and making sure that each of the original `Condition` labels is selected once and only once. The new, randomly selected order of selected labels provides the permuted labels. Stepping through the process helps to understand how it works: after the initial random sample of one label, there would $n-1$ choices possible; on the n^{th} selection, there would only be one label remaining to select. This makes sure that all original labels are re-used but that the order is random. Sampling without replacement is like picking names out of a hat, one-at-a-time, and not putting the names back in after they are selected. It is an exhaustive process for all the original observations. ***Sampling with replacement***, in contrast, involves sampling from the specified list with each observation having an equal chance of selection for each sampled observation – in other words, observations can be selected more than once. This is like picking n names out of a hat that contains n names, except that every time a name is selected, it goes back into the hat – we'll use this technique in Section 2.9 to do what is called ***bootstrapping***. Both sampling mechanisms can be used to generate inferences but each has particular situations where they are most useful. For hypothesis testing, we will use permutations (sampling without replacement) as its mechanism most closely matches the null hypotheses we will be testing.

The comparison of the pirate-plots between the real $n = 30$ data set and permuted version is what is really interesting (Figure 2.7). The original difference in the sample means of the two groups was -25.93 cm (*commute* - *casual*). The sample means are the ***statistics*** that estimate the parameters for the true means of the two groups and the difference in the sample means is a way to create a single number that tracks a quantity directly related to the difference between the null and alternative models. In the permuted data set, the difference in the means is 12.07 cm in the opposite direction (the *commute* group had a higher mean than *casual* in the permuted data).

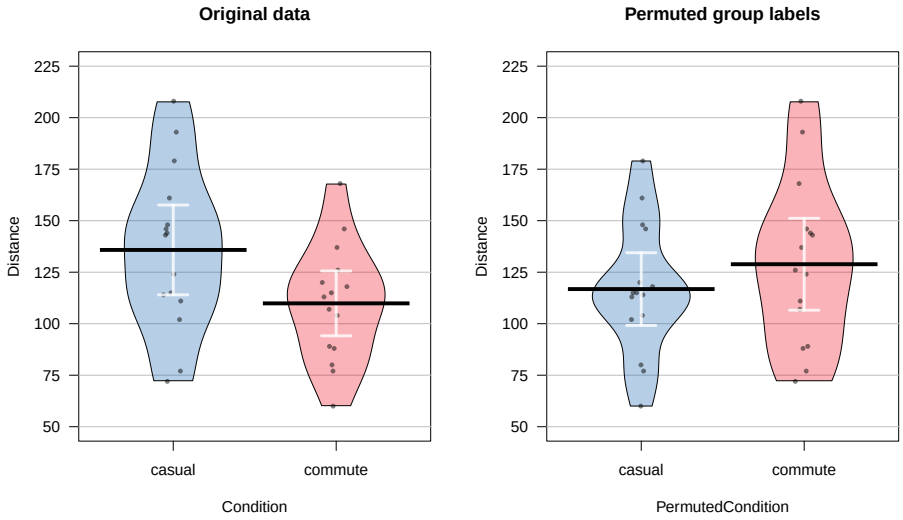

Figure 2.7: Pirate-plots of Distance responses versus actual treatment groups and permuted groups. Note how the responses are the same but that they are shuffled between the two groups differently in the permuted data set. With the smaller sample size, the 95% confidence intervals for each of the means are more clearly visible than with the original large data set.

```
mean(Distance ~ PermutedCondition, data = Perm1)
```

```
##   casual  commute
## 116.8000 128.8667
```

```
diffmean(Distance ~ PermutedCondition, data = Perm1)
```

```
## diffmean
## 12.06667
```

The `diffmean` function is a simple way to get the differences in the means, but we can also start to learn about using the `lm` function – that will be used for every chapter except for Chapter **??**. The `lm` stands for ***linear model*** and, as we will see moving forward, encompasses a wide array of different models and scenarios. The ability to estimate the difference in the mean of two groups is among its simplest uses.[18] Notationally, it is very similar to other functions we have considered, `lm(y ~ x, data = ...)` where `y` is the response variable and `x` is the explanatory variable. Here that is `lm(Distance ~ Condition, data = dsample)` with `Condition` defined as a factor variable. With linear models, we will need to interrogate them to obtain a variety of useful information and our first "interrogation" function is usually the `summary` function. To use it, it is best to have stored the model into an object, something like `lm1`, and then we can apply the `summary()` function to the stored model object to get a suite of output:

```
lm1 <- lm(Distance ~ Condition, data = dsample)
summary(lm1)
```

```
##
## Call:
```

[18]This is a bit like getting a new convertible sports car and driving it to the grocery store – there might be better ways to get groceries, but we probably would want to drive our new car as soon as we got it.

```
## lm(formula = Distance ~ Condition, data = dsample)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -63.800 -21.850   4.133  15.150  72.200
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       135.800      8.863  15.322 3.83e-15
## Conditioncommute  -25.933     12.534  -2.069   0.0479
##
## Residual standard error: 34.33 on 28 degrees of freedom
## Multiple R-squared:  0.1326, Adjusted R-squared:  0.1016
## F-statistic: 4.281 on 1 and 28 DF,  p-value: 0.04789
```

This output is explored more in Chapter **??**, but for the moment, focus on the row labeled as `Conditioncommute` in the middle of the output. In the first (`Estimate`) column, there is -25.933. This is a number we saw before – it is the difference in the sample means between *commute* and *casual* (*commute* - *casual*). When `lm` denotes a category in the row of the output (here `commute`), it is trying to indicate that the information to follow relates to the difference between this category and a baseline or reference category (here `casual`). The first (`(Intercept)`) row also contains a number we have seen before: - 135.8 is the sample mean for the *casual* group. So the `lm` is generating a coefficient for the mean of one of the groups and another as the difference in the two groups[19]. In developing a test to assess evidence against the null hypothesis, we will focus on the difference in the sample means. So we want to be able to extract that number from this large suite of information. It ends up that we can apply the `coef` function to `lm` models and then access that second coefficient using the bracket notation. Specifically:

```
coef(lm1)[2]
```

```
## Conditioncommute
##        -25.93333
```

This is the same result as using the `diffmean` function, so either could be used here. The estimated difference in the sample means in the permuted data set of 12.07 cm is available with:

```
lmP <- lm(Distance ~ PermutedCondition, data = Perm1)
coef(lmP)[2]
```

```
## PermutedConditioncommute
##                 12.06667
```

Comparing the pirate-plots and the estimated difference in the sample means suggests that the observed difference was larger than what we got when we did a single permutation. Conceptually, permuting observations between group labels is consistent with the null hypothesis – this is a technique to generate results that we might have gotten if the null hypothesis were true since the true models for the responses are the same in the two groups if the null is true. We just need to repeat the permutation process many times and track how unusual our observed result is relative to this distribution of potential responses if the null were true. If the observed differences are unusual relative to the results under permutations, then there is evidence against the null hypothesis, and we can conclude, in the direction of the alternative hypothesis, that the true means differ. If the observed differences are similar to (or at least not unusual relative to) what we get under random shuffling under the null model, we would have a tough time concluding that there is any real

[19]This will be formalized and explained more in the next chapter when we encounter more than two groups in these same models. For now, it is recommended to start with the sample means from `favstats` for the two groups and then use that to sort out which direction the differencing was done in the `lm` output.

difference between the groups based on our observed data set. This is formalized using the ***p-value*** as a measure of the strength of evidence against the null hypothesis and how we use it.

2.4 Permutation testing for the two sample mean situation

In any testing situation, you must define some function of the observations that gives us a single number that addresses our question of interest. This quantity is called a ***test statistic***. These often take on complicated forms and have names like t or z statistics that relate to their parametric (named) distributions so we know where to look up ***p-values***[20]. In randomization settings, they can have simpler forms because we use the data set to find the distribution of the statistic under the null hypothesis and don't need to rely on a named distribution. We will label our test statistic $\boldsymbol{T}$ (for **T**est statistic) unless the test statistic has a commonly used name. Since we are interested in comparing the means of the two groups, we can define

$$T = \bar{x}_{\text{commute}} - \bar{x}_{\text{casual}},$$

which coincidentally is what the `diffmean` function and the second coefficient from the `lm` provided us previously. We label our ***observed test statistic*** (the one from the original data set) as

$$T_{obs} = \bar{x}_{\text{commute}} - \bar{x}_{\text{casual}},$$

which happened to be -25.933 cm here. We will compare this result to the results for the test statistic that we obtain from permuting the group labels. To denote permuted results, we will add an * to the labels:

$$T^* = \bar{x}_{\text{commute}^*} - \bar{x}_{\text{casual}^*}.$$

We then compare the $T_{obs} = \bar{x}_{\text{commute}} - \bar{x}_{\text{casual}} = -25.933$ to the distribution of results that are possible for the permuted results (T^*) which corresponds to assuming the null hypothesis is true.

We need to consider lots of permutations to do a permutation test. In contrast to your introductory statistics course where, if you did this, it was just a click away, we are going to learn what was going on "under the hood" of the software you were using. Specifically, we need a ***for loop*** in R to be able to repeatedly generate the permuted data sets and record T^* for each one. Loops are a basic programming task that make randomization methods possible as well as potentially simplifying any repetitive computing task. To write a "for loop", we need to choose how many times we want to do the loop (call that `B`) and decide on a counter to keep track of where we are at in the loops (call that `b`, which goes from 1 up to `B`). The simplest loop just involves printing out the index, `print(b)` at each step. This is our first use of curly braces, { and }, that are used to group the code we want to repeatedly run as we proceed through the loop. By typing the following code in a code chunk and then highlighting it all and hitting the run button, R will go through the loop $B = 5$ times, printing out the counter:

```
B <- 5
for (b in (1:B)){
  print(b)
}
```

Note that when you highlight and run the code, it will look about the same with "+" printed after the first line to indicate that all the code is connected when it appears in the console, looking like this:

```
> for(b in (1:B)){
+   print(b)
+ }
```

[20] P-values are the probability of obtaining a result as extreme as or more extreme than we observed given that the null hypothesis is true.

When you run these three lines of code (or compile a .Rmd file that contains this), the console will show you the following output:

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

Instead of printing the counter, we want to use the loop to repeatedly compute our test statistic across B random permutations of the observations. The `shuffle` function performs permutations of the group labels relative to responses and the `coef(lmP)[2]` extracts the estimated difference in the two group means in the permuted data set. For a single permutation, the combination of shuffling `Condition` and finding the difference in the means, storing it in a variable called `Ts` is:

```
lmP <- lm(Distance ~ shuffle(Condition), data = dsample)
Ts <- coef(lmP)[2]
Ts
```

```
## shuffle(Condition)commute
##               -0.06666667
```

And putting this inside the `print` function allows us to find the test statistic under 5 different permutations easily:

```
B <- 5
for (b in (1:B)){
  lmP <- lm(Distance~shuffle(Condition), data=dsample)
  Ts <- coef(lmP)[2]
  print(Ts)
}
```

```
## shuffle(Condition)commute
##                      -1.4
## shuffle(Condition)commute
##                  1.133333
## shuffle(Condition)commute
##                  20.86667
## shuffle(Condition)commute
##                  3.133333
## shuffle(Condition)commute
##                 -2.333333
```

Finally, we would like to store the values of the test statistic instead of just printing them out on each pass through the loop. To do this, we need to create a variable to store the results, let's call it `Tstar`. We know that we need to store `B` results so will create a vector[21] of length B, which contains B elements, full of missing values (NA) using the `matrix` function with the `nrow` option specifying the number of elements:

```
Tstar <- matrix(NA, nrow = B)
Tstar
```

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

[21] In statistics, vectors are one dimensional lists of numeric elements – basically a column from a matrix of our tibble.

```
## [2,]   NA
## [3,]   NA
## [4,]   NA
## [5,]   NA
```

Now we can run our loop B times and store the results in `Tstar`.

```
for (b in (1:B)){
  lmP <- lm(Distance ~ shuffle(Condition), data = dsample)
  Tstar[b] <- coef(lmP)[2]
}
#Print out the results stored in Tstar with the next line of code
```

```
Tstar
```

```
##           [,1]
## [1,] -5.400000
## [2,] -3.266667
## [3,] -7.933333
## [4,] 13.133333
## [5,] -6.466667
```

Five permutations are still not enough to assess whether our T_{obs} of -25.933 is unusual and we need to do many permutations to get an accurate assessment of the possibilities under the null hypothesis. It is common practice to consider something like 1,000 permutations. The `Tstar` vector when we set B to be large, say `B=1000`, contains the permutation distribution for the selected test statistic under[22] the null hypothesis – what is called the ***null distribution*** of the statistic. The null distribution is the distribution of possible values of a statistic under the null hypothesis. We want to visualize this distribution and use it to assess how unusual our T_{obs} result of -25.933 cm was relative to all the possibilities under permutations (under the null hypothesis). So we repeat the loop, now with $B = 1000$ and generate a histogram (modified to add counts to the bars using `stat_bin`[23]), density curve, and summary statistics of the results:

```
B <- 1000
Tstar <- matrix(NA, nrow = B)
for (b in (1:B)){
  lmP <- lm(Distance ~ shuffle(Condition), data = dsample)
  Tstar[b] <- coef(lmP)[2]
}
tibble(Tstar) %>%  ggplot(aes(x = Tstar)) +
  geom_histogram(aes(y = ..ncount..), bins = 15, col = 1, fill = "skyblue",
                 center = 0) +
  stat_bin(aes(y = ..ncount.., label = ..count..), bins = 15,
           geom = "text", vjust=-0.75) +
  geom_density(aes(y = ..scaled..)) + theme_bw() + labs(y = "Density")
```

```
favstats(Tstar)
```

```
##        min        Q1     median  Q3      max       mean       sd    n missing
##  -41.26667 -10.06667 -0.3333333 8.6 37.26667 -0.5054667 13.17156 1000       0
```

[22] We often say "under" in statistics and we mean "given that the following is true".

[23] This is another place where the code is a bit criptic when you are starting - just copy this entire chunk of code - you only ever need to modify the `lm` line in this code!

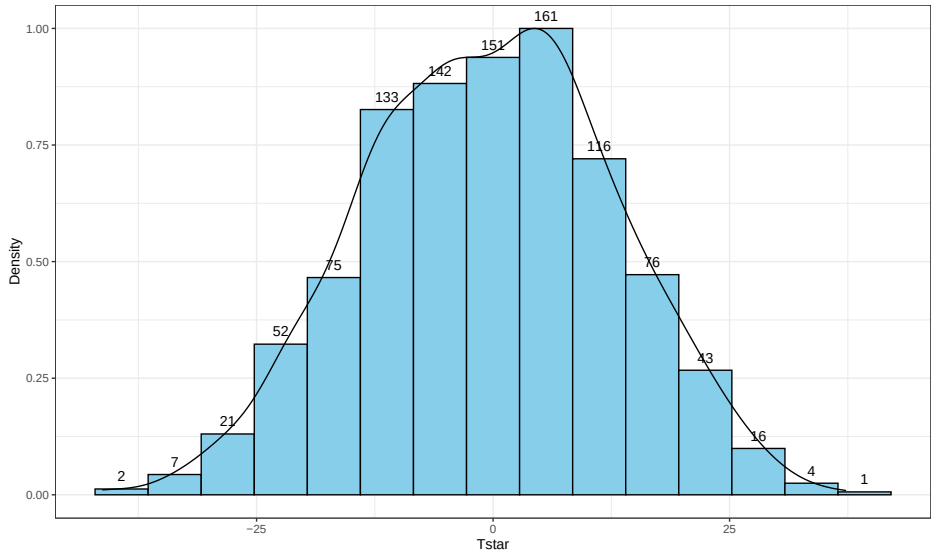

Figure 2.8: Histogram (left, with counts in bars) and density curve (right) of values of test statistic for $B =$ 1,000 permutations.

Figure 2.8 contains visualizations of T^* and the `favstats` summary provides the related numerical summaries. Our observed T_{obs} of -25.933 seems somewhat unusual relative to these results with only 30 T^* values smaller than -25 based on the histogram. We need to make more specific comparisons of the permuted results versus our observed result to be able to clearly decide whether our observed result is really unusual.

To make the comparisons more concrete, first we can enhance the previous graphs by adding the value of the test statistic from the real data set, as shown in Figure 2.9, using the `geom_vline` function to draw a vertical line at our T_{obs} value specified in the `xintercept` option.

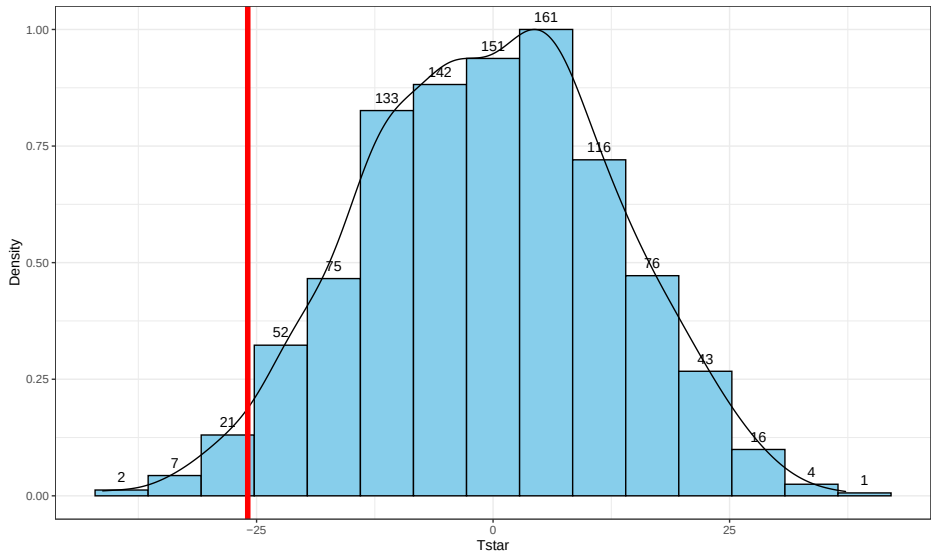

Figure 2.9: Histogram (left) and density curve (right) of values of test statistic for 1,000 permutations with bold vertical line for value of observed test statistic.

```
Tobs <- -25.933
tibble(Tstar) %>%  ggplot(aes(x = Tstar)) +
  geom_histogram(aes(y = ..ncount..), bins = 15, col = 1, fill = "skyblue",
                 center = 0) +
  stat_bin(aes(y = ..ncount.., label = ..count..), bins = 15,
           geom = "text", vjust=-0.75) +
  geom_density(aes(y = ..scaled..)) + theme_bw() + labs(y = "Density") +
  geom_vline(xintercept = Tobs, col = "red", lwd = 2)
```

Second, we can calculate the exact number of permuted results that were as small or smaller than what we observed. To calculate the proportion of the 1,000 values that were as small or smaller than what we observed, we will use the `pdata` function. To use this function, we need to provide the distribution of values to compare to the cut-off (`Tstar`), the cut-off point (`Tobs`), and whether we want calculate the proportion that are below (left of) or above (right of) the cut-off (`lower.tail=T` option provides the proportion of values to the left of (below) the cutoff of interest).

```
pdata(Tstar, Tobs, lower.tail=T)[[1]]
```

```
## [1] 0.027
```

The proportion of 0.027 tells us that 27 of the 1,000 permuted results (2.7%) were as small or smaller than what we observed. This type of work is how we can generate ***p-values*** using permutation distributions. P-values, as you should remember, are the probability of getting a result as extreme as or more extreme than what we observed, given that the null is true. Finding only 27 permutations of 1,000 that were as small or smaller than our observed result suggests that it is hard to find a result like what we observed if there really were no difference, although it is not impossible.

When testing hypotheses for two groups, there are two types of alternative hypotheses, one-sided or two-sided. ***One-sided tests*** involve only considering differences in one-direction (like $\mu_1 > \mu_2$) and are performed when researchers can decide ***a priori***[24] which group should have a larger mean if there is going to be any sort of difference. In this situation, we did not know enough about the potential impacts of the outfits to know which group should be larger than the other so should do a two-sided test. It is important to remember that you can't look at the responses to decide on the hypotheses. It is often safer and more ***conservative***[25] to start with a ***two-sided alternative*** ($\mathbf{H_A}: \mu_1 \neq \mu_2$). To do a 2-sided test, find the area smaller than what we observed as above (or larger if the test statistic had been positive). We also need to add the area in the other tail (here the right tail) similar to what we observed in the right tail. Some statisticians suggest doubling the area in one tail but we will collect information on the number that were as or more extreme than the same value in the other tail[26]. In other words, we count the proportion below -25.933 and over 25.933. So we need to find how many of the permuted results were larger than or equal to 25.933 cm to add to our previous proportion. Using `pdata` with `-Tobs` as the cut-off and `lower.tail =F` provides this result:

```
pdata(Tstar, -Tobs, lower.tail=F)[[1]]
```

```
## [1] 0.017
```

So the p-value to test our null hypothesis of no difference in the true means between the groups is 0.027 + 0.017, providing a p-value of 0.044. Figure 2.10 shows both cut-offs on the histogram and density curve.

[24] This is a fancy way of saying "in advance", here in advance of seeing the observations.

[25] Statistically, a conservative method is one that provides less chance of rejecting the null hypothesis in comparison to some other method or less than some pre-defined standard. A liberal method provides higher rates of false rejections.

[26] Both approaches are reasonable. By using both tails of the distribution we can incorporate potential differences in shape in both tails of the permutation distribution.

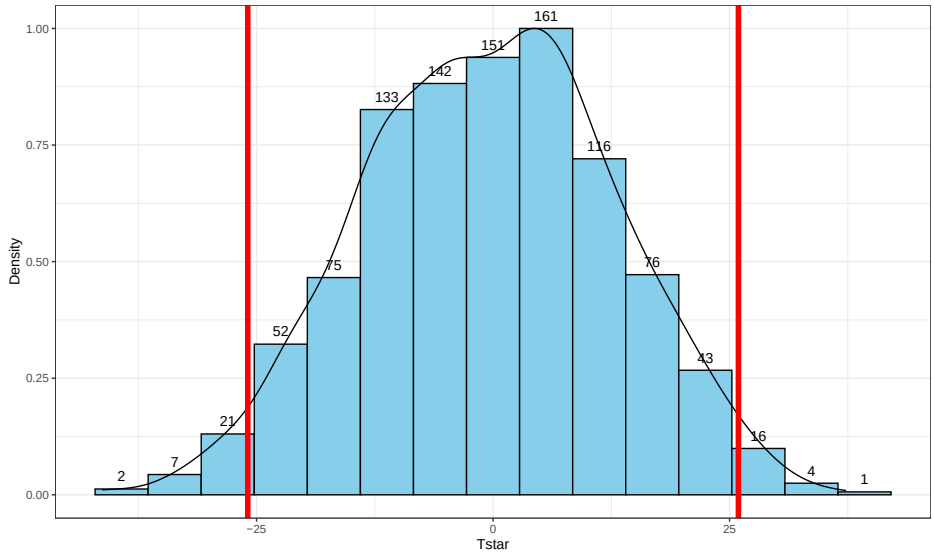

Figure 2.10: Histogram and density curve of values of test statistic for 1,000 permutations with bold lines for value of observed test statistic (-25.933) and its opposite value (25.933) required for performing the two-sided test.

```
tibble(Tstar) %>%  ggplot(aes(x = Tstar)) +
  geom_histogram(aes(y = ..ncount..), bins = 15, col = 1, fill = "skyblue",
                 center = 0) +
  stat_bin(aes(y = ..ncount.., label = ..count..), bins = 15,
           geom = "text", vjust=-0.75) +
  geom_density(aes(y = ..scaled..)) + theme_bw() + labs(y = "Density") +
  geom_vline(xintercept = c(-1,1)*Tobs, col = "red", lwd = 2)
```

In general, the ***one-sided test p-value*** is the proportion of the permuted results that are as extreme or more extreme than observed in the direction of the *alternative* hypothesis (lower or upper tail, remembering that this also depends on the direction of the difference taken). For the two-sided test, the p-value is the proportion of the permuted results that are *less than or equal to the negative version of the observed statistic and greater than or equal to the positive version of the observed statistic.* Using absolute values (| |), we can simplify this: the ***two-sided p-value*** is the *proportion of the |permuted statistics| that are as large or larger than |observed statistic|.* This will always work and finds areas in both tails regardless of whether the observed statistic is positive or negative. In R, the `abs` function provides the ***absolute value*** and we can again use `pdata` to find our p-value in one line of code:

```
pdata(abs(Tstar), abs(Tobs), lower.tail=F)[[1]]
```

```
## [1] 0.044
```

We will encourage you to think through what might constitute strong evidence against your null hypotheses and then discuss how strong you feel the evidence is against the null hypothesis in the p-value that you obtained. Basically, p-values present a measure of evidence against the null hypothesis, with smaller values presenting more evidence against the null. They range from 0 to 1 and you should interpret them on a graded scale from strong evidence (close to 0) to little evidence to no evidence (1). We will discuss the use of a fixed ***significance level*** below as it is still commonly used in many fields and is necessary to discuss to think about the theory of hypothesis testing, but, for the moment, we can say that there is moderate evidence against the null hypothesis presented by having a p-value of 0.044 because our observed result is somewhat

rare relative to what we would expect if the null hypothesis was true. And so we might conclude (in the direction of the alternative) that there is a difference in the population means in the two groups, but that depends on what you think about how unusual that result was. It is also reasonable to feel that this is not sufficient evidence to conclude that there is a difference in the true means even though many people feel that p-values less than 0.05 are fairly strong evidence against the null hypothesis. If you do not rate this as strong enough evidence (or in general obtain weak evidence) to conclude that there is a difference, then you can only say that there might not be a difference in the means. We can't conclude that the null hypothesis is true – we just failed to find enough evidence to be sure that it is wrong. It might still be wrong but we couldn't detect it, either as a mistake because of an unusual sample from our population, or because our sample size was not large enough to detect the size of difference in the populations, or results with larger p-values could happen because there really isn't a difference. We don't know which of these might be the truth and certainly don't know that the null hypothesis is true even if the p-value obtained is 1[27].

Before we move on, let's note some interesting features of the permutation distribution of the difference in the sample means shown in Figure 2.10.

1. It is basically centered at 0. Since we are performing permutations assuming the null model is true, we are assuming that $\mu_1 = \mu_2$ which implies that $\mu_1 - \mu_2 = 0$. This also suggests that 0 should be the center of the permutation distribution and it was.

2. It is approximately normally distributed. This is due to the ***Central Limit Theorem***[28], where the ***sampling distribution*** (distribution of all possible results for samples of this size) of the difference in sample means $(\bar{x}_1 - \bar{x}_2)$ becomes more normally distributed as the sample sizes increase. With 15 observations in each group, we have no guarantee to have a relatively normal looking distribution of the difference in the sample means but with the distributions of the original observations looking somewhat normally distributed, the sampling distribution of the sample means likely will look fairly normal. This result will allow us to use a parametric method to approximate this sampling distribution under the null model if some assumptions are met, as we'll discuss below.

3. Our observed difference in the sample means (-25.933) is a fairly unusual result relative to the rest of these results but there are some permuted data sets that produce more extreme differences in the sample means. When the observed differences are really large, we may not see any permuted results that are as extreme as what we observed. When `pdata` gives you 0, the p-value should be reported to be smaller than 0.001 (**not 0!**) if B is 1,000 since it happened in less than 1 in 1,000 tries but does occur once – in the actual data set. This applies to any p-values when they are very small – just report them as less than 0.001, or 0.0001 if you prefer that next smaller upper limit, when they are under these values.

4. Since our null model is not specific about the direction of the difference, considering a result like ours but in the other direction (25.933 cm) needs to be included. The observed result seems to put about the same area in both tails of the distribution but it is not exactly the same. The small difference in the tails is a useful aspect of this approach compared to the parametric method discussed below as it accounts for potential asymmetry in the sampling distribution.

Earlier, we decided that the p-value provided moderate evidence against the null hypothesis. You should use your own judgment about whether the p-value obtain is sufficiently small to conclude that you think the null hypothesis is wrong. Remembering that the p-value is the probability you would observe a result like you did (or more extreme), assuming the null hypothesis is true; this tells you that the smaller the p-value is, the more evidence you have against the null. Figure 2.11 provides a diagram of some suggestions for the graded p-value interpretation that you can use. The next section provides a more formal review of the hypothesis testing infrastructure, terminology, and some of things that can happen when testing hypotheses. P-values have been (validly) criticized for the inability of studies to be reproduced, for the bias in publications to only include studies that have small p-values, and for the lack of thought that often accompanies using a fixed

[27] P-values of 1 are the only result that provide no evidence against the null hypothesis but this still doesn't prove that the null hypothesis is true.

[28] We'll leave the discussion of the CLT to your previous statistics coursework or an internet search. For this material, just remember that it has something to do with distributions of statistics looking more normal as the sample size increases.

significance level to make decisions (and only focusing on that decision). To alleviate some of these criticisms, we recommend reporting the strength of evidence of the result based on the p-value and also reporting and discussing the size of the estimated results (with a measure of precision of the estimated difference). We will explore the implications of how p-values are used in scientific research in Section 2.8.

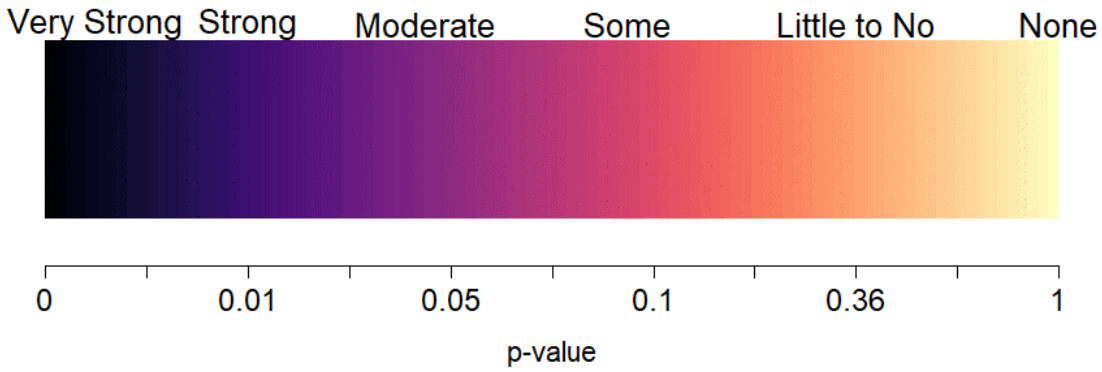

Figure 2.11: Graphic suggesting potential interpretations of strength of evidence based on gradient of p-values. P-values range from 0 to 1, with only a p-value of 1.0 providing no evidence against the null hypothesis.

2.5 Hypothesis testing (general)

In hypothesis testing (sometimes more explicitly called "Null Hypothesis Significance Testing" or NHST), it is formulated to answer a specific question about a population or true parameter(s) using a statistic based on a data set. In your previous statistics course, you (hopefully) considered one-sample hypotheses about population means and proportions and the two-sample mean situation we are focused on here. Hypotheses relate to trying to answer the question about whether the population mean overtake distances between the two groups are different, with an initial assumption of no difference.

NHST is much like a criminal trial with a jury where you are in the role of a jury member. Initially, the defendant is assumed innocent. In our situation, the true means are assumed to be equal between the groups. Then evidence is presented and, as a juror, you analyze it. In statistical hypothesis testing, data are collected and analyzed. Then you have to decide if we had "enough" evidence to reject the initial assumption ("innocence" that is initially assumed). To make this decision, you want to have thought about and decided on the standard of evidence required to reject the initial assumption. In criminal cases, "beyond a reasonable doubt" is used. Wikipedia's definition (https://en.wikipedia.org/wiki/Reasonable_doubt) suggests that this standard is that "there can still be a doubt, but only to the extent that it would not affect a reasonable person's belief regarding whether or not the defendant is guilty". In civil trials, a lower standard called a "preponderance of evidence" is used. Based on that defined and pre-decided (*a priori*) measure, you decide that the defendant is guilty or not guilty. In statistics, the standard is set by choosing a significance level, α, and then you compare the p-value to it. In this approach, if the p-value is less than α, we reject the null hypothesis. The choice of the significance level is like the variation in standards of evidence between criminal and civil trials – and in all situations everyone should know the standards required for rejecting the initial assumption before any information is "analyzed". Once someone is found guilty, then there is the matter of sentencing which is related to the impacts ("size") of the crime. In statistics, this is similar to the estimated size of differences and the related judgments about whether the differences are practically important or not. If the crime is proven beyond a reasonable doubt but it is a minor crime, then the sentence will be small. With the same level of evidence and a more serious crime, the sentence will be more dramatic. This latter step is more critical than the p-value as it directly relates to actions to be taken based on the research but

unfortunately p-values and the related decisions get most of the attention.

There are some important aspects of the testing process to note that inform how we interpret statistical hypothesis test results. When someone is found "not guilty", it does not mean "innocent", it just means that there was not enough evidence to find the person guilty "beyond a reasonable doubt". Not finding enough evidence to reject the null hypothesis does not imply that the true means are equal, just that there was not enough evidence to conclude that they were different. There are many potential reasons why we might fail to reject the null, but the most common one is that our sample size was too small (which is related to having too little evidence). Other reasons include simply the variation in taking a random sample from the population(s). This randomness in samples and the differences in the sample means also implies that p-values are random and can easily vary if the data set had been slightly different. This also relates to the suggestion of using a graded interpretation of p-values instead of the fixed α usage – if the p-value is an estimated quantity, is there really any difference between p-values of 0.049 and 0.051? We probably shouldn't think there is a big difference in results for these two p-values even though the standard NHST reject/fail to reject the null approach considers these as completely different results. So where does that leave us? Interpret the p-values using strength of evidence against the null hypothesis, remembering that smaller (but not really small) p-values can still be interesting. And if you think the p-value is small enough, then you can reject the null hypothesis and conclude that the alternative hypothesis is a better characterization of the truth – and then make sure to estimate and think about the size of the differences.

Throughout this material, we will continue to re-iterate the distinctions between parameters and statistics and want you to be clear about the distinctions between estimates based on the sample and inferences for the population or true values of the parameters of interest. Remember that statistics are summaries of the sample information and parameters are characteristics of populations (which we rarely know). In the two-sample mean situation, the sample means are always at least a little different – that is not an interesting conclusion. What is interesting is whether we have enough evidence to feel like we have proven that the population or true means differ "beyond a reasonable doubt".

The scope of any inferences is constrained based on whether there is a ***random sample*** (RS) and/or ***random assignment*** (RA). Table 2.1 contains the four possible combinations of these two characteristics of a given study. Random assignment of treatment levels to subjects allows for causal inferences for differences that are observed – the difference in treatment levels is said to cause differences in the mean responses. Random sampling (or at least some sort of representative sample) allows inferences to be made to the population of interest. If we do not have RA, then causal inferences cannot be made. If we do not have a representative sample, then our inferences are limited to the sampled subjects.

Table 2.1: Scope of inference summary.

Random Sampling/ Random Assignment	**Random Assignment (RA) – Yes (controlled experiment)**	**Random Assignment (RA) – No (observational study)**
Random Sampling (RS) – Yes (or some method that results in a representative sample of population of interest)	Because we have RS, we can generalize inferences to the population the RS was taken from. Because we have RA we can assume the groups were equivalent on all aspects except for the treatment and can establish causal inference.	Can generalize inference to population the RS was taken from but cannot establish causal inference (no RA – cannot isolate treatment variable as only difference among groups, could be confounding variables).

Random Sampling/ Random Assignment	**Random Assignment (RA) – Yes (controlled experiment)**	**Random Assignment (RA) – No (observational study)**
Random Sampling (RS) – No (usually a convenience sample)	Cannot generalize inference to the population of interest because the sample was not random and could be biased – may not be "representative" of the population of interest. Can establish causal inference due to RA → the inference from this type of study applies only to the sample.	Cannot generalize inference to the population of interest because the sample was not random and could be biased – may not be "representative" of the population of interest. Cannot establish causal inference due to lack of RA of the treatment.

A simple example helps to clarify how the scope of inference can change based on the study design. Suppose we are interested in studying the GPA of students. If we had taken a random sample from, say, Intermediate Statistics students in a given semester at a university, our scope of inference would be the population of students in that semester taking that course. If we had taken a random sample from the entire population of students at that school, then the inferences would be to the entire population of students in that semester. These are similar types of problems but the two populations are very different and the group you are trying to make conclusions about should be noted carefully in your results – it does matter! If we did not have a representative sample, say the students could choose to provide this information or not and some chose not to, then we can only make inferences to volunteers. These volunteers might differ in systematic ways from the entire population of Intermediate Statistics students (for example, they are proud of their GPA) so we cannot safely extend our inferences beyond the group that volunteered.

To consider the impacts of RA versus results from purely observational studies, we need to be comparing groups. Suppose that we are interested in differences in the mean GPAs for different sections of Intermediate Statistics and that we take a random sample of students from each section and compare the results and find evidence of some difference. In this scenario, we can conclude that there is some difference in the population of these statistics students but we can't say that being in different sections caused the differences in the mean GPAs. Now suppose that we randomly assigned every student to get extra training in one of three different study techniques and found evidence of differences among the training methods. We could conclude that the training methods caused the differences in these students. These conclusions would only apply to Intermediate Statistics students at this university in this semester and could not be generalized to a larger population of students. If we took a random sample of Intermediate Statistics students (say only 10 from each section) and then randomly assigned them to one of three training programs and found evidence of differences, then we can say that the training programs caused the differences. But we can also say that we have evidence that those differences pertain to the population of Intermediate Statistics students in that semester at this university. This seems similar to the scenario where all the students participated in the training programs except that by using random sampling, only a fraction of the population needs to actually be studied to make inferences to the entire population of interest – saving time and money.

A quick summary of the terminology of hypothesis testing is useful at this point. The ***null hypothesis*** (H_0) states that there is no difference or no relationship in the population. This is the statement of no effect or no difference and the claim that we are trying to find evidence against in NHST. In this chapter, H_0: $\mu_1 = \mu_2$. When doing two-group problems, you always need to specify which group is 1 and which one is 2 because the order does matter. The ***alternative hypothesis*** (H_1 or H_A) states a specific difference between parameters. This is the research hypothesis and the claim about the population that we often hope to demonstrate is more reasonable to conclude than the null hypothesis. In the two-group situation, we can have ***one-sided alternatives*** $H_A : \mu_1 > \mu_2$ (greater than) or $H_A : \mu_1 < \mu_2$ (less than) or, the more common, ***two-sided alternative*** $H_A : \mu_1 \neq \mu_2$ (not equal to). We usually default to using two-sided tests because we often do not know enough to know the direction of a difference *a priori*, especially in more complicated situations. The ***sampling distribution under the null*** is the distribution of all possible values of a statistic under the assumption that H_0 is true. It is used to calculate the ***p-value***, the probability of obtaining a result as extreme or more extreme (defined by the alternative) than what we observed given that the null hypothesis is

true. We will find sampling distributions using ***nonparametric*** approaches (like the permutation approach used previously) and ***parametric*** methods (using "named" distributions like the t, F, and χ^2).

Small p-values are evidence against the null hypothesis because the observed result is unlikely due to chance if H_0 is true. Large p-values provide little to no evidence against H_0 but do not allow us to conclude that the null hypothesis is correct – just that we didn't find enough evidence to think it was wrong. The ***level of significance*** is an *a priori* definition of how small the p-value needs to be to provide "enough" (sufficient) evidence against H_0. This is most useful to prevent sliding the standards after the results are found but you can interpret p-values as strength of evidence against the null hypothesis without employing the fixed significance level. If using a fixed significance level, we can compare the p-value to the level of significance to decide if the p-value is small enough to constitute sufficient evidence to reject the null hypothesis. We use α to denote the level of significance and most typically use 0.05 which we refer to as the 5% significance level. We can compare the p-value to this level and make a decision, focusing our interpretation on the strength of evidence we found based on the p-value from very strong to little to none. If we are using the strict version of NHST, the two options for *decisions* are to either *reject the null hypothesis* if the p-value $\leq \alpha$ or *fail to reject the null hypothesis* if the p-value $> \alpha$. When interpreting hypothesis testing results, remember that the p-value is a measure of how unlikely the observed outcome was, assuming that the null hypothesis is true. It is **NOT** the probability of the data or the probability of either hypothesis being true. The p-value, simply, is a measure of evidence against the null hypothesis.

Although we want to use graded evidence to interpret p-values, there is one situation where thinking about comparisons to fixed α levels is useful for understanding and studying statistical hypothesis testing. The specific definition of α is that it is the probability of rejecting H_0 when H_0 is true, the probability of what is called a ***Type I error***. Type I errors are also called ***false rejections*** or ***false detections***. In the two-group mean situation, a Type I error would be concluding that there is a difference in the true means between the groups when none really exists in the population. In the courtroom setting, this is like falsely finding someone guilty. We don't want to do this very often, so we use small values of the significance level, allowing us to control the rate of Type I errors at α. We also have to worry about **Type II errors**, which are failing to reject the null hypothesis when it's false. In a courtroom, this is the same as failing to convict a truly guilty person. This most often occurs due to a lack of evidence that could be due to a small sample size or merely just an unusual sample from the population. You can use the Table 2.2 to help you remember all the possibilities.

Table 2.2: Table of decisions and truth scenarios in a hypothesis testing situation. But we never know the truth in a real situation.

	H_0 True	**H_0 False**
FTR H_0	Correct decision	Type II error
Reject H_0	Type I error	Correct decision

In comparing different procedures or in planning studies, there is an interest in studying the rate or probability of Type I and II errors. The probability of a Type I error was defined previously as α, the significance level. The ***power*** of a procedure is the probability of rejecting the null hypothesis when it is false. Power is defined as

$$\text{Power} = 1 - \text{Probability(Type II error)} = \text{Probability(Reject } H_0 | H_0 \text{ is false)},$$

or, in words, the probability of detecting a difference when it actually exists. We want to use a statistical procedure that controls the Type I error rate at the pre-specified level and has high power to detect false null hypotheses. Increasing the sample size is one of the most commonly used methods for increasing the power in a given situation. Sometimes we can choose among different procedures and use the power of the procedures to help us make that selection. Note that there are many ways H_0 can be false and the power changes based on how false the null hypothesis actually is. To make this concrete, suppose that the true

mean overtake distances differed by either 1 or 30 cm in previous example. The chances of rejecting the null hypothesis are much larger when the group means actually differ by 30 cm than if they differ by just 1 cm, given the same sample size. The null hypothesis is false in both cases. Similarly, for a given difference in the true means, the larger the sample, the higher the power of the study to actually find evidence of a difference in the groups. We will see this difference when we return to using the entire overtake data set instead of the sample of $n = 30$ used to illustrate the permutation procedures.

After making a decision (was there enough evidence to reject the null or not), we want to make the conclusions specific to the problem of interest. If we reject H_0, then we can conclude that there was sufficient evidence at the α-level that the null hypothesis is wrong (and the results point in the direction of the alternative). If we fail to reject H_0 (FTR H_0), then we can conclude that there was insufficient evidence at the α-level to say that the null hypothesis is wrong. We are **NOT** saying that the null is correct and we **NEVER** accept the null hypothesis. We just failed to find enough evidence to say it's wrong. If we find sufficient evidence to reject the null, then we need to revisit the method of data collection and design of the study to discuss the scope of inference. Can we discuss causality (due to RA) and/or make inferences to a larger group than those in the sample (due to RS)?

To perform a hypothesis test, there are some steps to remember to complete to make sure you have thought through and reported all aspects of the results.

Outline of 6+ steps to perform a Hypothesis Test
Preliminary steps:
* Define research question (RQ) and consider study design - what question can the data collected address?
* What graphs are appropriate to visualize the data?
* What model/statistic (T) is needed to address RQ?
1. Write the null and alternative hypotheses.
2. Plot the data and assess the "Validity Conditions" for the procedure being used (discussed below).
3. Find the value of the appropriate test statistic and p-value for your hypotheses.
4. Write a conclusion specific to the problem based on the p-value, reporting the strength of evidence against the null hypothesis (include test statistic, its distribution under the null hypothesis, and p-value).
5. Report and discuss an estimate of the size of the differences, with confidence interval(s) if appropriate.
6. Scope of inference discussion for results.

2.6 Connecting randomization (nonparametric) and parametric tests

In developing statistical inference techniques, we need to define the test statistic, T, that measures the quantity of interest. To compare the means of two groups, a statistic is needed that measures their differences. In general, for comparing two groups, the choice is simple – a difference in the means often works well and is a natural choice. There are other options such as tracking the ratio of means or possibly the difference in medians. Instead of just using the difference in the means, we also could "standardize" the difference in the means by dividing by an appropriate quantity that reflects the variation in the difference in the means. All of these are valid and can sometimes provide similar results - it ends up that there are many possibilities for testing using the randomization (nonparametric) techniques introduced previously. Parametric statistical methods focus on means because the statistical theory surrounding means is quite a bit easier (not easy, just easier) than other options. There are just a couple of test statistics that you can use and end up with named distributions to use for generating inferences. Randomization techniques allow inference for other quantities (such as ratios of means or differences in medians) but our focus here will be on using randomization for inferences on means to see the similarities with the more traditional parametric procedures used in these situations.

In two-sample mean situations, instead of working just with the difference in the means, we often calculate a test statistic that is called the ***equal variance two-independent samples t-statistic***. The test statistic is

$$t = \frac{\bar{x}_1 - \bar{x}_2}{s_p\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}},$$

where s_1^2 and s_2^2 are the sample variances for the two groups, n_1 and n_2 are the sample sizes for the two groups, and the ***pooled sample standard deviation***,

$$s_p = \sqrt{\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2}}.$$

The t-statistic keeps the important comparison between the means in the numerator that we used before and standardizes (re-scales) that difference so that t will follow a t-distribution (a parametric "named" distribution) if certain assumptions are met. But first we should see if standardizing the difference in the means had an impact on our permutation test results. It ends up that, while not too obvious, the `summary` of the `lm` we fit earlier contains this test statistic[29]. Instead of using the second model coefficient that estimates the difference in the means of the groups, we will extract the test statistic from the table of summary output that is in the `coef` object in the summary – using `$` to reference the `coef` information only. In the `coef` object in the summary, results related to the `ConditionCommute` are again useful for the comparison of two groups.

```
summary(lm1)$coef
```

```
##                   Estimate Std. Error   t value     Pr(>|t|)
## (Intercept)      135.80000   8.862996 15.322133 3.832161e-15
## Conditioncommute -25.93333  12.534169 -2.069011 4.788928e-02
```

The first column of numbers contains the estimated difference in the sample means (-25.933 here) that was used before. The next column is the `Std. Error` column that contains the standard error (SE) of the estimated difference in the means, which is $s_p\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$ and also the denominator used to form the t-test statistic (12.53 here). It will be a common theme in this material to take the ratio of the estimate (-25.933) to its SE (12.53) to generate test statistics, which provides -2.07 – this is the "standardized" estimate of the difference in the means. It is also a test statistic (T) that we can use in a permutation test. This value is in the second row and third column of `summary(lm1)$coef` and to extract it the bracket notation is again employed. Specifically we want to extract `summary(lm1)$coef[2,3]` and using it and its permuted data equivalents to calculate a p-value. Since we are doing a two-sided test, the code resembles the permutation test code in Section 2.4 with the new t-statistic replacing the difference in the sample means that we used before.

```
Tobs <- summary(lm1)$coef[2,3]
Tobs
```

```
## [1] -2.069011
```

```
B <- 1000
set.seed(406)
Tstar <- matrix(NA, nrow = B)
for (b in (1:B)){
  lmP <- lm(Distance ~ shuffle(Condition), data = dsample)
  Tstar[b] <- summary(lmP)$coef[2,3]
```

[29] The `t.test` function with the `var.equal=T` option is the more direct route to calculating this statistic (here that would be `t.test(Distance~Condition, data=dsamp, var.equal=T)`), but since we can get the result of interest by fitting a linear model, we will use that approach.

```
}
pdata(abs(Tstar), abs(Tobs), lower.tail = F)
```

```
## [1] 0.041
```

The permutation distribution in Figure 2.12 looks similar to the previous results with slightly different x-axis scaling. The observed t-statistic was -2.07 and the proportion of permuted results that were as or more extreme than the observed result was 0.041. This difference is due to a different set of random permutations being selected. If you run permutation code, you will often get slightly different results each time you run it. If you are uncomfortable with the variation in the results, you can run more than $B = 1{,}000$ permutations (say 10,000) and the variability in the resulting p-values will be reduced further. Usually this uncertainty will not cause any substantive problems – but do not be surprised if your results vary if you use different random number seeds.

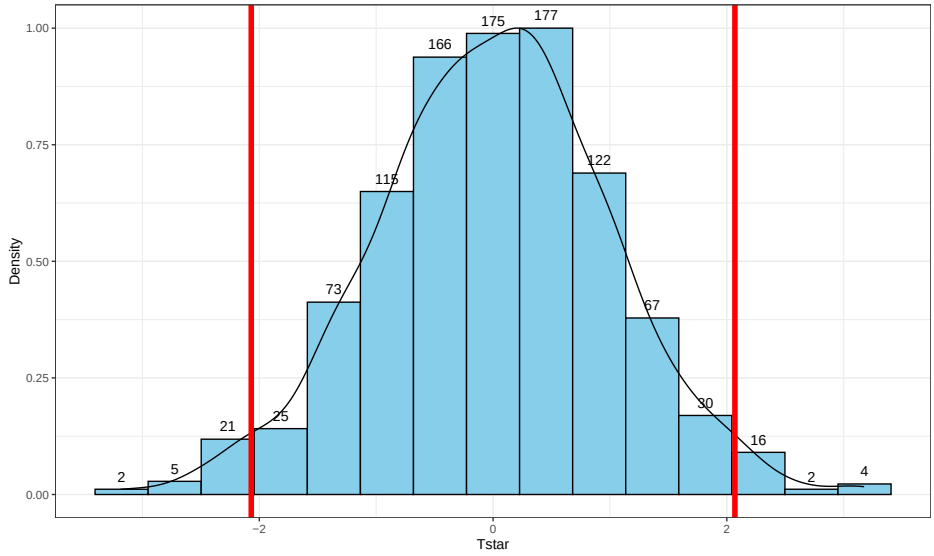

Figure 2.12: Permutation distribution of the t-statistic.

```
tibble(Tstar) %>%  ggplot(aes(x = Tstar)) +
  geom_histogram(aes(y = ..ncount..), bins = 15, col = 1, fill = "skyblue",
                 center = 0) +
  stat_bin(aes(y = ..ncount.., label = ..count..), bins = 15,
           geom = "text", vjust=-0.75) +
  geom_density(aes(y = ..scaled..)) + theme_bw() + labs(y = "Density") +
  geom_vline(xintercept = c(-1,1)*Tobs, col = "red", lwd = 2)
```

The parametric version of these results is based on using what is called the ***two-independent sample t-test***. There are actually two versions of this test, one that assumes that variances are equal in the groups and one that does not. There is a rule of thumb that if the **ratio of the larger standard deviation over the smaller standard deviation is less than 2, the equal variance procedure is OK**. It ends up that this assumption is less important if the sample sizes in the groups are approximately equal and more important if the groups contain different numbers of observations. In comparing the two potential test statistics, the procedure that assumes equal variances has a complicated denominator (see the formula above for t involving s_p) but a simple formula for ***degrees of freedom*** (***df***) for the t-distribution ($df = n_1 + n_2 - 2$) that approximates the distribution of the test statistic, t, under the null hypothesis. The procedure that assumes unequal variances has a simpler test statistic and a very complicated degrees of freedom formula. The equal variance procedure is equivalent to the methods we will consider in Chapters **??** and **??** so that

will be our focus for the two group problem and is what we get when using the `lm` model to estimate the differences in the group means. The unequal variance version of the two-sample t-test is available in the `t.test` function if needed.

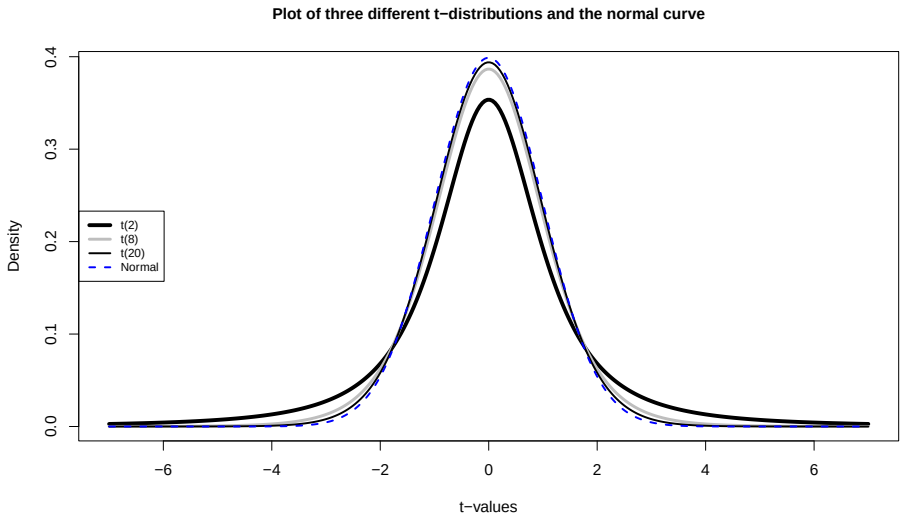

Figure 2.13: Plots of t-distributions with 2, 8, and 20 degrees of freedom and a normal distribution (dashed line). Note how the t-distributions get closer to the normal distribution as the degrees of freedom increase and at 20 degrees of freedom, the t-distribution *almost* matches a standard normal curve.

If the assumptions for the equal variance t-test and the null hypothesis are true, then the sampling distribution of the test statistic should follow a t-distribution with $n_1 + n_2 - 2$ degrees of freedom (so the total sample size, n, minus 2). The ***t-distribution*** is a bell-shaped curve that is more spread out for smaller values of degrees of freedom as shown in Figure 2.13. The t-distribution looks more and more like a ***standard normal distribution*** ($N(0, 1)$) as the degrees of freedom increase.

To get the p-value for the parametric t-test, we need to calculate the test statistic and df, then look up the areas in the tails of the t-distribution relative to the observed t-statistic. We'll learn how to use R to do this below, but for now we will allow the `summary` of the `lm` function to take care of this. In the `ConditionCommute` row of the summary and the `Pr(>|t|)` column, we can find the p-value associated with the test statistic. We can either calculate the degrees of freedom for the t-distribution using $n_1 + n_2 - 2 = 15 + 15 - 2 = 28$ or explore the full suite of the model summary that is repeated below. In the first row below the `ConditionCommute` row, it reports "... 28 degrees of freedom" and these are the same df that are needed to report and look up for any of the t-statistics in the model summary.

```
summary(lm1)
```

```
##
## Call:
## lm(formula = Distance ~ Condition, data = dsample)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -63.800 -21.850   4.133  15.150  72.200
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      135.800      8.863  15.322 3.83e-15
```

```
## Conditioncommute  -25.933     12.534  -2.069   0.0479
##
## Residual standard error: 34.33 on 28 degrees of freedom
## Multiple R-squared:  0.1326, Adjusted R-squared:  0.1016
## F-statistic: 4.281 on 1 and 28 DF,  p-value: 0.04789
```

So the parametric t-test gives a p-value of 0.0479 from a test statistic of -2.07. The p-value is very similar to the two permutation results found before. The reason for this similarity is that the permutation distribution looks like a t-distribution with 28 degrees of freedom. Figure 2.14 shows how similar the two distributions happened to be here, where the only difference in shape is near the peak of the distributions with a slight difference of the permutation distribution to shift to the right.

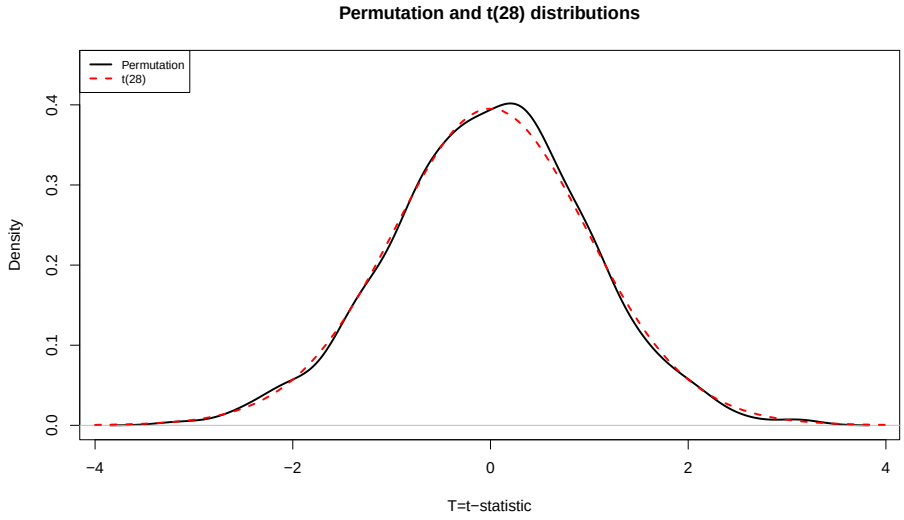

Figure 2.14: Plot of permutation and t-distribution with $df = 28$. Note the close match in the two distributions, especially in the tails of the distributions where we are obtaining the p-values.

In your previous statistics course, you might have used an applet or a table to find p-values such as what was provided in the previous R output. When not directly provided in the output of a function, R can be used to look up p-values[30] from named distributions such as the t-distribution. In this case, the distribution of the test statistic under the null hypothesis is a $t(28)$ or a t with 28 degrees of freedom. The `pt` function is used to get p-values from the t-distribution in the same manner that `pdata` could help us to find p-values from the permutation distribution. We need to provide the `df = ...` and specify the tail of the distribution of interest using the `lower.tail` option along with the cutoff of interest. If we want the area to the left of -2.07:

```
pt(-2.069, df = 28, lower.tail = T)
```

```
## [1] 0.02394519
```

And we can double it to get the p-value that was in the output, because the t-distribution is symmetric:

```
2*pt(-2.069, df = 28, lower.tail = T)
```

```
## [1] 0.04789038
```

[30] On exams, you might be asked to describe the area of interest, sketch a picture of the area of interest, and/or note the distribution you would use. Make sure you think about what you are trying to do here as much as learning the mechanics of how to get p-values from R.

More generally, we could always make the test statistic positive using the absolute value (`abs`), find the area to the right of it (`lower.tail = F`), and then double that for a two-sided test p-value:

```
2*pt(abs(-2.069), df=28, lower.tail=F)
```

```
## [1] 0.04789038
```

Permutation distributions do not need to match the named parametric distribution to work correctly, although this happened in the previous example. The parametric approach, the *t*-test, requires certain conditions to be true (or at least not be clearly violated) for the sampling distribution of the statistic to follow the named distribution and provide accurate p-values. The conditions for the *t*-test are:

1. **Independent observations**: Each observation obtained is unrelated to all other observations. To assess this, consider whether anything in the data collection might lead to clustered or related observations that are un-related to the differences in the groups. For example, was the same person measured more than once[31]?
2. **Equal variances** in the groups (because we used a procedure that assumes equal variances! – there is another procedure that allows you to relax this assumption if needed...). To assess this, compare the standard deviations and variability in the pirate-plots and see if they look noticeably different. Be particularly critical of this assessment if the sample sizes differ greatly between groups.
3. **Normal distributions** of the observations in each group. We'll learn more diagnostics later, but the pirate-plots are a good place to start to help you look for potential skew or outliers. If you find skew and/or outliers, that would suggest a problem with the assumption of normality as normal distributions are symmetric and extreme observations occur very rarely.

For the permutation test, we relax the third condition and replace it with:

3. ***Similar distributions for the groups:*** The permutation approach allows valid inferences as long as the two groups have similar shapes and only possibly differ in their centers. In other words, the distributions need not look normal for the procedure to work well, but they do need to look similar.

In the bicycle overtake study, the independent observation condition is violated because of multiple measurements taken on the same ride. The fact that the same rider was used for all observations is not really a violation of independence here because there was only one subject used. If multiple subjects had been used, then that also could present a violation of the independence assumption. This violation is important to note as the inferences may not be correct due to the violation of this assumption and more sophisticated statistical methods would be needed to complete this analysis correctly. The equal variance condition does not appear to be violated. The standard deviations are 28.4 vs 39.4, so this difference is not "large" according to the rule of thumb noted above (ratio of SDs is about 1.4). There is also little evidence in the pirate-plots to suggest a violation of the normality condition for each of the groups (Figure 2.5). Additionally, the shapes look similar for the two groups so we also could feel comfortable using the permutation approach based on its version of condition (3) above. Note that when assessing assumptions, it is important to never state that assumptions are met – we never know the truth and can only look at the information in the sample to look for evidence of problems with particular conditions. Violations of those conditions suggest a need for either more sophisticated statistical tools[32] or possibly transformations of the response variable (discussed in Chapter **??**).

The permutation approach is resistant to impacts of violations of the normality assumption. It is not resistant to impacts of violations of any of the other assumptions. In fact, it can be quite sensitive to unequal variances as it will detect differences in the variances of the groups instead of differences in the means. Its scope of inference is the same as the parametric approach. It also provides similarly inaccurate conclusions in the presence of non-independent observations as for the parametric approach. In this example, we discover

[31] In some studies, the same subject is measured in both conditions and this violates the assumptions of this procedure.

[32] At this level, it is critical to learn the tools and learn where they might provide inaccurate inferences. If you explore more advanced statistical resources, you will encounter methods that can allow you to obtain valid inferences in even more scenarios.

that parametric and permutation approaches provide very similar inferences, but both are subject to concerns related to violations of the independent observations condition. And we haven't directly addressed the size and direction of the differences, which is addressed in the coming discussion of confidence intervals.

For comparison, we can also explore the original data set of all $n = 1,636$ observations for the two outfits. The estimated difference in the means is -3.003 cm (*commute* minus *casual*), the standard error is 1.472, the t-statistic is -2.039 and using a t-distribution with 1634 df, the p-value is 0.0416. The estimated difference in the means is much smaller but the p-value is similar to the results for the sub-sample we analyzed. The SE is much smaller with the large sample size which corresponds to having higher power to detect smaller differences.

```
lm_all <- lm(Distance ~ Condition, data = ddsub)
summary(lm_all)
```

```
##
## Call:
## lm(formula = Distance ~ Condition, data = ddsub)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -106.608  -17.608    0.389   16.392  127.389
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        117.611      1.066 110.357   <2e-16
## Conditioncommute    -3.003      1.472  -2.039   0.0416
##
## Residual standard error: 29.75 on 1634 degrees of freedom
## Multiple R-squared:  0.002539,   Adjusted R-squared:  0.001929
## F-statistic:  4.16 on 1 and 1634 DF,  p-value: 0.04156
```

The permutations take a little more computing power with almost two thousand observations to shuffle, but this is manageable on a modern laptop as it only has to be completed once to fill in the distribution of the test statistic under 1,000 shuffles. And the p-value obtained is a close match to the parametric result at 0.045 for the permutation version and 0.042 for the parametric approach. So we would get similar inferences for strength of evidence against the null with either the smaller data set or the full data set but the estimated size of the differences is quite a bit different. It is important to note that other random samples from the larger data set would give different p-values and this one happened to match the larger set more closely than one might expect in general.

```
Tobs <- summary(lm_all)$coef[2,3]
Tobs
```

```
## [1] -2.039491
```

```
B <- 1000
set.seed(406)
Tstar <- matrix(NA, nrow = B)
for (b in (1:B)){
  lmP <- lm(Distance ~ shuffle(Condition), data = ddsub)
  Tstar[b] <- summary(lmP)$coef[2,3]
}
pdata(abs(Tstar), abs(Tobs), lower.tail = F)
```

```
## [1] 0.045
```

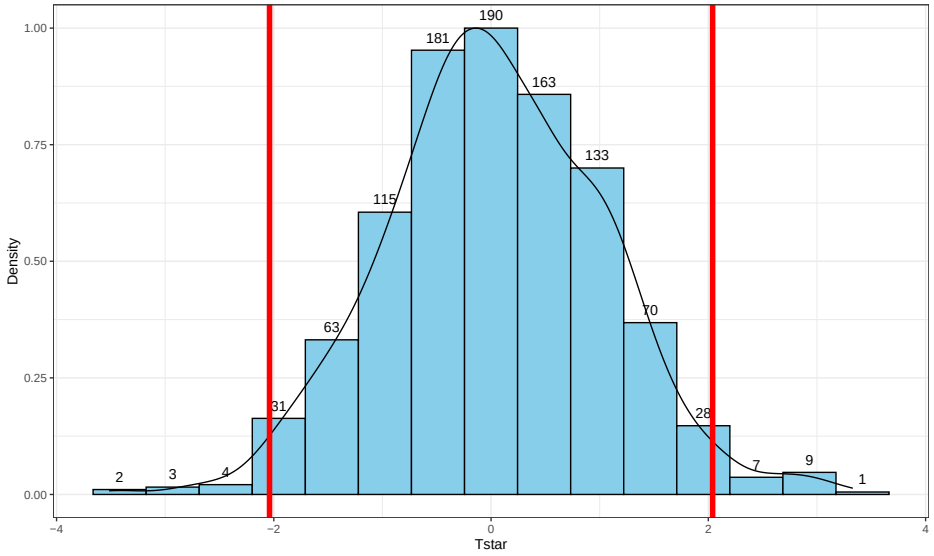

Figure 2.15: Permutation distribution of the t-statistic for $n = 1,636$ overtake data set.

2.7 Second example of permutation tests

In every chapter, the first example, used to motivate and explain the methods, is followed with a "worked" example where we focus just on the results. In a previous semester, some of the Intermediate Statistics (STAT 217) students at Montana State University (n=79) provided information on their *Sex*[33], *Age*, and current cumulative *GPA*. We might be interested in whether Males and Females had different average GPAs. First, we can take a look at the difference in the responses by groups based on the output and as displayed in Figure 2.16.

```
s217 <- read_csv("http://www.math.montana.edu/courses/s217/documents/s217.csv")
library(mosaic)
library(yarrr)
```

```
mean(GPA ~ Sex, data = s217)
```

```
##        F        M
## 3.338378 3.088571
```

```
favstats(GPA ~ Sex, data = s217)
```

```
##   Sex  min  Q1 median   Q3 max     mean        sd  n missing
## 1   F 2.50 3.1  3.400 3.70   4 3.338378 0.4074549 37       0
## 2   M 1.96 2.8  3.175 3.46   4 3.088571 0.4151789 42       0
```

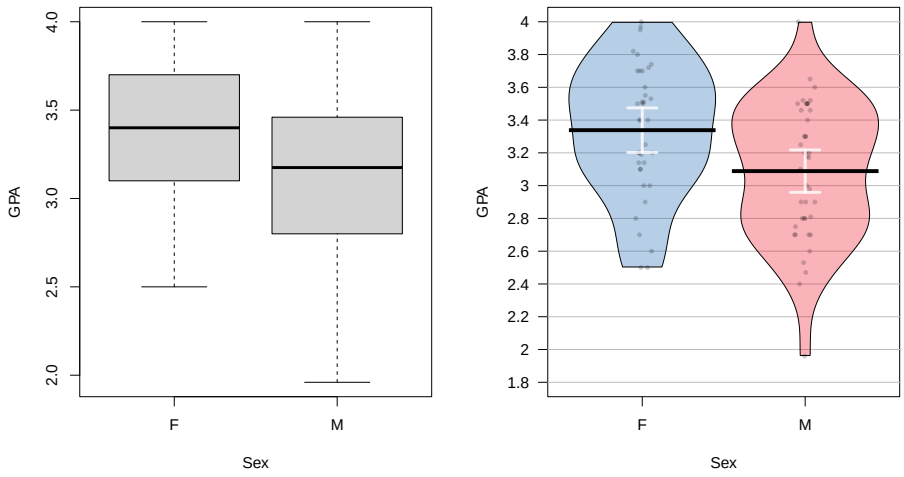

Figure 2.16: Side-by-side boxplot and pirate-plot of GPAs of Intermediate Statistics students by gender.

```
boxplot(GPA ~ Sex, data = s217)
pirateplot(GPA ~ Sex, data = s217, inf.method = "ci", inf.disp = "line")
```

In these data, the distributions of the GPAs look to be left skewed. The Female GPAs look to be slightly higher than for Males (0.25 GPA difference in the means) but is that a "real" difference? We need our inference tools to more fully assess these differences.

[33]Only male and female were provided as options on the survey. These data were collected as part of a project to study learning of material using online versus paper versions of this book but we focus just on the gender differences in GPA here.

First, we can try the parametric approach:

```
lm_GPA <- lm(GPA ~ Sex, data = s217)
summary(lm_GPA)
```

```
##
## Call:
## lm(formula = GPA ~ Sex, data = s217)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.12857 -0.28857  0.06162  0.36162  0.91143
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.33838    0.06766  49.337  < 2e-16
## SexM        -0.24981    0.09280  -2.692  0.00871
##
## Residual standard error: 0.4116 on 77 degrees of freedom
## Multiple R-squared:  0.08601,    Adjusted R-squared:  0.07414
## F-statistic: 7.246 on 1 and 77 DF,  p-value: 0.008713
```

So the test statistic was observed to be $t = 2.69$ and it hopefully follows a $t(77)$ distribution under the null hypothesis. This provides a p-value of 0.008713 that we can trust if the conditions to use this procedure are at least not clearly violated. Compare these results to the permutation approach, which relaxes that normality assumption, with the results that follow. In the permutation test, $T = -2.692$ and the p-value is 0.011 which is a little larger than the result provided by the parametric approach. The general agreement of the two approaches, again, provides some re-assurance about the use of either approach when there are not dramatic violations of validity conditions.

```
B=1000
Tobs <- summary(lm_GPA)$coef[2,3]
Tstar <- matrix(NA, nrow = B)
for (b in (1:B)){
  lmP <- lm(GPA ~ shuffle(Sex), data = s217)
  Tstar[b] <- summary(lmP)$coef[2,3]
}
pdata(abs(Tstar), abs(Tobs), lower.tail = F)[[1]]
```

```
tibble(Tstar) %>%  ggplot(aes(x = Tstar)) +
  geom_histogram(aes(y = ..ncount..), bins = 15, col = 1, fill = "skyblue",
                 center = 0) +
  stat_bin(aes(y = ..ncount.., label = ..count..), bins = 15,
           geom = "text", vjust=-0.75) +
  geom_density(aes(y = ..scaled..)) + theme_bw() + labs(y = "Density") +
  geom_vline(xintercept = c(-1,1)*Tobs, col = "red", lwd = 2)
```

Here is a full write-up of the results using all 6+ hypothesis testing steps, using the permutation results for the grade data:

0. The research question involves exploring differences in GPAs between males and females. With data collected from both groups, we should be able to assess this RQ. The pirate-plot with GPAs by gender is a useful visualization. We could use either differences in the sample means or the t-statistic for the

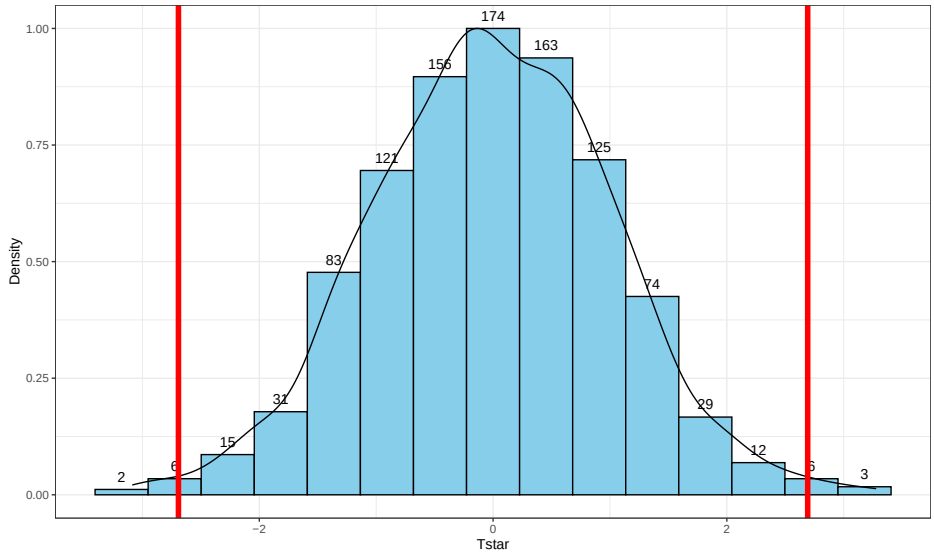

Figure 2.17: Histogram and density curve of permutation distribution of test statistic for Intermediate Statistics student GPAs.

test statistic here.

1. Write the null and alternative hypotheses:
   - $H_0 : \mu_{\text{male}} = \mu_{\text{female}}$
     - where μ_{male} is the true mean GPA for males and μ_{female} is true mean GPA for females.
   - $H_A : \mu_{\text{male}} \neq \mu_{\text{female}}$
2. Plot the data and assess the "Validity Conditions" for the procedure being used:
   - **Independent observations condition**: It does not appear that this assumption is violated because there is no reason to assume any clustering or grouping of responses that might create dependence in the observations. The only possible consideration is that the observations were taken from different sections and there could be some differences among the sections. However, for overall GPA there is not too much likelihood that the overall GPAs would vary greatly so this not likely to be a big issue. However, it is possible that certain sections (times of day) attract students with different GPA levels.
   - **Equal variance condition**: There is a small difference in the range of the observations in the two groups but the standard deviations are very similar (close to 0.41) so there is little evidence that this condition is violated.
   - **Similar distribution condition**: Based on the side-by-side boxplots and pirate-plots, it appears that both groups have slightly left-skewed distributions, which could be problematic for the parametric approach. The two distributions are not exactly alike but they are similar enough that the permutation approach condition is not clearly violated.
3. Find the value of the appropriate test statistic and p-value for your hypotheses:
   - $T = -2.69$ from the previous R output.
   - p-value = 0.011 from the permutation distribution results.
   - This means that there is about a 1.1% chance we would observe a difference in mean GPA (female-male or male-female) of 0.25 points or more if there in fact is no difference in true mean GPA between females and males in Intermediate Statistics in a particular semester.

4. Write a conclusion specific to the problem based on the p-value:
    - There is strong evidence against the null hypothesis of no difference in the true mean GPA between males and females for the Intermediate Statistics students in this semester and so we conclude that there is a difference in the mean GPAs between males and females in these students.
5. Report and discuss an estimate of the size of the differences, with confidence interval(s) if appropriate.
    - Females were estimated to have a higher mean GPA by 0.25 points. The next section discusses confidence intervals that we could add to this result to quantify the uncertainty in this estimate since an estimate without any idea of its precision is only a partial result. This difference of 0.25 on a GPA scale does not seem like a very large difference in the means even though we were able to detect a difference in the groups.
6. Scope of inference:
    - Because this was not a randomized experiment in our explanatory variable, we can't say that the difference in gender causes the difference in mean GPA. Because it was not a random sample from a larger population (they were asked to participate but not required to and not all the students did participate), our inferences only pertain the Intermediate Statistics students that responded to the survey in that semester.

2.8 Reproducibility Crisis: Moving beyond $p < 0.05$, publication bias, and multiple testing issues

In the previous examples, some variation in p-values was observed as different methods (parametric, non-parametric) were applied to the same data set and in the permutation approach, the p-values can vary as well from one set of permutations to another. P-values also vary based on randomness in the data that were collected – take a different (random) sample and you will get different data and a different p-value. We want the best estimate of a p-value we can obtain, so should use the best sampling method and inference technique that we can. But it is just an estimate of the evidence against the null hypothesis. These sources of variability make fixed α NHST especially worry-some as sampling variability could take a p-value from just below to just above α and this would lead to completely different inferences if the only focus is on rejecting the null hypothesis at a fixed significance level. But viewing p-values on a gradient from extremely strong (close to 0) to no (1) evidence against the null hypothesis, p-values of, say, 0.046 and 0.054 provide basically the same evidence against the null hypothesis. The fixed α decision-making is tied into the use of the terminology of "significant results" or, slightly better, "statistically significant results" that are intended to convey that there was sufficient evidence to reject the null hypothesis at some pre-decided α level. You will notice that this is the only time that the "s-word" (significant) is considered here.

The focus on p-values has been criticized for a suite of reasons [Wasserstein and Lazar, 2016]. There are situations when p-values do not address the question of interest or the fact that a small p-value was obtained is so un-surprising that one wonders why it was even reported. For example, in Smith [Smith, 2014] the researcher considered bee sting pain ratings across 27 different body locations[34]. I don't think anyone would be surprised to learn that there was strong evidence against the null hypothesis of no difference in the true mean pain ratings across different body locations. What is really of interest are the differences in the means – especially which locations are most painful and how much more painful those locations were than others, on average.

As a field, Statistics is trying to encourage a move away from the focus on p-values and the use of the term "significant", even when modified by "statistically". There are a variety of reasons for this change. Science (especially in research going into academic journals and in some introductory statistics books) has taken to using p-value < 0.05 and rejected null hypotheses as the only way to "certify" that a result is interesting. It has (and unfortunately still is) hard to publish a paper with a primary result with a p-value that is higher than 0.05, even if the p-value is close to that "magical" threshold. One thing that is lost when

[34]The data are provided and briefly discussed in the Practice Problems for Chapter **??**.

using that strict cut-off for decisions is that any p-value that is not exactly 1 suggests that there is at least some evidence against the null hypothesis in the data and that evidence is then on a continuum from none to very strong. And that p-values are both a function of the size of the difference and the sample size. It is easy to get small p-values for small size differences with large data sets. A small p-value can be associated with an unimportant (not practically meaningful) size difference. And large p-values, especially in smaller sample situations, could be associated with very meaningful differences in size even though evidence is not strong against the null hypothesis. It is critical to always try to estimate and discuss the size of the differences, whether a large or small p-value is encountered.

There are some other related issues to consider in working with p-values that help to illustrate some of the issues with how p-values and "statistical significance" are used in practice. In many studies, researchers have a suite of outcome variables that they measure on their subjects. For example, in an agricultural experiment they might measure the yield of the crops, the protein concentration, the digestibility, and other characteristics of the crops. In various "omics" fields such as genomics, proteomics, and metabolomics, responses for each subject on hundreds, thousands, or even millions of variables are considered and a p-value may be generated for each of those variables. In education, researchers might be interested in impacts on grades (as in the previous discussion) but we could also be interested in reading comprehension, student interest in the subject, and the amount of time spent studying, each as response variables in their own right. In each of these situations it means that we are considering not just one null hypothesis and assessing evidence against it, but are doing it many times, from just a few to millions of repetitions. There are two aspects of this process and implications for research to explore further: the impacts on scientific research of focusing solely on "statistically significant" results and the impacts of considering more than one hypothesis test in the same study.

There is the systematic bias in scientific research that has emerged from scientists having a difficult time publishing research if p-values for their data are not smaller than 0.05. This has two implications. Many researchers have assumed that results with "large" p-values are not interesting – so they either exclude these results from papers (they put them in *their* file drawer instead of into their papers - the so-called "file-drawer" bias) or reviewers reject papers because they did not have small p-values to support their discussions (only results with small p-values are judged as being of interest for publication - the so-called "publication bias"). Some also include bias from researchers only choosing to move forward with attempting to publish results if they are in the same direction that the researchers expect/theorized as part of this problem – ignoring results that contradict their theories is an example of "confirmation bias" but also would hinder the evolution of scientific theories to ignore contradictory results. But since most researchers focus on p-values and not on estimates of size (and direction) of differences, that will be our focus here.

We will use some of our new abilities in R to begin to study some of the impacts of systematically favoring only results with small p-values using a "simulation study" inspired by the explorations in Schneck [2017]. Specifically, let's focus on the bicycle passing data. We start with assuming that there really is no difference in the two groups, so the true mean is the same in both groups, the variability is the same around the means in the two groups, and all responses follow normal distributions. This is basically like the permutation idea where we assumed the group labels could be equivalently swapped among responses if the null hypothesis were true except that observations will be generated by a normal distribution instead of shuffling the original observations among groups. This is a little stronger assumption than in the permutation approach but makes it possible to study Type I error rates, power, and to explore a process that is similar to how statistical results are generated and used in academic research settings.

Now let's suppose that we are interested in what happens when we do ten independent studies of the same research question. You could think of this as ten different researchers conducting their own studies of the same topic (say passing distance) or ten times the same researchers did the the same study or (less obviously) a researcher focusing on ten different response variables in the same study[35]. Now suppose that one of two things happens with these ten unique response variables – we just report one of them (any could

[35]Researchers often measure multiple related response variables on the same subjects while they are conducting a study, so these would not meet the "independent studies" assumption that is used here, but we can start with the assumption of independent results across these responses as the math is easier and the results are conservative. You can consult a statistician for other related approaches that incorporate the dependency of the different responses.

be used, but suppose the first one is selected) OR we only report the one of the ten with the smallest p-value. This would correspond to reporting the results of *a* study or to reporting the "most significant" of ten tries at (or in) the same study – either because nine researchers decided not to publish/ got their papers rejected by journals or because one researcher put the other nine results into their drawer of "failed studies" and never even tried to report the results.

The following code generates one realization of this process to explore both the p-values that are created and the estimated differences. To simulate new observations with the null hypothesis true, there are two new ideas to consider. First, we need to fit a model that makes the means the same in both groups. This is called the "mean-only" model and is implemented with `lm(y~1, data=...)`, with the `~1` indicating that no predictor variable is used and that a common mean is considered for all observations. Note that this notation also works in the `favstats` function to get summary statistics for the response variable without splitting it apart based on a grouping variable. In the $n = 30$ passing distance data set, the mean of all the observations is 116.04 cm and this estimate is present in the `(Intercept)` row in the `lm_commonmean` model summary.

```
lm_commonmean <- lm(Distance ~ 1, data = ddsub)
summary(lm_commonmean)
```

```
##
## Call:
## lm(formula = Distance ~ 1, data = ddsub)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -108.038  -17.038   -0.038   16.962  128.962
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 116.0379     0.7361   157.6   <2e-16
##
## Residual standard error: 29.77 on 1635 degrees of freedom
```

```
favstats(Distance ~ 1, data = ddsub)
```

```
##   1 min Q1 median  Q3 max     mean       sd    n missing
## 1 1   8 99    116 133 245 116.0379 29.77388 1636       0
```

The second new R code needed is the `simulate` function that can be applied to `lm`-objects; it generates a new data set that contains the same number of observations as the original one but assumes that all the aspects of the estimated model (mean(s), variance, and normal distributions) are true to generate the new observations. In this situation that implies generating new observations with the same mean (116.04) and standard deviation (29.77, also found as the "residual standard error" in the model summary). The new responses are stored in `SimDistance` in `ddsub` and then plotted in Figure 2.18.

The following code chunk generates one run through generating ten data sets as the loop works through the index `c`, simulates a new set of responses (`ddsub$SimDistance`), fits a model that explores the difference in the means of the two groups (`lm_sim`), and extracts the ten p-values (stored in `pval10`) and estimated difference in the means (stored in `diff10`). The smallest p-value of the ten p-values (`min(pval10)`) is 0.00576. By finding the value of `diff10` where `pval10` is equal to (`==`) the `min(pval10)`, the estimated difference in the means from the simulated responses that produced the smallest p-value can be extracted. The difference was -4.17 here. As in the previous initial explorations of permutations, this is just one realization of this process and it needs to be repeated many times to study the impacts of using (1) the first realization of the responses to estimate the difference and p-value and (2) the result with the smallest p-value from ten different realizations of the responses to estimate the difference and p-value. In the following code, we added

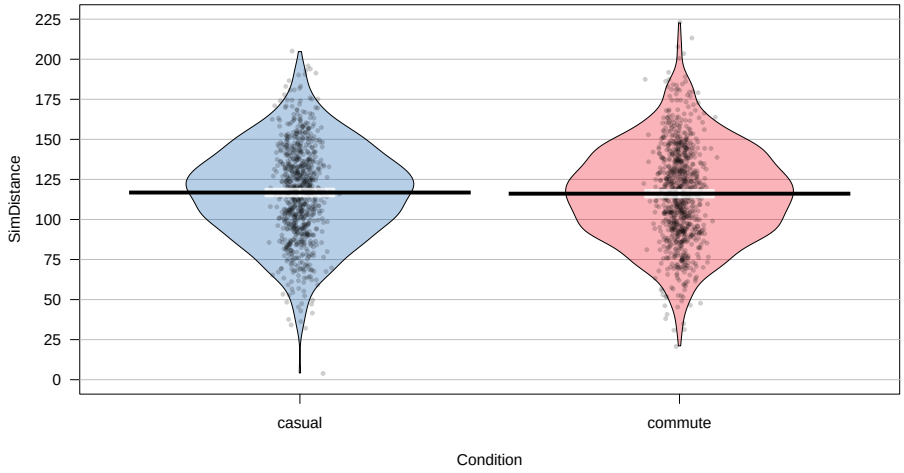

Figure 2.18: Pirate-plot of a simulated data set that assumes the same mean for both groups. The means in the two groups are very similar.

octothorpes (#)[36] and then some text to explain what is being calculated. In computer code, octothorpes provide a way of adding comments that tell the software (here R) to ignore any text after a "#" on a given line. In the color version of the text, comments are even more clearly distinguished.

```
#For one iteration through generating 10 data sets:
  diff10 <- pval10 <- matrix(NA, nrow=10) #Create empty vectors to store 10 results
  set.seed(222)
  #Create 10 data sets, keep estimated differences and p-values in diff10 and pval10
  for (c in (1:10)){
    ddsub$SimDistance <- simulate(lm_commonmean)[[1]]
    #Estimate two group model using simulated responses
    lm_sim <- lm(SimDistance ~ Condition, data = ddsub)
    diff10[c] <- coef(lm_sim)[2]
    pval10[c] <- summary(lm_sim)$coef[2,4]
  }

tibble(pval10, diff10)
```

```
## # A tibble: 10 x 2
##    pval10[,1] diff10[,1]
##         <dbl>      <dbl>
##  1    0.735      -0.492
##  2    0.326       1.44
##  3    0.158      -2.06
##  4    0.265      -1.66
##  5    0.153       2.09
##  6    0.00576    -4.17
##  7    0.915       0.160
##  8    0.313      -1.50
```

[36] You can correctly call octothorpes *number* symbols or, in the twitter verse, *hashtags*. For more on this symbol, see "http://blog.dictionary.com/octothorpe/". Even after reading this, I call them number symbols.

```
##  9    0.983       0.0307
## 10    0.268      -1.69
```

```
min(pval10) #Smallest of 10 p-values
```

```
## [1] 0.005764602
```

```
diff10[pval10 == min(pval10)] #Estimated difference for data set with smallest p-value
```

```
## [1] -4.170526
```

In these results, the first data set shows little evidence against the null hypothesis with a p-value of 0.735 and an estimated difference of -0.49. But if you repeat this process and focus just on the "top" p-value result, you think that there is moderate evidence against the null hypothesis with a p-value from the sixth data set due to its p-value of 0.0057. Remember that these are all data sets simulated with the null hypothesis being true, so we should not reject the null hypothesis. But we would expect an occasional false detection (Type I error – rejecting the null hypothesis when it is true) due to sampling variability in the data sets. But by exploring many results and selecting a single result from that suite of results (and not accounting for that selection process in the results), there is a clear issue with exaggerating the strength of evidence. While not obvious yet, we also create an issue with the estimated mean difference in the groups that is demonstrated below.

To fully explore the impacts of either the office drawer or publication bias (they basically have the same impacts on published results even though they are different mechanisms), this process must be repeated many times. The code is a bit more complex here, as the previous code that created ten data sets needs to be replicated $B = 1{,}000$ times and four sets of results stored (estimated mean differences and p-values for the first data set and the smallest p-value one). This involves a loop that is very similar to our permutation loop but with more activity inside that loop, with the code for generating and extracting the realization of ten results repeated B times. Figure 2.19 contains the results for the simulation study. In the left plot that contains the p-values we can immediately see some important differences in the distribution of p-values. In the "first" result, the p-values are evenly spread from 0 to 1 – this is what happens when the null hypothesis is true and you simulate from that scenario one time and track the p-values. A good testing method should make a mistake at the α-level at a rate around α (a 5% significance level test should make a mistake 5% of the time). If the p-values are evenly spread from 0 to 1, then about 0.05 will be between 0 and 0.05 (think of areas in rectangles with a height of 1 where the total area from 0 to 1 has to add up to 1). But when a researcher focuses only on the top result of ten, then the p-value distribution is smashed toward 0. Using `favstats` on each distribution of p-values shows that the median for the p-values from taking the first result is around 0.5 but for taking the minimum of ten results, the median p-value is 0.065. So half the results are at the "moderate" evidence level or better when selection of results is included. This gets even worse as more results are explored but seems quite problematic here.

The estimated difference in the means also presents an interesting story. When just reporting the first result, the distribution of the estimated means in panel b of Figure 2.19 shows a symmetric distribution that is centered around 0 with results extending just past $\pm$ 4 in each tail. When selection of results is included, only more extreme estimated differences are considered and no results close to 0 are even reported. There are two modes here around $\pm$ 2.5 and multiple results close to $\pm$ 5 are observed. Interestingly, the mean of both distributions is close to 0 so both are "unbiased" [37] estimators but the distribution for the estimated difference from the selected "top" result is clearly flawed and would not give correct inferences for differences when the null hypothesis is correct. If a one-sided test had been employed, the selection of the top result would result is a clearly biased estimator as only one of the two modes would be selected. The presentation of these results is a great example of why pirate-plots are better than boxplots as a boxplot of these results would not allow the viewer to notice the two distinct groups of results.

[37] An unbiased estimator is a statistic that is on average equal to the population parameter.

```
# Simulation study of generating 10 data sets and either using the first
# or "best p-value" result:
set.seed(1234)

B <- 1000 # # of simulations
# To store results
Diffmeans <- pvalues <- Diffmeans_Min <- pvalues_Min <- matrix(NA, nrow=B)
for (b in (1:B)){ #Simulation study loop to repeat process B times
  # Create empty vectors to store 10 results for each b
  diff10 <- pval10 <- matrix(NA, nrow = 10)
  for (c in (1:10)){ #Loop to create 10 data sets and extract results
    ddsub$SimDistance <- simulate(lm_commonmean)[[1]]
    # Estimate two group model using simulated responses
    lm_sim <- lm(SimDistance ~ Condition, data = ddsub)
    diff10[c] <- coef(lm_sim)[2]
    pval10[c] <- summary(lm_sim)$coef[2,4]
  }

  pvalues[b] <- pval10[1] #Store first result p-value
  Diffmeans[b] <- diff10[1] #Store first result estimated difference

  pvalues_Min[b] <- min(pval10) #Store smallest p-value
  Diffmeans_Min[b] <- diff10[pval10 == min(pval10)] #Store est. diff of smallest p-value

}

#Put results together
results <- tibble(pvalue_results = c(pvalues,pvalues_Min),
                  Diffmeans_results = c(Diffmeans, Diffmeans_Min),
                  Scenario = rep(c("First", "Min"), each = B))

par(mfrow=c(1,2)) #Plot results
pirateplot(pvalue_results ~ Scenario, data = results, inf.f.o = 0, inf.b.o = 0,
           avg.line.o = 0, main = "(a) P-value results")
abline(h = 0.05, lwd = 2, col = "red", lty = 2)
pirateplot(Diffmeans_results ~ Scenario, data = results, inf.f.o = 0, inf.b.o = 0,
           avg.line.o = 0, main = "(b) Estimated difference in mean results")
```

```
#Numerical summaries of results
favstats(pvalue_results ~ Scenario, data = results)
```

```
##   Scenario          min         Q1    median        Q3       max       mean
## 1    First 0.0017051496 0.27075755 0.5234412 0.7784957 0.9995293 0.51899179
## 2      Min 0.0005727895 0.02718018 0.0646370 0.1273880 0.5830232 0.09156364
##           sd    n missing
## 1 0.28823469 1000       0
## 2 0.08611836 1000       0
```

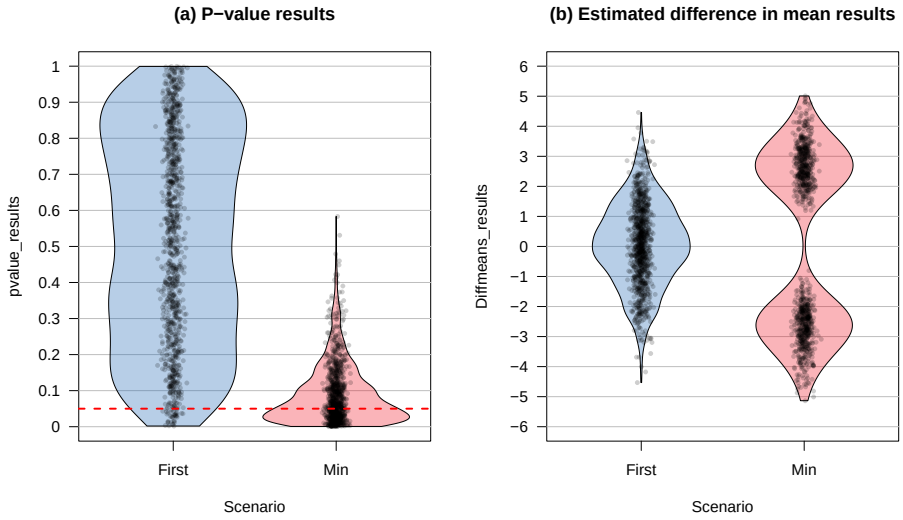

Figure 2.19: Pirate-plot of a simulation study results. Panel (a) contains the $B = 1{,}000$ p-values and (b) contains the B=1,000 estimated differences in the means. Note that the estimated means and confidence intervals normally present in pirate-plots are suppressed here with `inf.f.o = 0, inf.b.o = 0, avg.line.o = 0` because these plots are being used to summarize simulation results instead of an original data set.

```
favstats(Diffmeans_results ~ Scenario, data = results)
```

```
##   Scenario       min         Q1     median       Q3      max       mean
## 1    First -4.531864 -0.8424604 0.07360378 1.002228 4.458951 0.05411473
## 2      Min -5.136510 -2.6857436 1.24042295 2.736930 5.011190 0.03539750
##         sd    n missing
## 1 1.392940 1000       0
## 2 2.874454 1000       0
```

Generally, the challenge in this situation is that if you perform many tests (ten were the focus before) at the same time (instead of just one test), you inflate the Type I error rate across the tests. We can define the ***family-wise error rate*** as the probability that at least one error is made on a set of tests or, more compactly, Pr(At least 1 error is made) where Pr() is the probability of an event occurring. The family-wise error is meant to capture the overall situation in terms of measuring the likelihood of making a mistake if we consider many tests, each with some chance of making their own mistake, and focus on how often we make at least one error when we do many tests. A quick probability calculation shows the magnitude of the problem. If we start with a 5% significance level test, then Pr(Type I error on one test) = 0.05 and the Pr(no errors made on one test) = 0.95, by definition. This is our standard hypothesis testing situation. Now, suppose we have m independent tests, then

$$\begin{aligned}&\Pr(\text{make at least 1 Type I error given all null hypotheses are true})\\&= 1 - \Pr(\text{no errors made})\\&= 1 - 0.95^m.\end{aligned}$$

Figure 2.20 shows how the probability of having at least one false detection grows rapidly with the number of tests, m. The plot stops at 100 tests since it is effectively a 100% chance of at least one false detection. It might seem like doing 100 tests is a lot, but, as mentioned before, some researchers consider situations where millions of tests are considered. Researchers want to make sure that when they report a "significant" result that it is really likely to be a real result and will show up as a difference in the next data set they collect.

Some researchers are now collecting multiple data sets to use in a single study and using one data set to identify interesting results and then using a validation or test data set that they withheld from initial analysis to try to verify that the first results are also present in that second data set. This also has problems but the only way to develop an understanding of a process is to look across a suite of studies and learn from that accumulation of evidence. This is a good start but needs to be coupled with complete reporting of all results, even those that have p-values larger than 0.05 to avoid the bias identified in the previous simulation study.

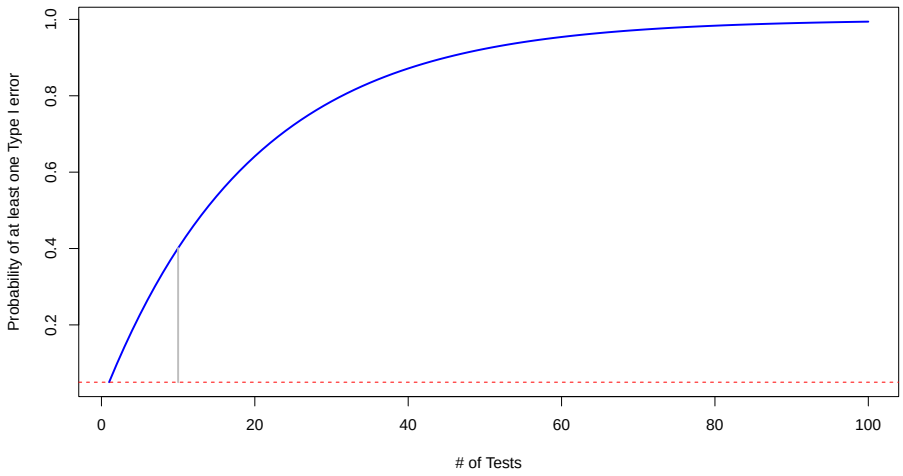

Figure 2.20: Plot of family-wise error rate (bold solid line) as the number of tests performed increases. Dashed line indicates 0.05 and grey solid line highlights the probability of at least on error on m=10 tests.

All hope is not lost when multiple tests are being considered in the same study or by a researcher and exploring more than one result need not lead to clearly biased and flawed results being reported. To account for multiple testing in the same study/analysis, there are many approaches that adjust results to acknowledge that multiple tests are being considered. A simple approach called the "Bonferroni Correction" [Bland and Altman, 1995] is a good starting point for learning about these methods. It works to control the family-wise error rate of a suite of tests by either dividing α by the number of tests (α/m) or, equivalently and more usefully, multiplying the p-value by the number of tests being considered ($p - value_{adjusted} = p - value \cdot m$ or 1 if $p - value \cdot m > 1$). The "Bonferroni adjusted p-values" are then used as regular p-values to assess evidence against each null hypothesis but now accounting for exploring many of them together. There are some assumptions that this adjustment method makes that make it to generally be a conservative adjustment method. In particular, it assumes that all m tests are independent of each other and that the null hypothesis was true for all m tests conducted. While all p-values should be reported in this situation when considering ten results, the impacts of using a Bonferroni correction are that the resulting p-values are not driving inflated Type I error rates even if the smallest p-value is the main focus of the results. The correction also provides a suggestion of decreasing evidence in the first test result because it is now incorporated in considering ten results instead of one.

The following code repeats the simulation study but with the p-values adjusted for multiple testing within each simulation but does not repeat tracking the estimated differences in the means as this is not impacted by the p-value adjustment process. The `p.adjust` function provides Bonferroni corrections to a vector of p-values (here ten are collected together) using the `bonferroni` method option (`p.adjust(pval10, method="bonferroni")`) and then stores those results. Figure 2.21 shows the results for the first result and minimum result again, but now with these corrections incorporated. The plots may look a bit odd, but in the first data set, so many of the first data sets had p-values that were "large" that they were adjusted to have p-values of 1 (so no evidence against the null once we account for multiple testing). The distribution for the minimum p-value results with adjustment more closely resembles the distribution of the first result

p-values from Figure 2.19, except for some minor clumping up at adjusted p-values of 1.

```
# Simulation study of generating 10 data sets and either using the first
# or "best p-value" result:
set.seed(1234)

B <- 1000 # # of simulations
pvalues <- pvalues_Min <- matrix(NA, nrow = B) #To store results
for (b in (1:B)){ #Simulation study loop to repeat process B times
  # Create empty vectors to store 10 results for each b
  pval10 <- matrix(NA, nrow = 10)
  for (c in (1:10)){ #Loop to create 10 data sets and extract results
    ddsub$SimDistance <- simulate(lm_commonmean)[[1]]
    # Estimate two group model using simulated responses
    lm_sim <- lm(SimDistance ~ Condition, data = ddsub)
    pval10[c] <- summary(lm_sim)$coef[2,4]
  }

  pval10 <- p.adjust(pval10, method = "bonferroni")

  pvalues[b] <- pval10[1] #Store first result adjusted p-value

  pvalues_Min[b] <- min(pval10) #Store smallest adjusted p-value
}

#Put results together
results <- tibble(pvalue_results = c(pvalues, pvalues_Min),
                  Scenario = rep(c("First", "Min"), each=B))

pirateplot(pvalue_results ~ Scenario, data = results, inf.f.o = 0, inf.b.o = 0,
           avg.line.o = 0, main = "P-value results")
abline(h=0.05, lwd=2, col="red", lty=2)
```

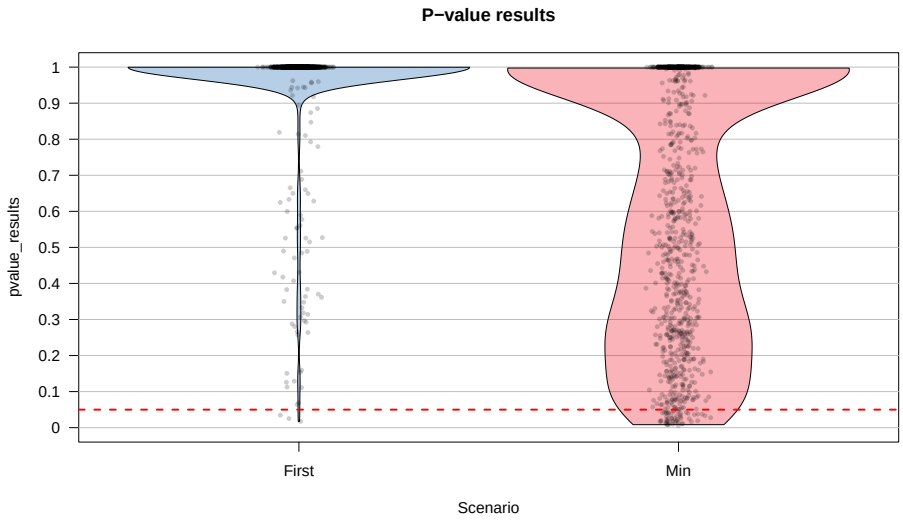

Figure 2.21: Pirate-plot of a simulation study results of p-values with Bonferroni correction.

By applying the `pdata` function to the two groups of results, we can directly assess how many of each type ("First" or "Min") resulted in p-values less than 0.05. It ends up that if we adjust for ten tests and just focus on the first result, it is really hard to find moderate or strong evidence against the null hypothesis as only 3 in 1,000 results had adjusted p-values less than 0.05. When the focus is on the "best" (or minimum) p-value result when ten are considered and adjustments are made, 52 out of 1,000 results (0.052) show at least moderate evidence against the null hypothesis. This is the rate we would expect from a well-behaved hypothesis test when the null hypothesis is true – that we would only make a mistake 5% of the time when α is 0.05.

```
#Numerical summaries of results
favstats(pvalue_results ~ Scenario, data = results)
```

```
##   Scenario         min        Q1  median Q3 max      mean        sd    n missing
## 1    First 0.017051496 1.0000000 1.00000  1   1 0.9628911 0.1502805 1000       0
## 2      Min 0.005727895 0.2718018 0.64637  1   1 0.6212932 0.3597701 1000       0
```

```
#Proportion of simulations with adjusted p-values less than 0.05
pdata(pvalue_results ~ Scenario, data = results, .05, lower.tail = T)
```

```
##   Scenario pdata_v
## 1    First   0.003
## 2      Min   0.052
```

So adjusting for multiple testing is suggested when multiple tests are being considered "simultaneously". The Bonferroni adjustment is easy but also crude and can be conservative in applications, especially when the number of tests grows very large (think of multiplying all your p-values by m=1,000,000). So other approaches are considered in situations with many tests (there are six other options in the `p.adjust` function and other functions for doing similar things in R) and there are other approaches that are customized for particular situations with one example discussed in Chapter **??**. The biggest lesson as a statistics student to take from this is that all results are of interest and should be reported and that adjustment of p-values should be considered in studies where many results are being considered. If you are reading results that seem to have walked discretely around these issues you should be suspicious of the real strength of their evidence.

While it wasn't used here, the same general code used to explore this multiple testing issue could be used to explore the power of a particular procedure. If simulations were created from a model with a difference in the means in the groups, then the null hypothesis would have been false and the rate of correctly rejecting the null hypothesis could be studied. The rate of correct rejections is the *power* of a procedure for a chosen version of a true alternative hypothesis (there are many ways to have it be true and you have to choose one to study power) and simply switching the model being simulated from would allow that to be explored. We could also use similar code to compare the power and Type I error rates of parametric versus permutation procedures or to explore situations where an assumption is not true. The steps would be similar – decide on what you need to simulate from and track a quantity of interest across repeated simulated data sets.

2.9 Confidence intervals and bootstrapping

Up to this point the focus has been on hypotheses, p-values, and estimates of the size of differences. But so far this has not explored inference techniques for the size of the difference. ***Confidence intervals*** provide an interval where we are ___% ***confident*** that the true parameter lies. The idea of "confidence" is that if we repeated randomly sampling from the same population and made a similar confidence interval, the collection of all these confidence intervals would contain the true parameter at the specified confidence level (usually 95%). We only get to make one interval and so it either has the true parameter in it or not, and we don't know the truth in real situations.

Confidence intervals can be constructed with parametric and a nonparametric approaches. The nonparametric approach will be using what is called ***bootstrapping*** and draws its name from "pull yourself up by your bootstraps" where you improve your situation based on your own efforts. In statistics, we make our situation or inferences better by re-using the observations we have by assuming that the sample represents the population. Since each observation represents other similar observations in the population that we didn't get to measure, if we ***sample with replacement*** to generate a new data set of size n from our data set (also of size n) it mimics the process of taking repeated random samples of size n from our population of interest. This process also ends up giving us useful sampling distributions of statistics even when our standard normality assumption is violated, similar to what we encountered in the permutation tests. Bootstrapping

is especially useful in situations where we are interested in statistics other than the mean (say we want a confidence interval for a median or a standard deviation) or when we consider functions of more than one parameter and don't want to derive the distribution of the statistic (say the difference in two medians). Here, bootstrapping is used to provide more trustworthy inferences when some of our assumptions (especially normality) might be violated for our parametric confidence interval procedure.

To perform bootstrapping, the `resample` function from the `mosaic` package will be used. We can apply this function to a data set and get a new version of the data set by sampling new observations *with replacement* from the original one[38]. The new, bootstrapped version of the data set (called `dsample_BTS` below) contains a new variable called `orig.id` which is the number of the subject from the original data set. By summarizing how often each of these id's occurred in a bootstrapped data set, we can see how the re-sampling works. The `table` function will count up how many times each observation was used in the bootstrap sample, providing a row with the id followed by a row with the count[39]. In the first bootstrap sample shown, the 1^{st}, 14^{th}, and 26^{th} observations were sampled twice, the 9^{th} and 28^{th} observations were sampled four times, and the 4^{th}, 5^{th}, 6^{th}, and many others were not sampled at all. Bootstrap sampling thus picks some observations multiple times and to do that it has to ignore some[40] observations.

```
set.seed(406)
dsample_BTS <- resample(dsample)
```

```
table(as.numeric(dsample_BTS$orig.id))
```

```
##
##  1  2  3  7  8  9 10 11 12 13 14 16 18 19 23 24 25 26 27 28 30
##  2  1  1  1  1  4  1  1  1  1  2  1  1  1  1  1  1  2  1  4  1
```

Like in permutations, one randomization isn't enough. A second bootstrap sample is also provided to help you get a sense of what bootstrap data sets contain. It did not select observations two through five but did select eight others more than once. You can see other variations in the resulting re-sampling of subjects with the most sampled observation used four times. With $n = 30$, the the chance of selecting any observation for any slot in the new data set is $1/30$ and the expected or mean number of appearances we expect to see for an observation is the number of random draws times the probably of selection on each so $30 * 1/30 = 1$. So we expect to see each observation in the bootstrap sample on average once but random variability in the samples then creates the possibility of seeing it more than once or not all.

```
dsample_BTS2 <- resample(dsample)
table(as.numeric(dsample_BTS2$orig.id))
```

```
##
##  1  6  7  8  9 10 11 12 13 16 17 20 22 23 24 25 26 28 30
##  2  2  1  1  2  1  4  1  3  1  1  1  2  2  1  1  2  1  1
```

We can use the two results to get an idea of distribution of results in terms of number of times observations might be re-sampled when sampling with replacement and the variation in those results, as shown in Figure 2.22. We could also derive the expected counts for each number of times of re-sampling when we start with all observations having an equal chance and sampling with replacement but this isn't important for using bootstrapping methods.

[38] Some perform bootstrap sampling in this situation by re-sampling within each of the groups. We will discuss using this technique in situations without clearly defined groups, so prefer to sample with replacement from the entire data set. It also directly corresponds to situations where the data came from one large sample and then the grouping variable of interest was measured on the n subjects.

[39] The `as.numeric` function is also used here. It really isn't important but makes sure the output of `table` is sorted by observation number by first converting the *orig.id* variable into a numeric vector.

[40] In any bootstrap sample, about 1/3 of the observations are not used at all.

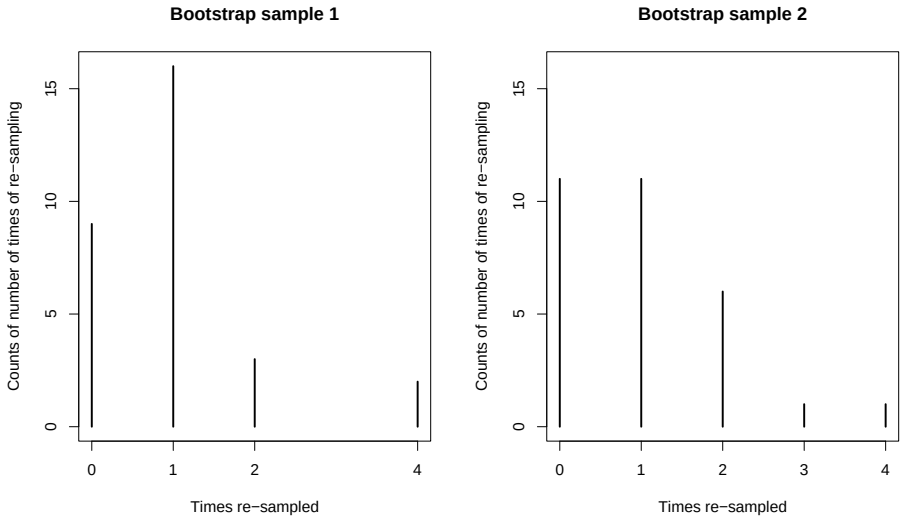

Figure 2.22: Counts of number of times of observation (or not observed for times re-sampled of 0) for two bootstrap samples.

The main point of this exploration was to see that each run of the `resample` function provides a new version of the data set. Repeating this B times using another `for` loop, we will track our quantity of interest, say T, in all these new "data sets" and call those results T^*. The distribution of the bootstrapped T^* statistics tells us about the range of results to expect for the statistic. The middle **% of the T^*'s provides a %** ***bootstrap confidence interval***[41] for the true parameter – here the *difference in the two population means*.

To make this concrete, we can revisit our previous examples, starting with the `dsample` data created before and our interest in comparing the mean passing distances for the *commuter* and *casual* outfit groups in the $n = 30$ stratified random sample that was extracted. The bootstrapping code is very similar to the permutation code except that we apply the `resample` function to the entire data set used in `lm` as opposed to the `shuffle` function that was applied only to the explanatory variable.

```
lm1 <- lm(Distance ~ Condition, data = dsample)
Tobs <- coef(lm1)[2]; Tobs
```

```
## Conditioncommute
##        -25.93333
```

```
B <- 1000
set.seed(1234)
Tstar <- matrix(NA, nrow = B)
for (b in (1:B)){
  lmP <- lm(Distance ~ Condition, data = resample(dsample))
  Tstar[b] <- coef(lmP)[2]
}
```

```
favstats(Tstar)
```

```
##        min        Q1    median        Q3       max      mean        sd     n missing
```

[41] There are actually many ways to use this information to make a confidence interval. We are using the simplest method that is called the "percentile" method.

```
##  -66.96429 -34.57159 -25.65881 -17.12391 17.17857 -25.73641 12.30987 1000       0
```

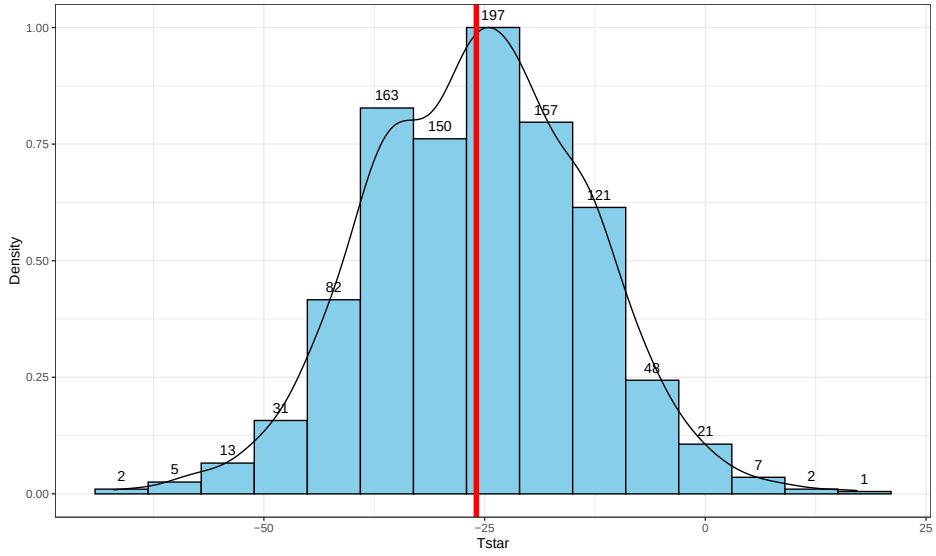

Figure 2.23: Histogram and density curve of bootstrap distributions of difference in sample mean `Distances` with vertical line for the observed difference in the means of -25.933.

```
tibble(Tstar) %>%  ggplot(aes(x = Tstar)) +
  geom_histogram(aes(y = ..ncount..), bins = 15, col = 1, fill = "skyblue",
                 center = 0) +
  stat_bin(aes(y = ..ncount.., label = ..count..), bins = 15,
           geom = "text", vjust=-0.75) +
  geom_density(aes(y = ..scaled..)) + theme_bw() + labs(y = "Density") +
  geom_vline(xintercept = Tobs, col = "red", lwd = 2)
```

In this situation, the observed difference in the mean passing distances is -25.933 cm (*commute* - *casual*), which is the bold vertical line in Figure 2.23. The bootstrap distribution shows the results for the difference in the sample means when fake data sets are re-constructed by sampling from the original data set with replacement. The bootstrap distribution is approximately centered at the observed value (difference in the sample means) and is relatively symmetric.

The permutation distribution in the same situation (Figure 2.10) had a similar shape but was centered at 0. Permutations create sampling distributions based on assuming the null hypothesis is true, which is useful for hypothesis testing. Bootstrapping creates distributions centered at the observed result, which is the sampling distribution "under the alternative" or when no null hypothesis is assumed; bootstrap distributions are useful for generating confidence intervals for the true parameter values.

To create a 95% bootstrap confidence interval for the difference in the true mean distances ($\mu_{\text{commute}} - \mu_{\text{casual}}$), select the middle 95% of results from the bootstrap distribution. Specifically, find the 2.5^{th} percentile and the 97.5^{th} percentile (values that put 2.5 and 97.5% of the results to the left) in the bootstrap distribution, which leaves 95% in the middle for the confidence interval. To find percentiles in a distribution in R, functions are of the form `q[Name of distribution]`, with the function `qt` extracting percentiles from a t-distribution (examples below). From the bootstrap results, use the `qdata` function on the `Tstar` results that contain the bootstrap distribution of the statistic of interest.

```
qdata(Tstar, 0.025)
```

```
##      2.5%
```

```
## -50.0055
```

```
qdata(Tstar, 0.975)
```

```
##     97.5%
## -2.248774
```

These results tell us that the 2.5$^{\text{th}}$ percentile of the bootstrap distribution is at -50.01 cm and the 97.5$^{\text{th}}$ percentile is at -2.249 cm. We can combine these results to provide a 95% confidence for $\mu_{\text{commute}} - \mu_{\text{casaual}}$ that is between -50 and -2.25 cm. This interval is interpreted as with any confidence interval, that we are 95% confident that the difference in the true mean distances (*commute* minus *casual* groups) is between -50 and -2.25 cm. Or we can switch the direction of the comparison and say that we are 95% confident that the difference in the true means is between 2.25 and 50 cm (*casual* minus *commute*). This result would be incorporated into step 5 of the hypothesis testing protocol to accompany discussing the size of the estimated difference in the groups or used as a result of interest in itself. Both percentiles can be obtained in one line of code using:

```
quantiles <- qdata(Tstar, c(0.025,0.975))
```

```
quantiles
```

```
##       2.5%      97.5%
## -50.005502  -2.248774
```

Figure 2.24 displays those same percentiles on the bootstrap distribution residing in `Tstar`.

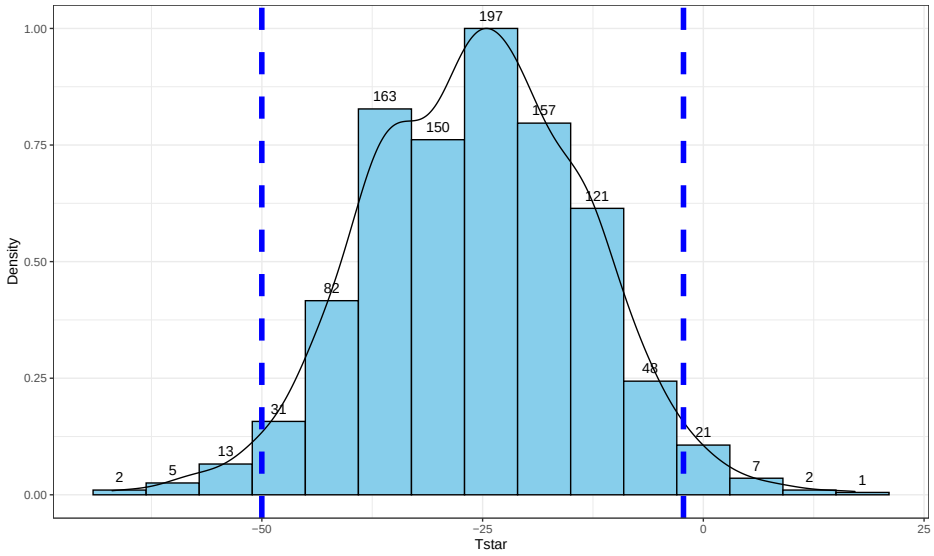

Figure 2.24: Histogram and density curve of bootstrap distribution with 95% bootstrap confidence intervals displayed (bold, dashed vertical lines).

```
tibble(Tstar) %>%  ggplot(aes(x = Tstar)) +
  geom_histogram(aes(y = ..ncount..), bins = 15, col = 1, fill = "skyblue",
                 center = 0) +
  stat_bin(aes(y = ..ncount.., label = ..count..), bins = 15,
           geom = "text", vjust=-0.75) +
```

```
  geom_density(aes(y = ..scaled..)) + theme_bw() + labs(y = "Density") +
  geom_vline(xintercept = quantiles, col = "blue", lwd = 2, lty = 2)
```

Although confidence intervals can exist without referencing hypotheses, we can revisit our previous hypotheses and see what this confidence interval tells us about the test of $H_0 : \mu_{\text{commute}} = \mu_{\text{casual}}$. This null hypothesis is equivalent to testing $H_0 : \mu_{\text{commute}} - \mu_{\text{casual}} = 0$, that the difference in the true means is equal to 0 cm. And the difference in the means was the scale for our confidence interval, which did not contain 0 cm. The 0 cm values is an interesting ***reference value*** for the confidence interval, because here it is the value where the true means are equal to each other (have a difference of 0 cm). In general, if our confidence interval does not contain 0, then it is saying that 0 is not one of the likely values for the difference in the true means at the selected confidence level. This implies that we should reject a claim that they are equal. This provides the same inferences for the hypotheses that we considered previously using both parametric and permutation approaches using a fixed α approach where $\alpha = 1$ - confidence level.

The general summary is that we can use confidence intervals to test hypotheses by assessing whether the reference value under the null hypothesis is in the confidence interval (suggests insufficient evidence against H_0 to reject it, at least at the α level and equivalent to having a p-value larger than α) or outside the confidence interval (sufficient evidence against H_0 to reject it and equivalent to having a p-value that is less than α). P-values are more informative about hypotheses (measure of evidence against the null hypothesis) but confidence intervals are more informative about the size of differences, so both offer useful information and, as shown here, can provide consistent conclusions about hypotheses. But it is best practice to use p-values to assess evidence against null hypotheses and confidence intervals to do inferences for the size of differences.

As in the previous situation, we also want to consider the parametric approach for comparison purposes and to have that method available, especially to help us understand some methods where we will only consider parametric inferences in later chapters. The parametric confidence interval is called the ***equal variance, two-sample t confidence interval*** and additionally assumes that the populations being sampled from are normally distributed instead of just that they have similar shapes in the bootstrap approach. The parametric method leads to using a t-distribution to form the interval with the degrees of freedom for the t-distribution of $n - 2$ although we can obtain it without direct reference to this distribution using the `confint` function applied to the `lm` model. This function generates two confidence intervals and the one in the second row is the one we are interested as it pertains to the difference in the true means of the two groups. The parametric 95% confidence interval here is from -51.6 to -0.26 cm which is a bit different in width from the nonparametric bootstrap interval that was from -50 and -2.25 cm.

```
confint(lm1)
```

```
##                       2.5 %      97.5 %
## (Intercept)       117.64498 153.9550243
## Conditioncommute -51.60841  -0.2582517
```

The bootstrap interval was narrower by almost 4 cm and its upper limit was much further from 0. The bootstrap CI can vary depending on the random number seed used and additional runs of the code produced intervals of (-49.6, -2.8), (-48.3, -2.5), and (-50.9, -1.1) so the differences between the parametric and nonparametric approaches was not just due to an unusual bootstrap distribution. It is not entirely clear why the two intervals differ but there are slightly more results in the left tail of Figure 2.24 than in the right tail and this shifts the 95% confidence slightly away from 0 as compared to the parametric approach. All intervals have the same interpretation, only the methods for calculating the intervals and the assumptions differ. Specifically, the bootstrap interval can tolerate different distribution shapes other than normal and still provide intervals that work well[42]. The other assumptions are all the same as for the hypothesis test,

[42]When hypothesis tests "work well" they have high power to detect differences while having Type I error rates that are close to what we choose *a priori*. When confidence intervals "work well", they contain the true parameter value in repeated random samples at around the selected confidence level, which is called the ***coverage rate***.

where we continue to assume that we have independent observations with equal variances for the two groups and maintain concerns about inferences here due to the violation of independence in these responses.

The formula that `lm` is using to calculate the parametric ***equal variance, two-sample t-based confidence interval*** is:

$$\bar{x}_1 - \bar{x}_2 \mp t^*_{df} s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$$

In this situation, the df is again $n_1 + n_2 - 2$ (the total sample size - 2) and $s_p = \sqrt{\frac{(n_1-1)s_1^2+(n_2-1)s_2^2}{n_1+n_2-2}}$. The t^*_{df} is a multiplier that comes from finding the percentile from the t-distribution that puts $C\%$ in the middle of the distribution with C being the confidence level. It is important to note that this t^* has nothing to do with the previous test statistic t. It is confusing and students first engaging these two options often happily take the result from a test statistic calculation and use it for a multiplier in a t-based confidence interval – try to focus on which t you are interested in before you use either. Figure 2.25 shows the t-distribution with 28 degrees of freedom and the cut-offs that put 95% of the area in the middle.

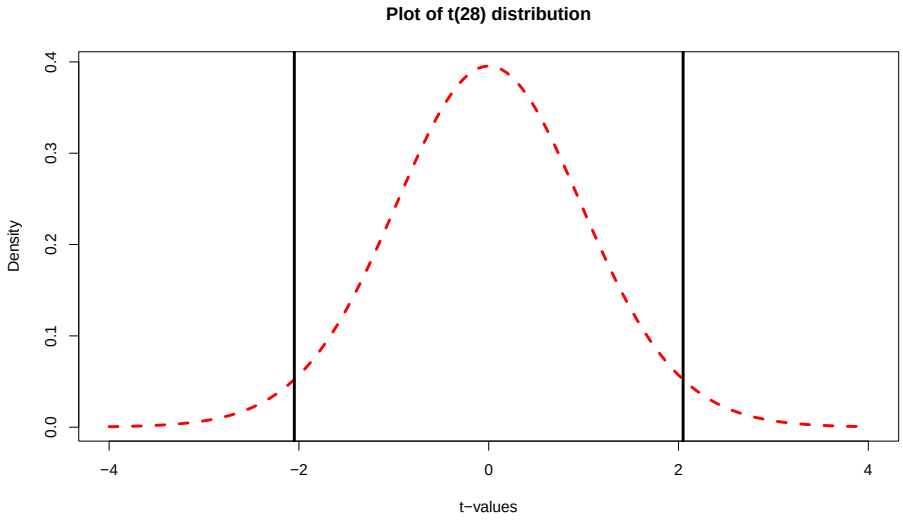

Figure 2.25: Plot of $t(28)$ with cut-offs for putting 95% of distribution in the middle that delineate the t^* multiplier to make a 95% confidence interval.

For 95% confidence intervals, the multiplier is going to be close to 2 and anything else is a likely indication of a mistake. We can use R to get the multipliers for confidence intervals using the `qt` function in a similar fashion to how `qdata` was used in the bootstrap results, except that this new value must be used in the previous confidence interval formula. This function produces values for requested percentiles, so if we want to put 95% in the middle, we place 2.5% in each tail of the distribution and need to request the 97.5^{th} percentile. Because the t-distribution is always symmetric around 0, we merely need to look up the value for the 97.5^{th} percentile and know that the multiplier for the 2.5^{th} percentile is just $-t^*$. The t^* multiplier to form the confidence interval is 2.0484 for a 95% confidence interval when the $df = 28$ based on the results from `qt`:

```
qt(0.975, df=28)
```

```
## [1] 2.048407
```

Note that the 2.5^{th} percentile is just the negative of this value due to symmetry and the real source of the minus in the minus/plus in the formula for the confidence interval.

```
qt(0.025, df=28)
```

```
## [1] -2.048407
```

We can also re-write the confidence interval formula into a slightly more general forms as

$$\bar{x}_1 - \bar{x}_2 \mp t^*_{df} SE_{\bar{x}_1 - \bar{x}_2} \quad \text{OR} \quad \bar{x}_1 - \bar{x}_2 \mp ME$$

where $SE_{\bar{x}_1 - \bar{x}_2} = s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$ and $ME = t^*_{df} SE_{\bar{x}_1 - \bar{x}_2}$. The SE is available in the `lm` model `summary` for the line related to the difference in groups in the "Std. Error" column. In some situations, researchers will report the ***standard error*** (SE) or ***margin of error*** (ME) as a method of quantifying the uncertainty in a statistic. The SE is an estimate of the standard deviation of the statistic (here $\bar{x}_1 - \bar{x}_2$) and the ME is an estimate of the precision of a statistic that can be used to directly form a confidence interval. The ME depends on the choice of confidence level although 95% is almost always selected.

To finish this example, R can be used to help you do calculations much like a calculator except with much more power "under the hood". You have to make sure you are careful with using `( )` to group items and remember that the asterisk (*) is used for multiplication. We need the pertinent information which is available from the `favstats` output repeated below to calculate the confidence interval "by hand"[43] using R.

```
favstats(Distance ~ Condition, data = dsample)
```

```
##   Condition min    Q1 median    Q3 max     mean       sd  n missing
## 1    casual  72 112.5    143 154.5 208 135.8000 39.36133 15       0
## 2   commute  60  88.5    113 123.0 168 109.8667 28.41244 15       0
```

Start with typing the following command to calculate s_p and store it in a variable named `sp`:

```
sp <- sqrt(((15-1)*(39.36133^2)+(15-1)*(28.4124^2))/(15+15-2))
sp
```

```
## [1] 34.32622
```

Then calculate the confidence interval that `confint` provided using:

```
109.8667-135.8 + c(-1,1)*qt(0.975, df=28)*sp*sqrt(1/15+1/15)
```

```
## [1] -51.6083698  -0.2582302
```

Or using the information from the model summary:

```
-25.933 + c(-1,1)*qt(0.975, df=28)*12.534
```

```
## [1] -51.6077351  -0.2582649
```

The previous results all use `c(-1, 1)` times the margin of error to subtract and add the ME to the difference in the sample means ($109.8667 - 135.8$), which generates the lower and then upper bounds of the confidence interval. If desired, we can also use just the last portion of the calculation to find the margin of error, which is 25.675 here.

[43] We will often use this term to indicate perform a calculation using the `favstats` results – not that you need to go back to the data set and calculate the means and standard deviations yourself.

```
qt(0.975, df=28)*sp*sqrt(1/15+1/15)
```

```
## [1] 25.67507
```

For the entire $n = 1,636$ data set for these two groups, the results are obtained using the following code. The estimated difference in the means is -3 cm (*commute* minus *casual*). The t-based 95% confidence interval is from -5.89 to -0.11.

```
lm_all <- lm(Distance ~ Condition, data = ddsub)
confint(lm_all) #Parametric 95% CI
```

```
##                       2.5 %      97.5 %
## (Intercept)      115.520697 119.7013823
## Conditioncommute  -5.891248  -0.1149621
```

The bootstrap 95% confidence interval is from -5.82 to -0.076. With this large data set, the differences between parametric and permutation approaches decrease and they essentially equivalent here. The bootstrap distribution (not displayed) for the differences in the sample means is relatively symmetric and centered around the estimated difference of -3 cm. So using all the observations we would be 95% confident that the true mean difference in overtake distances (*commute* - *casual*) is between -5.89 and -0.11 cm, providing additional information about the estimated difference in the sample means of -3 cm.

```
Tobs <- coef(lm_all)[2]; Tobs
```

```
## Conditioncommute
##        -3.003105
```

```
B <- 1000
set.seed(1234)
Tstar <- matrix(NA, nrow = B)
for (b in (1:B)){
  lmP <- lm(Distance ~ Condition, data = resample(ddsub))
  Tstar[b] <- coef(lmP)[2]
}
```

```
qdata(Tstar, c(0.025, 0.975))
```

```
##        2.5%       97.5%
## -5.81626474 -0.07606663
```

2.10 Bootstrap confidence intervals for difference in GPAs

We can now apply the new confidence interval methods on the STAT 217 grade data. This time we start with the parametric 95% confidence interval "by hand" in R and then use `lm` to verify our result. The `favstats` output provides us with the required information to calculate the confidence interval, with the estimated difference in the sample mean GPAs of $3.338 - 3.0886 = 0.2494$:

```
favstats(GPA~Sex, data=s217)
```

```
##   Sex  min  Q1 median   Q3 max     mean        sd  n missing
## 1   F 2.50 3.1  3.400 3.70   4 3.338378 0.4074549 37       0
```

```
## 2   M 1.96 2.8  3.175 3.46   4 3.088571 0.4151789 42       0
```

The df are $37 + 42 - 2 = 77$. Using the SDs from the two groups and their sample sizes, we can calculate s_p:

```
sp <- sqrt(((37-1)*(0.4075^2)+(42-1)*(0.41518^2))/(37+42-2))
sp
```

```
## [1] 0.4116072
```

The margin of error is:

```
qt(0.975, df=77)*sp*sqrt(1/37+1/42)
```

```
## [1] 0.1847982
```

All together, the 95% confidence interval is:

```
3.338-3.0886+c(-1,1)*qt(0.975, df=77)*sp*sqrt(1/37+1/42)
```

```
## [1] 0.0646018 0.4341982
```

So we are 95% confident that the difference in the true mean GPAs between females and males (females minus males) is between 0.065 and 0.434 GPA points. We get a similar result from `confint` on `lm`, except that `lm` switched the direction of the comparison from what was done "by hand" above, with the estimated mean difference of -0.25 GPA points (male - female) and similarly switched CI:

```
lm_GPA <- lm(GPA ~ Sex, data = s217)
summary(lm_GPA)
```

```
##
## Call:
## lm(formula = GPA ~ Sex, data = s217)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.12857 -0.28857  0.06162  0.36162  0.91143
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.33838    0.06766  49.337  < 2e-16
## SexM        -0.24981    0.09280  -2.692  0.00871
##
## Residual standard error: 0.4116 on 77 degrees of freedom
## Multiple R-squared:  0.08601,    Adjusted R-squared:  0.07414
## F-statistic: 7.246 on 1 and 77 DF,  p-value: 0.008713
```

```
confint(lm_GPA)
```

```
##                 2.5 %      97.5 %
## (Intercept)  3.2036416  3.47311517
## SexM        -0.4345955 -0.06501838
```

Note that we can easily switch to 90% or 99% confidence intervals by simply changing the percentile in `qt` or changing the `level` option in the `confint` function.

```
qt(0.95, df = 77) #For 90% confidence and 77 df
```

```
## [1] 1.664885
```

```
qt(0.995, df = 77) #For 99% confidence and 77 df
```

```
## [1] 2.641198
```

```
confint(lm_GPA, level = 0.9) #90% confidence interval
```

```
##                   5 %        95 %
## (Intercept)  3.2257252  3.45103159
## SexM        -0.4043084 -0.09530553
```

```
confint(lm_GPA, level = 0.99) #99% confidence interval
```

```
##                 0.5 %       99.5 %
## (Intercept)  3.1596636  3.517093108
## SexM        -0.4949103 -0.004703598
```

As a review of some basic ideas with confidence intervals make sure you can answer the following questions:

1. What is the impact of increasing the confidence level in this situation?
2. What happens to the width of the confidence interval if the size of the SE increases or decreases?
3. What about increasing the sample size – should that increase or decrease the width of the interval?

All the general results you learned before about impacts to widths of CIs hold in this situation whether we are considering the parametric or bootstrap methods...

To finish this example, we will generate the comparable bootstrap 90% confidence interval using the bootstrap distribution in Figure 2.26.

```
Tobs <- coef(lm_GPA)[2]; Tobs
```

```
##       SexM
## -0.2498069
```

```
B <- 1000
set.seed(1234)
Tstar <- matrix(NA, nrow = B)
for (b in (1:B)){
  lmP <- lm(GPA ~ Sex, data = resample(s217))
  Tstar[b] <- coef(lmP)[2]
}

quantiles <- qdata(Tstar, c(0.05, 0.95))
quantiles
```

```
##          5%         95%
## -0.39290566 -0.09622185
```

The output tells us that the 90% confidence interval is from -0.393 to -0.096 GPA points. The bootstrap distribution with the observed difference in the sample means and these cut-offs is displayed in Figure 2.26 using this code:

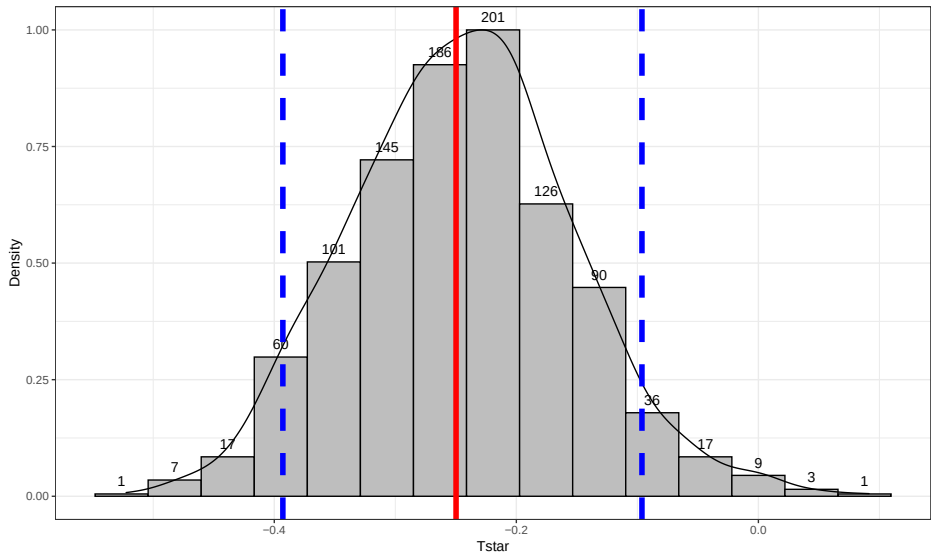

Figure 2.26: Histogram and density curve of bootstrap distribution of difference in sample mean GPAs (male minus female) with observed difference (solid vertical line) and quantiles that delineate the 90% confidence intervals (dashed vertical lines).

```
tibble(Tstar) %>%  ggplot(aes(x = Tstar)) +
  geom_histogram(aes(y = ..ncount..), bins = 15, col = 1, fill = "grey",
                 center = 0) +
  stat_bin(aes(y = ..ncount.., label = ..count..), bins = 15,
           geom = "text", vjust=-0.75) +
  geom_density(aes(y = ..scaled..)) + theme_bw() + labs(y = "Density") +
  geom_vline(xintercept = quantiles, col = "blue", lwd = 2, lty = 2) +
  geom_vline(xintercept = Tobs, col = "red", lwd = 2)
```

In the previous output, the parametric 90% confidence interval is from -0.404 to -0.095, suggesting similar results again from the two approaches. Based on the bootstrap CI, we can say that we are 90% confident that the difference in the true mean GPAs for STAT 217 students is between -0.393 to -0.094 GPA points

(male minus females). This result would be usefully added to step 5 in the 6+ steps of the hypothesis testing protocol with an updated result of:

5. Report and discuss an estimate of the size of the differences, with confidence interval(s) if appropriate.
    - Females were estimated to have a higher mean GPA by 0.25 points (*90% bootstrap confidence interval: 0.094 to 0.393*). This difference of 0.25 on a GPA scale does not seem like a very large difference in the means even though we were able to detect a difference in the groups.

Throughout the text, pay attention to the distinctions between parameters and statistics, focusing on the differences between estimates based on the sample and inferences for the population of interest in the form of the parameters of interest. Remember that statistics are summaries of the sample information and parameters are characteristics of populations (which we rarely know). And that our inferences are limited to the population that we randomly sampled from, if we randomly sampled.

2.11 Chapter summary

In this chapter, we reviewed basic statistical inference methods in the context of a two-sample mean problem using linear models and the `lm` function. You were introduced to using R to do enhanced visualizations (pirate-plots), permutation testing, and generate bootstrap confidence intervals as well as obtaining parametric t-test and confidence intervals. You should have learned how to use a `for` loop for doing the nonparametric inferences and the `lm` and `confint` functions for generating parametric inferences. In the examples considered, the parametric and nonparametric methods provided similar results, suggesting that the assumptions were not too violated for the parametric procedures. When parametric and nonparametric approaches disagree, the nonparametric methods are likely to be more trustworthy since they have less restrictive assumptions but can still make assumptions and can have problems.

When the noted conditions are violated in a hypothesis testing situation, the Type I error rates can be inflated, meaning that we reject the null hypothesis more often than we have allowed to occur by chance. Specifically, we could have a situation where our assumed 5% significance level test might actually reject the null when it is true 20% of the time. If this is occurring, we call a procedure ***liberal*** (it rejects too easily) and if the procedure is liberal, how could we trust a small p-value to be a "real" result and not just an artifact of violating the assumptions of the procedure? Likewise, for confidence intervals we hope that our 95% confidence level procedure, when repeated, will contain the true parameter 95% of the time. If our assumptions are violated, we might actually have an 80% confidence level procedure and it makes it hard to trust the reported results for our observed data set. Statistical inference relies on a belief in the methods underlying our inferences. If we don't trust our assumptions, we shouldn't trust the conclusions to perform the way we want them to. As sample sizes increase and/or violations of conditions lessen, then the procedures will perform better. In Chapter **??**, some new tools for doing diagnostics are introduced to help us assess how and how much those validity conditions are violated.

It is good to review how to report hypothesis test conclusions and compare those for when we have strong, moderate, or weak evidence. Suppose that we are doing parametric inferences with `lm` for differences between groups A and B, are extracting the t-statistics, have 15 degrees of freedom, and obtain the following test statistics and p-values:

- $t_{15} = 3.5$, p-value=0.0016: There is strong evidence against the null hypothesis of no difference in the true means of the response between A and B ($t_{15} = 3.5$, p-value=0.0016), so we would conclude that there is a difference in the true means.
- $t_{15} = 1.75$, p-value=0.0503: There is moderate evidence against the null hypothesis of no difference in the true means of the response between A and B ($t_{15} = 1.75$, p-value=0.0503), so we would conclude that there is likely[44] a difference in the true means.

[44]Note that this modifier is added to note less certainty than when we encounter strong evidence against the null. Also note that someone else might decide that this more like weak evidence against the null and might choose to interpret it as in the "weak" case. In cases that are near boundaries for evidence levels, it becomes difficult to find a universal answer and it is best to report that the evidence is both not strong and not weak and is somewhere in between and let the reader decide what they think

- $t_{15} = 0.75$, p-value=0.232: There is weak evidence against the null hypothesis of no difference in the true means of the response between A and B ($t_{15} = 1.75$, p-value=0.0503), so we would conclude that there is likely not a difference in the true means.

The last conclusion also suggests an action to take when we encounter weak evidence against null hypotheses – we could potentially model the responses using the null model since we couldn't prove it was wrong. We would take this action knowing that we could be wrong, but the "simpler" model that the null hypothesis suggests is often an attractive option in very complex models, such as what we are going to encounter in the coming chapters, especially in Chapters **??** and **??**.

2.12 Summary of important R code

The main components of R code used in this chapter follow with components to modify in lighter and/or ALL CAPS text, remembering that any R packages mentioned need to be installed and loaded for this code to have a chance of working:

- **summary(DATASETNAME)**
  - Provides numerical summaries of all variables in the data set.
- **summary(lm(Y ~ X, data = DATASETNAME))**
  - Provides estimate, SE, test statistic, and p-value for difference in second row of coefficient table.
- **confint(lm(Y ~ X, data = DATASETNAME), level = 0.95)**
  - Provides 95% confidence interval for difference in second row of output.
- **2*pt(abs(Tobs), df = DF, lower.tail = F)**
  - Finds the two-sided test p-value for an observed 2-sample t-test statistic of `Tobs`.
- **hist(DATASETNAME$Y)**
  - Makes a histogram of a variable named `Y` from the data set of interest.
- **boxplot(Y~X, data = DATASETNAME)**
  - Makes a boxplot of a variable named Y for groups in X from the data set.
- **pirateplot(Y~X, data = DATASETNAME, inf.method = "ci", inf.disp = "line")**
  - Requires the `yarrr` package is loaded.
  - Makes a pirate-plot of a variable named Y for groups in X from the data set with estimated means and 95% confidence intervals for each group.
  - Add `theme=2` if the confidence intervals extend outside the density curves and you can't see how far they extend.
- **mean(Y~X, data = DATASETNAME); sd(Y~X, data = DATASETNAME)**
  - This usage of `mean` and `sd` requires the `mosaic` package.
  - Provides the mean and sd of responses of Y for each group described in X.
- **favstats(Y~X, data = DATASETNAME)**
  - Provides numerical summaries of Y by groups described in X.

it means to them. This is complicated by often needing to make decisions about next steps based on p-values where we might choose to focus on the model with a difference or without it.

- **Tobs <- coef(lm(Y~X, data=DATASETNAME))[2]; Tobs**
  B <- 1000
  Tstar <- matrix(NA, nrow = B)
  for (b in (1:B)){
  lmP <- lm(Y ~ shuffle(X), data = DATASETNAME)
  Tstar[b] <- coef(lmP)[2]
  }
  - Code to run a `for` loop to generate 1000 permuted versions of the test statistic using the `shuffle` function and keep track of the results in `Tstar`
- **pdata(Tstar, abs(Tobs), lower.tail = F)[[1]]**
  - Finds the proportion of the permuted test statistics in Tstar that are less than -|Tobs| or greater than |Tobs|, useful for finding the two-sided test p-value.
- **Tobs <- coef(lm(Y~X, data=DATASETNAME))[2]; Tobs**
  B <- 1000
  Tstar <- matrix(NA, nrow = B)
  for (b in (1:B)){
  lmP <- lm(Y ~ X, data = resample(DATASETNAME))
  Tstar[b] <- coef(lmP)[2]
  }
  - Code to run a `for` loop to generate 1000 bootstrapped versions of the data set using the `resample` function and keep track of the results of the statistic in `Tstar`.
- **qdata(Tstar, c(0.025, 0.975))**
  - Provides the values that delineate the middle 95% of the results in the bootstrap distribution (`Tstar`).

2.13 Practice problems

2.1. **Overtake Distance Analysis** The tests for the overtake distance data were performed with two-sided alternatives and so two-sided areas used to find the p-values. Suppose that the researchers expected that the average passing distance would be less (closer) for the commute clothing than for the casual clothing group. Repeat obtaining the permutation-based p-value for the one-sided test for either the full or smaller sample data set. Hint: Your p-value should be just about half of what it was before and in the direction of the alternative.

2.2. **HELP Study Data Analysis** Load the `HELPrct` data set from the `mosaicData` package [Pruim et al., 2021a] (you need to install the `mosaicData` package once to be able to load it). The HELP study was a clinical trial for adult inpatients recruited from a detoxification unit. Patients with no primary care physician were randomly assigned to receive a multidisciplinary assessment and a brief motivational intervention or usual care and various outcomes were observed. Two of the variables in the data set are `sex`, a factor with levels *male* and *female* and `daysanysub` which is the time (in days) to first use of any substance post-detox. We are interested in the difference in mean number of days to first use of any substance post-detox between males and females. There are some missing responses and the following code will produce `favstats` with the missing values and then provide a data set that by applying the `drop_na()` function to the piped data set removes any observations with missing values.

```
library(mosaicData)
data(HELPrct)
HELPrct2 <- HELPrct %>% select(daysanysub, sex) #Just focus on two variables
HELPrct3 <- HELPrct2 %>% drop_na() #Removes subjects (complete rows) with any missing values
favstats(daysanysub ~ sex, data = HELPrct2)
favstats(daysanysub ~ sex, data = HELPrct3)
```

2.2.1. Based on the results provided, how many observations were missing for males and females? Missing values here likely mean that the subjects didn't use any substances post-detox in the time of the study but might have at a later date – the study just didn't run long enough. This is called ***censoring***. What is the problem with the numerical summaries here if the missing responses were all something larger than the largest observation?

2.2.2. Make a pirate-plot and a boxplot of `daysanysub` ~ `sex` using the `HELPrct3` data set created above. Compare the distributions, recommending parametric or nonparametric inferences.

2.2.3. Generate the permutation results and write out the 6+ steps of the hypothesis test.

2.2.4. Interpret the p-value for these results.

2.2.5. Generate the parametric test results using `lm`, reporting the test-statistic, its distribution under the null hypothesis, and compare the p-value to those observed using the permutation approach.

2.2.6. Make and interpret a 95% bootstrap confidence interval for the difference in the means.

Chapter 3

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