Answering questions with data: Lab Manual

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Contents

Preface

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This is the companion lab to our free introductory statistics for undergraduates in psychology textbook, Answering questions with data.

This lab manual involves step by-step tutorials to solve data-analysis problems in software. We use open-data sets that are usually paired with a primary research article.

Each lab is designed to be solved in R & R-studio.

The manual is a free and open resource. See below for more information about copying, making change, or contributing to the lab manual.

0.1 Important notes

This lab manual is based on the OER course package for teaching undergraduate statistics in Psychology, customized for Environmental Science Graduate students by Mallory Barnes. The source code for all material is contained in the GitHub repositories for each, and they are a written in R-markdown, so they are relatively easy to copy and edit. Have Fun!

0.1.1 Attributions

This lab manual was authored by Matt Crump (R exercises), updated by Mallory Barnes.

Labs 6, 7, and 8 were adapted and expanded from Open Stats Labs. Thanks to Open Stats Labs (Dr. Kevin P. McIntyre) for their fantastic work.

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0.1.3 Copying the lab manual

This lab manual was written in R-Studio, using R Markdown, and compiled into a web-book format using the bookdown package.

All of the source code for compiling the book is available in the GitHub repository for this book:

https://github.com/CrumpLab/statisticsLab

In principle, anybody could fork or otherwise download this repository. Load the Rproj file in R-studio, and then compile the entire book. Then, the individual .rmd files for each chapter could be edited for content and style to better suit your needs.

If you want to contribute to this version of the lab manual, you could make pull requests on GitHub, or discuss issues and request on the issues tab.

0.1.4 Acknowledgments

Thanks to the librarians at Brooklyn College of CUNY, especially Miriam Deutch, and Emily Fairey, for their support throughout the process. Thanks to CUNY for supporting OER development, and for the grant we received to develop this work.

Software

0.2 Data

Data files used for the labs are all taken from open data sources. Links are provided for each lab. For convenience, all of the data files are also available here as single files in the github repository for this lab manual

0.2.1 Data Repository

https://github.com/CrumpLab/statisticsLab/tree/master/data

0.2.2 CSV format

All of the data files in .csv format are also available to download as a .zip file

0.3 R

In this course we will be using R as a tool to analyze data, and as a tool to help us gain a better understanding of what our analyses are doing. Throughout each lab we will show you how to use R to solve specific problems, and then you will use the examples to solve homework and lab assignments. R is a very deep programming language, and in many ways we will only be skimming the surface of what R can do. Along the way, there will be many pointers to more advanced techniques that interested students can follow to become experts in using R for data-analysis, and computer programming in general.

R is primarily a computer programming language for statistical analysis. It is *free*, and *open-source* (many people contribute to developing it), and runs on most operating systems. It is a powerful language that can be used for all sorts

of mathematical operations, data-processing, analysis, and graphical display of data. I even used R to write this lab manual. And, I use R all the time for my own research, because it makes data-analyis fast, efficient, transparent, reproducible, and exciting.

Statistics Software

- SPSS
- SAS
- JMP
- R
- Julia
- Matlab

0.3.1 Why R?

There are lots of different options for using computers to analyze data, why use R?. The options all have pros and cons, and can be used in different ways to solve a range of different problems. Some software allows you to load in data, and then analyze the data by clicking different options in a menu. This can sometimes be fast and convenient. For example, once the data is loaded, all you have to do is click a couple buttons to analyse the data! However, many aspects of data-analysis are not so easy. For example, particular analyses often require that the data be formatted in a particular way so that the program can analyze it properly. Often times when a researcher wants to ask a new question of an existing data set, they have to spend time re-formatting the data. If the data is large, then reformatting by hand is very slow, and can lead to errors. Another option, is to use a scripting language to instruct the computer how reformat the data. This is very fast and efficient. R provides the ability to everything all in one place. You can load in data, reformat it any way you like, then anlayze it anyway you like, and create beautiful graphs and tables (publication quality) to display your findings. Once you get the hang of R, it becomes very fast and efficient.

0.3.2 R studio notes and tips

0.3.2.1 Console

When you open up R studio you will see three or four main windows (the placement of each are configurable). In the above example, the bottom left window is the command line (terminal or console) for R. This is used to directly enter commands into R. Once you have entered a command here, press enter to execute the command. The console is useful for entering single lines of code and running them. Oftentimes this occurs when you are learning how to correctly

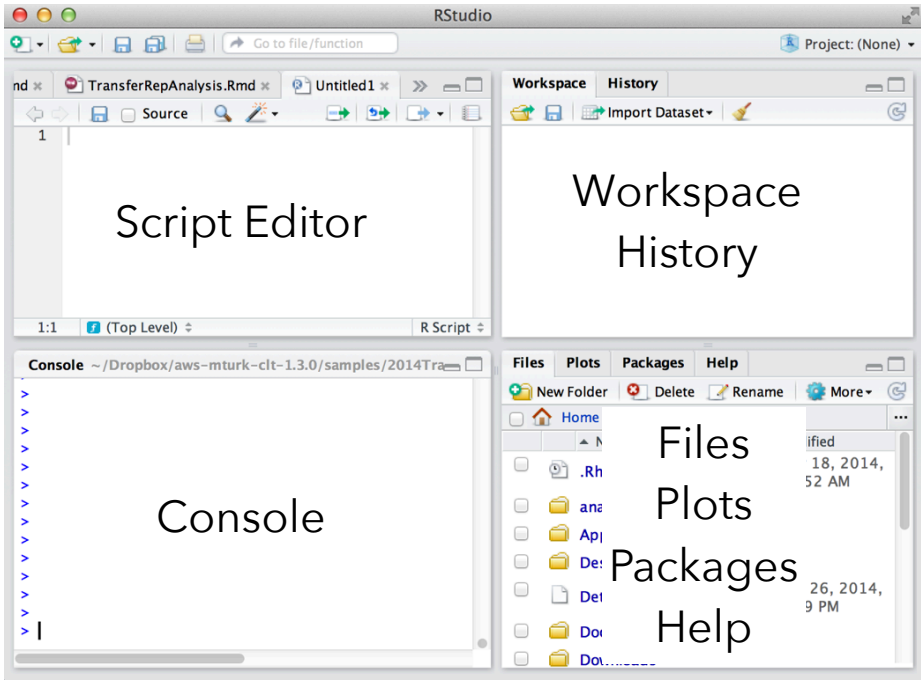


Figure 1: The R-studio workspace

execute a line of code in R. Your first few attempts may be incorrect resulting in errors, but trying out different variations on your code in the command line can help you produce the correct code. Pressing the up arrow while in the console will scroll through the most recently executed lines of code.

0.3.2.2 Script Editor

The top left corner contains the script editor. This is a simple text editor for writing and saving R scripts with many lines. Several tabs can be opened at once, with each tab representing a different R script. R scripts can be saved from the editor (resulting in a .r file). Whole scripts can be run by copy and pasting them into the console and pressing enter. Alternatively, you can highlight portions of the script that you want to run (in the script editor) and press command-enter to automatically run that portion in the console (or press the button for running the current line/section: green arrow pointing right).

0.3.2.3 Workspace and History

The top right panel contains two tabs, one for the workspace and another for history. The workspace lists out all of the variables and functions that are currently loaded in R's memory. You can inspect each of the variables by clicking on them. This is generally only useful for variables that do not contain large amounts of information. The history tab provides a record of the recent commands executed in the console.

0.3.2.4 File, Plot, Packages, Help

The bottom-right window has four tabs for files, plots, packages, and help. The files tab allows browsing of the computers file directory. An important concept in R is the **current working directory**. This is file folder that R points to by default. Many functions in R will save things directly to this direct, or attempt to read files from this directory. The current working directory can be changed by navigating to the desired folder in the file menu, and then clicking on the more option to set that folder to the current working directory. This is especially important when reading in data to R. The current working directory should be set to the folder containing the data to be inputted into R. The plots tab will show recent plots and figures made in R. The packages tab lists the current R libraries loaded into memory, and provides the ability to download and enable new R packages. The help menu is an invaluable tool. Here, you can search for individual R commands to see examples of how they are used. Sometimes the help files for individual commands are opaque and difficult to understand, so it is necessary to do a Google search to find better examples of using these commands.

0.3.3 How to complete the R Labs

Each of the labs focuses on particular data-analysis problems, from graphing data, computing descriptive statistics, to running inferential tests in R. All of the labs come in three parts, a training part, a generalization part, and a writing part. The training part includes step-by-step examples of R code that solves particular problems. The R code is always highlighted in grey. The generalization part gives short assignments to change parts of the provided code to solve a new problem. The writing part tasks you with answering questions about statitiscal concepts.

The way to complete each lab is to open a new R Markdown document in R-studio, and then document your progression through each of the parts. By doing this, you will become familiar with how R and R-studio works, and how to create documents that preserve both the code and your notes all in one place. There are a few tricks to getting started that are outline below.

1. Open R-studio

0.3.3.1 R projects

2. Create a new R project
    a. Go to the file menu and select new project, or go to the top right-hand corner of R-studio, you should see a blue cube with an R in it, then select New project from the dropdown menu
3. Save the new R project somewhere that you can find it. If you are working on a lab computer, then save the new R project to the desktop.

What is an R project? When you create a new R project you are creating two things, 1) a new folder on your computer, and 2) a ".Rproj" file. For example, if you gave your R project the name "Lab1", then you will have created a folder title "Lab1", and inside the folder you will find an R project file called "Lab1.Rproj".

As you work inside R-studio you will be creating text documents, and you will be doing things like loading data, and saving the results of your analyses. As your work grows and becomes more complex, you can often find yourself creating many different files. **The R project folder is a very useful way of organizing your files all in one place so you can find them later.** If you double-clik an R project file, R-studio will automatically load and restore your last session. In the labs, you will be using your R project folder to:

1. save data files into this folder
2. save R-markdown files that you will use to write your R-code and lab notes
3. save the results of your analysis

0.3.3.2 Installing libraries

When you install R and R-studio, you get what is called Base R. Base R contains many libraries that allow you to conduct statistical anlayses. Because R is free and open-source, many other developers have created add-on libraries that extend the functionality of R. **We use some of these libraries, and you need to install them before you can do the labs**.

For example, in any of the labs, whenever you see a line code that uses the word library like this `library(libraryname)`, this line of code telling R to load up that library so it can be used. The `libraryname` would be replaced with the actual name of the library. For example, you will see code like this in the labs:

```
library(data.table)
```

This line of code is saying that the `data.table` library needs to be loaded. You can check to see if any library is already loaded by clicking on the "packages" tab in the bottom right hand panel. You will see many packages listed in alphabetical order. Packages that are currently loaded and available have a checkmark. If you scroll down and find that you **do not** have `data.table` installed, then you need to install it. To install any package follow these steps:

1. Click on the packages tab
2. Find the "install" button in the top left hand corner of the packages tab.
3. Click the install button
4. Make sure "install from:" is set to CRAN repository
5. Make sure "dependencies" is clicked on (with a checkmark)
6. type the name of the library into the search bar.
7. As you type, you should see the names of different packages you can install pop-up in a drop-down menu. **You must be connected to the internet to install packages from CRAN**
8. Once you find the package (e.g., `data.table`), click it, or just make sure the full, correctly spelled name, is in the search bar
9. Press the install button

You should see some text appear in the console while R installs the package.

10. After you have installed the package, you should now see that it is listed in the packages tab.
11. You can turn the package on by clicking it in the package tab.
12. OR, you can turn the packge on by running the command `library(data.table)` in the console, to do this type `library(data.table)` into the console, and press enter.

0.3.3.3 Quick install

If you are using R on one of the lab computers, you may find that some of the packages are not installed. The lab computers get wiped everynight, so it may be necessary to install packages each time you come back to the lab. Fortunately, we can tell R to install all of the packages we need in one go. Copy the following lines of code into the console, and press enter. Note you can select all of the lines at once, then copy them, then paste all of them into the console, and press enter to run them all. After each of the packages are installed, you will then be able to load them using `library()`.

```
install.packages(ggplot2)
install.packages(dplyr)
install.packages(data.table)
install.packages(summarytools)
install.packages(gapminder)
install.packages(ggpubr)
```

0.3.3.4 R markdown

Once you have the necessary packages installed you can begin creating R markdown documents for each lab. We admit that at the beginning, R markdown documents might seem a little bit confusing, but you will find they are extremely useful and flexible. Basically, what R markdown allows you to do is combine two kinds of writing, 1) writing R code to conduct analyses, and 2) writing normal text, with headers, sub-headers, and paragraphs. You can think of this like a lab journal, that contains both your writing about what you are doing (e.g., notes to self), and the code that you use for analysis. Additionally, when your code does something like make a graph, or run a statistical test, you can ask R markdown to print the results.

The R markdown website has an excellent tutorial that is well worth your time to check out: https://rmarkdown.rstudio.com/lesson-1.html

0.3.3.5 R markdown lab templates

1. Go to Canvas and download RMarkdownLab1.zip file to your computer.
2. Unzip the file, this will produce a new folder with three important parts
    a. data folder (contains data files for Lab 1)
    b. Blank template (.Rmd file) for completing Lab 1: Lab 01 Graphing_Student Name.Rmd
    c. RMarkdownsLab1.Rproj A file with a little blue cube with an R in it.

3. Double-click the RMarkdownsLab1.Rproj file, this will automatically open R-studio
4. Open the template .rmd, and use it to begin adding your code and notes for lab 1.

One you've downloaded R-studio on your computer, you'll Just need to find it and double-click. Now you have R-studio. Your lab instructor will also walk you through the steps to get started completing the first lab.

To get started with Lab 1, follow these steps:

1. copy the template file for lab 1, "Lab 01 Graphing_Student Name.Rmd", and place it into the "RMarkdownsLab" (copy it out of the template folder, and into the RMarkdownsLab folder).
2. Rename the file to add your own name, eg., "Lab1GraphingMattCrump.Rmd"
3. double-click the "RMarkdownsLab.Rproj" file
4. R-studio will now load up.
5. If you click the files tab, you will see all of the files and folders inside the "RMarkdownsLab" folder
6. Click on your .rmd file, it will now load into the editor window.

Each lab template .rmd file contains three main sections, one for each part of the lab. You will write things inside each section to complete the lab.

0.3.4 R-studio Cloud

R-studio is also in the cloud. This means that if you want to use R and R-studio through your web-browser you can do that without even installing R or R-studio on your computer. It's also free!

1. sign up for an R-studio cloud account here: https://rstudio.cloud
2. You can make new R projects, work inside them, and everything is saved in the cloud!
3. To see how everything would work, follow the steps in this video. You will need to download this .zip file to your computer to get started

The link to the video is https://www.youtube.com/watch?v=WsbnV0t7FE4, or you can watch it here:

Chapter 1

Lab 1: Graphing Data

The commonality between science and art is in trying to see profoundly - to develop strategies of seeing and showing. —Edward Tufte

As we have found out from the textbook and lecture, when we measure things, we get lots of numbers. Too many. Sometimes so many your head explodes just thinking about them. One of **the most helpful things** you can do to begin to make sense of these numbers, is to look at them in graphical form. Unfortunately, for sight-impaired individuals, graphical summary of data is much more well-developed than other forms of summarizing data for our human senses. Some researchers are developing auditory versions of visual graphs, a process called **sonification**, but we aren't prepared to demonstrate that here. Instead, we will make charts, and plots, and things to look at, rather than the numbers themselves, mainly because these are tools that are easiest to get our hands on, they are the most developed, and they work really well for visual summary. If time permits, at some point I would like to come back here and do the same things with sonification. I think that would be really, really cool!

1.1 General Goals

Our general goals for this first lab are to get your feet wet, so to speak. We'll do these things:

1. Download the statistical software program R and the RStudio (Integrated Development Environment for R) on your personal computers
2. Load in some data to a statistical software program
3. Talk a little bit about how the data is structured
4. Make graphs of the data so we can look at it and make sense of it.

1.1.1 Important info

1. Data for NYC film permits was obtained from the NYC open data website. The .csv file can be found here: Film_Permits.csv
2. Gapminder data from the gapminder project (copied from the R gapminder library) can be downloaded in .csv format here: gapminder.csv

1.2 R

1.2.1 Install R and R Studio

First, we need to install R and R-studio. Download and install R onto your computer. The R website is: http://www.r-project.org

Find the download R using the link. This will take you to a page with many different mirror links. You can click any of these links to download a version of R that will work on your computer. After you have installed R you can continue.

After you have installed R on your computer, you should want to install another program called R studio. This program provides a user-friendly interface for using R. You must already have installed R before you perform this step. The R-studio website is: http://www.rstudio.com

Find the download link on the front-page, and then download R studio desktop version for your computer. After you have installed R studio you will be ready to start using R.

1.2.2 Download the lab template

You will be completing each lab by writing your code and notes in an R Markdown document.

1. Go to Canvas and download RMarkdownLab1.zip file to your computer.
2. Unzip the file, this will produce a new folder with three important parts
    a. data folder (contains data files for Lab 1)
    b. Blank template (.Rmd file) for completing Lab 1: Lab 01 Graphing_Student Name.Rmd
    c. RMarkdownsLab1.Rproj A file with a little blue cube with an R in it.
3. Double-click the RMarkdownsLab1.Rproj file, this will automatically open R-studio

4. Open the template .rmd, and use it to begin adding your code and notes for lab 1.

One you've downloaded R-studio on your computer, you'll Just need to find it and double-click. Now you have R-studio. Your lab instructor will also walk you through the steps to get started completing the first lab. The steps are here.

There are numerous resources for learning about R, and I've put some of them on the course Canvas, under the Resources module. You will find these resources helpful as you learn.The Crump lab also has a helpful general introduction to R and Rstudio here. This shows you how to download R and R-studio at home (it's free). Throughout the labs you will be writing things called R Markdown documents. You will learn how to do this throughout the labs, but it can also be worthwhile reading other tutorials, such as the one provided by R Markdown.

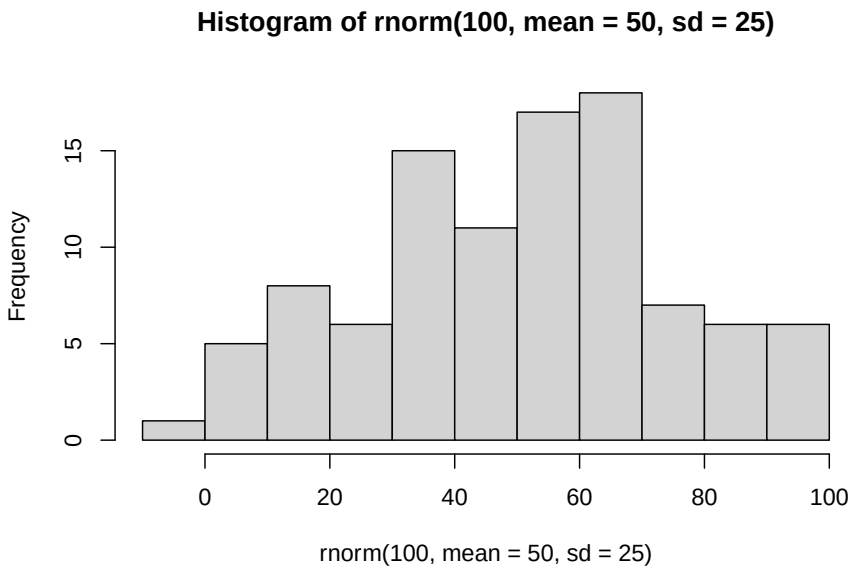
When I designed this course, I considered that many students might be unfamiliar with R and RStudio. The idea of diving into a computer programming language might seem daunting or even intimidating. But I assure you, there's no need to panic or consider dropping the course! In reality, learning R is going to be much more accessible and enjoyable than you might think. Together, we'll demystify the process and make it an engaging experience. Let's compare to other statistics courses where you would learn something like SPSS or SAS. That is also a limited programming language, but you would mostly learn how to point with a mouse, and click with button. I bet you already know how to do that. I bet you also already know how to copy and paste text, and press enter. That's mostly what we'll be doing to learn R. We will be doing statistics by typing commands, rather than by clicking buttons. However, lucky for you, all of the commands are already written for you. You just have to copy/paste them.

I know that this will seem challenging at first. But, I think that with lots of working examples, you will get the hang of it, and by the end of the course you will be able to do things you might never have dreamed you can do. It's really a fantastic skill to learn, even if you aren't planning on going on to do research (in which case, this kind of thing is necessary skill to learn). With that, let's begin.

1.2.3 Get some data

In order to graph data, we need to have some data first…Actually, with R, that's not quite true. Run this bit of code and see what happens:

```
hist(rnorm(100, mean=50, sd=25))
```



You just made R sample 100 numbers, and then plot the results in a histogram. Pretty neat. We'll be doing some of this later in the course, where get R to make fake data for us, and then we learn to think about how data behaves under different kinds of assumptions.

For now, let's do something that might be a little bit more interesting…what movies are going to be filming in NYC? It turns out that NYC makes a lot of data about a lot things open and free for anyone to download and look at. This is the NYC Open Data website: https://opendata.cityofnewyork.us. I searched through the data, and found a data file that lists the locations of film permits for shooting movies all throughout the Burroughs. There are multiple ways to load this data into R.

1. If you have downloaded the RMarkdownLab1.zip file, then you already have the data file in the data folder. Assuming you are working in your main directory (your .rmd file is saved in the main folder that contains both the data and template folders), then use the following commands to load the data.

```
library(data.table)
nyc_films <-fread("data/Film_Permits.csv")
```

2. If the above method doesn't work, you can try loading the data from my github:

```
library(data.table)
nyc_films <- fread("https://raw.githubusercontent.com/malloryb/statisticsLabE538/master/data/Film
```

If you are having issues getting the data loaded, then talk to your lab instructor

1.2.4 Look at the data

You will be downloading and analyzing all kinds of data files this semester. We will follow the very same steps every time. The steps are to load the data, then look at it. You want to see what you've got.

In R-studio, you will now see a variable called `nyc_films` in the top right-hand corner of the screen, in the environment tab. If you click this thing, it will show you the contents of the data in a new window. The data is stored in something we call a `data frame`. It's R lingo, for the thing that contains the data. Notice is a square, with rows going across, and columns going up and down. It looks kind of like an excel spreadsheet if you are familiar with Excel.

It's useful to know you can look at the data frame this way if you need to. But, this data frame is really big, it has 50,728 rows of data. That's a lot too much to look at.

1.2.4.1 summarytools

The summarytools packages give a quick way to summarize all of the data in a data frame. Here's how. When you run this code you will see the summary in the viewer on the bottom right hand side. There's a little browser button (arrow on top of little window) that you can click to expand and see the whole thing in a browser.

```
library(summarytools)
view(dfSummary(nyc_films))
```

That is super helpful, but it's still a lot to look at. Because there is so much data here, it's pretty much mind-boggling to start thinking about what to do with it.

1.2.5 Make Plots to answer questions

Let's walk through a couple questions we might have about this data. We can see that there were 50,728 film permits made. We can also see that there are different columns telling us information about each of the film permits. For example, the `Borough` column lists the Borough for each request, whether it was made for: Manhattan, Brooklyn, Bronx, Queen's, or Staten Island. Now we can ask our first question, and learn how to do some plotting in R.

1.2.5.1 Where are the most film permits being requested?

Do you have any guesses? Is it Manhattan, or Brooklyn, of the Bronx? Or Queen's or Staten Island? We can find out by plotting the data using a bar plot. We just need to count how many film permits are made in each borough, and then make different bars represent the the counts.

First, we do the counting in R. Run the following code.

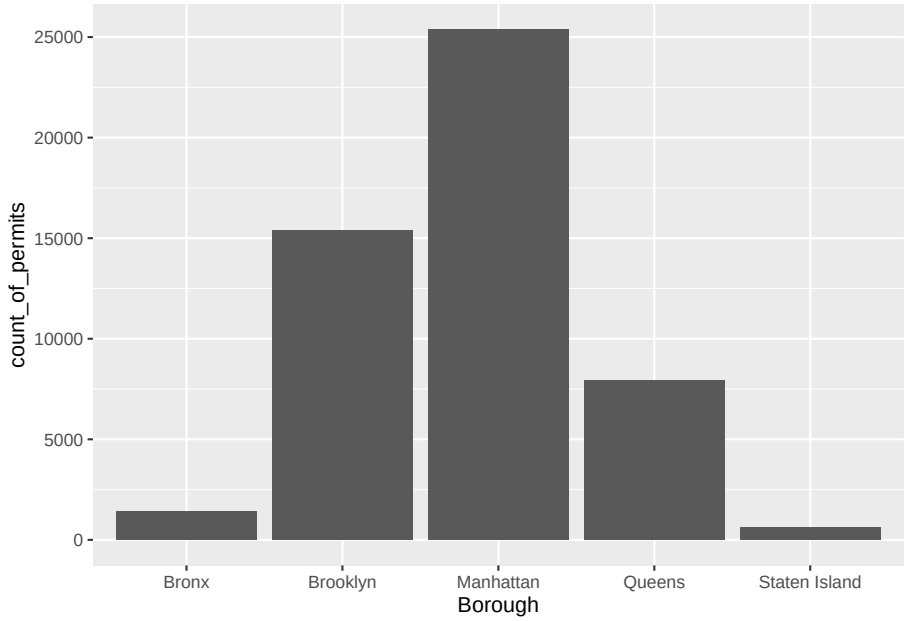
```
library(dplyr)

counts <- nyc_films %>%
          group_by(Borough) %>%
          summarize(count_of_permits = length(Borough))
```

The above grouped the data by each of the five Borough's, and then counted the number of times each Borough occurred (using the `length` function). The result is a new variable called `count`. I chose to name this variable `count`. You can see that it is now displayed in the top-right hand corned in the environment tab. If you gave `count` a different name, like `muppets`, then it would be named what you called it.

If you click on the `counts` variable, you will see the five boroughs listed, along with the counts for how many film permits were requested in each Borough. These are the numbers that we want to plot in a graph.

We do the plot using a fantastic package called `ggplot2`. It is very powerful once you get the hand of it, and when you do, you will be able to make all sorts of interesting graphs. Here's the code to make the plot

```
library(ggplot2)

ggplot(counts, aes(x = Borough, y = count_of_permits )) +
  geom_bar(stat="identity")
```

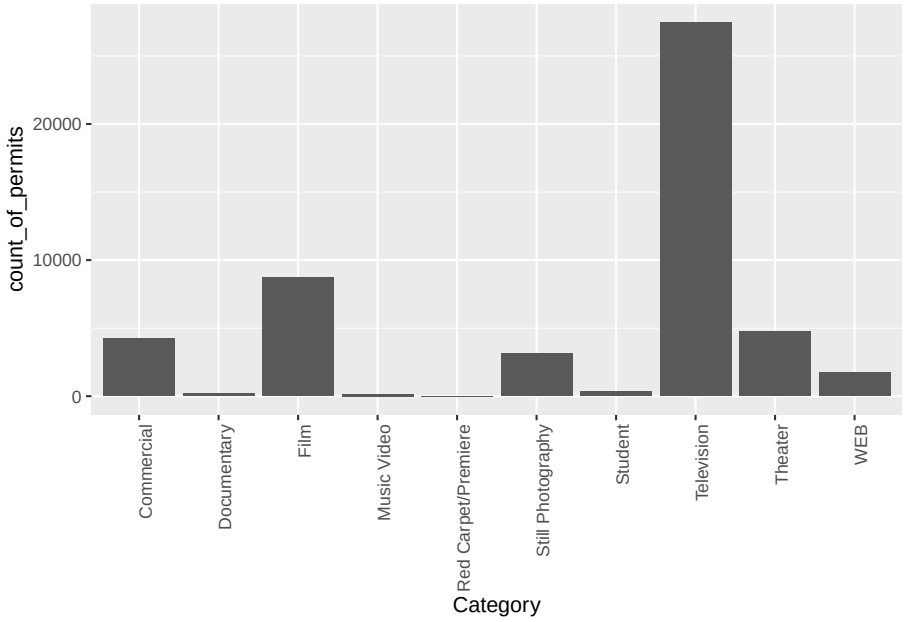


There it is, we're done here! We can easily look at this graph, and answer our question. Most of the film permits were requested in Manhattan, followed by Brooklyn, then Queen's, the Bronx, and finally Staten Island.

1.2.5.2 What kind of "films" are being made, what is the category?

We think you might be skeptical of what you are doing here, copying and pasting things. Soon you'll see just how fast you can do things by copying and pasting, and make a few little changes. Let's quickly ask another question about what kinds of films are being made. The column `Category`, gives us some information about that. Let's just copy paste the code we already made, and see what kinds of categories the films fall into. See if you can tell what I changed in the code to make this work, I'll do it all at once:

```
counts <- nyc_films %>%
          group_by(Category) %>%
          summarize(count_of_permits = length(Category))

ggplot(counts, aes(x = Category, y = count_of_permits )) +
  geom_bar(stat="identity")+
  theme(axis.text.x = element_text(angle = 90, hjust = 1))
```



OK, so this figure might look a bit weird because the labels on the bottom are running into each other. We'll fix that in a bit. First, let's notice the changes.

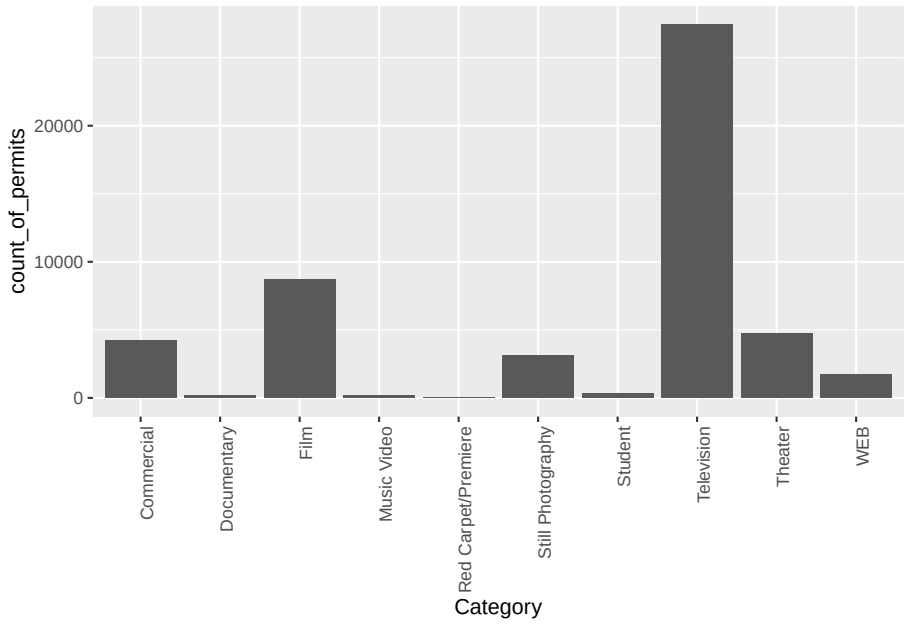
1. I changed `Borough` to `Category`. That was the main thing
2. I left out a bunch of things from before. None of the `library()` commands are used again, and I didn't re-run the very early code to get the data. R already has those things in it's memory, so we don't need to do that first. If you ever clear the memory of R, then you will need to reload those things. First-things come first.

Fine, so how do we fix the graph? Good question. To be honest, I don't know right now. I totally forgot how. But, I know ggplot2 can do this, and I'm going to Google it, right now. Then I'm going to find the answer, and use it here. The googling of your questions is a fine way to learn. It's what everybody does these days….[goes to Google…].

Found it, actually found a lot of ways to do this. The trick is to add the last line. I just copy-pasted it from the solution I found on stack overflow (you will become friend's with stack overflow, there are many solutions there to all of your questions)

```
counts <- nyc_films %>%
          group_by(Category) %>%
          summarize(count_of_permits = length(Category))
```

```
ggplot(counts, aes(x = Category, y = count_of_permits )) +
  geom_bar(stat="identity")+
  theme(axis.text.x = element_text(angle = 90, hjust = 1))
```



1.2.6 ggplot2 basics

Before we go further, I want to point out some basic properties of ggplot2, just to give you a sense of how it is working. This will make more sense in a few weeks, so come back here to remind yourself. We'll do just a bit a basics, and then move on to making more graphs, by copying and pasting.

The ggplot function uses layers. Layers you say? What are these layers? Well, it draws things from the bottom up. It lays down one layer of graphics, then you can keep adding on top, drawing more things. So the idea is something like: Layer 1 + Layer 2 + Layer 3, and so on. If you want Layer 3 to be Layer 2, then you just switch them in the code.

Here is a way of thinking about ggplot code

```
ggplot(name_of_data, aes(x = name_of_x_variable, y = name_of_y_variable)) +
    geom_layer()+
    geom_layer()+
    geom_layer()
```

What I want you to focus on in the above description is the + signs. What we are doing with the plus signs is adding layers to plot. The layers get added in the order that they are written. If you look back to our previous code, you will see we add a `geom_bar` layer, then we added another layer to change the rotation of the words on the x-axis. This is how it works.

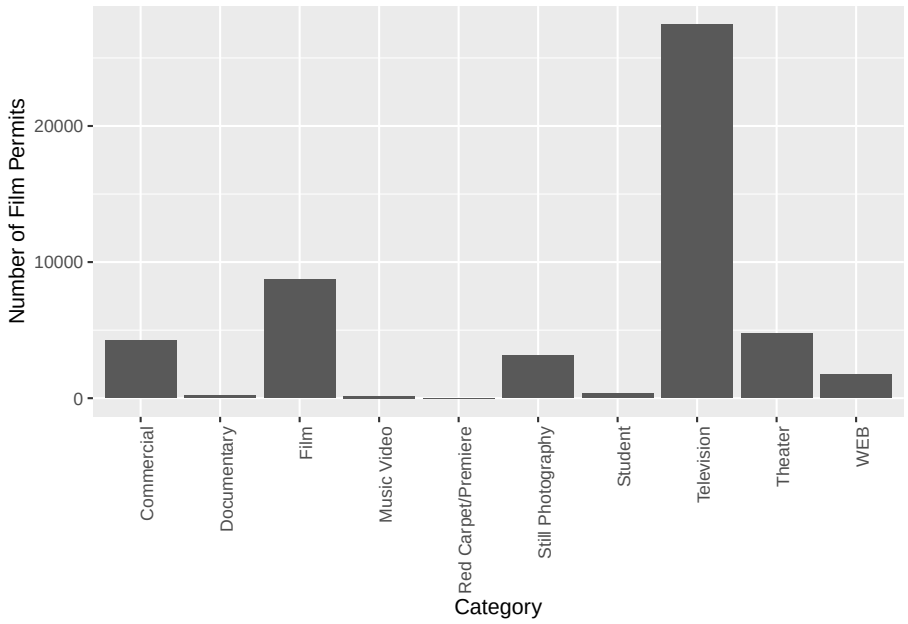
BUT WAIT? How am I supposed to know what to add? This is nuts! We know. You're not supposed to know just yet, how could you? We'll give you lots of examples where you can copy and paste, and they will work. That's how you'll learn. If you really want to read the help manual you can do that too. It's on the ggplot2 website. This will become useful after you already know what you are doing, before that, it will probably just seem very confusing. However, it is pretty neat to look and see all of the different things you can do, it's very powerful.

For now, let's the get the hang of adding things to the graph that let us change some stuff we might want to change. For example, how do you add a title? Or change the labels on the axes? Or add different colors, or change the font-size, or change the background? You can change all of these things by adding different lines to the existing code.

1.2.6.1 ylab() changes y label

The last graph had `count_of_permits` as the label on the y-axis. That doesn't look right. ggplot2 automatically took the label from the column, and made it be the name on the y-axis. We can change that by adding `ylab("what we want")`. We do this by adding a + to the last line, then adding `ylab()`

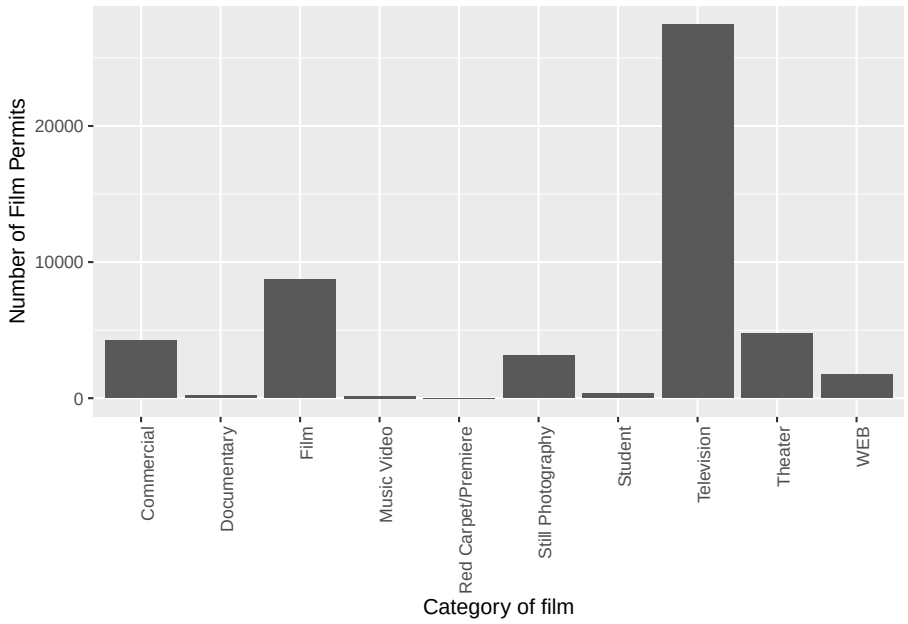
```
ggplot(counts, aes(x = Category, y = count_of_permits )) +
  geom_bar(stat="identity") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits")
```



1.2.6.2 xlab() changes x label

Let's slightly modify the x label too:

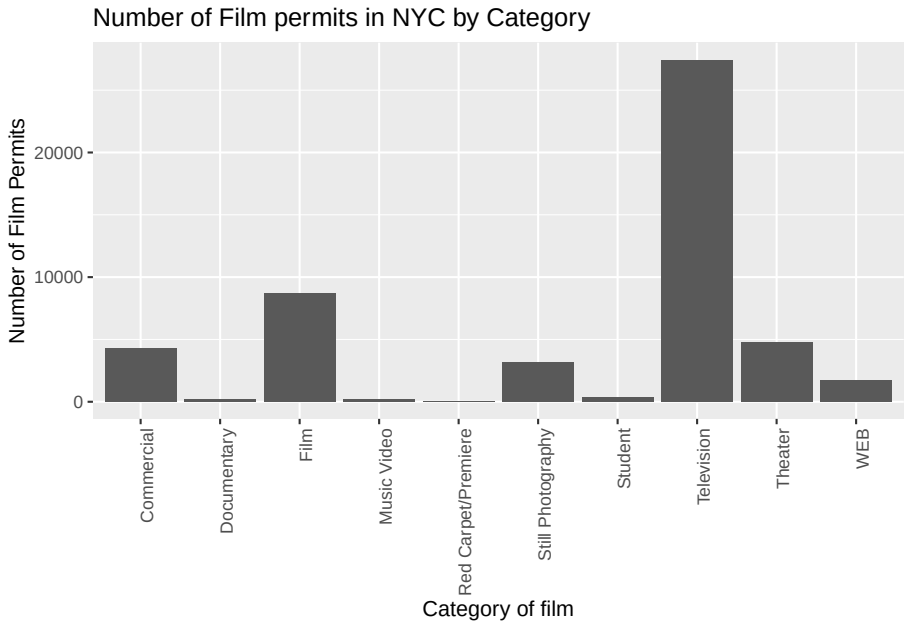
```
ggplot(counts, aes(x = Category, y = count_of_permits )) +
  geom_bar(stat="identity") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Category of film")
```



1.2.6.3 ggtitle() adds title

Let's give our graph a title

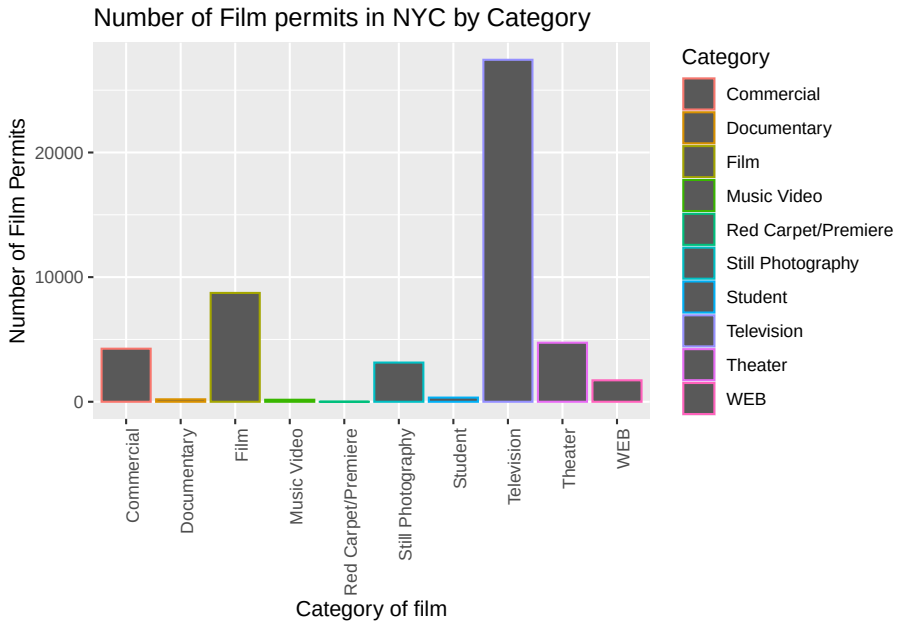
```
ggplot(counts, aes(x = Category, y = count_of_permits )) +
  geom_bar(stat="identity") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Category of film") +
  ggtitle("Number of Film permits in NYC by Category")
```



1.2.6.4 color adds color

Let's make the bars different colors. To do this, we add new code to the inside of the `aes()` part:

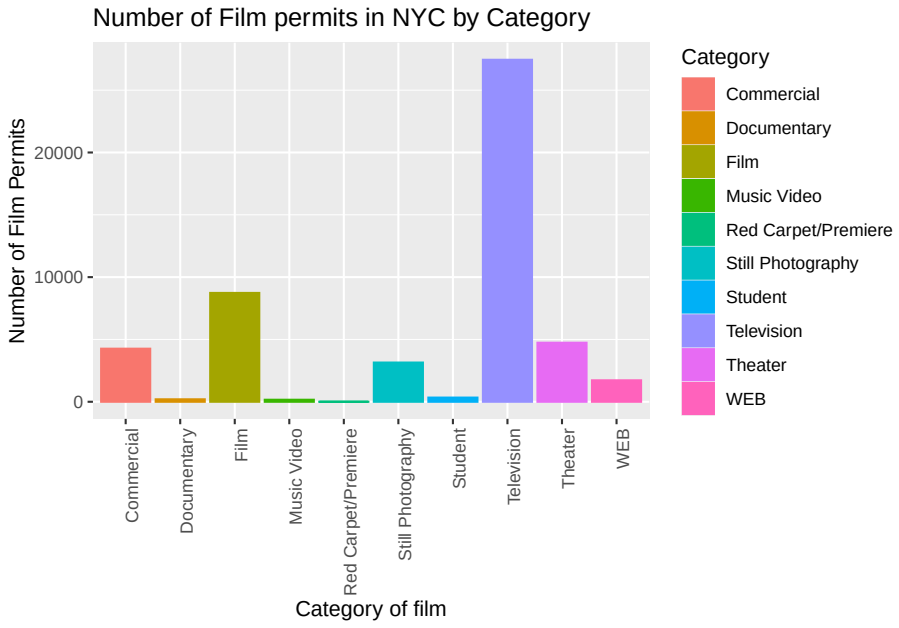
```
ggplot(counts, aes(x = Category, y = count_of_permits, color=Category )) +
  geom_bar(stat="identity") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Category of film") +
  ggtitle("Number of Film permits in NYC by Category")
```



1.2.6.5 fill fills in color

Let's make the bars different colors. To do this, we add new code to the inside of the `aes()` part...Notice I've started using new lines to make the code more readable.

```
ggplot(counts, aes(x = Category, y = count_of_permits,
                   color=Category,
                   fill= Category )) +
  geom_bar(stat="identity") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Category of film") +
  ggtitle("Number of Film permits in NYC by Category")
```

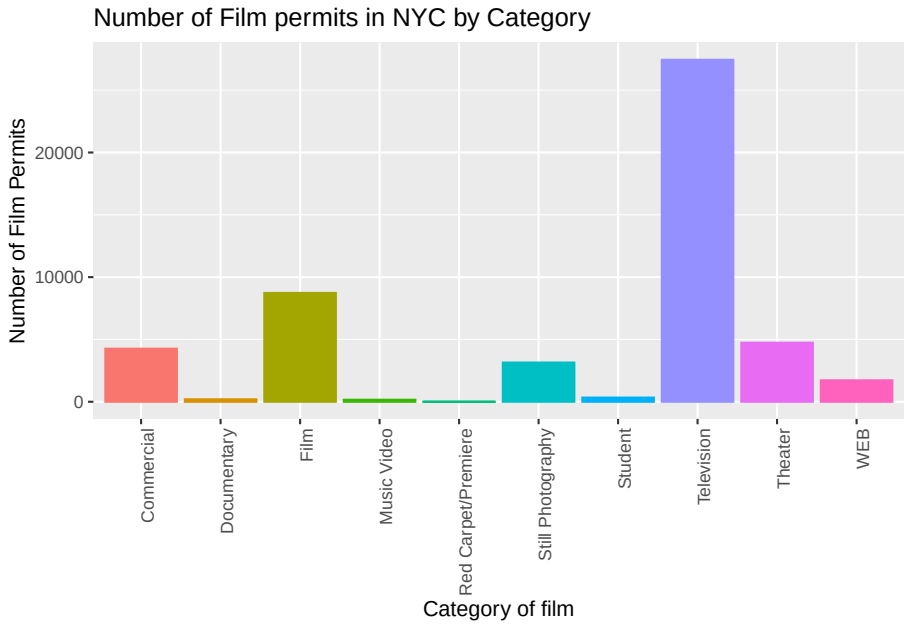


1.2.6.6 get rid of the legend

Sometimes you just don't want the legend on the side, to remove it add

```
theme(legend.position="none")
```

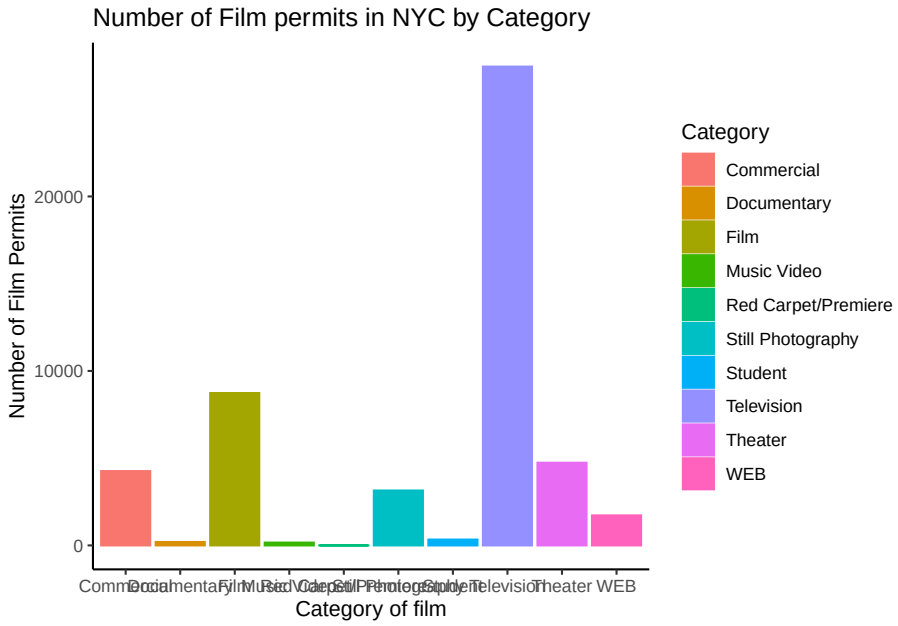
```
ggplot(counts, aes(x = Category, y = count_of_permits,
                   color=Category,
                   fill= Category )) +
  geom_bar(stat="identity") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Category of film") +
  ggtitle("Number of Film permits in NYC by Category") +
  theme(legend.position="none")
```



1.2.6.7 theme_classic() makes white background

The rest is often just visual preference. For example, the graph above has this grey grid behind the bars. For a clean classic no nonsense look, use `theme_classic()` to take away the grid.

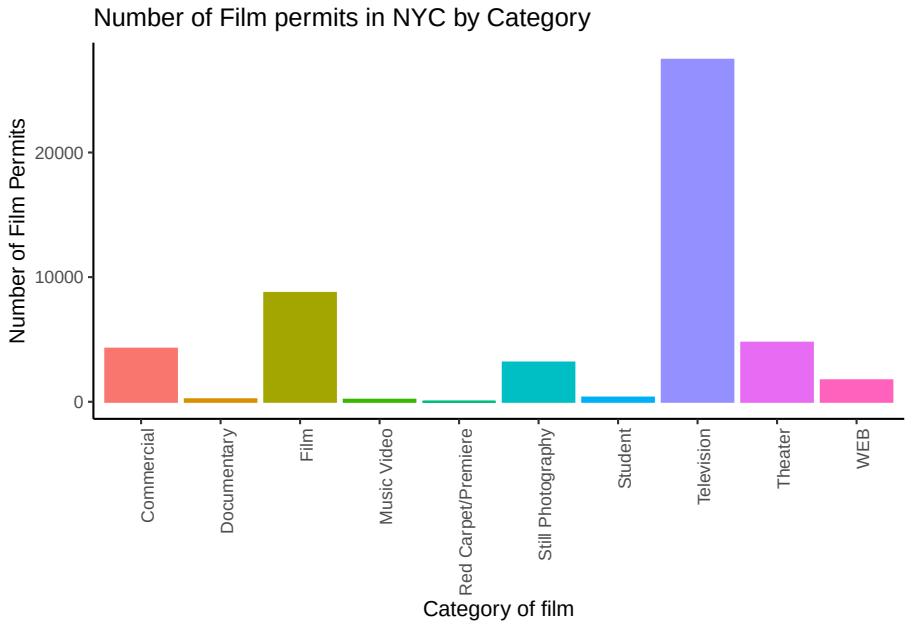
```
ggplot(counts, aes(x = Category, y = count_of_permits,
                   color=Category,
                   fill= Category )) +
  geom_bar(stat="identity") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Category of film") +
  ggtitle("Number of Film permits in NYC by Category") +
  theme(legend.position="none") +
  theme_classic()
```



1.2.6.8 Sometimes layer order matters

Interesting, `theme_classic()` is misbehaving a little bit. It looks like we have some of our layer out of order, let's re-order. I just moved `theme_classic()` to just underneath the `geom_bar()` line. Now everything get's drawn properly.

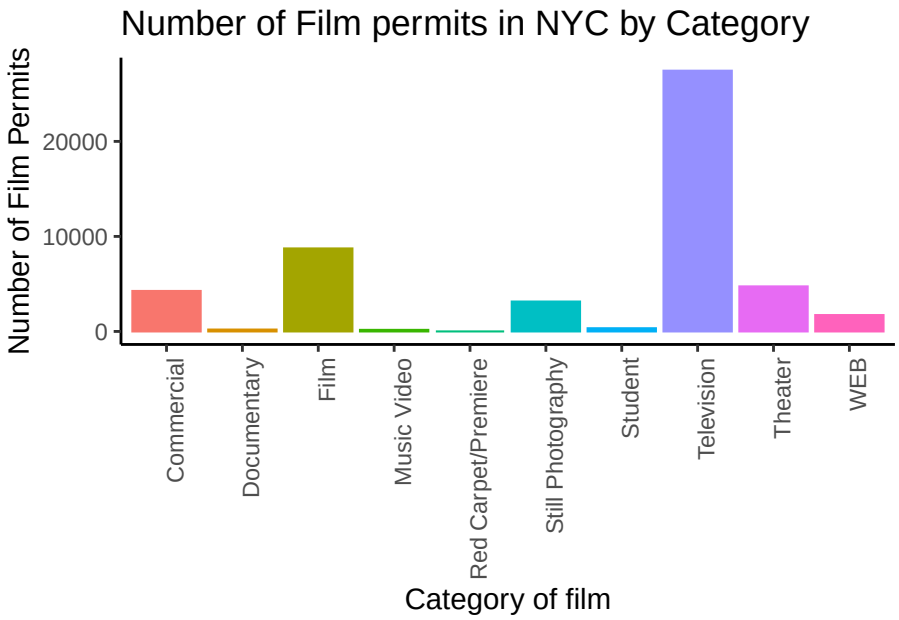
```
ggplot(counts, aes(x = Category, y = count_of_permits,
                   color=Category,
                   fill= Category )) +
  geom_bar(stat="identity") +
  theme_classic() +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Category of film") +
  ggtitle("Number of Film permits in NYC by Category") +
  theme(legend.position="none")
```



1.2.6.9 Font-size

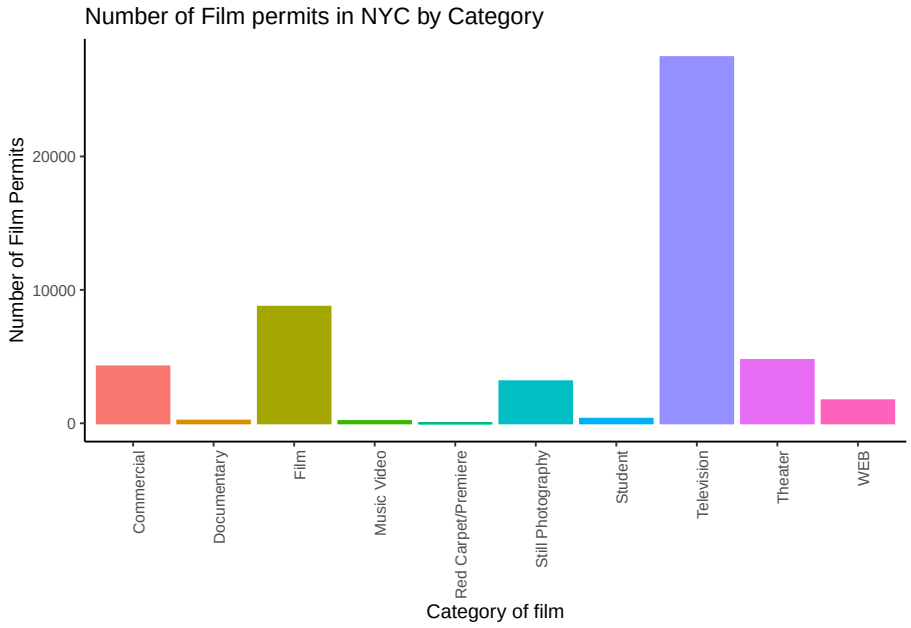
Changing font-size is often something you want to do. ggplot2 can do this in different ways. I suggest using the `base_size` option inside `theme_classic()`. You set one number for the largest font size in the graph, and everything else gets scaled to fit with that that first number. It's really convenient. Look for the inside of `theme_classic()`

```
ggplot(counts, aes(x = Category, y = count_of_permits,
                   color=Category,
                   fill= Category )) +
  geom_bar(stat="identity") +
  theme_classic(base_size = 15) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Category of film") +
  ggtitle("Number of Film permits in NYC by Category") +
  theme(legend.position="none")
```



or make things small... just to see what happens

```
ggplot(counts, aes(x = Category, y = count_of_permits,
                   color=Category,
                   fill= Category )) +
  geom_bar(stat="identity") +
  theme_classic(base_size = 10) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Category of film") +
  ggtitle("Number of Film permits in NYC by Category") +
  theme(legend.position="none")
```



1.2.6.10 ggplot2 summary

That's enough of the ggplot2 basics for now. You will discover that many things are possible with ggplot2. It is amazing. We are going to get back to answering some questions about the data with graphs. But, now that we have built the code to make the graphs, all we need to do is copy-paste, and make a few small changes, and boom, we have our graph.

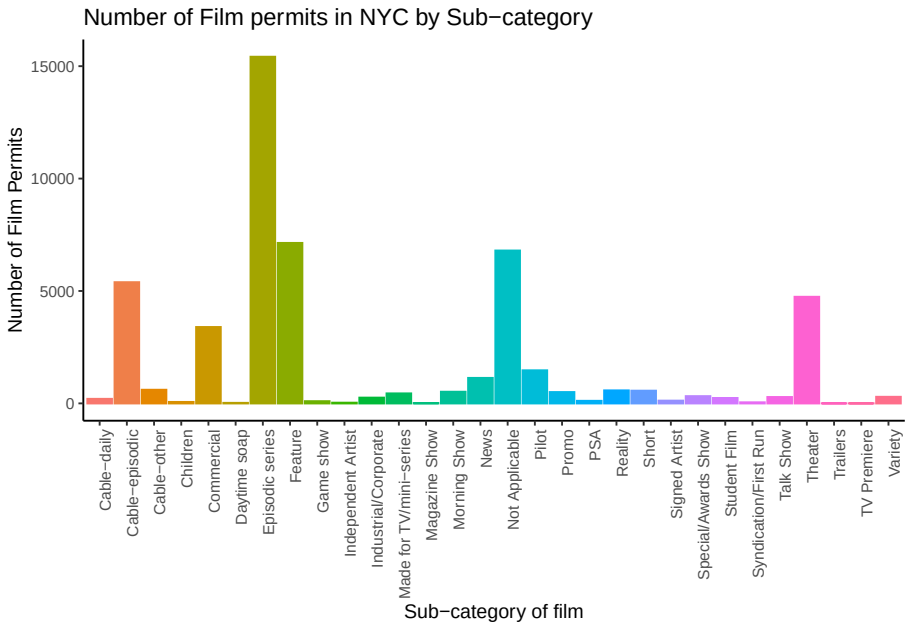
1.2.7 More questions about NYC films

1.2.7.1 What are the sub-categories of films?

Notice the `nyc_films` data frame also has a column for `SubCategoryName`. Let's see what's going on there with a quick plot.

```
# get the counts (this is a comment it's just here for you to read)

counts <- nyc_films %>%
          group_by(SubCategoryName) %>%
          summarize(count_of_permits = length(SubCategoryName))

# make the plot
```

```
ggplot(counts, aes(x = SubCategoryName, y = count_of_permits,
                   color=SubCategoryName,
                   fill= SubCategoryName )) +
  geom_bar(stat="identity") +
  theme_classic(base_size = 10) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Sub-category of film") +
  ggtitle("Number of Film permits in NYC by Sub-category") +
  theme(legend.position="none")
```



I guess "episodic series" are the most common. Using a graph like this gave us our answer super fast.

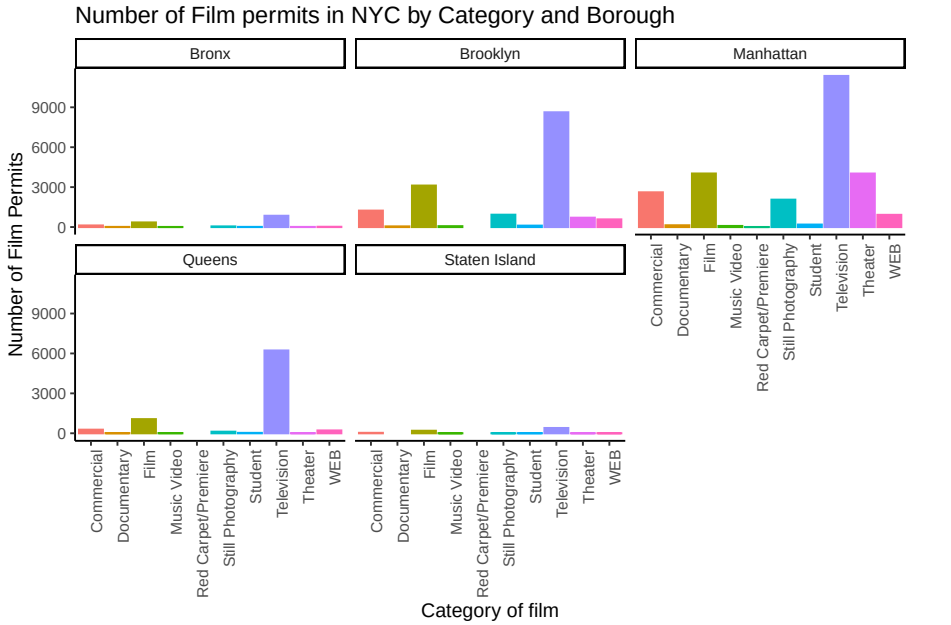
1.2.7.2 Categories by different Boroughs

Let's see one more really useful thing about ggplot2. It's called `facet_wrap()`. It's an ugly word, but you will see that it is very cool, and you can do next-level-super-hero graph styles with `facet_wrap` that other people can't do very easily.

Here's our question. We know that some films are made in different Boroughs, and that same films are made in different categories, but do different Boroughs have different patterns for the kinds of categories of films they request permits

for? Are their more TV shows in Brooklyn? How do we find out? Watch, just like this:

```
# get the counts (this is a comment it's just here for you to read)

counts <- nyc_films %>%
          group_by(Borough,Category) %>%
          summarize(count_of_permits = length(Category))

# make the plot

ggplot(counts, aes(x = Category, y = count_of_permits,
                   color=Category,
                   fill= Category )) +
  geom_bar(stat="identity") +
  theme_classic(base_size = 10) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Category of film") +
  ggtitle("Number of Film permits in NYC by Category and Borough") +
  theme(legend.position="none") +
  facet_wrap(~Borough, ncol=3)
```

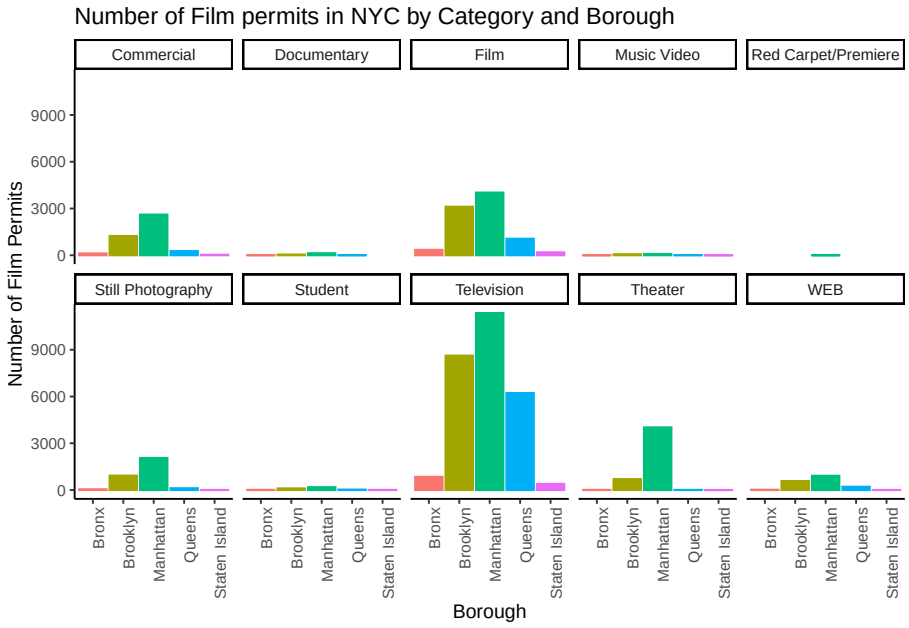


We did two important things. First we added `Borough` and `Category` into the `group_by()` function. This automatically gives separate counts for each

category of film, for each Borough. Then we added `facet_wrap(~Borough, ncol=3)` to the end of the plot, and it automatically drew us 5 different bar graphs, one for each Borough! That was fast. Imagine doing that by hand.

The nice thing about this is we can switch things around if we want. For example, we could do it this way by switching the `Category` with `Borough`, and facet-wrapping by Category instead of Borough like we did above. Do what works for you.

```
ggplot(counts, aes(x = Borough, y = count_of_permits,
                   color=Borough,
                   fill= Borough )) +
  geom_bar(stat="identity") +
  theme_classic(base_size = 10) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ylab("Number of Film Permits") +
  xlab("Borough") +
  ggtitle("Number of Film permits in NYC by Category and Borough") +
  theme(legend.position="none") +
  facet_wrap(~Category, ncol=5)
```



1.2.8 Gapminder Data

https://www.gapminder.org is an organization that collects some really interesting worldwide data. They also make cool visualization tools for look-

ing at the data. There are many neat examples, and they have visualization tools built right into their website that you can play around with https://www.gapminder.org/tools/. That's fun check it out.

There is also an R package called `gapminder`. When you install this package, it loads in some of the data from gapminder, so we can play with it in R.

If you don't have the gapminder package installed, you can install it by running this code

```
install.packages("gapminder")
```

Once the package is installed, you need to load the new library, like this. Then, you can put the `gapminder` data into a data frame, like we do here: `gapminder_df`.

```
library(gapminder)
gapminder_df<-gapminder
```

1.2.8.1 Look at the data frame

You can look at the data frame to see what is in it, and you can use `summarytools` again to view a summary of the data.

```
view(dfSummary(gapminder_df))
```

There are 1704 rows of data, and we see some columns for country, continent, year, life expectancy, population, and GDP per capita.

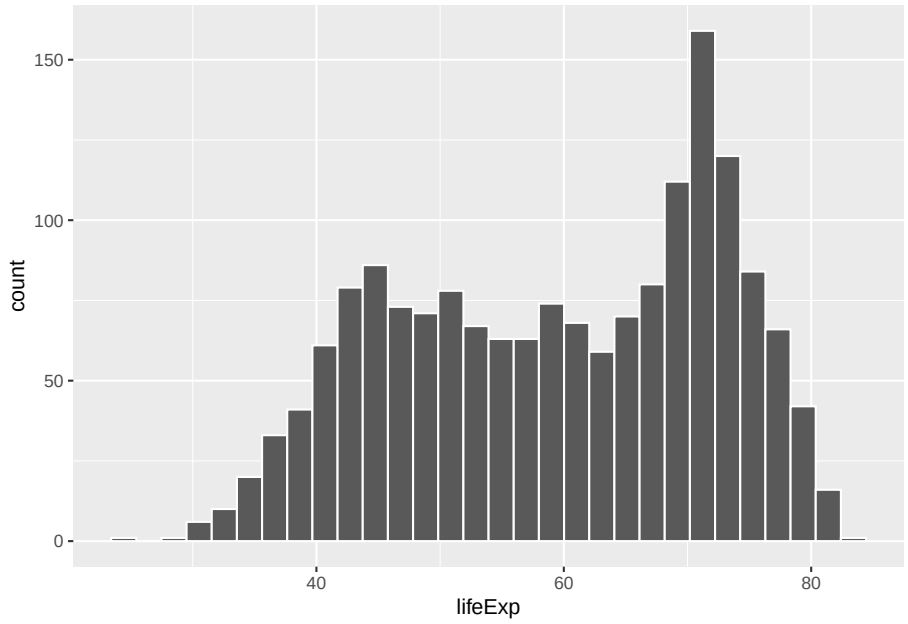
1.2.9 Asking Questions with the gap minder data

We will show you how to graph some the data to answer a few different kinds of questions. Then you will form your own questions, and see if you can answer them with ggplot2 yourself. All you will need to do is copy and paste the following examples, and change them up a little bit

1.2.9.1 Life Expectancy histogram

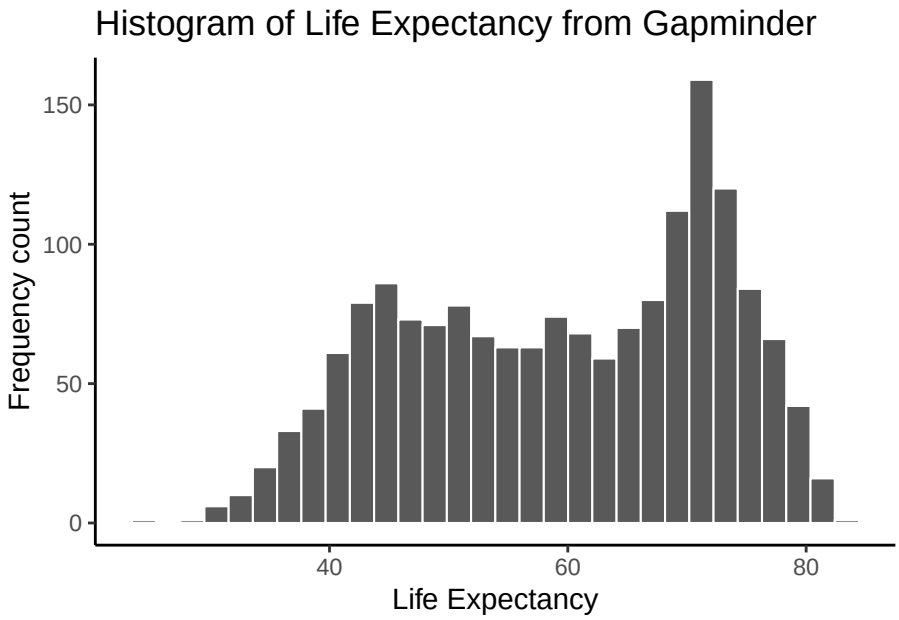
How long are people living all around the world according to this data set? There are many ways we could plot the data to find out. The first way is a histogram. We have many numbers for life expectancy in the column `lifeExp`. This is a big sample, full of numbers for 142 countries across many years. It's easy to make a histogram in ggplot to view the distribution:

```
ggplot(gapminder_df, aes(x=lifeExp))+
  geom_histogram(color="white")
```



See, that was easy. Next, is a code block that adds more layers and settings if you wanted to modify parts of the graph:

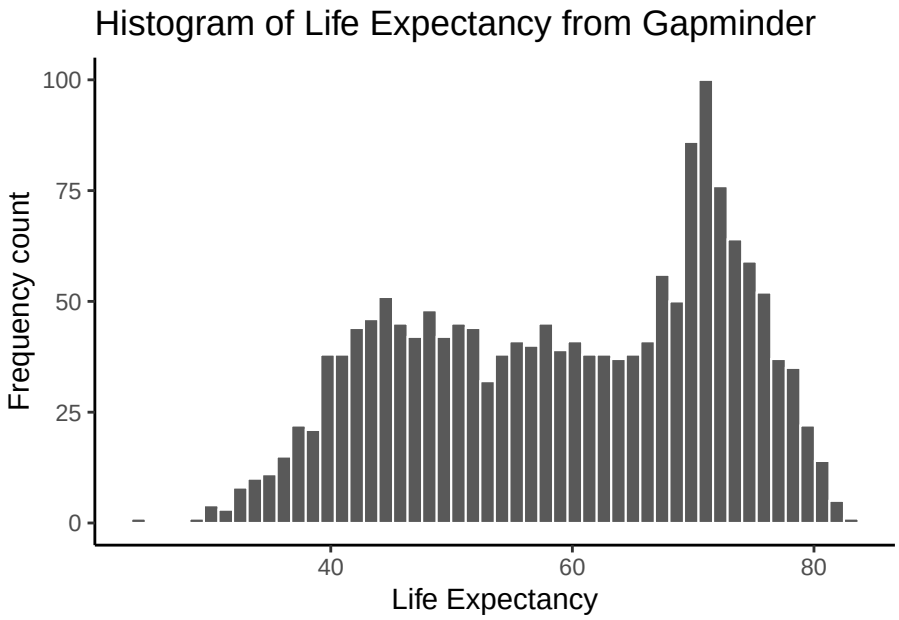
```
ggplot(gapminder_df, aes(x = lifeExp)) +
  geom_histogram(color="white")+
  theme_classic(base_size = 15) +
  ylab("Frequency count") +
  xlab("Life Expectancy") +
  ggtitle("Histogram of Life Expectancy from Gapminder")
```



The histogram shows a wide range of life expectancies, from below 40 to just over 80. Histograms are useful, they can show you what kinds of values happen more often than others.

One final thing about histograms in ggplot. You may want to change the bin size. That controls how wide or narrow, or the number of bars (how they split across the range), in the histogram. You need to set the `bins=` option in `geom_histogram()`.

```
ggplot(gapminder_df, aes(x = lifeExp)) +
  geom_histogram(color="white", bins=50)+
  theme_classic(base_size = 15) +
  ylab("Frequency count") +
  xlab("Life Expectancy") +
  ggtitle("Histogram of Life Expectancy from Gapminder")
```



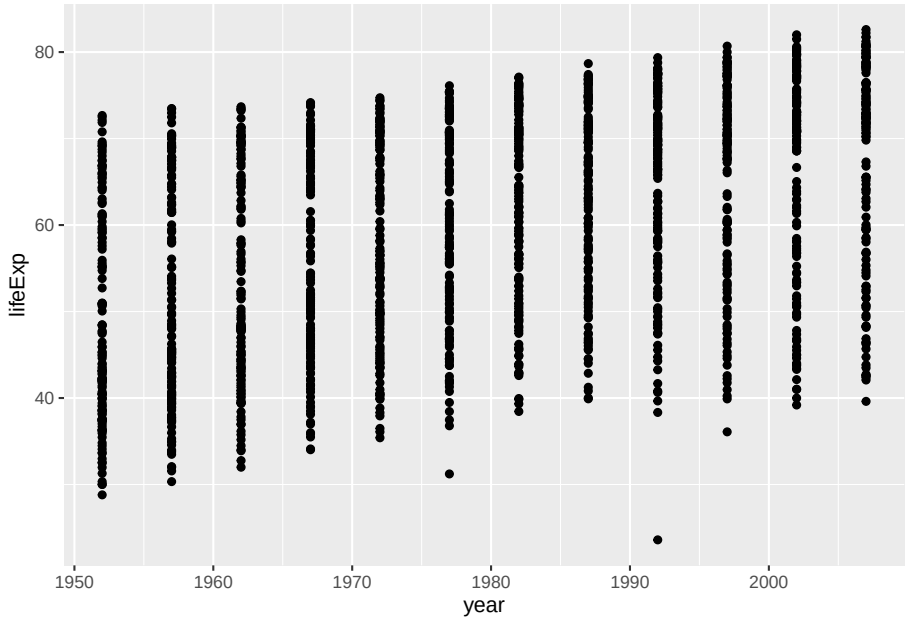
See, same basic patter, but now breaking up the range into 50 little equal sized bins, rather than 30, which is the default. You get to choose what you want to do.

1.2.9.2 Life Expectancy by year Scatterplot

We can see we have data for life expectancy and different years. So, does worldwide life expectancy change across the years in the data set? As we go into the future, are people living longer?

Let's look at this using a scatter plot. We can set the x-axis to be year, and the y-axis to be life expectancy. Then we can use `geom_point()` to display a whole bunch of dots, and then look at them. Here's the simple code:

```
ggplot(gapminder_df, aes(y= lifeExp, x= year))+
  geom_point()
```

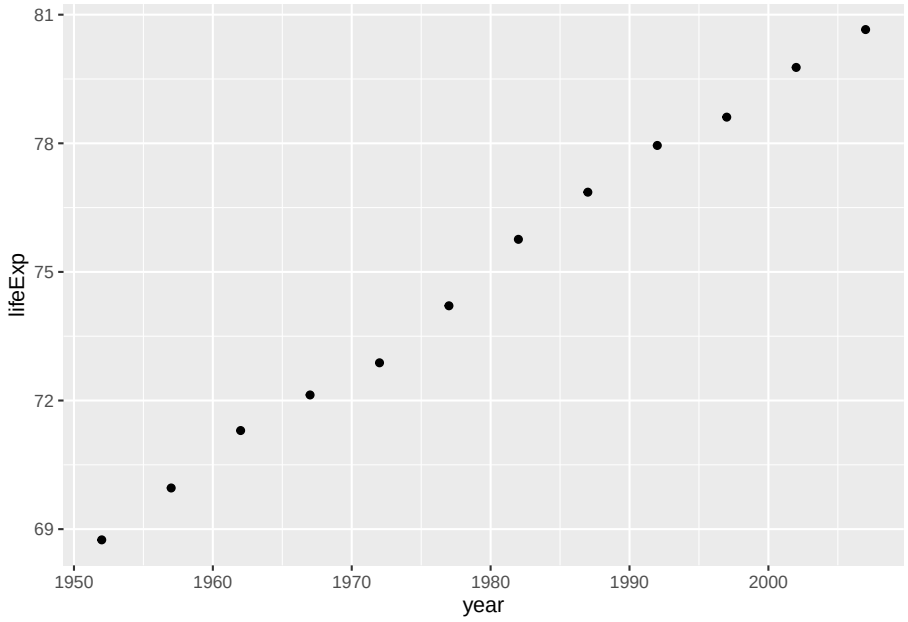


Whoa, that's a lot of dots! Remember that each country is measured each year. So, the bands of dots you see, show the life expectancies for the whole range of countries within each year of the database. There is a big spread inside each year. But, on the whole it looks like groups of dots slowly go up over years.

1.2.9.3 One country, life expectancy by year

Let's say I'm from Canada, so maybe I want to know if life expectancy for Canadians is going up over the years. To find out the answer for one country, we first need to split the full data set, into another smaller data set that only contains data for Canada. In other words, we want only the rows where the word "Canada" is found in the `country` column. We will use the `filter` function from `dplyr` for this:

```
# filter rows to contain Canada

smaller_df <- gapminder_df %>%
                filter(country == "Canada")

# plot the new data contained in smaller_df

ggplot(smaller_df, aes(y= lifeExp, x= year))+
  geom_point()
```

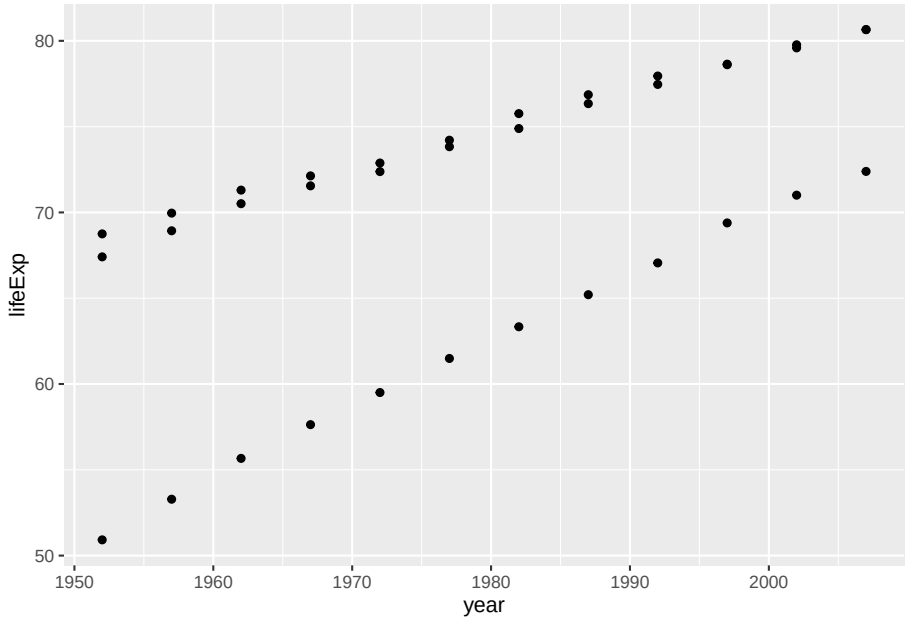


I would say things are looking good for Canadians, their life expectancy is going up over the years!

1.2.9.4 Multiple countries scatterplot

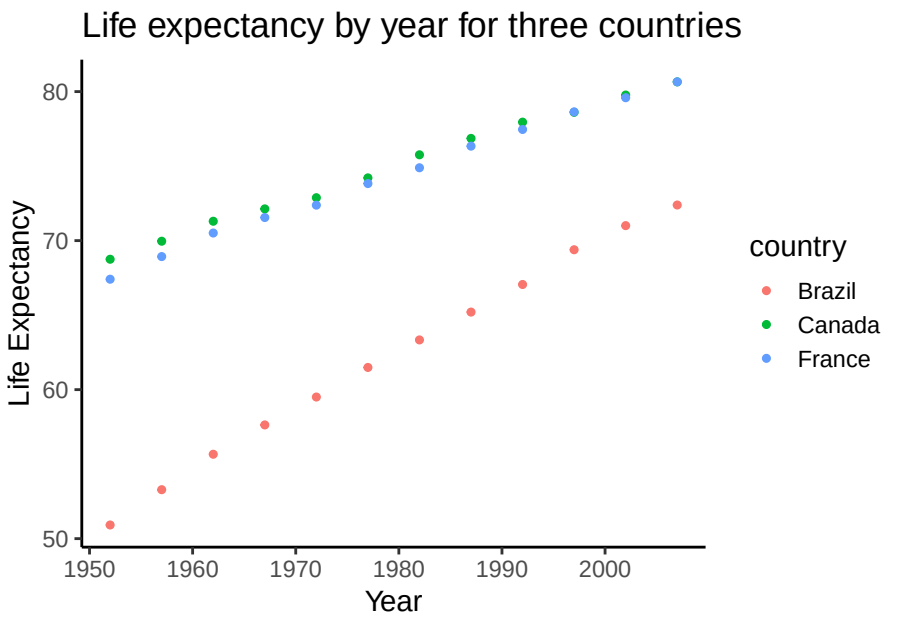
What if we want to look at a few countries altogether. We can do this too. We just change how we filter the data so more than one country is allowed, then we plot the data. We will also add some nicer color options and make the plot look pretty. First, the simple code:

```
# filter rows to contain countries of choice

smaller_df <- gapminder_df %>%
                filter(country %in% c("Canada","France","Brazil") == TRUE)

# plot the new data contained in smaller_df

ggplot(smaller_df, aes(y= lifeExp, x= year, group= country))+
  geom_point()
```



Nice, we can now see three sets of dots, but which are countries do they represent? Let's add a legend, and make the graph better looking.

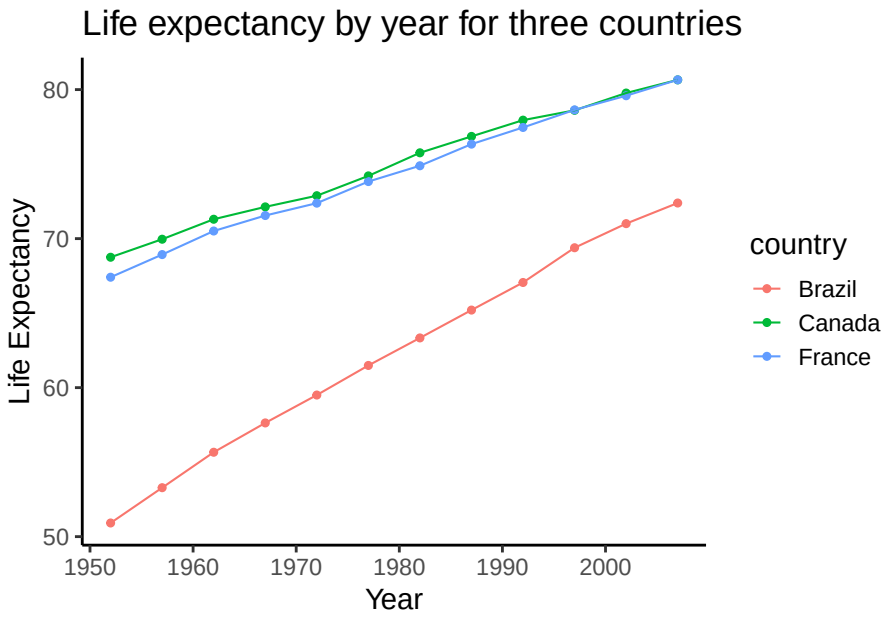
```
ggplot(smaller_df,aes(y= lifeExp, x= year,
                      group= country, color = country)) +
  geom_point()+
  theme_classic(base_size = 15) +
  ylab("Life Expectancy") +
  xlab("Year") +
  ggtitle("Life expectancy by year for three countries")
```



1.2.9.5 geom_line() connecting the dots

We might also want to connect the dots with a line, to make it easier to see the connection! Remember, ggplot2 draws layers on top of layers. So, we add in a new `geom_line()` layer.

```
ggplot(smaller_df,aes(y= lifeExp, x= year,
                      group= country, color = country)) +
  geom_point()+
  geom_line()+
  theme_classic(base_size = 15) +
  ylab("Life Expectancy") +
  xlab("Year") +
  ggtitle("Life expectancy by year for three countries")
```



1.2.10 Generalization Exercise

The following generalization exercise and writing assignment is also in your lab R Markdown document for this lab. Complete your work in that document and hand it in.

(4 points - Pass/Fail)

Use the code from above to attempt to solve the extra things we ask you do for this assignment. You generalization exercises are as follows:

1. Make a graph plotting Life Expectancy by year for the five continents, using the `continent` factor. Make sure you change the title so it reads correctly

2. Make a graph plotting GDP per capita by year for the USA, Canada, and Mexico. Use the `gdpPercap` column for the GDP per capita data

3. Make a new graph plotting anything you are interested in using the gapminder dataset. It just needs to be a plot that we have not given an example for

1.2.11 Writing assignment

Complete the writing assignment described here in your R Markdown document for this lab. When you have finished everything, knit the document and submit to Canvas.

Note: It's vital that the work submitted is entirely your own. Utilizing chatGPT or other AI to complete this portion of the lab assignment is not permissible. These responses must reflect your own words and thoughts. Using external assistance not only constitutes plagiarism but also undermines the educational value of this exercise, hindering your opportunity to learn and grasp the concepts intended.

The question for this lab is a long answer question about histograms. Here is the question:

Describe what histograms are, how to interpret them, and what they are useful for. You should answer each of these questions:

The answers to each of these questions are worth 1 point each, for a total of 8 points

a. What do the bars on a histogram represent?
b. How many bars can a histogram have?
c. What do the heights of the bars tell you
d. What is on the x-axis and y-axis of a histogram
e. What does the tallest bar on a histogram tell you?
f. What does the shortest bar on a histogram tell you?
g. What are some uses for histograms, why would you want to look at a histogram of some numbers that you collected?
h. Imagine you had two histograms, one was very wide and spread out, the other was very narrow with a very tall peak. Which histogram would you expect to contain more consistent numbers (numbers that are close to each other), explain why.

Rubric

General grading.

- You will receive 0 points for missing answers (say, if you do not answer question c, then you will receive 0 points for that question)
- You must write in complete sentences. Point form sentences will be given 0 points.
- Completely incorrect answers will receive 0 points. For example, if you incorrectly describe what the x and y-axes refer to, then you will receive 0 points for that question.
- If your answer is generally correct but very difficult to understand and unclear you may receive half points for the question.

Chapter 2

Lab 2: Descriptive Statistics

Describing comic sensibility is near impossible. It's sort of an abstract silliness, that sometimes the joke isn't the star. —Dana Carvey

The purpose of this lab is to show you how to compute basic descriptive statistics, including measures of central tendency (mean, mode, median) and variation (range, variance, standard deviation).

2.1 General Goals

1. Compute measures of central tendency using software
2. Compute measures of variation using software
3. Ask some questions of a data set using descriptive statistics

2.1.1 Important info

We will be using data from the gapminder project. You can download a small snippet of the data in .csv format from this link (note this dataset was copied from the gapminder library for R) gapminder.csv. If you are using R, then you can install the gapminder package. This method is described later in the R section.

2.2 R

2.2.1 Descriptives basics in R

We learned in lecture and from the textbook that data we want to use ask and answer questions often comes with loads of numbers. Too many numbers to look at all at once. That's one reason we use descriptive statistics. To reduce the big set of numbers to one or two summary numbers that tell use something about all of the numbers. R can produce descriptive statistics for you in many ways. There are base functions for most of the ones that you want. We'll go over some R basics for descriptive statistics, and then use our new found skills to ask some questions about real data.

2.2.1.1 Making numbers in R

In order to do descriptive statistics we need to put some numbers in a variable. You can also do this using the `c()` command, which stands for combine

```
my_numbers <- c(1,2,3,4)
```

There a few other handy ways to make numbers. We can use `seq()` to make a sequence. Here's making the numbers from 1 to 100

```
one_to_one_hundred <- seq(1,100,1)
```

We can repeat things, using rep. Here's making 10 5s, and 25 1s:

```
rep(10,5)
```

```
## [1] 10 10 10 10 10
```

```
rep(1,25)
```

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

```
all_together_now <- c(rep(10,5),rep(1,25))
```

2.2.1.2 Sum

Let's play with the number 1 to 100. First, let's use the `sum()` function to add them up

```
one_to_one_hundred <- seq(1,100,1)
sum(one_to_one_hundred)
```

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

2.2.1.3 Length

We put 100 numbers into the variable `one_to_one_hundred`. We know how many numbers there are in there. How can we get R to tell us? We use `length()` for that.

```
length(one_to_one_hundred)
```

```
## [1] 100
```

2.2.2 Central Tendency

2.2.2.1 Mean

Remember the mean of some numbers is their sum, divided by the number of numbers. We can compute the mean like this:

```
sum(one_to_one_hundred)/length(one_to_one_hundred)
```

```
## [1] 50.5
```

Or, we could just use the `mean()` function like this:

```
mean(one_to_one_hundred)
```

```
## [1] 50.5
```

2.2.2.2 Median

The median is the number in the exact middle of the numbers ordered from smallest to largest. If there are an even number of numbers (no number in the middle), then we take the number in between the two (decimal .5). Use the `median` function. There's only 3 numbers here. The middle one is 2, that should be the median

```
median(c(1,2,3))
```

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

2.2.2.3 Mode

R does not a base function for the Mode. You would have to write one for yourself. Here is an example of writing your own mode function, and then using it. Note I searched how to do this on Google, and am using the mode defined by this answer on stack overflow

Remember, the mode is the most frequently occurring number in the set. Below 1 occurs the most, so the mode will be one.

```
my_mode <- function(x) {
  ux <- unique(x)
  ux[which.max(tabulate(match(x, ux)))]
}

my_mode(c(1,1,1,1,1,1,1,2,3,4))
```

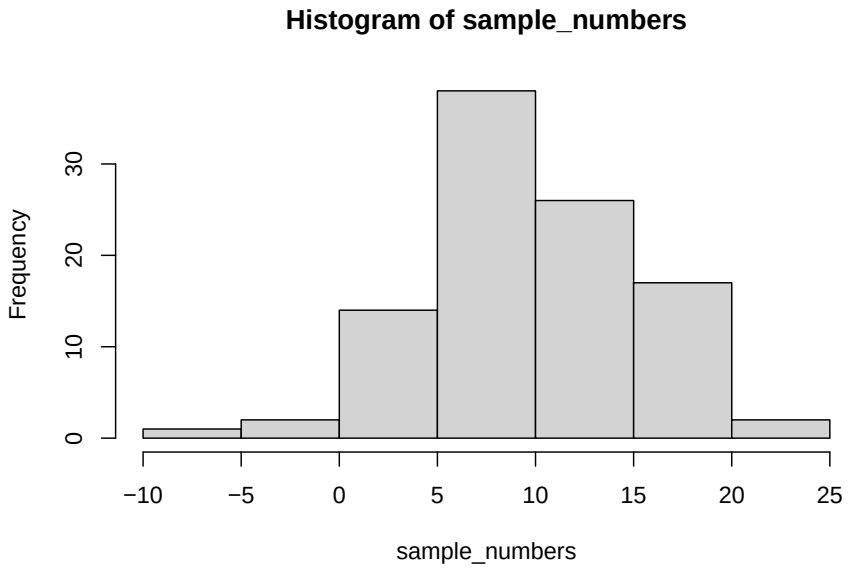
```
## [1] 1
```

2.2.3 Variation

We often want to know how variable the numbers are. We are going to look at descriptive statistics to describe this such as the **range**, **variance**, the **standard deviation**, and a few others.

First, let's remind ourselves what variation looks like (it's when the numbers are different). We will sample 100 numbers from a normal distribution (don't worry about this yet), with a mean of 10, and a standard deviation of 5, and then make a histogram so we can see the variation around 10..

```
sample_numbers <- rnorm(100,10,5)
hist(sample_numbers)
```



2.2.3.1 range

The range is the minimum and maximum values in the set, we use the `range` function.

```
range(sample_numbers)
```

```
## [1] -6.116085 21.120523
```

2.2.3.2 var = variance

We can find the sample variance using `var`. Note, divides by (n-1)

```
var(sample_numbers)
```

```
## [1] 27.49566
```

2.2.3.3 sd = standard deviation

We find the sample standard deviation us SD. Note, divides by (n-1)

```
sd(sample_numbers)
```

```
## [1] 5.243631
```

Remember that the standard deviation is just the square root of the variance, see:

```
sqrt(var(sample_numbers))
```

```
## [1] 5.243631
```

2.2.3.4 All Descriptives

Let's put all of the descriptives and other functions so far in one place:

```
sample_numbers <- rnorm(100,10,5)

sum(sample_numbers)
```

```
## [1] 1002.548
```

```
length(sample_numbers)
```

```
## [1] 100
```

```
mean(sample_numbers)
```

```
## [1] 10.02548
```

```
median(sample_numbers)
```

```
## [1] 10.16463
```

```
my_mode(sample_numbers)
```

```
## [1] 10.54972
```

```
range(sample_numbers)
```

```
## [1] -0.3067084 26.5661968
```

```
var(sample_numbers)
```

```
## [1] 25.48026
```

```
sd(sample_numbers)
```

```
## [1] 5.047797
```

2.2.4 Descriptives by conditions

Sometimes you will have a single variable with some numbers, and you can use the above functions to find the descriptives for that variable. Other times (most often in this course), you will have a big data frame of numbers, with different numbers in different conditions. You will want to find descriptive statistics for each the sets of numbers inside each of the conditions. Fortunately, this is where R really shines, it does it all for you in one go.

Let's illustrate the problem. Here I make a date frame with 10 numbers in each condition. There are 10 conditions, each labelled, A, B, C, D, E, F, G, H, I, J.

```
scores <- rnorm(100,10,5)
conditions <- rep(c("A","B","C","D","E","F","G","H","I","J"), each =10)
my_df <- data.frame(conditions,scores)
```

If you look at the `my_df` data frame, you will see it has 100 rows, there are 10 rows for each condition with a label in the `conditions` column, and 10 scores for each condition in the `scores` column. What if you wanted to know the mean of the scores in each condition? You would want to find 10 means.

The slow way to do it would be like this:

```
mean(my_df[my_df$conditions=="A",]$scores)
```

```
## [1] 9.636791
```

```
mean(my_df[my_df$conditions=="B",]$scores)
```

```
## [1] 7.364333
```

```
mean(my_df[my_df$conditions=="C",]$scores)
```

```
## [1] 12.85212
```

```
# and then keep going
```

Nobody wants to do that! Not, me I stopped doing it that way, you should to.

2.2.4.1 group_by and summarise

We can easily do everything all at once using the `group_by` and `summarise` function from the `dplyr` package. Just watch

```
library(dplyr)

my_df %>%
  group_by(conditions) %>%
  summarise(means = mean(scores))
```

```
## # A tibble: 10 x 2
##    conditions means
##    <chr>      <dbl>
##  1 A           9.64
##  2 B           7.36
##  3 C          12.9
##  4 D           8.05
##  5 E           6.94
##  6 F           9.47
##  7 G           7.94
##  8 H           9.49
##  9 I           9.59
## 10 J           9.82
```

A couple things now. First, the print out of this was ugly. Let's fix that. we put the results of our code into a new variable, then we use `knitr::kable` to print it out nicely when we `knit` the document

```
summary_df <- my_df %>%
               group_by(conditions) %>%
               summarise(means = mean(scores))

knitr::kable(summary_df)
```

conditions	means
A	9.636791
B	7.364333
C	12.852121
D	8.046196
E	6.944765
F	9.468628
G	7.937272
H	9.491867
I	9.585712
J	9.823514

2.2.4.2 multiple descriptives

The best thing about the `dplyr` method, is that we can add more than one function, and we'll get more than one summary returned, all in a nice format, let's add the standard deviation:

```
summary_df <- my_df %>%
                group_by(conditions) %>%
                summarise(means = mean(scores),
                          sds = sd(scores))

knitr::kable(summary_df)
```

conditions	means	sds
A	9.636791	4.863356
B	7.364333	3.122062
C	12.852121	4.996556
D	8.046196	3.303041
E	6.944765	3.546821
F	9.468628	5.443471
G	7.937272	2.800717
H	9.491867	5.070831
I	9.585712	4.190495
J	9.823514	3.098157

We'll add the min and the max too:

```
summary_df <- my_df %>%
                group_by(conditions) %>%
                summarise(means = mean(scores),
                          sds = sd(scores),
                          min = min(scores),
                          max = max(scores))
```

```
knitr::kable(summary_df)
```

conditions	means	sds	min	max
A	9.636791	4.863356	0.1364273	17.64975
B	7.364333	3.122062	3.6478959	12.42980
C	12.852121	4.996556	2.0882922	18.39466
D	8.046196	3.303041	2.4214303	11.46234
E	6.944765	3.546821	-1.1854933	11.79227
F	9.468628	5.443471	1.2916955	16.47118
G	7.937272	2.800717	3.9929287	12.80781
H	9.491867	5.070831	1.2040815	17.31615
I	9.585712	4.190495	3.0639624	16.48314
J	9.823514	3.098157	5.4935171	14.78114

2.2.5 Describing gapminder

Now that we know how to get descriptive statistics from R, we cam do this will some real data. Let's quickly ask a few question about the gapminder data.

```
library(gapminder)
gapminder_df <- gapminder
```

Note: The above code will only work if you have installed the gapminder package. Make sure you are connected to the internet, then choose the Packages tab from the bottom right panel, and choose install. Thens search for gapminder, choose it, and install it.

2.2.5.1 What are some descriptive for Life expectancy by continent?

Copy the code from the last part of descriptives using `dplyr`, then change the names like this:

```
summary_df <- gapminder_df %>%
               group_by(continent) %>%
               summarise(means = mean(lifeExp),
                         sds = sd(lifeExp),
                         min = min(lifeExp),
                         max = max(lifeExp))

knitr::kable(summary_df)
```

continent	means	sds	min	max
Africa	48.86533	9.150210	23.599	76.442
Americas	64.65874	9.345088	37.579	80.653
Asia	60.06490	11.864532	28.801	82.603
Europe	71.90369	5.433178	43.585	81.757
Oceania	74.32621	3.795611	69.120	81.235

2.2.6 Generalization Exercise

(1 point - Pass/Fail)

Complete the generalization exercise described in your R Markdown document for this lab.

1. What is the mean, standard deviation, minimum and maximum life expectancy for all the gapminder data (across all the years and countries). Hint: do not use `group_by`
2. What is the mean, standard deviation, minimum and maximum life expectancy for all of the continents in 2007, the most recent year in the dataset. Hint: add another pipe using `filter(year==2007) %>%`

2.2.7 Writing assignment

(2 points - Graded)

Complete the writing assignment described in your R Markdown document for this lab. When you have finished everything. Knit the document and hand in your stuff (you can submit your .RMD file to blackboard if it does not knit.)

Your writing assignment is to answer these questions in full sentences using simple plain langauge:

1. Define the mode.
2. Explain what would need to happen in order for a set of numbers to have two modes
3. Define the median
4. Define the mean
5. Define the range
6. When calculating the standard deviation, explain what the difference scores represent
7. Explain why the difference scores are squared when calculating the standard deviation
8. If one set of numbers had a standard deviation of 5, and another had a standard deviation of 10, which set of numbers would have greater variance, explain why.

Rubric

General grading.

- You will receive 0 points for missing answers (say, if you do not answer question c, then you will receive 0 out .25 points for that question)
- You must write in complete sentences. Point form sentences will be given 0 points.
- Completely incorrect answers will receive 0 points.
- If your answer is generally correct but very difficult to understand and unclear you may receive half points for the question

2.2.8 Practice Problems

---

1. Using the life expectancy data set, produce a table of output showing the descriptive statistics (measures of central tendency and variability) for both years 1800 and 1934 (during the Great Depression).

2. Plot histograms of life expectancy for both years. How are these distributions different? (Hint: Plot these on the same axes so that they are comparable).

Chapter 3

Lab 3: Correlation

If … we choose a group of social phenomena with no antecedent knowledge of the causation or absence of causation among them, then the calculation of correlation coefficients, total or partial, will not advance us a step toward evaluating the importance of the causes at work. —Sir Ronald Fisher

In lecture and in the textbook, we have been discussing the idea of correlation. This is the idea that two things that we measure can be somehow related to one another. For example, your personal happiness, which we could try to measure say with a questionnaire, might be related to other things in your life that we could also measure, such as number of close friends, yearly salary, how much chocolate you have in your bedroom, or how many times you have said the word Nintendo in your life. Some of the relationships that we can measure are meaningful, and might reflect a causal relationship where one thing causes a change in another thing. Some of the relationships are spurious, and do not reflect a causal relationship.

In this lab you will learn how to compute correlations between two variables in software, and then ask some questions about the correlations that you observe.

3.1 General Goals

1. Compute Pearson's r between two variables using software
2. Discuss the possible meaning of correlations that you observe

3.1.1 Important Info

We use data from the World Happiness Report. A .csv of the data can be found here: WHR2018.csv

3.2 R

In this lab we use explore to explore correlations between any two variables, and also show how to do a regression line. There will be three main parts. Getting R to compute the correlation, and looking at the data using scatter plots. We'll look at some correlations from the World Happiness Report. Then you'll look at correlations using data we collect from ourselves. It will be fun.

3.2.1 cor for correlation

R has the `cor` function for computing Pearson's r between any two variables. In fact this same function computes other versions of correlation, but we'll skip those here. To use the function you just need two variables with numbers in them like this:

```
x  <- c(1,3,2,5,4,6,5,8,9)
y  <- c(6,5,8,7,9,7,8,10,13)
cor(x,y)
```

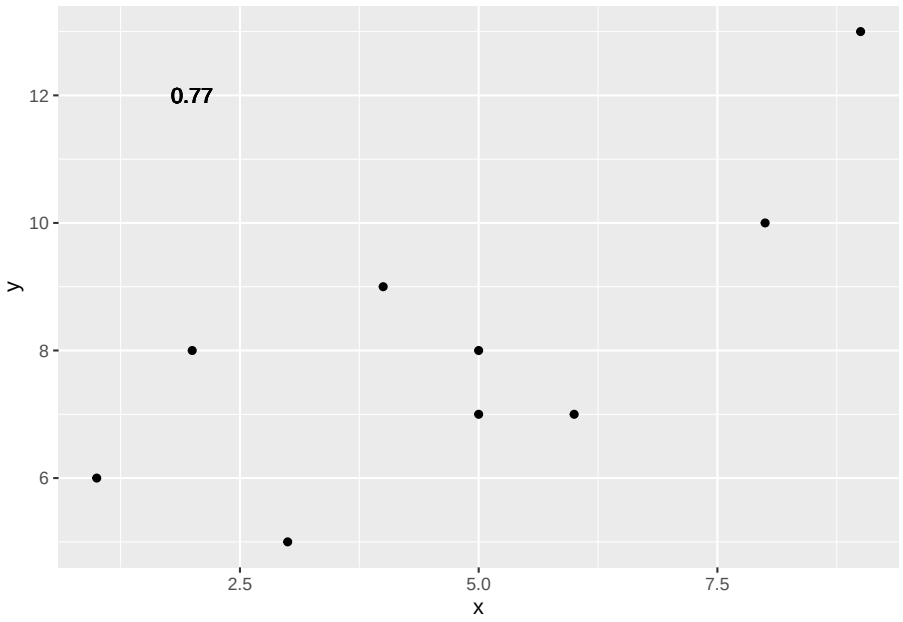
```
## [1] 0.76539
```

Well, that was easy.

3.2.1.1 scatterplots

Let's take our silly example, and plot the data in a scatter plot using ggplot2, and let's also return the correlation and print it on the scatter plot. Remember, ggplot2 wants the data in a data.frame, so we first put our x and y variables in a data frame.

```
library(ggplot2)

# create data frame for plotting
my_df <- data.frame(x,y)

# plot it
ggplot(my_df, aes(x=x,y=y))+
  geom_point()+
  geom_text(aes(label = round(cor(x,y), digits=2), y=12, x=2 ))
```

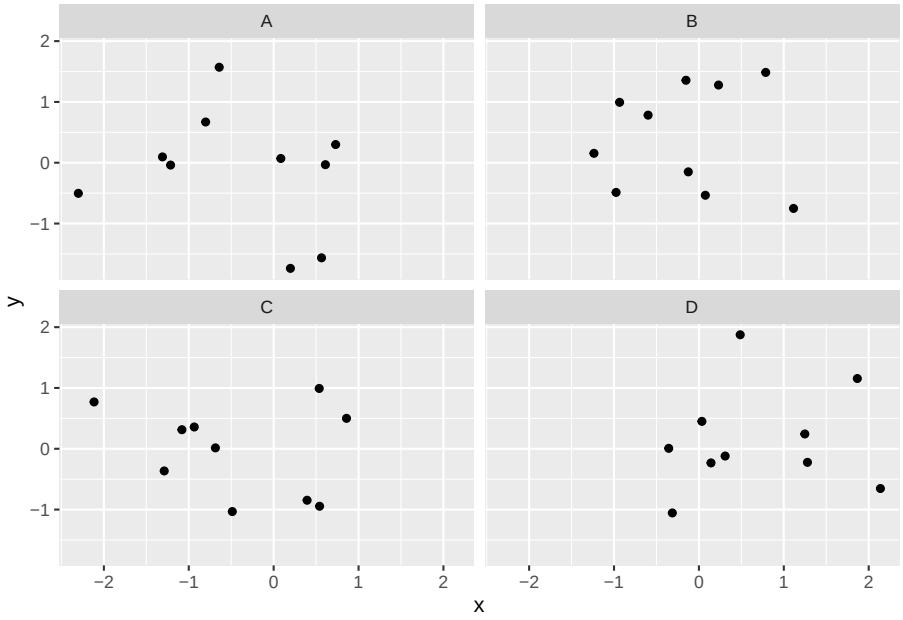


Wow, we're moving fast here.

3.2.1.2 lots of scatterplots

Before we move on to real data, let's look at some fake data first. Often we will have many measures of X and Y, split between a few different conditions, for example, A, B, C, and D. Let's make some fake data for X and Y, for each condition A, B, C, and D, and then use facet_wrapping to look at four scatter plots all at once

```
x<-rnorm(40,0,1)
y<-rnorm(40,0,1)
conditions<-rep(c("A","B","C","D"), each=10)

all_df <- data.frame(conditions, x, y)

ggplot(all_df, aes(x=x,y=y))+
  geom_point()+
  facet_wrap(~conditions)
```



3.2.1.3 computing the correlations all at once

We've seen how we can make four graphs at once. Facet_wrap will always try to make as many graphs as there are individual conditions in the column variable. In this case there are four, so it makes four.

Notice, the scatter plots don't show the correlation (r) values. Getting these numbers on there is possible, but we have to calculate them first. We'll leave it to you to Google how to do this, if it's something you want to do. Instead, what we will do is make a table of the correlations in addition to the scatter plot. We again use `dplyr` to do this:

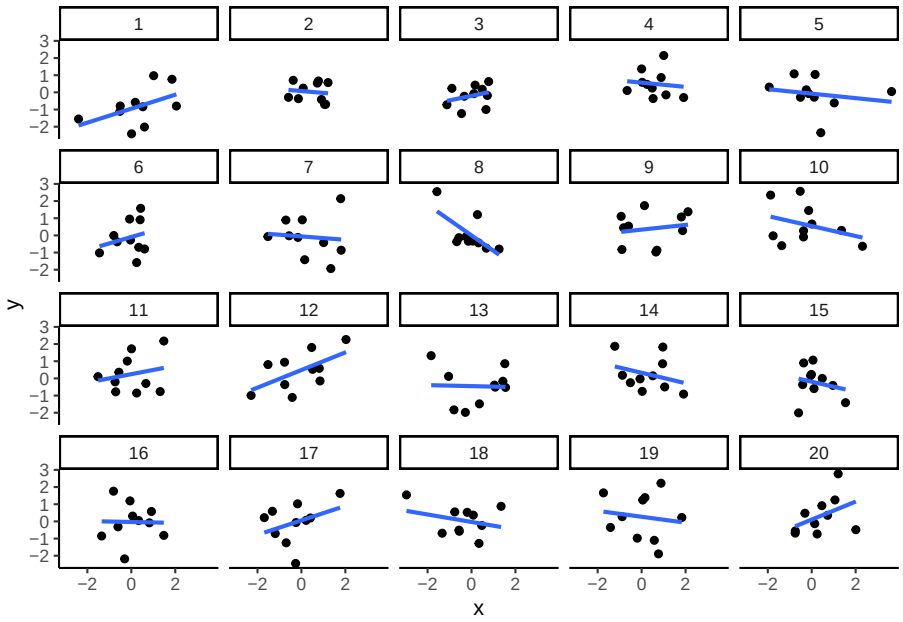
OK, we are basically ready to turn to some real data and ask if there are correlations between interesting variables…You will find that there are some… But before we do that, we do one more thing. This will help you become a little bit more skeptical of these "correlations".

3.2.1.4 Chance correlations

As you learned from the textbook. We can find correlations by chance alone, even when there is no true correlation between the variables. For example, if we sampled randomly into x, and then sampled some numbers randomly into y. We know they aren't related, because we randomly sampled the numbers. However, doing this creates some correlations some of the time just by chance.

You can demonstrate this to yourself with the following code. It's a repeat of what we already saw, jut with a few more conditions added. Let's look at 20 conditions, with random numbers for x and y in each. For each, sample size will be 10. We'll make the fake data, then make a big graph to look at all. And, even though we get to regression later in the lab, I'll put the best fit line onto each scatter plot, so you can "see the correlations".

```
x<-rnorm(10*20,0,1)
y<-rnorm(10*20,0,1)
conditions<-rep(1:20, each=10)

all_df <- data.frame(conditions, x, y)

ggplot(all_df, aes(x=x,y=y))+
  geom_point()+
  geom_smooth(method=lm, se=FALSE)+
  facet_wrap(~conditions)+
  theme_classic()
```



You can see that the slope of the blue line is not always flat. Sometimes it looks like there is a correlation, when we know there shouldn't be. You can keep re-doing this graph, by re-knitting your R Markdown document, or by pressing the little green play button. This is basically you simulating the outcomes as many times as you press the button.

The point is, now you know you can find correlations by chance. So, in the next

section, you should always wonder if the correlations you find reflect meaningful association between the x and y variable, or could have just occurred by chance.

3.2.2 World Happiness Report

Let's take a look at some correlations in real data. We are going to look at responses to a questionnaire about happiness that was sent around the world, from the world happiness report

3.2.2.1 Load the data

We load the data into a data frame. Reminder, the following assumes that you have downloaded the RMarkdownsLab.zip file which contains the data file in the data folder.

```
library(data.table)
whr_data <- fread('data/WHR2018.csv')
```

You can also load the data using the following URL

```
library(data.table)
whr_data <- fread("https://raw.githubusercontent.com/CrumpLab/statisticsLab/master/data
```

3.2.2.2 Look at the data

```
library(summarytools)
view(dfSummary(whr_data))
```

You should be able to see that there is data for many different countries, across a few different years. There are lots of different kinds of measures, and each are given a name. I'll show you some examples of asking questions about correlations with this data, then you get to ask and answer your own questions.

3.2.2.3 My Question #1

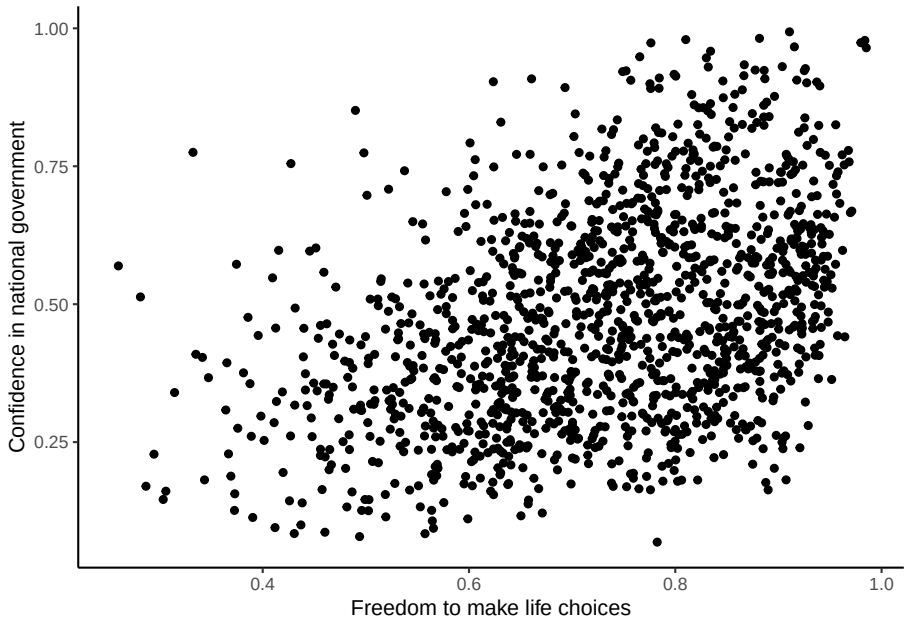
For the year 2017 only, does a countries measure for "freedom to make life choices" correlate with that countries measure for " Confidence in national government"?

Let's find out. We calculate the correlation, and then we make the scatter plot.

```
cor(whr_data$`Freedom to make life choices`,
    whr_data$`Confidence in national government`)
```

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

```
ggplot(whr_data, aes(x=`Freedom to make life choices`,
                     y=`Confidence in national government`))+
  geom_point()+
  theme_classic()
```



Interesting, what happened here? We can see some dots, but the correlation was NA (meaning undefined). This occurred because there are some missing data points in the data. We can remove all the rows with missing data first, then do the correlation. We will do this a couple steps, first creating our own data.frame with only the numbers we want to analyse. We can select the columns we want to keep using `select`. Then we use `filter` to remove the rows with NAs.

```
library(dplyr)

smaller_df <- whr_data %>%
               select(country,
                      `Freedom to make life choices`,
                      `Confidence in national government`) %>%
```

```
                filter(!is.na(`Freedom to make life choices`),
                       !is.na(`Confidence in national government`))

cor(smaller_df$`Freedom to make life choices`,
    smaller_df$`Confidence in national government`)
```

```
## [1] 0.4080963
```

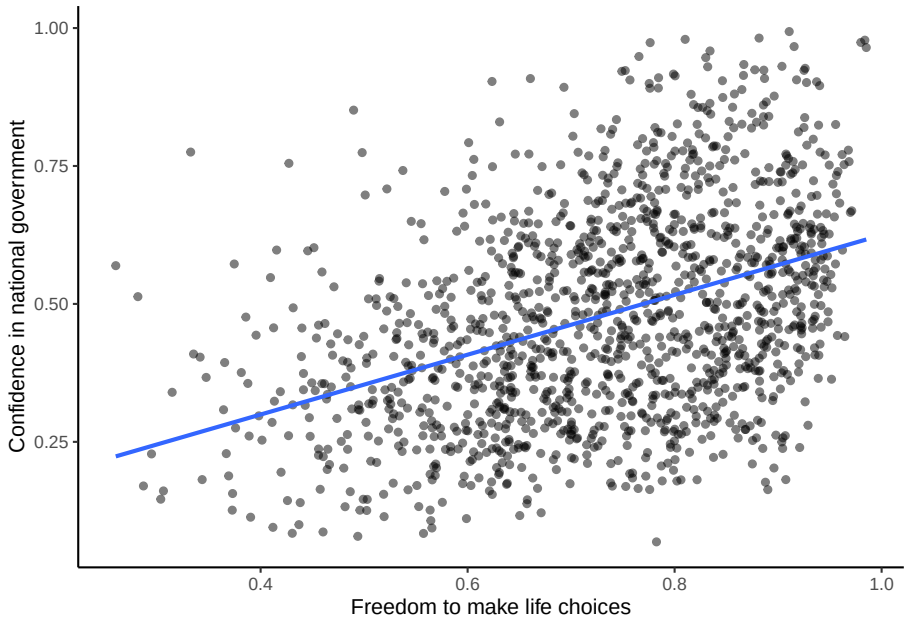
Now we see the correlation is .408.

Although the scatter plot shows the dots are everywhere, it generally shows that as Freedom to make life choices increases in a country, that countries confidence in their national government also increase. This is a positive correlation. Let's do this again and add the best fit line, so the trend is more clear, we use `geom_smooth(method=lm, se=FALSE)`. I also change the `alpha` value of the dots so they blend it bit, and you can see more of them.

```
# select DVs and filter for NAs

smaller_df <- whr_data %>%
                select(country,
                       `Freedom to make life choices`,
                       `Confidence in national government`) %>%
                filter(!is.na(`Freedom to make life choices`),
                       !is.na(`Confidence in national government`))

# calcualte correlation

cor(smaller_df$`Freedom to make life choices`,
    smaller_df$`Confidence in national government`)
```

```
## [1] 0.4080963
```

```
# plot the data with best fit line

ggplot(smaller_df, aes(x=`Freedom to make life choices`,
                       y=`Confidence in national government`))+
  geom_point(alpha=.5)+
  geom_smooth(method=lm, se=FALSE)+
  theme_classic()
```



3.2.2.4 My Question #2

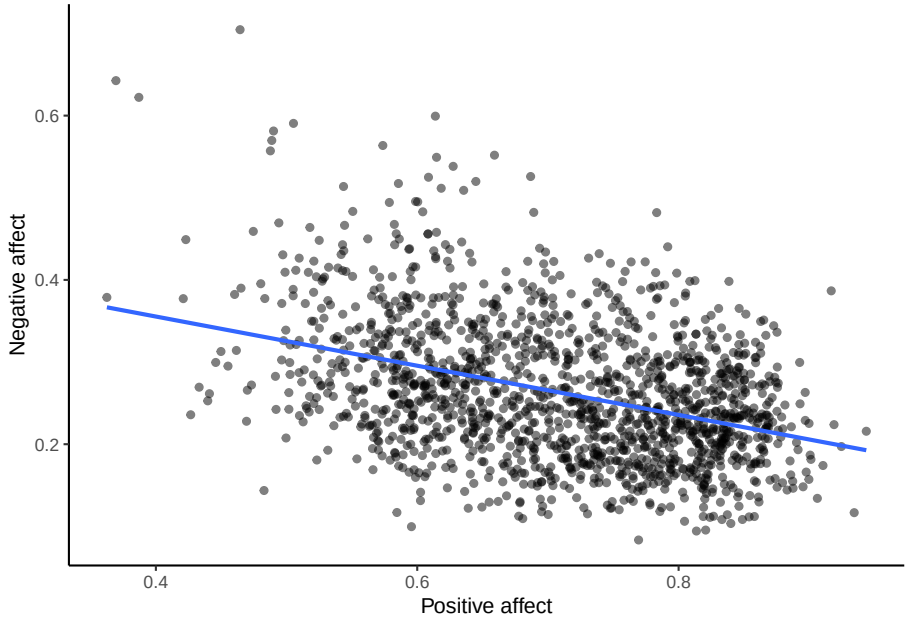
After all that work, we can now speedily answer more questions. For example, what is the relationship between positive affect in a country and negative affect in a country. I wouldn't be surprised if there was a negative correlation here: when positive feelings generally go up, shouldn't negative feelings generally go down?

To answer this question, we just copy paste the last code block, and change the DVs to be `Positive affect`, and `Negative affect`

```
# select DVs and filter for NAs

smaller_df <- whr_data %>%
                select(country,
                       `Positive affect`,
                       `Negative affect`) %>%
                filter(!is.na(`Positive affect`),
                       !is.na(`Negative affect`))

# calcualte correlation

cor(smaller_df$`Positive affect`,
    smaller_df$`Negative affect`)
```

```
## [1] -0.3841123
```

```
# plot the data with best fit line

ggplot(smaller_df, aes(x=`Positive affect`,
                       y=`Negative affect`))+
  geom_point(alpha=.5)+
  geom_smooth(method=lm, se=FALSE)+
  theme_classic()
```



Bam, there we have it. As positive affect goes up, negative affect goes down. A negative correlation.

3.2.3 Generalization Exercise

This generalization exercise will explore the idea that correlations between two measures can arise by chance alone. There are two questions to answer. For each question you will be sampling random numbers from uniform distribution. To conduct the estimate, you will be running a simulation 100 times. The questions are:

1. Estimate the range (minimum and maximum) of correlations (using pearons's r) that could occur by chance between two variables with n=10.

2. Estimate the range (minimum and maximum) of correlations (using pearons's r) that could occur bychance between two variables with n = 100.

Use these tips to answer the question.

Tip 1: You can use the `runif()` function to sample random numbers between a minimum value, and maximum value. The example below sample 10 (n=10) random numbers between the range 0 (min = 0) and 10 (max=10). Everytime you run this code, the 10 values in x will be re-sampled, and will be 10 new random numbers

```
x <- runif(n=10, min=0, max=10)
```

Tip 2: You can compute the correlation between two sets of random numbers, by first sampling random numbers into each variable, and then running the `cor()` function.

```
x <- runif(n=10, min=0, max=10)
y <- runif(n=10, min=0, max=10)
cor(x,y)
```

```
## [1] -0.1745448
```

Running the above code will give different values for the correlation each time, because the numbers in x and y are always randomly different. We might expect that because x and y are chosen randomly that there should be a 0 correlation. However, what we see is that random sampling can produce "fake" correlations just by chance alone. We want to estimate the range of correlations that chance can produce.

Tip 3: One way to estimate the range of correlations that chance can produce is to repeat the above code many times. For example, if you ran the above code 100 times, you could save the correlations each time, then look at the smallest and largest correlation. This would be an estimate of the range of correlations that can be produced by chance. How can you repeat the above code many times to solve this problem?

We can do this using a `for` loop. The code below shows how to repeat everything inside the for loop 100 times. The variable `i` is an index, that goes from 1 to 100. The `saved_value` variable starts out as an empty variable, and then we put a value into it (at index position i, from 1 to 100). In this code, we put the sum of the products of x and y into the `saved_value` variable. At the end of the simulation, the `save_value` variable contains 100 numbers. The `min()` and `max()` functions are used to find the minimum and maximum values for each of the 100 simulations. You should be able to modify this code by replacing

`sum(x*y)` with `cor(x,y)`. Doing this will allow you to run the simulation 100 times, and find the minimum correlation and maximum correlation that arises by chance. This will be estimate for question 1. To provide an estimate for question 2, you will need to change `n=10` to `n=100`.

```
saved_value <- c() #make an empty variable
for (i in 1:100){
  x <- runif(n=10, min=0, max=10)
  y <- runif(n=10, min=0, max=10)
  saved_value[i] <- sum(x*y)
}

min(saved_value)
```

```
## [1] 93.29848
```

```
max(saved_value)
```

```
## [1] 424.6493
```

3.2.4 Writing assignment

Answer the following questions with complete sentences. When you have finished everything. Knit the document and hand in your stuff (you can submit your .RMD file to blackboard if it does not knit.)

1. Imagine a researcher found a positive correlation between two variables, and reported that the r value was +.3. One possibility is that there is a true correlation between these two variables. Discuss one alternative possibility that would also explain the observation of +.3 value between the variables.
2. Explain the difference between a correlation of r = .3 and r = .7. What does a larger value of r represent?
3. Explain the difference between a correlation of r = .5, and r = -.5.

3.2.5 Practice Problems

---

1. For the year 2005 ONLY, find the correlation between "perceptions of corruption" and "positive affect". Create a scatterplot to visualize this relationship. What are your conclusions about the relationship between affect and perceived corruption? Is this surprising to you?

2. What has happened to log GDP (consider this a measure of GDP) in the United States ONLY with time (as the year has increased)? Explain this relationship and provide a scatterplot.

3. Which country (or countries) have seen a more consistent and strong increase in log GDP over time? Which country (or countries) have seen a decrease over time?

Chapter 4

Lab 4: Normal Distribution & Central Limit Theorem

By a small sample, we may judge of the whole piece. —Miguel de Cervantes from Don Quixote

4.1 General Goals

1. Distributions
2. Sampling from distributions
3. Sampling distribution of the mean
4. Sampling statistics (statistics of many samples)
5. Central limit theorem
6. Normal Distribution
7. z-scores

4.2 R

This is one of two special labs where we don't use too much real data. We will mostly fake everything. Yes, you will learn how to fake data in this course. Be a superhero, and only use these skills for good and not for evil.

As we progress through the course, you will learn that generating simulated data can be very useful to help you understand real data. In fact, I will say this right now. If you can't simulate the data you expect to find, then you probably can't understand the data that you do find very well. That's a bold statement. It's probably partly true.

4.2.1 Generating Numbers in R

There are many ways to make R generate numbers for you. In all cases you define how the numbers are generated. We'll go through a few of the many ways.

4.2.1.1 sample

The sample function is like an endless gumball machine. You put the gumballs inside with different properties, say As and Bs, and then you let sample endlessly take gumballs out. Check it out:

```
gumballs <- c("A","B")
sample_of_gumballs <-sample(gumballs, 10, replace=TRUE)
sample_of_gumballs
```

```
##  [1] "B" "B" "A" "B" "B" "B" "B" "B" "A" "B"
```

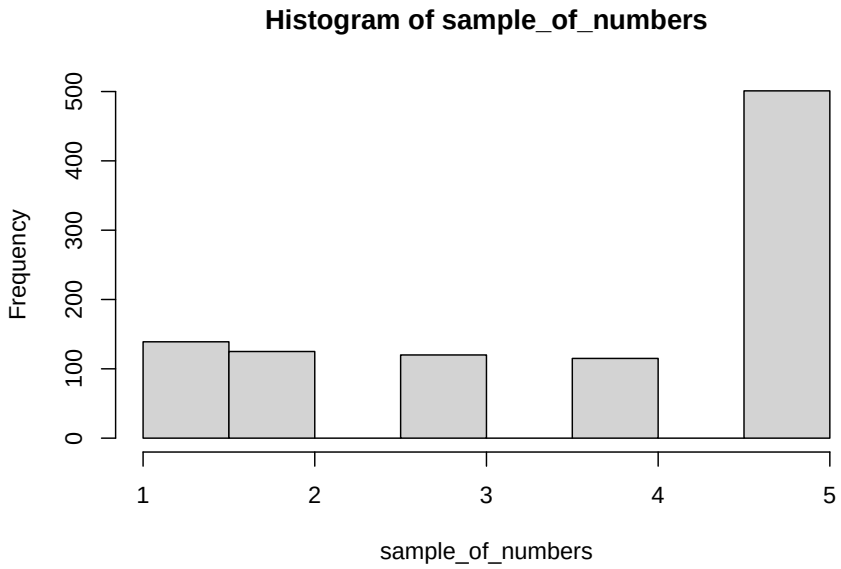
Here the sample function randomly picks A or B each time. We set it do this 10 times, so our sample has 10 things in it. We set `replace=TRUE` so that after each sample, we put the item back into the gumball machine and start again. Here's another example with numbers

```
some_numbers <- c(1,2,3,4,5,5,5,5)
sample_of_numbers <-sample(some_numbers, 20, replace=TRUE)
sample_of_numbers
```

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

Let's do one more thing with sample. Let's sample 1000 times from our `some_numbers` variable, and then look at the histogram

```
library(ggplot2)
some_numbers <- c(1,2,3,4,5,5,5,5)
sample_of_numbers <-sample(some_numbers, 1000, replace=TRUE)
hist(sample_of_numbers)
```

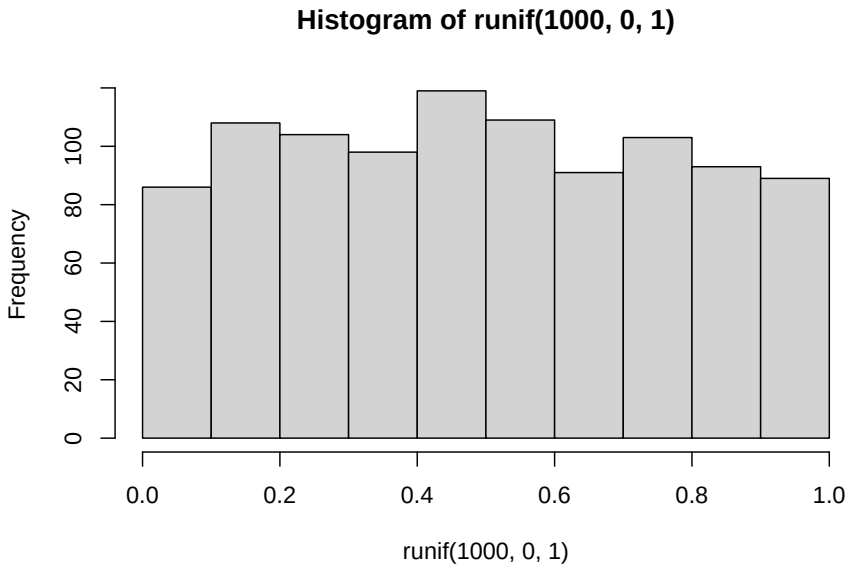


We are looking at lots of samples from our little gumball machine of numbers. We put more 5s in, and voila, more 5s come out of in our big sample of 1000.

4.2.1.2 runif uniform distribution

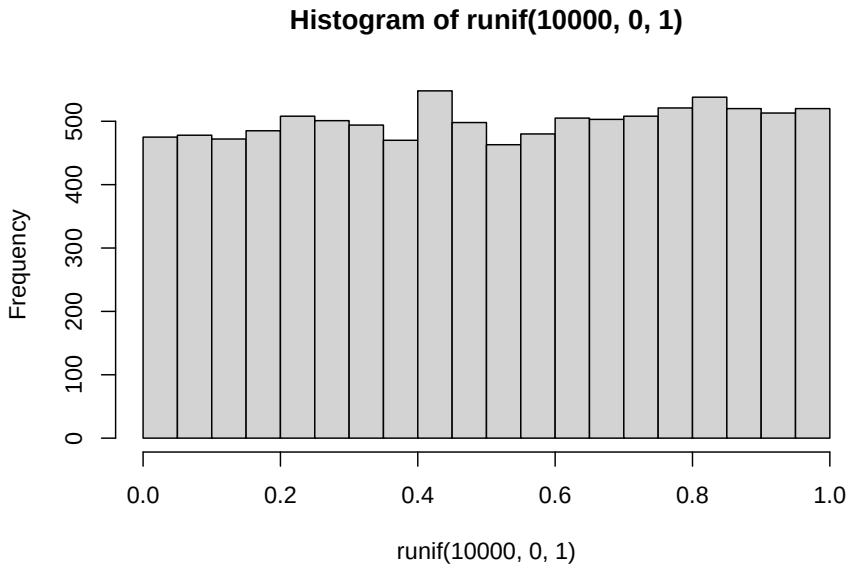
We can sample random numbers between any range using the `runif(n, min=0, max = 1)` function for the uniform distribution. We discussed this in the textbook. A uniform distribution is flat, and all the numbers between the min and max should occur roughly equally frequently. Let's take 1000 random numbers between 0 and 1 and plot the histogram. We'll just do it all in one line for speed.

```
hist(runif(1000,0,1))
```



This is histogram is flattish. Not perfectly flat, after all we only took 1000 samples. What if we took many more, say 10,000 total samples? Now it looks more flat, each bin is occurring about 500 times each, which is pretty close to the same amount.

```
hist(runif(10000,0,1))
```



4.2.1.3 rbinom the binomial distribution

The binomial distribution sounds like a scary word… binomial (AAGGGGHHHHH, stay away!). The binomial can be a coin flipping distribution. You use `rbinom(n, size, prob)`. `n` gives the number of samples you want to take. We'll keep `size = 1` for now, it's the number of trials (forget this for now, it's more useful for more complicated things than what we are doing, if you want to know what it does, try it out, and see if you figure it out). `prob` is a little list you make of probabilities, that define how often certain things happen.

For example, consider flipping a coin. It will be heads or tails, and the coin, if it is fair, should have a 50% chance of being heads or tails. Here's how we flip a coin 10 times using `rbinom`.

```
coin_flips <- rbinom(10,1,.5)
coin_flips
```

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

We get a bunch of 0s, and 1s. We can pretend 0 = tails, and 1 = heads. Great, now we can do coin flipping if we want. For example, if you flip 10 coins, how many heads do you get? We can can do the above again, and then `sum(coin_flips)`. All the 1s are heads, so it will work out.

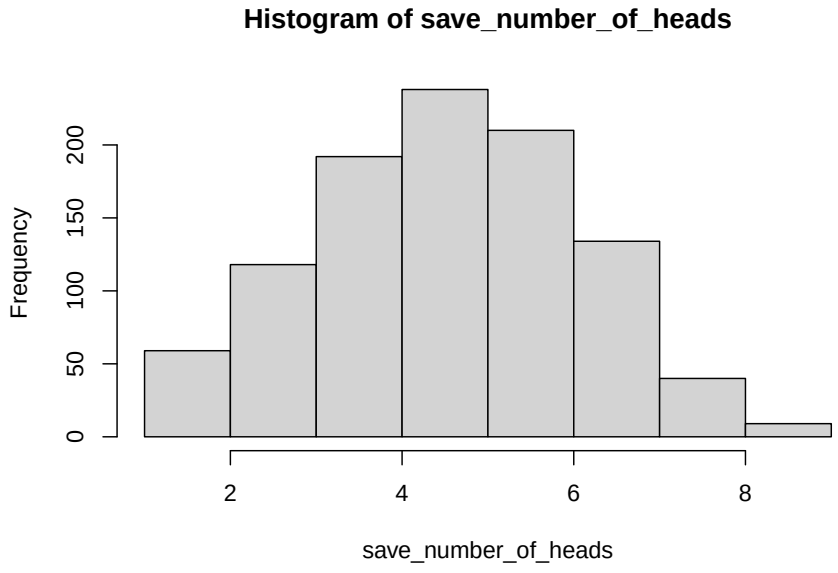
```
coin_flips <- rbinom(10,1,.5)
sum(coin_flips)
```

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

Alright, so we get the sum, which tells us the number of heads. But, should we always get that number of heads if we flipped a coin 10 times? If you keep redoing the above, you'll get different answers. 5 heads will be the most frequent answer, but you will get lots of other answers too.

Hold on to your seats for this next one. With R, we can simulate the flipping of a coin 10 times (you already know that, you just did it), and we can do that over and over as many times as we want. For example, we could do it 100 times over, saving the number of heads for each set of 10 flips. Then we could look at the distribution of those sums. That would tell us about the range of things that can happen when we flip a coin 10 times. We can do that in loop like this:

```
save_number_of_heads<-length(1000) # make an empty variable to save things in

for(i in 1:1000){
  save_number_of_heads[i] <- sum(rbinom(10,1,.5))
}

hist(save_number_of_heads)
```

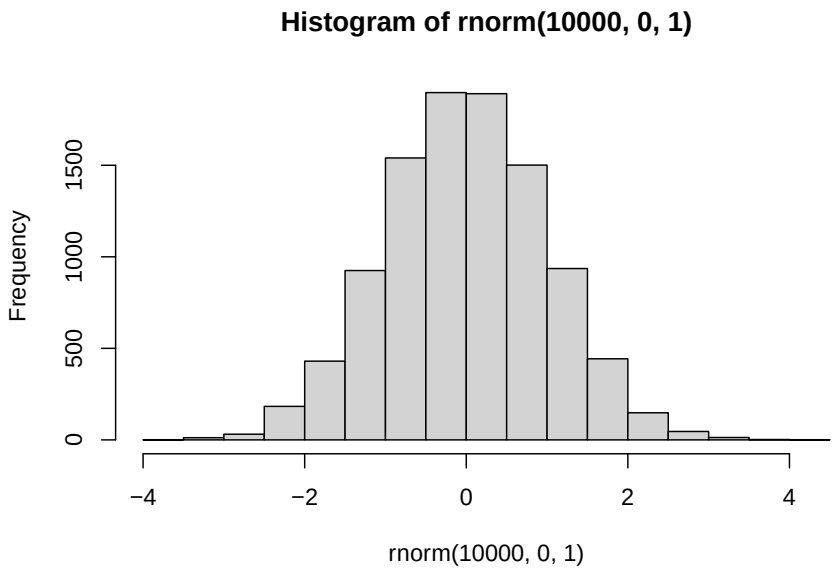


See, that wasn't too painful. Now we see another histogram. The histogram shows us the frequency observing different numbers of heads (for 10 flips) across the 1000 simulations. 5 happens the most, but 2 happens sometimes, and so does 8. All of the possibilities seem to happen sometimes, some more than others.

4.2.1.4 rnorm the normal distribution

We'll quickly show how to use `rnorm(n, mean=0, sd=1)` to sample numbers from a normal distribution. And, then we'll come back to the normal distribution later, because it is so important.

```
hist(rnorm(10000,0,1))
```

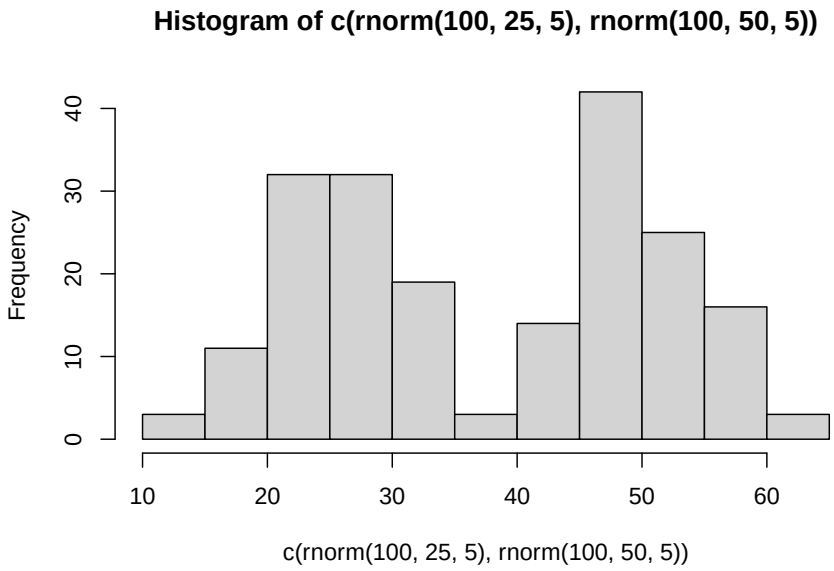


There it is, a bell-shaped normal distribution with a mean of 0, and a standard deviation of 1. You've probably seen things like this before. Now you can sample numbers from normal distributions with any mean or standard deviation, just by changing those parts of the `rnorm` function.

4.2.1.5 mixing it up

The r functions are like Legos, you can put them together and come up with different things. What if wanted to sample from a distribution that looked like a two-humped camel's back? Just sample from `rnorm` twice like this… mix away.

```
hist( c( rnorm(100,25,5), rnorm(100,50,5)) )
```



4.2.1.6 summary

You can generate as many numbers as your computer can handle with R. PSA: Don't ask R to generate a bajillion numbers or it will explode (or more likely just crash, probably won't explode, that's a metaphor).

4.2.2 sampling distribution of the mean.

Remember the sampling distribution of the sample means from the textbook? Now, you will see the R code that made the graphs from before. As we've seen, we can take samples from distributions in R. We can take as many as we want. We can set our sample-size to be anything we want. And, we can take multiple samples of the same size as many times as we want.

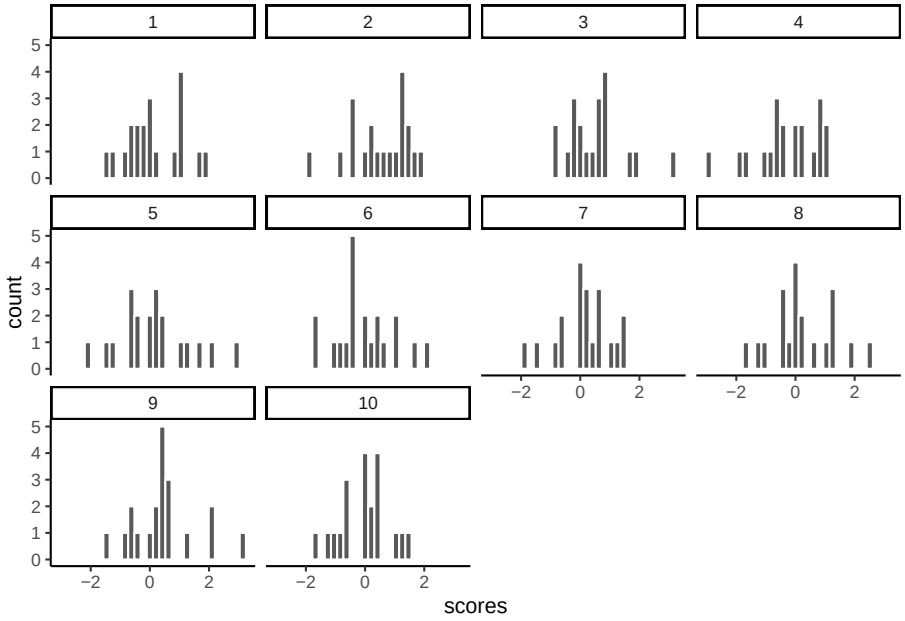
4.2.2.1 Taking multiple samples of the same size

Let's take 10 samples from a normal distribution (mean = 0, and SD = 1). Let's set the sample-size for each to be 20. Then, we'll put them all in a data frame and look at 10 different histograms, one for each sample.

```
scores <- rnorm(10*20,0,1)
samples <- rep(1:10,each=20)
my_df <- data.frame(samples,scores)
```

First, look at the new my_df data frame. You can see there is a column with numbers 1 to 10, these are the sample names. There are also 20 scores for each in the scores column. Let's make histograms for each sample, so we can see what all of the samples look like:

```
ggplot(my_df, aes(x=scores))+
  geom_histogram(color="white")+
  facet_wrap(~samples)+
  theme_classic()
```



Notice, all of the samples do not have the same looking histogram. This is because of random sampling error. All of the samples are coming from the same normal distributions, but random chance makes each sample a little bit different (e.g., you don't always get 5 heads and 5 tails when you flip a coin right)

4.2.2.2 Getting the means of the samples

Now, let's look at the means of the samples, we will use `dplyr` to get the means for each sample, and put them in a table:

```
library(dplyr)

sample_means <- my_df %>%
                group_by(samples) %>%
                summarise(means=mean(scores))

knitr::kable(sample_means)
```

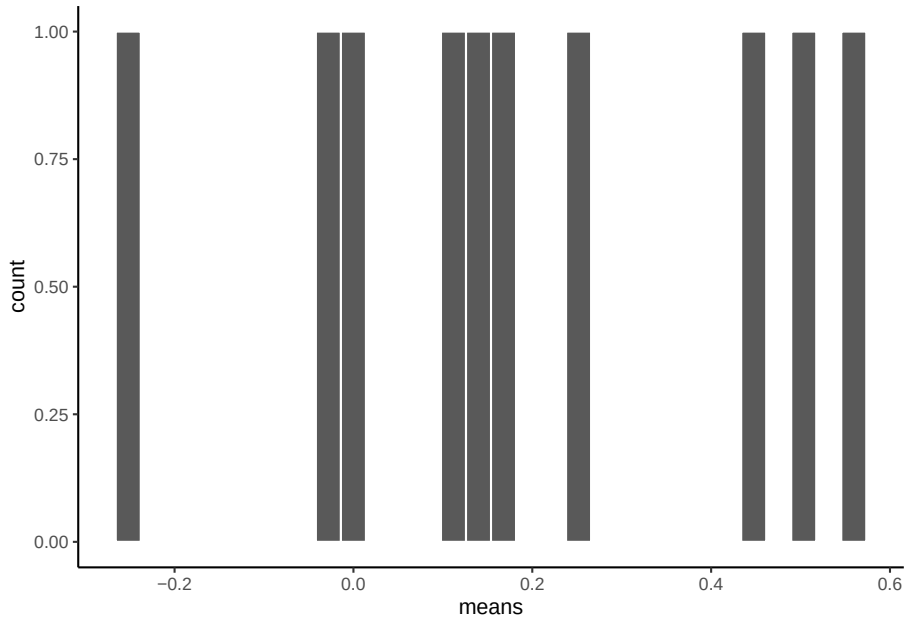
samples	means
1	0.1242773
2	0.5616046
3	0.5163987
4	-0.2496774
5	0.1534819
6	0.0060566
7	0.1632529
8	0.2536639
9	0.4376141
10	-0.0357752

So, those are the means of our samples. What should the means be? Well, we would hope they are estimating the mean of the distribution they came from, which was 0. Notice, the numbers are all not 0, but they are kind of close to 0.

4.2.2.3 histogram for the means of the samples

What if we now plot these 10 means (of each of the samples) in their own distribution?

```
ggplot(sample_means, aes(x=means))+
 geom_histogram(color="white")+
 theme_classic()
```



That is the distribution of the sample means. It doesn't look like much eh? That's because we only took 10 samples right.

Notice one more thing…What is the mean of our 10 sample means? This is a mean of means. Remember that.

```
mean(sample_means$means)
```

```
## [1] 0.1930898
```

Well, that's pretty close to zero. Which is good. When we average over our samples, they better estimate the mean of the distribution they came from.

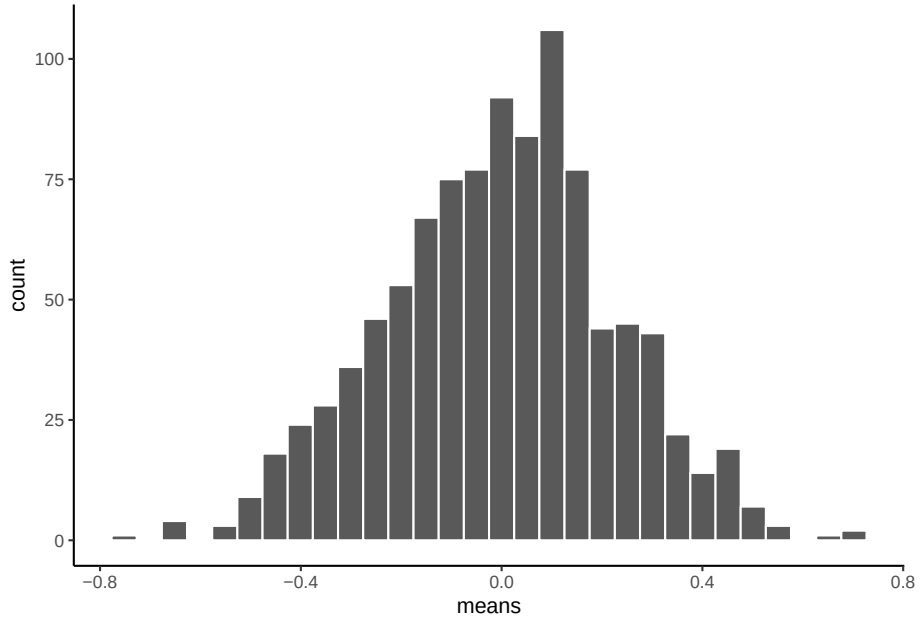
4.2.2.4 simulating the distribution of sample means

Our histogram with 10 sample means looked kind of sad. Let's give it some more friends. How about we repeat our little sampling experiment 1000 times.

Explain…We take 1000 samples. Each sample takes 20 scores from a normal distribution (mean=0, SD=1). Then we find the means of each sample (giving us 1000 sample means). Then, we plot that distribution.

```
# get 1000 samples with 20 scores each
```

```
scores <- rnorm(1000*20,0,1)
samples <- rep(1:1000,each=20)
my_df <- data.frame(samples,scores)

# get the means of the samples

sample_means <- my_df %>%
                group_by(samples) %>%
                summarise(means=mean(scores))

# make a histogram

 ggplot(sample_means, aes(x=means))+
  geom_histogram(color="white")+
  theme_classic()
```



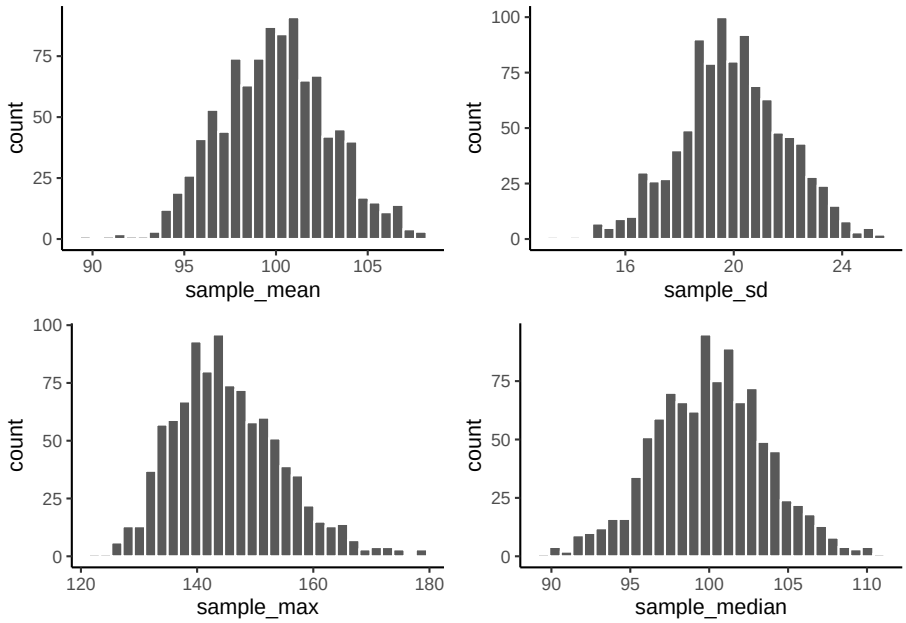
There, that looks more like a sampling distribution of the sample means. Notice it's properties. It is centered on 0, which tells us that sample means are mostly around zero. It is also bell-shaped, like the normal distribution it came from. It is also quite narrow. The numbers on the x-axis don't go much past -.5 to +.5.

We will use things like the sampling distribution of the mean to make inferences about what chance can do in your data later on in this course.

4.2.3 Sampling distributions for any statistic

Just for fun here are some different sampling distributions for different statistics. We will take a normal distribution with mean = 100, and standard deviation =20. Then, we'll take lots of samples with n = 50 (50 observations per sample). We'll save all of the sample statistics, then plot their histograms. We do the sample means, standard deviations, maximum values, and medians. Let's do it.

```
all_df<-data.frame()
for(i in 1:1000){
  sample<-rnorm(50,100,20)
  sample_mean<-mean(sample)
  sample_sd<-sd(sample)
  sample_max<-max(sample)
  sample_median<-median(sample)
  t_df<-data.frame(i,sample_mean,sample_sd,sample_max,sample_median)
  all_df<-rbind(all_df,t_df)
}

library(ggpubr)
a<-ggplot(all_df,aes(x=sample_mean))+
  geom_histogram(color="white")+
  theme_classic()
b<-ggplot(all_df,aes(x=sample_sd))+
  geom_histogram(color="white")+
  theme_classic()
c<-ggplot(all_df,aes(x=sample_max))+
  geom_histogram(color="white")+
  theme_classic()
d<-ggplot(all_df,aes(x=sample_median))+
  geom_histogram(color="white")+
  theme_classic()

ggarrange(a,b,c,d,
          ncol = 2, nrow = 2)
```



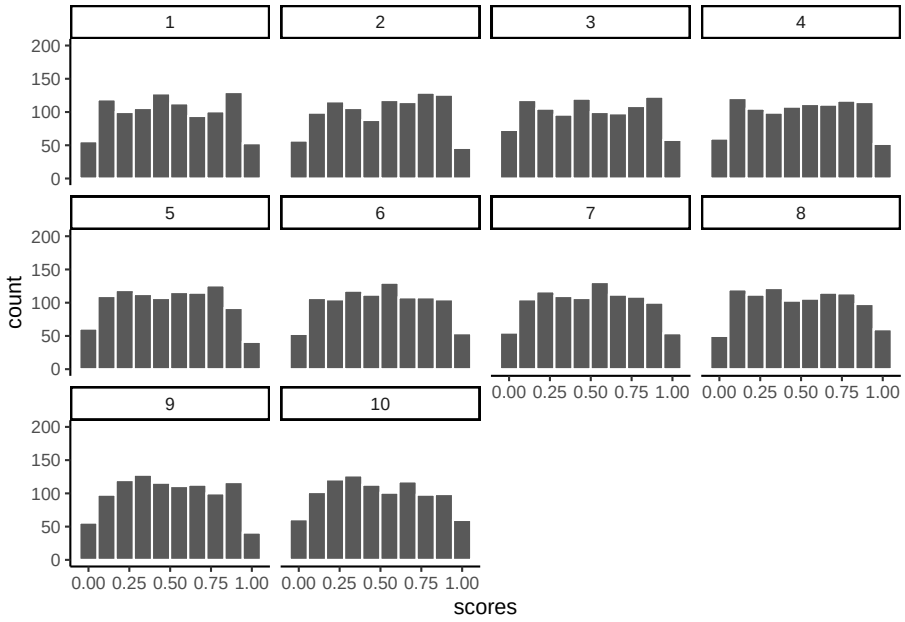
From reading the textbook and attending lecture, you should be able to start thinking about why these sampling statistic distributions might be useful…For now, just know that you can make a sampling statistic for pretty much anything in R, just by simulating the process of sampling, measuring the statistic, doing it over a bunch, and then plotting the histogram. This gives you a pretty good estimate of the distribution for that sampling statistic.

4.2.4 Central limit theorem

We have been building you up for the central limit theorem, described in the textbook and in class. The central limit theorem is basically that the distribution of sample means will be a normal curve. We already saw that before. But, the interesting thing about it, is that the distribution of your sample means will be normal, even if the distribution the samples came from is not normal. Huh what?

To demonstrate this the next bit of code is modified from what we did earlier. We create 100 samples. Each sample has 1000 observations. All of them come from a uniform distribution between 0 to 1. This means all of the numbers between 0 and 1 should occur equally frequently. Below I plot histograms for the first 10 samples (out of the 100 total, 100 is too many to look at). Notice the histograms are not normal, they are roughly flat.

```
scores <- runif(100*1000,0,1)
samples <- rep(1:100,each=1000)
my_df <- data.frame(samples,scores)

ggplot(my_df[1:(10*1000),], aes(x=scores))+
  geom_histogram(color="white", bins=10)+
  facet_wrap(~samples)+
  theme_classic()+
  ylim(0,200)
```

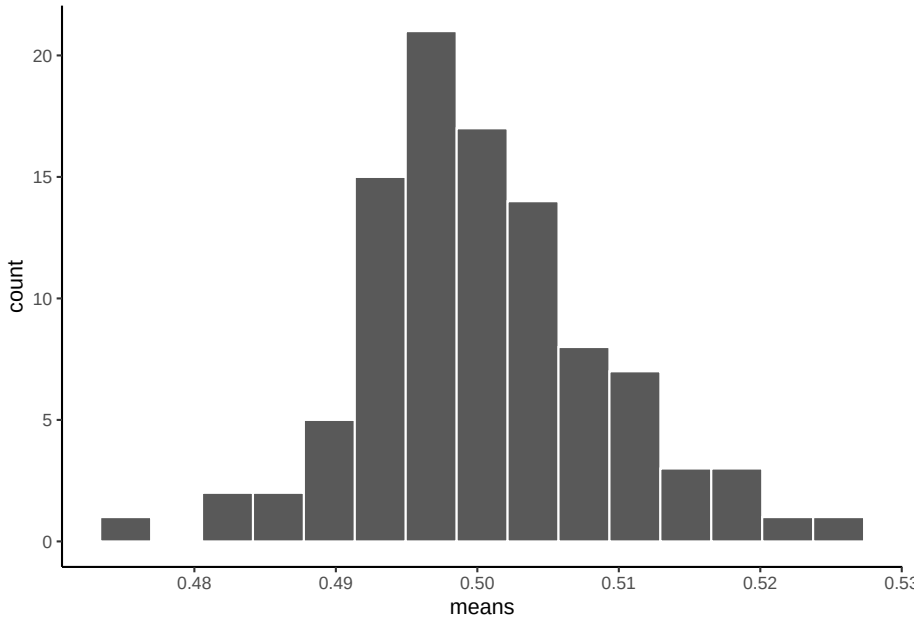


We took samples from a flat uniform distribution, and the samples themselves look like that same flat distribution.

HOWEVER, if we now do the next step, and compute the means of each of our 100 samples, we could then look at the sampling distribution of the sample means. Let's do that:

```
sample_means <- my_df %>%
                group_by(samples) %>%
                summarise(means=mean(scores))

# make a histogram

 ggplot(sample_means, aes(x=means))+
```

```
  geom_histogram(color="white", bins=15)+
  theme_classic()
```



As you can see, the sampling distribution of the sample means is not flat. It's shaped kind of normal-ish. If we had taken many more samples, found their means, and then looked at a histogram, it would become even more normal looking. Because that's what happens according to the central limit theorem.

4.2.5 The normal distribution

"Why does any of this matter, why are we doing this, can we stop now!!!!!! PLEEEEAASSEE, somebody HELP".

We are basically just repeating what was said in the textbook, and the lecture, so that you get the concept explained in a bunch of different ways. It will sink in.

The reason the central limit theorem is important, is because researchers often take many samples, then analyse the means of their samples. That's what they do.

An experiment might have 20 people. You might take 20 measurements from each person. That's taking 20 samples. Then, because we know that samples are noisy. We take the means of the samples.

So, what researchers are often looking at, (and you too, very soon) are means of samples. Not just the samples. And, now we know that means of samples (if we had a lot of samples), look like they are distributed normally (the central limit theorem says the should be).

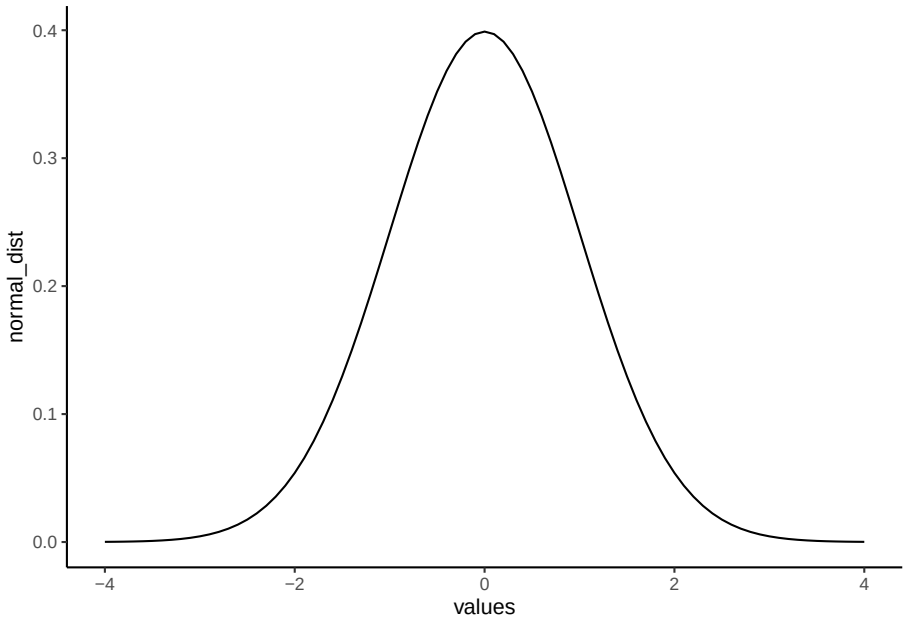
We can use this knowledge. If we learn a little bit more about normal distributions, and how they behave and work, we can take that and use it to understand our sample means better. This will become more clear as head into the topic of statistical inference next week. This is all a build up for that.

To continue the build-up we now look at some more properties of the normal distribution.

4.2.5.1 Graphing the normal distribution

"Wait, I thought we already did that". We sort of did. We sampled numbers and made histograms that looked like normal distributions. But, a "normal distribution" is more of an abstract idea. It looks like this in the abstract:

```
normal_dist <- dnorm(seq(-4,4,.1), 0, 1)
values <-seq(-4,4,.1)
normal_df <-data.frame(values,normal_dist)

ggplot(normal_df, aes(x=values,y=normal_dist))+
  geom_line()+
  theme_classic()
```



A really nice shaped bell-like thing. This normal distribution has a mean of 0, and standard deviation of 1. The heights of the lines tell you roughly how likely each value is. Notice, it is centered on 0 (most likely that numbers from this distribution will be near 0), and it goes down as numbers get bigger or smaller (so bigger or smaller numbers get less likely). There is a range to it. Notice the values don't go much beyond -4 and +4. This because those values don't happen very often. Theoretically any value could happen, but really big or small values have really low probabilities.

4.2.5.2 calculating the probability of specific ranges.

We can use R to tell us about the probability of getting numbers in a certain range. For example, when you think about. It should be obvious that you have a 50% probability of getting the number 0 or greater. Half of the distribution is 0 or greater, so you have a 50% probability.

We can use the `pnorm` function to confirm this:

```
pnorm(0, mean = 0, sd= 1, lower.tail=FALSE)
```

```
## [1] 0.5
```

Agreed, `pnorm` tells us the probability of getting 0 or greater is .5.

Well, what is the probability of getting a 2 or greater? That's a bit harder to judge, obviously less than 50%. Use R like this to find out:

```
pnorm(2, mean = 0, sd= 1, lower.tail=FALSE)
```

```
## [1] 0.02275013
```

The probability of getting a 2 or greater is .0227 (not very probable)

What is the probability of getting a score between -1 and 1?

```
ps<-pnorm(c(-1,1), mean = 0, sd= 1, lower.tail=FALSE)
ps[1]-ps[2]
```

```
## [1] 0.6826895
```

About 68%. About 68% of all the numbers would be between -1 and 1. So naturally, about 34% of the numbers would be between 0 and 1. Notice, we are just getting a feeling for this, you'll see why in a bit when we do z-scores (some of you may realize we are already doing that…)

What about the numbers between 1 and 2?

```
ps<-pnorm(c(1,2), mean = 0, sd= 1, lower.tail=FALSE)
ps[1]-ps[2]
```

```
## [1] 0.1359051
```

About 13.5% of numbers fall in that range, not much.

How about between 2 and 3?

```
ps<-pnorm(c(2,3), mean = 0, sd= 1, lower.tail=FALSE)
ps[1]-ps[2]
```

```
## [1] 0.02140023
```

Again a very small amount, only 2.1 % of the numbers, not a a lot.

4.2.5.3 summary pnorm

You can always use `pnorm` to figure how the probabilities of getting certain values from any normal distribution. That's great.

4.2.6 z-scores

We just spent a bunch of time looking at a very special normal distribution, the one where the mean = 0, and the standard deviation = 1. Then we got a little bit comfortable with what those numbers mean. 0 happens a lot. Numbers between -1 and 1 happen a lot. Numbers bigger or smaller than 1 also happen fairly often, but less often. Number bigger than 2 don't happen a lot, numbers bigger than 3 don't happen hardly at all.

We can use this knowledge for our convenience. Often, we are not dealing with numbers exactly like these. For example, someone might say, I got a number, it's 550. It came from a distribution with mean = 600, and standard deviation = 25. So, does 545 happen a lot or not? The numbers don't tell you right away.

If we were talking about our handy distribution with mean = 0 and standard deviation = 1, and I told I got a number 4.5 from that distribution. You would automatically know that 4.5 doesn't happen a lot. Right? Right!

z-scores are a way of transforming one set of numbers into our neato normal distribution, with mean = 0 and standard deviation = 1.

Here's a simple example, like what we said in the textbook. If you have a normal distribution with mean = 550, and standard deviation 25, then how far from the mean is the number 575? It's a whole 25 away (550+25 = 575). How many standard deviations is that? It's 1 whole standard deviation. So does a number like 575 happen a lot? Well, based on what you know about normal distributions, 1 standard deviation of the mean isn't that far, and it does happen fairly often. This is what we are doing here.

4.2.6.1 Calculating z-scores

1. get some numbers

```
some_numbers <- rnorm(20,50,25)
```

2. Calculate the mean and standard deviation

```
my_mean <- mean(some_numbers)
my_sd <-sd(some_numbers)

print(my_mean)
```

```
## [1] 58.05807
```

```
print(my_sd)
```

```
## [1] 29.28992
```

3. subtract the mean from your numbers

```
differences<-some_numbers-my_mean
print(differences)
```

```
##  [1] -48.167182  14.980089  42.267161  29.866269 -25.555337 -24.259125
##  [7]  23.072389  29.735354 -23.105184 -44.203498   3.726066   2.305146
## [13]  33.643191  26.586656 -20.377513 -32.471566  16.368551 -28.228258
## [19] -13.144142  36.960934
```

4. divide by the standard deviation

```
z_scores<-differences/my_sd
print(z_scores)
```

```
##  [1] -1.64449664  0.51144172  1.44306147  1.01967723 -0.87249583 -0.82824131
##  [7]  0.78772444  1.01520761 -0.78884410 -1.50917080  0.12721323  0.07870098
## [13]  1.14862678  0.90770653 -0.69571752 -1.10862582  0.55884579 -0.96375318
## [19] -0.44875986  1.26189926
```

Done. Now you have converted your original numbers into what we call standardized scores. They are standardized to have the same properties (assumed properties) as a normal distribution with mean = 0, and SD = 1.

You could look at each of your original scores, and try to figure out if they are likely or unlikely numbers. But, if you make them into z-scores, then you can tell right away. Numbers close to 0 happen a lot, bigger numbers closer to 1 happen less often, but still fairly often, and numbers bigger than 2 or 3 hardly happen at all.

4.2.7 Generalization Exercise

(1 point - Pass/Fail)

Complete the generalization exercise described in your R Markdown document for this lab.

1. Simulate the sampling distribution of the mean for sample-size =10, from a normal distribution with mean =100, and standard deviation = 25. Run the simulation 1000 times, taking 1000 samples, and computing the sample mean each time.

a. Plot the sampling distribution of the mean in a histogram
b. Report the mean of the sampling distribution of the mean
c. Report the standard deviation of the sampling distribution of the mean

2. Repeat all of the above, except change the sample-size to 100 for all simulations

a. Plot the sampling distribution of the mean in a histogram
b. Report the mean of the sampling distribution of the mean
c. Report the standard deviation of the sampling distribution of the mean

4.2.8 Writing assignment

(2 points - Graded)

Complete the writing assignment described in your R Markdown document for this lab. When you have finished everything. Knit the document and hand in your stuff (you can submit your .RMD file to blackboard if it does not knit.)

1. Explain the concept of sampling error (1 point)

2. Explain why the standard deviation of the sampling distribution of mean gets smaller as sample-size increases (1 point)

General grading.

- You must write in complete sentences. Point form sentences will be given 0 points.
- Completely incorrect answers will receive 0 points.
- If your answer is generally correct but very difficult to understand and unclear you may receive half points for the question

4.2.9 Practice Problems

"Professor, do you grade on a curve?"

This is probably the most commonly-asked question in Statistics class. Everyone assumes that grading on a curve will benefit them. But does it?

Here is a link to an SPSS file containing 50 students' exam grades (let's say it's the final exam for a Statistics class).

1. Create a table containing the mean and standard deviation for this sample of scores. Now, produce a frequency histogram of the score data. Describe the distribution.

2. Transform each student's score into a Z-score (you can use either method shown in this tutorial). Now, plot the frequency histogram of this Z-score distribution. Compare it to the raw score distribution. How are they the same? How are they different?

3. Imagine you are a student in this class who received a 90 on this exam. However, the Professor has decided to GRADE ON A CURVE (shock! awe!), such that only the top 10% of the class receives an A (this professor only gives whole grades, no minuses or pluses). Calculate the z-score that corresponds to a raw score of 90 on this exam. Will you get an A with this grade? Why or why not?

Chapter 5

Lab 5: Fundamentals of Hypothesis Testing

The null hypothesis is never proved or established, but is possibly disproved, in the course of experimentation. Every experiment may be said to exist only to give the facts a chance of disproving the null hypothesis. —R. A. Fisher

5.1 R

From here on, we will be focusing on making sense of data from experiments. In all of this, we use experiments to ask a question about whether one thing causes change (influences) another thing. Then, we look at the data to help us answer that question. In general, we expect to find a difference in our measurement between the conditions of the experimental manipulation. We expect to find a difference when the manipulation works, and causes change in our measure. We expect not to find a difference when the manipulation does not work, and does not cause change.

However, as you well know from reading the textbook, and attending the lectures. Experimental manipulations are not the only thing that can cause change in our measure. Chance alone can cause change. Our measures are usually variable themselves, so they come along with some change in them due to sampling error.

At a minimum, when we conduct an experiment, we want to know **if the change we observed is bigger than the change that can be produced by chance**. Theoretically, random chance could produce most any change we might measure in our experiment. So, there will always be uncertainty about whether our manipulation caused the change, or chance caused the change. But, we can

reduce and evaluate that uncertainty. When we do this, we make **inferences** about what caused change in our experiments. This process is called **statistical inference**. We use **inferential statistics** as tools to help us make these inferences.

In this lab we introduce you to foundational concepts in **statistical inference**. This is also commonly termed **hypothesis testing**. But, for various reasons using that language to describe the process is tied to particular philosophies about doing statistical inference. We use some of that language here, so that you know what it means. But, we also use our own plain language, so you know what the point is, without the statistical jargon.

The textbook describes a few different statistical tests for building your conceptual understanding for statistical inference. In this lab, we work through some of them. In particular, we work through the Crump test, and the Randomization test. We show you how to conduct these tests in R on fake data, and real data.

5.1.1 The Crump Test

The Crump test is described more fully in the textbook here, but you already read that in preparation for this lab, right! I hope you did.

The big idea behind the Crump test is this. You find out what kind of differences between two conditions can be found by chance alone. This shows you what chance can do. Then, you compare what you actually found in one experiment, with the chance distribution, and make an inference about whether or not chance could have produced the difference.

5.1.1.1 Make assumptions about the distribution for your measurement

The first step in conducting the Crump test is to make a guess at the distribution behind your measurement. We will see in the next part how to do this from real data. For now, we just pick a distribution. For example, let's say we are measuring something that comes from a normal distribution with mean = 75 and standard deviation = 5. Perhaps, this is a distribution for how people perform on a particular test. The mean on the test is 75%, with a standard deviation of 5%. We know from last lab that 3 standard deviations away from the mean is pretty unlikely with this distribution. So, for example, most people never score above 90% (5*3=15, 75+15 = 90) on this test.

In this example situation, we might imagine an experiment that was conducted to determine whether manipulation A improves test performance, compared to a control condition where no manipulation took place. Using the Crump test, we can simulate differences that can occur by chance. We are formally simulating

the differences that could be obtained between two control conditions, where no manipulation took place.

To, restate our assumptions, we assume a single score for each subject is sampled from:

```
rnorm(n, mean=75, sd=5)
```

5.1.1.2 Make assumptions about N

In the real world, experiments have some number of subjects in each condition, this number is called N. For our simulation we, need to choose the number of subjects that we have. For this demonstration, we choose N = 20 in each condition.

5.1.1.3 Choose the number of simulations to run

We are going to run a fake experiment with no manipulation, and do this many times over (doing it many times over is called **monte carlo simulation**). Each time we will do this:

1. Sample 20 numbers for control group A using `rnorm(20, mean=75, sd=5)`
2. Sample 20 numbers for control group B using `rnorm(20, mean=75, sd=5)`
3. Compute the means for control group A and B
4. Compute the difference between the mean for group A and B
5. Save the differences score in a variable
6. Repeat as many times as we want

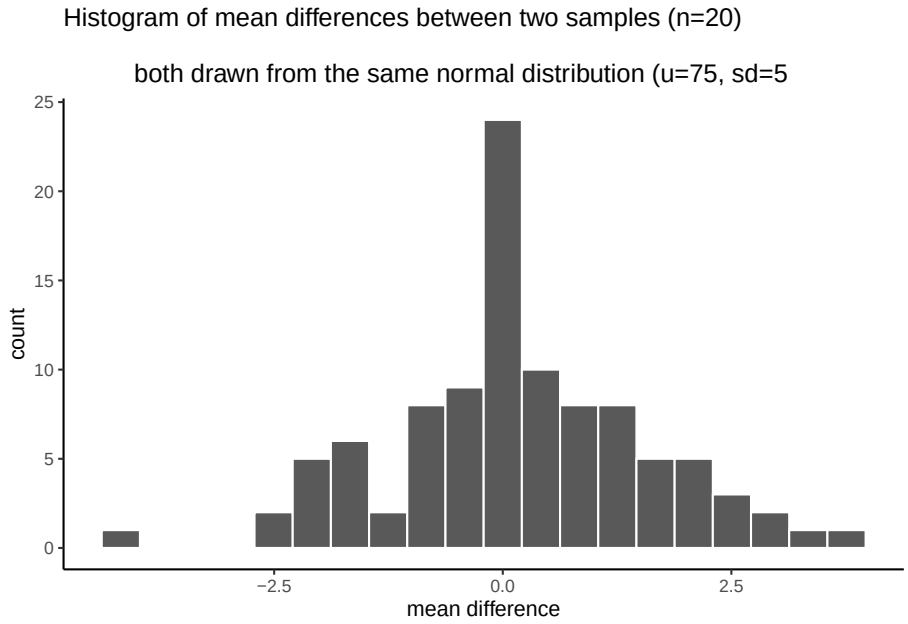
If we repeat the simulation 100 times, we will see the differences that can be produced by chance, when given the opportunity 100 times. For example, in a simulation like this, the biggest difference (the maximum value) only happens once. We can find that difference, and then roughly conclude that a difference of that big happens 1 out of 100 times just by chance. That's not a lot.

If we want to be more restrictive, we can make the simulation go to 1,000, or 10,000, or greater. Each time the maximum value will tell us what is the biggest thing chance did 1 out of 1000 times, or 1 out of 10,000 times.

The textbook uses 10,000 times. Let's use 100 times here to keep things simple.

5.1.1.4 Run the simluation

```r
library(ggplot2)

# set paramaters of simulation

sims_to_run <- 100
sample_n   <- 20
dist_mean  <- 75
dist_sd    <- 5

# run simulation

mean_differences <- length(sims_to_run)
for(i in 1:sims_to_run){
  mean_control_A      <- mean(rnorm(sample_n, dist_mean, dist_sd))
  mean_control_B      <- mean(rnorm(sample_n, dist_mean, dist_sd))
  mean_differences[i] <- mean_control_A - mean_control_B
}

# plot the  distribution of mean difference scores

plot_df <- data.frame(sim=1:sims_to_run,mean_differences)

ggplot(plot_df,aes(x=mean_differences))+
  geom_histogram(bins=20, color="white")+
  theme_classic()+
  ggtitle("Histogram of mean differences between two samples (n=20) \n
          both drawn from the same normal distribution (u=75, sd=5")+
  xlab("mean difference")
```



5.1.1.5 find the range

We can see that chance produces some differences that are non-zero. The histogram shows all the mean differences that were produced by chance. Most of the differences are between -2 and +2, but some of them are bit more negative, or a bit more positive. If we want to know what chance **did** do in this one simulation with 100 runs, then we need to find the range, the minimum and maximum value. This will tell us the most negative mean difference that chance did produce, and the most positive mean difference that chance did produce. Then, we will also know that chance **did not** produce any larger negative, or larger positive differences, in this simulation.

We use the `min()` and `max()` functions to get the minimum and maximum value.

```
min(mean_differences)
```

```
## [1] -4.228719
```

```
max(mean_differences)
```

```
## [1] 3.707135
```

We now know, that biggest negative difference was -4.229, and the biggest positive difference was 3.707. We also know that any mean difference inside the

range **was produced by chance** in our simulation, and any mean difference outside the range **was not produced by chance** in our simulation

5.1.1.6 Make inferences

This part requires you to think about the answers. Let's go through some scenario's.

1. You sample 20 numbers from a normal distribution with mean = 75, and standard deviation =5. The mean of your sample is 76. Then, you take another sample of the same size, from the same distribution, and the mean of your second sample is 78. The mean difference is +1 (or -1, depending on how you take the difference)

    a. **Question**: According to the histogram did a mean difference of 1 or -1 occur by chance?
    b. **Answer**: Yes, it is inside the range

2. Same as above, but the mean of your first sample is 74, and the mean of your second sample is 80, showing a mean difference of 6, or -6.

    a. **Question**: According to the histogram did a mean difference of 6 or -6 occur by chance?
    b. **Answer**: No, it is outside the range

3. You run an experiment. Group A receives additional instruction that should make them do better on a test. Group B takes the test, but without the instruction. There are 20 people in each group. You have a pretty good idea that group B's test scores will be coming from a normal distribution with mean = 75, and standard deviation = 5. You know this because you have given the test many times, and this is what the distribution usually looks like. You are making an educated guess. You find that the mean test performance for Group A (with additional instruction) was 76%, and the mean test performance for Group B (no additional instruction) was 75%. The mean difference has an absolute value of +1.

    a. **Question #1**: According to the histogram, could chance alone have produced a mean absolute difference of +1?
    b. **Answer**: Yes, it is inside the range
    c. **Question #2**: It looks like Group A did better on the test (on average), by 1%, compared to the control group B. Are you willing to believe that your additional instruction **caused the increase in test performance**?
    d. **Answer**: The answer is up to you. There is no correct answer. It could easily be the case that your additional instruction did not do anything at all, and that the difference in mean test performance

was produced by chance. My inference is that I do not know if my instruction did anything, I can't tell it's potential influence from chance.

4. Same as 3, except the group mean for A (receiving instruction) is 90%. The group mean for B (no instruction control) is 75%. The absolute mean difference is 15%.

    a. **Question #1**: According to the histogram, could chance alone have produced a mean absolute difference of +15?
    b. **Answer**: No, it is well outside the range
    c. **Question #2**: It looks like Group A did better on the test (on average), by 15%, compared to the control group B. Are you willing to believe that your additional instruction **caused the increase in test performance**?
    d. **Answer**: The answer is up to you. There is no correct answer. You know from the simulation that chance never produced a difference this big, and that producing a difference this big by chance would be like winning the lottery (almost never happens to you). My inference is that I believe chance did not produce the difference, I'm willing to believe that my instructional did cause the difference.

5.1.1.7 Planning your experiment

We've been talking about a hypothetical experiment where an instructor tests whether group A does better (when receiving additional instruction) on a test, compared to a group that does receives no additional instruction and just takes the test.

If this hypothetical instructor wanted to make an experiment, they would get to choose things like how many subjects they will put in each condition. How many subjects should they plan to get?

The number of subjects they plan to get will change what chance can do, and will change the sensitivity of their experiment to detect differences of various sizes, that are not due to chance.

We can use the simulation process to make informed decisions about how many subjects to recruit for an experiment. This is called **sample-size planning**. There are two goals here. The instructor might have a first goal in mind. They may be only interested in adopting a new method for instruction, if it actually improves test performance beyond more than 1% (compared to control). Differences of less than 1% are just not worth it for the instructor. They want bigger differences, they want to help their students improve more than 1%.

One problem for the instructor, is that they just don't know in advance how good their new teaching materials will be. Some of them will be good and

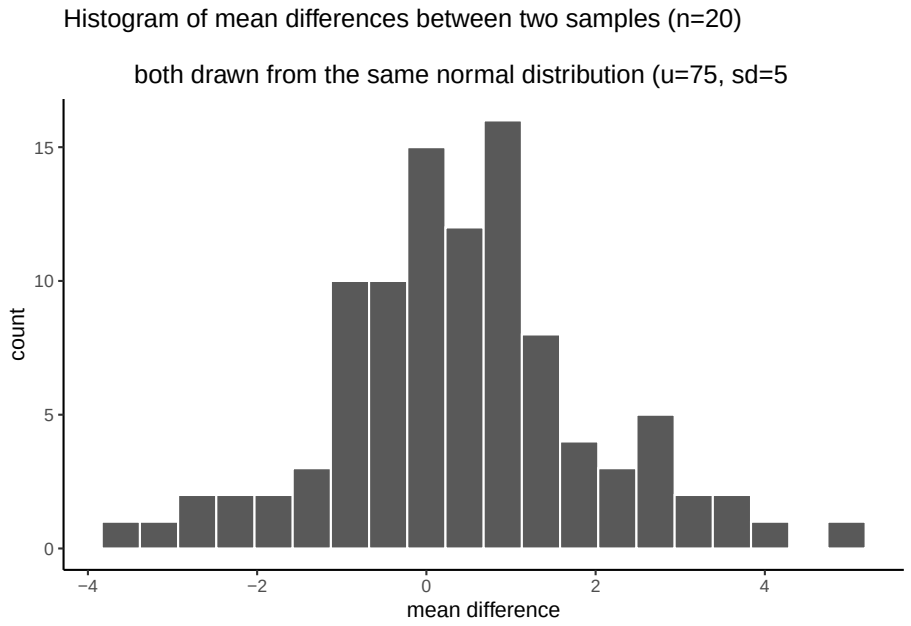
produce bigger differences, and some of them won't. The size of the difference from the manipulation can be unknown. However, this doesn't really matter for planning the experiment. The instructor wants to know that they can **find** or detect any real difference (not due to chance) that is say 2% or bigger. We can use the simulation to figure out roughly (or more exactly, depending on how much we work at it) how many subjects are needed to detect difference of at least 2%.

Notice, from our prior simulation, chance does produce differences of 2% some of the time (given 100 runs). The task now is to re-run the simulation, but use different numbers of subjects to figure out how many subjects are needed to always detect differences of 2%. To be simple about this, we are interested in producing a distribution of mean differences that never produces a mean difference of -2% to + 2% (not once out of 100 times). You can re-run this code, and change N until the min and max are always smaller than -2 to +2.

The code starts out exactly as it was before. You should change the number for `sample_n`. As you make the number bigger, the range (min and max) of the mean differences by chance will get smaller and smaller. Eventually it will be smaller than -2 to +2. When you get it this small, then the N that you used is your answer. Use that many subjects. If you run your experiment with that many subjects, **AND** you find a difference or 2 or greater, then you know that chance does not do this even 1 times out of 100.

```
library(ggplot2)

# set paramaters of simulation

sims_to_run <- 100
sample_n   <- 20
dist_mean  <- 75
dist_sd    <- 5

# run simulation

mean_differences <- length(sims_to_run)
for(i in 1:sims_to_run){
  mean_control_A      <- mean(rnorm(sample_n, dist_mean, dist_sd))
  mean_control_B      <- mean(rnorm(sample_n, dist_mean, dist_sd))
  mean_differences[i] <- mean_control_A - mean_control_B
}

# plot the  distribution of mean difference scores

plot_df <- data.frame(sim=1:sims_to_run,mean_differences)

ggplot(plot_df,aes(x=mean_differences))+
```

```
  geom_histogram(bins=20, color="white")+
  theme_classic()+
  ggtitle("Histogram of mean differences between two samples (n=20) \n
          both drawn from the same normal distribution (u=75, sd=5")+
  xlab("mean difference")
```




```
min(mean_differences)
```

```
## [1] -3.63058
```

```
max(mean_differences)
```

```
## [1] 4.94561
```

5.1.2 Crumping real data

In this example we look at how you can run a Crump test to evaluate the results in a published paper. The goal of this is to build up your intuitions about whether or not an observed difference could have been caused by chance. We take many liberties, and this is not an exact test of anything. However, we will see how a series of rough, and reasonable assumptions can be made to simulate the results of published experiments, even when exact information is not provided in the paper.

5.1.2.1 Test-enhanced learning

We have already been using an educational example. We've been talking about a manipulation that might be employed to help students learn something better than they otherwise would without the manipulation.

Research in Cognitive Psychology has discovered clear evidence of some teaching practices that really work to enhance memory and comprehension. One of these practices is called test-enhanced learning. Students who study material, and take a quick test (quiz) while they study, do better at remembering the material compared to students who just studied the whole time and did not take a quiz (why do you think we have so many quizzes, in the textbook and for this class? This is why. Prior research shows this will improve your memory for the content, so we are asking you to take the quizzes so that it helps you learn!).

Here is a link to a paper demonstrating the test-enhanced learning effect.

The citation is: Roediger III, H. L., & Karpicke, J. D. (2006). Test-enhanced learning: Taking memory tests improves long-term retention. Psychological science, 17(3), 249-255.

5.1.2.2 Brief summary

The subjects learned about some things in two conditions. In one condition (study-study) they studied some things, then studied them again. In the other condition (study-test) they studied some things, then took a quiz about the things rather then studying them one more time.

Everyone received follow up tests to see what they learned and remembered. They came back one week later and took the test. The researchers measured the mean proportion of things remembered in both conditions. They found the study-test condition had a higher mean proportion of remembered idea units than the study-study condition. So, the difference between the mean proportions suggest that taking a quick test after studying was beneficial for remembering the content. The researchers also conducted statistical tests, and they concluded the difference they found was not likely due to chance. Let's apply the Crump test to their findings, and see if we come to the same conclusion about the role of chance.

5.1.2.3 Estimate the paramaters of the distribution

To do the Crump test, we need to make assumptions about where the sample data is coming from. Download the paper from the link, then look at Figure 1. We will estimate our distribution by looking at this figure. We will be doing **informed guesstimation** (a real word I just made up).

Look only at the two bars for the `1 week` condition.

The mean for the study-study group is about .4. The mean for the study-test group is about .55. The results section reports that the actual mean for the study-study group was .42 (42%) and the mean for the study-test group was .56 (56%). Pretty close to our visual guesstimate.

The data show that the study-test group remembered .14 (14%, or .56-.42=.14) more idea units than the study-study group.

Estimating the mean

We can imagine for the moment that this difference could have been caused by chance. For example, in this case, both samples would have been drawn from the same distribution. For example, we might say that on average people remember about .49 idea units after a one week delay. I got .49 by averaging the .42 and the .56 together. We can use this as the mean for our distribution in the Crump test.

N

The paper says there were 120 subjects in total, and that different groups of subjects were measured in the three different delay conditions (5 minutes, 2 Days and 1 week). We will assume there were an equal number of subjects in each group. There were 3 groups, $120/3 = 40$, so we assume there were 40 subjects in the 1 week delay group

Estimating Standard Deviation

The paper doesn't directly report the standard deviation for the measurement of proportion idea units. But, we can guesstimate it visually. Look at the little bars with a line on them coming out of each bar. These are called error bars, and they represent the standard error of the mean.

These look like they are about .033 in length. We know the standard error of the mean (SEM) is the standard deviation divided by the sqare root of N. So, we can infer that the standard deviation is $.033 * \sqrt{40} = .21$.

The paper also reports cohen's D, which is a measure of effect size using the mean difference divided the standard deviation. Cohen's D was .83, so the standard deviation must have been $.14/.83 = .168$, which is pretty close to our guesstimate of .21.

5.1.2.4 Findings from the original study

One week after the initial learning conditions, subjects came back and took a retention test to see how much they learned. The mean proportion "idea units" recalled was:

1. study-study : 42% or .42
2. study-test : 56% or .56

The mean difference was .56-.42 = .14 or a whopping 14% improvements. That's actually pretty big.

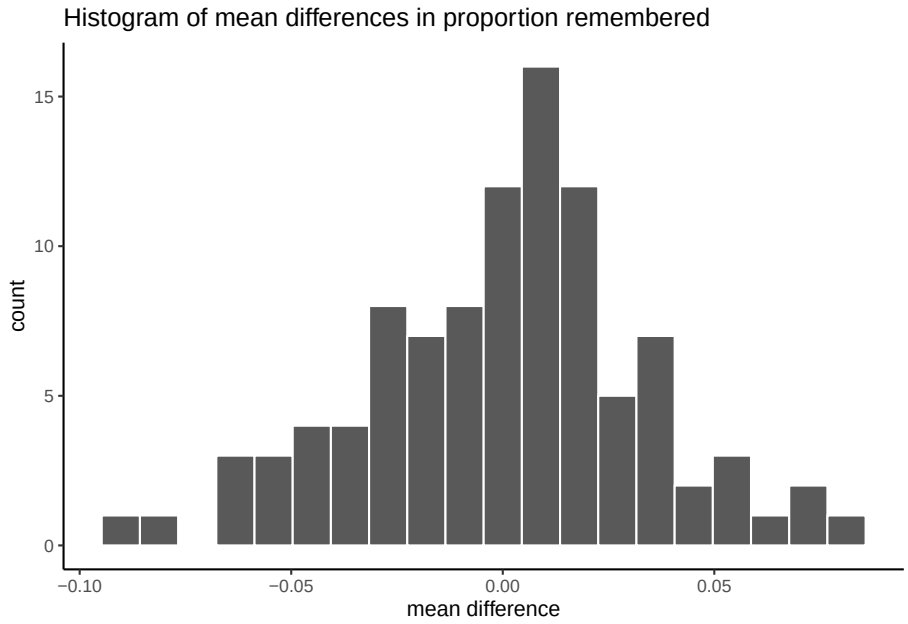
What we want to know is whether chance could produce a difference of 14%, or .14, just by itself.

5.1.2.5 Run the simulation

Now we can plug our numbers in to the Crump test simulation.

1. We run the simulation 100 times
2. Our sample N is 40
3. The mean of our distribution is .49
4. The standard deviation of the distribution is .168

```
# set paramaters of simulation

sims_to_run <- 100
sample_n   <- 40
dist_mean  <- .49
dist_sd    <- .168

# run simulation

mean_differences <- length(sims_to_run)
for(i in 1:sims_to_run){
  mean_control_A      <- mean(rnorm(sample_n, dist_mean, dist_sd))
  mean_control_B      <- mean(rnorm(sample_n, dist_mean, dist_sd))
  mean_differences[i] <- mean_control_A - mean_control_B
}

# plot the  distribution of mean difference scores

plot_df <- data.frame(sim=1:sims_to_run,mean_differences)

ggplot(plot_df,aes(x=mean_differences))+
  geom_histogram(bins=20, color="white")+
  theme_classic()+
  ggtitle("Histogram of mean differences in proportion remembered")+
  xlab("mean difference")
```




```
min(mean_differences)
```

```
## [1] -0.08802108
```

```
max(mean_differences)
```

```
## [1] 0.08350093
```

According to the simulation, the biggest negative difference was -0.088, and the biggest positive difference was 0.084. We also know that any mean difference inside the range **was produced by chance** in our simulation, and any mean difference outside the range **was not produced by chance** in our simulation.

A difference of .14 or 14% was never produced by chance, it was completely outside the range. Based on this analysis we can be fairly confident that the test-enhanced learning effect was not a fluke, it was not produced by chance. We have evidence to support the claim that testing enhances learning, and because of this we test you while you are learning to enhance your learning while you learn.

5.1.3 The Randomization Test

Unlike the Crump test, which was made to help you understand some basic ideas about how chance can do things, the Randomization test is a well-known,

very real, statistical test for making inferences about what chance can do. You will see that it is very similar to the Crump test in many respects. In fact, we might say that the Crump test is really just a randomization test.

You read about the randomization test in the textbook. We won't repeat much about that here, but we will show you how to do one in R.

To briefly remind you, in a randomization test we first obtain some data from an experiment. So we have a sample of numbers for group A, and Group B. We calculate the means for both groups (or other statistic we want to know about), and then see if they are different. We want to know if the difference we found could be produced by chance, so we conduct the randomization test on using the sample data that we have.

The major difference between the Crump test and the Randomization test, is that we make no assumption about the distribution that the sample data came from. We just randomize the sample data. We do:

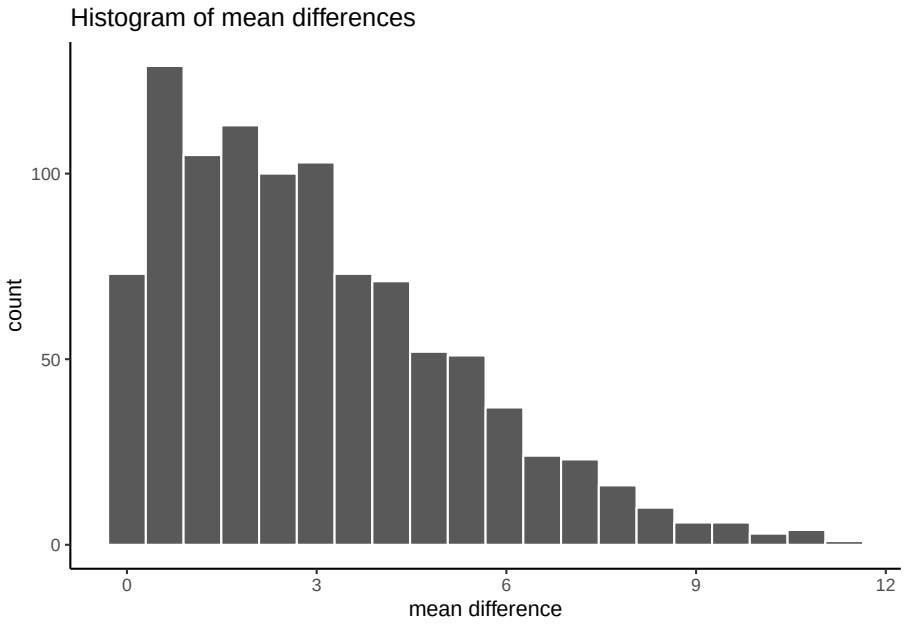
1. Take all the numbers from group A and B, put them in the same pot. Then randomly take the numbers out and assign them back into A and B. Then, compute the means, and the difference, and save the difference
2. Do this over and over
3. Plot the histogram of the mean differences obtained by shuffling the numbers. This shows you what chance can do.

5.1.3.1 Run the randomization test

Note, this time when we calculate the mean differences for each new group, we will take the absolute value of the mean difference.

```
# get sample numbers from one experiment
Group_A <- rnorm(20,50,10)
Group_B <- rnorm(20,50,10)

# randomize the numbers, compute mean difference, save the mean difference
mean_differences <- length(1000)
for(i in 1:1000){
  shuffle_numbers <- sample(c(Group_A, Group_B), replace=FALSE)
  new_group_A <- shuffle_numbers[1:20]
  new_group_B <- shuffle_numbers[21:40]
  mean_differences[i] <- abs(mean(new_group_A)-mean(new_group_B))
}

# plot the histogram
plot_df <- data.frame(sim=1:1000,mean_differences)
```

```
ggplot(plot_df,aes(x=mean_differences))+
  geom_histogram(bins=20, color="white")+
  theme_classic()+
  ggtitle("Histogram of mean differences")+
  xlab("mean difference")
```



The histogram shows us the kinds of absolute mean difference that happen by chance alone. So, in this data, a mean difference of 10 hardly wouldn't happen very often. A difference between 0 and 2.5 happens fairly often by chance.

5.1.3.2 Decision criteria

When you are determining whether or not chance could have produced a difference in your data, you might want to consider how stringent you want to be about accepting the possibility that chance did something. For example chance could produce a difference of 0 or greater 100% of the time. Or, it produces a difference of 10 or greater, a very small (less than .00001% of the time). How big does the difference need to be, before you will consider the possibility that chance probably didn't cause the difference.

Alpha. Researchers often set what is called an **alpha** criteria. This draws a line in the histogram, and says I will be comfortable assuming that chance did not produce my differences, when chance produces difference less than X percent of the time. This X percent, is the alpha value. For example, it is often set to 5%, or **p <= .05**.

Where is 5% of the time on our histogram? What mean difference or greater happens less than or equal to 5% of the time.

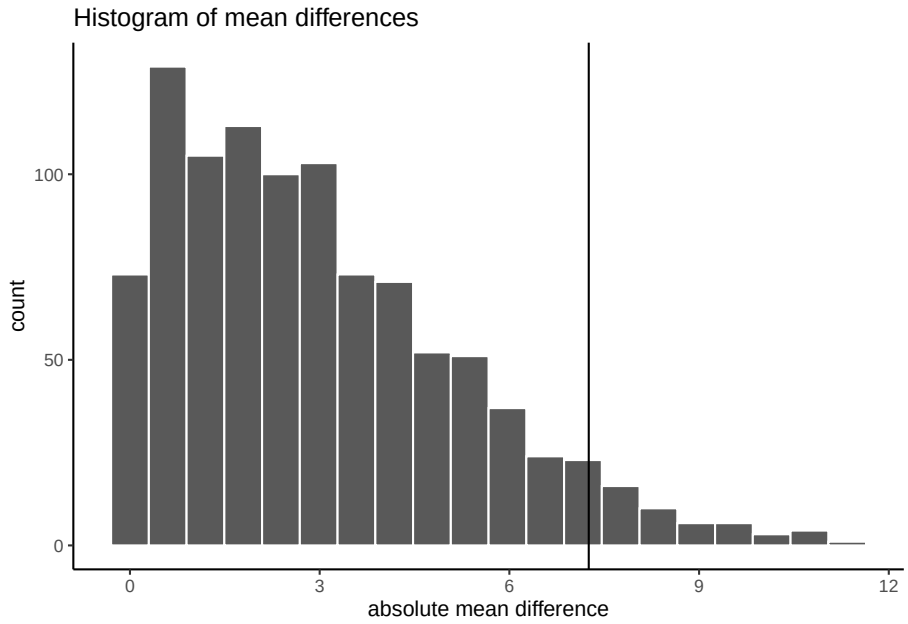
5.1.3.3 Finding the critical region

1. Take the simulated mean difference scores and order them from smallest to largest
2. We have 1000 numbers, ordered from smallest to largest.
3. The number in position 950 is the alpha location. All of the numbers from position 0 to 950, reflect 95% of the numbers. What is left over is 5% of the numbers.
4. Find the alpha cut-off, and plot it on the histogram

```
ordered_differences <- sort(mean_differences) # sort
alpha_cutoff <- ordered_differences[950] # pick 950th number
alpha_cutoff
```

```
## [1] 7.255284
```

```
# add to histogram using vline

ggplot(plot_df,aes(x=mean_differences))+
  geom_histogram(bins=20, color="white")+
  geom_vline(xintercept=alpha_cutoff)+
  theme_classic()+
  ggtitle("Histogram of mean differences")+
  xlab("absolute mean difference")
```



OK, so our alpha criterion or cutoff is located at 7.26 on the x-axis. This shows us that mean differences of 7.26 or larger happen only 5% of the time by chance.

You could use this information to make an inference about whether or not chance produced the difference in your experiments

1. When the mean difference is 7.26 or larger, you might conclude that chance did not produce the difference
2. When the mean difference is less than 7.26, you might conclude that chance could have produced the mean difference.

It's up to you to set your alpha criterion. In practice it is often set at p=.05. But, you could be more conservative and set it to p=.01. Or more liberal and set it to p=.1. It's up to you.

5.1.4 Generalization Exercise

Complete the generalization exercise described in your R Markdown document for this lab.

1. Consider taking measurements from a normal distribution with mean = 100 and standard deviation = 25. You will have 10 subjects in two conditions (20 subject total). You will take 1 measurement (sample 1 score) of each subject.

Use the process for simulating the Crump test. Pretend that there are now differences between the conditions. Run a Crump test simulation 100 times.

a. Report the maximum mean difference in the simulation
b. Report the minimum mean difference in the simulation
c. Report a mean difference that, according to the simulation, was not observed by chance
d. Report a mean difference that, according to the simulation was observed by chance
e. What is the smallest mean difference that, if you found this difference in an experiment, you would be willing to entertain the possibility that the difference was unlikely to be due to chance (note this is a subjective question, give your subjective answer)

5.1.5 Writing assignment

Complete the writing assignment described in your R Markdown document for this lab. When you have finished everything. Knit the document and hand in your stuff (you can submit your .RMD file to blackboard if it does not knit.)

Imagine you conduct an experiment. There is one independent variable with two levels, representing the manipulation. There is one dependent variable representing the measurement. Critically, the measurement has variability, so all of the samples will not be the same because of variability. The researcher is interested in whether the manipulation causes a change in the dependent measure. Explain how random chance, or sampling error, could produce a difference in the dependent measure even if the manipulation had no causal role.

a. Explain how the sampling distribution of the mean differences from the Crump or Randomization test relates to the concept that chance can produce differences (0.5 points)

b. Imagining a sampling distribution of the mean differences from a Crump test simulation, which values in the distribution are most likely to be produced by chance (0.5 points)

c. From above, which values are least likely to be produced by chance (0.5 points)

d. If you obtained a mean difference that was very large and it fell outside the range of the sampling distribution of the mean differences from a Crump test, what would you conclude about the possibility that chance produced your difference. Explain your decision. (0.5 points)

General grading.

- You will receive 0 points for missing answers
- You must write in complete sentences. Point form sentences will be given 0 points.
- Completely incorrect answers will receive 0 points.
- If your answer is generally correct but very difficult to understand and unclear you may receive half points for the question

5.1.6 Practice Problems

---

1. In this lab, you will be conducting a sign test to determine whether a coin is weighted. Individually or in small groups, take a coin out of your pocket. If working in groups, use only one coin for the whole group. Now, flip the coin 25 times. Write down how many heads and tails you observed.

2. Enter this into your SPSS spreadsheet and run a sign test using an alpha level of .05. What is your result?

3. Have students in the class (or groups) announce their results as well. Did anyone have a trick coin? Do you think some of the coins used were actually weighted? Why or why not?

Chapter 6

Lab 6: t-Test (one-sample, paired sample)

Any experiment may be regarded as forming an individual of a 'population' of experiments which might be performed under the same conditions. A series of experiments is a sample drawn from this population. —William Sealy Gossett

This lab is modified and extended from Open Stats Labs. Thanks to Open Stats Labs (Dr. Kevin P. McIntyre) for their fantastic work.

6.1 Does Music Convey Social Information to Infants?

This lab activity uses the open data from Experiment 1 of Mehr, Song, and Spelke (2016) to teach one-sample and paired samples t-tests. Results of the activity provided below should exactly reproduce the results described in the paper.

6.1.1 STUDY DESCRIPTION

Parents often sing to their children and, even as infants, children listen to and look at their parents while they are singing. Research by Mehr, Song, and Spelke (2016) sought to explore the psychological function that music has for parents and infants, by examining the hypothesis that particular melodies convey important social information to infants. Specifically, melodies convey information about social affiliation.

The authors argue that melodies are shared within social groups. Whereas children growing up in one culture may be exposed to certain songs as infants (e.g., "Rock-a-bye Baby"), children growing up in other cultures (or even other groups within a culture) may be exposed to different songs.Thus, when a novel person (someone who the infant has never seen before) sings a familiar song, it may signal to the infant that this new person is a member of their social group.

To test this hypothesis, the researchers recruited 32 infants and their parents to complete an experiment.During their first visit to the lab, the parents were taught a new lullaby (one that neither they nor their infants had heard before).The experimenters asked the parents to sing the new lullaby to their child every day for the next 1-2 weeks.

Following this 1-2 week exposure period, the parents and their infant returned to the lab to complete the experimental portion of the study.Infants were first shown a screen with side-by-side videos of two unfamiliar people, each of whom were silently smiling and looking at the infant.The researchers recorded the looking behavior (or gaze) of the infants during this 'baseline' phase. Next, one by one, the two unfamiliar people on the screen sang either the lullaby that the parents learned or a different lullaby (that had the same lyrics and rhythm, but a different melody).Finally, the infants saw the same silent video used at baseline, and the researchers again recorded the looking behavior of the infants during this 'test' phase.For more details on the experiment's methods, please refer to Mehr et al. (2016) Experiment 1.

6.2 Lab skills learned

1. Conducting a one-sample t-test
2. Conducting a two-sample t-test
3. Plotting the data
4. Discussing inferences and limitations

6.3 Important Stuff

- citation: Mehr, S. A., Song. L. A., & Spelke, E. S. (2016). For 5-month-old infants, melodies are social. Psychological Science, 27, 486-501.
- Link to .pdf of article
- Data in .csv format
- Data in SPSS format

6.4 R

6.4.1 Loading the data

The first thing to do is download the .csv formatted data file, using the link above, or just click here. It turns out there are lots of ways to load .csv files into R.

1. Load the data.table library. Then use the `fread` function and supply the web address to the file. Just like this. No downloading required.

```
library(data.table)
all_data <- fread("https://raw.githubusercontent.com/CrumpLab/statisticsLab/master/data/MehrSongS
```

2. Or, if you downloaded the .csv file. Then you can use `fread`, but you need to point it to the correct file location. The file location in this next example will not work for you, because the file is on my computer.

```
library(data.table)
all_data <- fread("data/MehrSongSpelke2016.csv")
```

6.4.2 Inspect the data frame

When you have loaded data it's always a good idea to check out what it looks like. You can look at all of the data in the environment tab on the top right hand corner. The data should be in a variable called `all_data`. Clicking on `all_data` will load it into a viewer, and you can scroll around. This can be helpful to see things. But, there is so much data, can be hard to know what you are looking for.

6.4.2.1 summarytools

The `summarytools` packages give a quick way to summarize all of the data in a data frame. Here's how. When you run this code you will see the summary in the viewer on the bottom right hand side. There's a little browser button (arrow on top of little window) that you can click to expand and see the whole thing in a browser.

```
library(summarytools)
view(dfSummary(all_data))
```

6.4.3 Get the data for Experiment one

The data contains all of the measurements from all five experiments in the paper. By searching through the `all_data` data frame, you should look for the variables that code for each experiment. For example, the third column is called `exp1`, which stands for experiment 1. Notice that it contains a series of 1s. If you keep scrolling down, the 1s stop. These 1s identify the rows associated with the data for Experiment 1. We only want to analyse that data. So, we need to filter our data, and put only those rows into a new variable. We do this with the `dplyr` library, using the `filter` function.

```
library(dplyr)
experiment_one <- all_data %>% filter(exp1==1)
```

Now if you look at the new variable `experiment_one`, there are only 32 rows of data. Much less than before. Now we have the data from experiment 1.

6.4.4 Baseline phase: Conduct a one sample t-test

You first want to show that infants' looking behavior did not differ from chance during the baseline trial. The baseline trial was 16 seconds long. During the baseline, infants watched a video of two unfamiliar people, one of the left and one on the right. There was no sound during the baseline. Both of the actors in the video smiled directly at the infant.

The important question was to determine whether the infant looked more or less to either person. If they showed no preference, the infant should look at both people about 50% of the time. How could we determine whether the infant looked at both people about 50% of the time?

The `experiment_one` data frame has a column called `Baseline_Proportion_Gaze_to_Singer`. All of these values show how the proportion of time that the infant looked to the person who would later sing the familiar song to them. If the average of these proportion is .5 across the infants, then we would have some evidence that the infants were not biased at the beginning of the experiment. However, if the infants on average had a bias toward the singer, then the average proportion of the looking time should be different than .5.

Using a one-sample t-test, we can test the hypothesis that our sample mean for the `Baseline_Proportion_Gaze_to_Singer` was not different from .5.

To do this in R, we just need to isolate the column of data called `Baseline_Proportion_Gaze_to_Singer`. We will do this using the `$` operator. The `$` operator is placed after any data frame variable, and allows you to select a column of the data. The next bit of code will select the column of data we want, and put it into a new variable called `Baseline`. Note, if you

type `exp1$` then R-Studio should automatically bring up all the columns you can choose from.

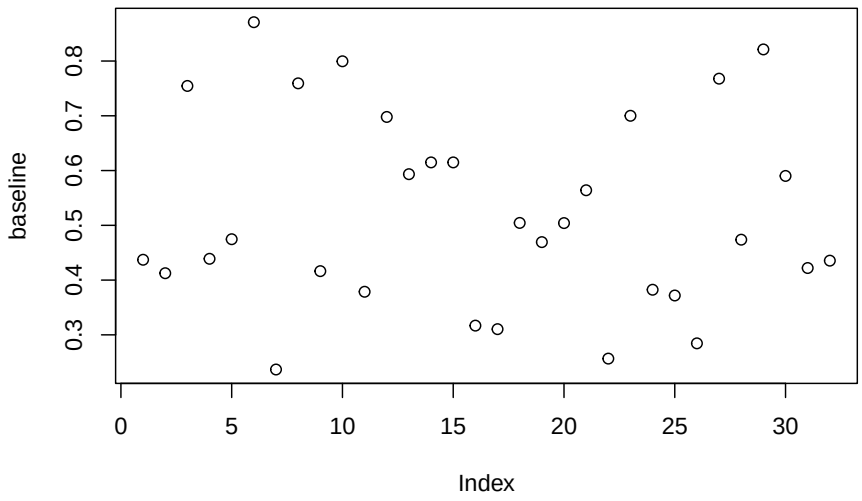
```
baseline <- experiment_one$Baseline_Proportion_Gaze_to_Singer
```

6.4.4.1 Look at the numbers

Question: Why is it important to look at your numbers? What could happen if you didn't?

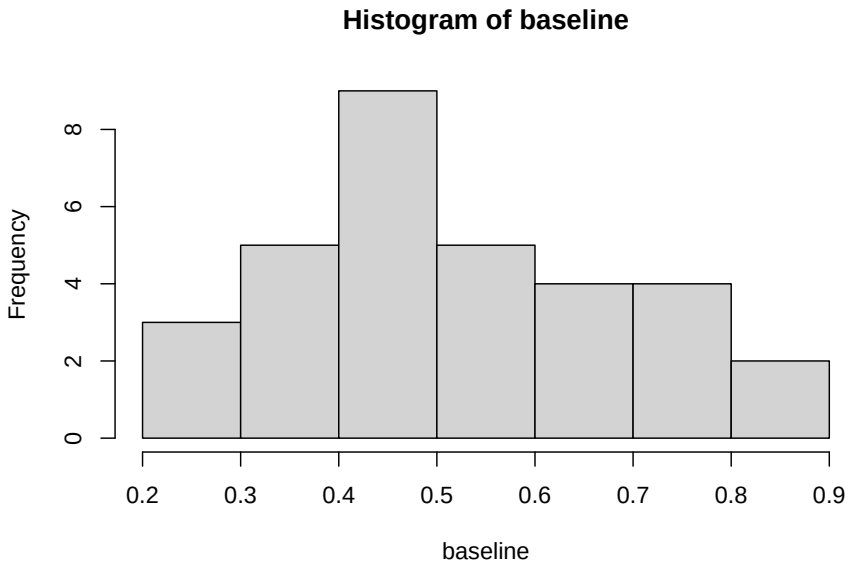
OK, we could just do the t-test right away, it's really easy, only one line of code. But, we haven't even looked at the numbers yet. Let's at least do that. First, we'll just use plot. It will show every data point for each infant as a dot.

```
plot(baseline)
```



That's helpful, we see that the dots are all over the place. Let's do a histogram, so we can get a better sense of the frequency of different proportions.

```
hist(baseline)
```



6.4.4.2 Look at the descriptives

Let's get the mean and standard deviation of the sample

```
mean(baseline)
```

```
## [1] 0.5210967
```

```
sd(baseline)
```

```
## [1] 0.1769651
```

OK, so just looking at the mean, we see the proportion is close to .5 (it's .521). And, we see there is a healthy amount of variance (the dots were all over the place), as the standard deviation was about .176.

Question: Based on the means and standard deviations can you make an educated guess about what the t and p values might be? Learn how to do this and you will be improving your data-sense.

Now, before we run the t-test, what do you think is going to happen? We are going to get a t-value, and an associated p-value. If you can make a guess at what those numbers would be right now in your head, and those end up being

pretty close to the ones we will see in a moment, then you should pat yourself on the back. You have learned how to have intuitions about the data. As I am writing this I will tell you that 1) I can't remember what the t and p was from the paper, and I haven't done the test yet, so I don't know the answer. So, I am allowed to guess what the answer will be. Here are my guesses t(31) = 0.2, p = .95. The numbers in the brackets are degrees of freedom, which we know are 31 (df= n-1 = 32-1= 31). More important than the specific numbers I am guessing (which will probably be wrong), I am guessing that the p-value will be pretty large, it will not be less than .05, which the author's set as their alpha rate. So, I am guessing we will not reject the hypothesis that .52 is different from .5.

Let's do the t-test and see what happens.

6.4.4.3 Conduct t.test

```
t.test(baseline, mu=.5)
```

```
##
##  One Sample t-test
##
## data:  baseline
## t = 0.67438, df = 31, p-value = 0.5051
## alternative hypothesis: true mean is not equal to 0.5
## 95 percent confidence interval:
##  0.4572940 0.5848994
## sample estimates:
## mean of x
## 0.5210967
```

Question: Why was the baseline condition important for the experiment? What does performance in this condition tell us?

So, there we have it. We did a one-sample t-test. Here's how you would report it, t(31) = .67, p = .505. Or, we might say something like:

> During the baseline condition, the mean proportion looking time toward the singer was .52, and was not significantly different from .5, according to a one-sample test, t(31) = .67, p = .505.

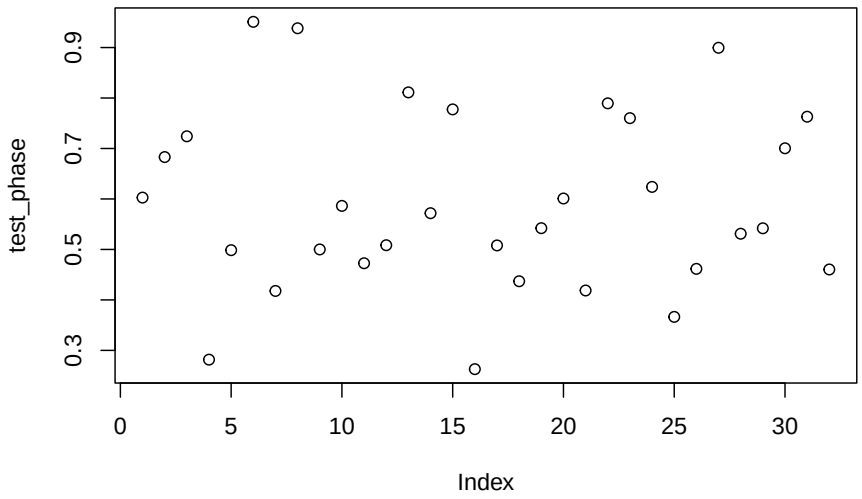
You should take the time to check this result, and see if it is the same one that was reported in the paper.

6.4.5 Test phase

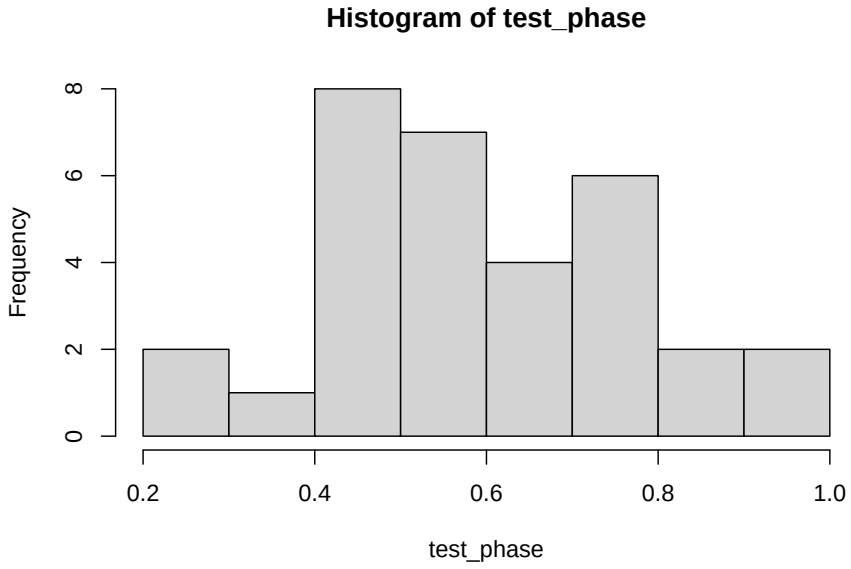
Remember how the experiment went. Infants watched silent video recordings of two women (Baseline). Then each person sung a song, one was familiar to the infant (their parents sung the song to them many times), and one was unfamiliar (singing phase). After the singing phase, the infants watched the silent video of the two singers again (test phase). The critical question was whether the infants would look more to the person who sung the familiar song compared to the person who sun the unfamiliar song. If the infants did this, they should look more than 50% of the time to the singer who sang the familiar song. We have the data, we can do another one sample t-test to find out. We can re-use all the code we already wrote to do this. I'll put it all in one place. If we run all of this code, we will see all of the things we want to see.

We only need to make two changes. We will change `experiment_one$Baseline_Proportion_Gaze_to_Si` to `experiment_one$Test_Proportion_Gaze_to_Singer`, because that column has the test phase data. And, instead of putting the data into the variable `baseline`. We will make a new variable called `test_phase` to store the data.

```
test_phase <- experiment_one$Test_Proportion_Gaze_to_Singer
plot(test_phase)
```




```
hist(test_phase)
```




```
mean(test_phase)
```

```
## [1] 0.5934913
```

```
sd(test_phase)
```

```
## [1] 0.1786884
```

```
t.test(test_phase, mu = .5)
```

```
##
##  One Sample t-test
##
## data:  test_phase
## t = 2.9597, df = 31, p-value = 0.005856
## alternative hypothesis: true mean is not equal to 0.5
## 95 percent confidence interval:
##  0.5290672 0.6579153
## sample estimates:
## mean of x
## 0.5934913
```

Question: Why was the test condition important for the experiment? What does performance in this condition tell us?

Alright. What did we find? You should take a stab at writing down what we found. You can use the same kind of language that I used from the first one sample-test. You should state the mean proportion, the t-value, the dfs, and the p-value. You should be able to answer the question, did the infants look longer at the singer who sang the familiar song? And, did they look longer than would be consist with chance at 50%.

6.4.6 Paired-samples t-test

The paired samples t-test is easy to do. We've already made two variables called `baseline`, and `test_phase`. These contain each of the infants looking time proportions to the singer for both parts of the experiment. We can see if the difference between them was likely or unlikely due to chance by running a paired samples t-test. We do it like this in one line:

```
t.test(test_phase, baseline, paired=TRUE, var.equal=TRUE)
```

```
##
##  Paired t-test
##
## data:  test_phase and baseline
## t = 2.4164, df = 31, p-value = 0.02175
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.01129217 0.13349698
## sample estimates:
## mean difference
##      0.07239457
```

Question: Why was the paired samples t-test necessary if we already did two one sample t-test? What new question is the paired samples t-test asking?

I'll leave it to you to interpret these values, and to see if they are the same as the ones in the paper. Based on these values what do you conclude? Is there a difference between the mean proportion looking times for the baseline and testing phase?

6.4.6.1 Relationship between one-sample and paired sample t-test

Question: Why is it that a paired samples t-test can be the same as the one sample t-test? What do you have to do the data in the paired samples t-test in order to conduct a one-sample t-test that would give you the same result?

We've discussed in the textbook that the one-sample and paired sample t-test are related, they can be the same test. The one-sample test whether a sample mean is different from some particular mean. The paired sample t-test, is to determine whether one sample mean is different from another sample mean. If you take the scores for each variable in a paired samples t-test, and subtract them from one another, then you have one list of difference scores. Then, you could use a one sample t-test to test whether these difference scores are different from 0. It turns out you get the same answer from a paired sample t-test testing the difference between two sample means, and the one sample t-test testing whether the mean difference of the difference scores between the samples are different from 0. We can show this in r easily like this:

```
t.test(test_phase, baseline, paired=TRUE, var.equal=TRUE)
```

```
##
##  Paired t-test
##
## data:  test_phase and baseline
## t = 2.4164, df = 31, p-value = 0.02175
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  0.01129217 0.13349698
## sample estimates:
## mean difference
##      0.07239457
```

```
difference_scores<-test_phase-baseline
t.test(difference_scores, mu=0)
```

```
##
##  One Sample t-test
##
## data:  difference_scores
## t = 2.4164, df = 31, p-value = 0.02175
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  0.01129217 0.13349698
## sample estimates:
##  mean of x
## 0.07239457
```

6.4.6.2 Usefulness of difference scores

OK fine, the paired samples t-test can be a one sample t-test if you use the difference scores. This might just seem like a mildly useful factoid you can use

for stats trivia games (which no one plays). The point of drawing your attention to the relationship, is to get you to focus on the difference scores. These are what we are actually interested in.

Let's use the difference scores to one more useful thing. Sometime the results of a t-test aren't intuitively obvious. By the t-test we found out that a small difference between the test phase and baseline was not likely produced by chance. How does this relate to the research question about infants using familiar songs as cues for being social? Let's ask a very simple question. How many infants actually showed the bias? How many infants out of 32 looked longer at the singer who sang the familiar song during test, compared to during baseline.

We can determine this by calculating the difference scores. Then, asking how many of them were greater than zero:

```
difference_scores <- test_phase-baseline
length(difference_scores[difference_scores>0])
```

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

So, 22 out of 32 infants showed the effect. To put that in terms of probability, 68.75% of infants showed the effect. These odds and percentages give us another way to appreciate how strong the effect is. It wasn't strong enough for all infants to show it.

6.4.7 Graphing the findings

It is often useful to graph the results of our analysis. We have already looked at dot plots and histograms of the individual samples. But, we also conducted some t-tests on the means of the baseline and test_phase samples. One of the major questions was whether these means are different. Now, we will make a graph that shows the means for each condition. Actually, we will make a few different graphs, so that you can think about what kinds of graphs are most helpful. There are two major important things to show: 1) the sample means, and 2) a visual aid for statistical inference showing whether the results were likely due to chance.

We will use the ggplot2 package to make our graphs. Remember, there are two steps to take when using ggplot2. 1) put your data in a long form data frame, where each measure has one row, and 2) define the layers of the ggplot.

6.4.7.1 Make the dataframe for plotting

To start we will need 2 columns. One column will code the experimental phase, Baseline or Test. There are 32 observations in each phase, so we want the word

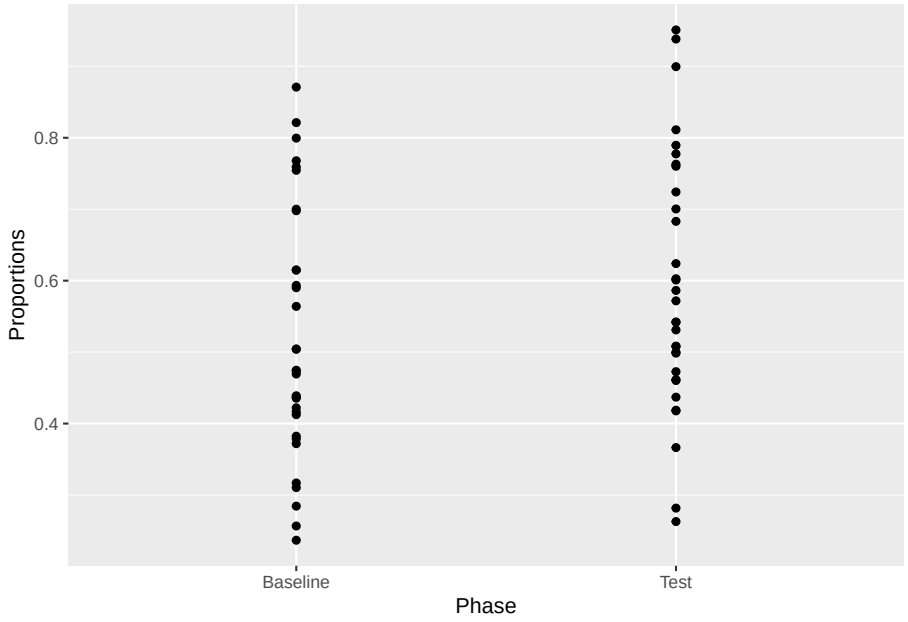
`Baseline` to appear 32 times, followed by the word `Test` 32 times. Then we want a single column with each of the proportions for each infant.

```
Phase <- rep(c("Baseline","Test"), each = 32)
Proportions <- c(baseline,test_phase)
plot_df <- data.frame(Phase,Proportions)
```

6.4.7.2 Dot plot of raw scores

This shows every scores value on the y-axis, split by the baseline and test groups. If you just looked at this, you might not think the test phase was different from the baseline phase. Still very useful to see the spread of individual scores. Supports the intuition that the scores are still kind of in a similar ballpark.

```
library(ggplot2)
ggplot(plot_df, aes(x=Phase, y=Proportions))+
  geom_point()
```



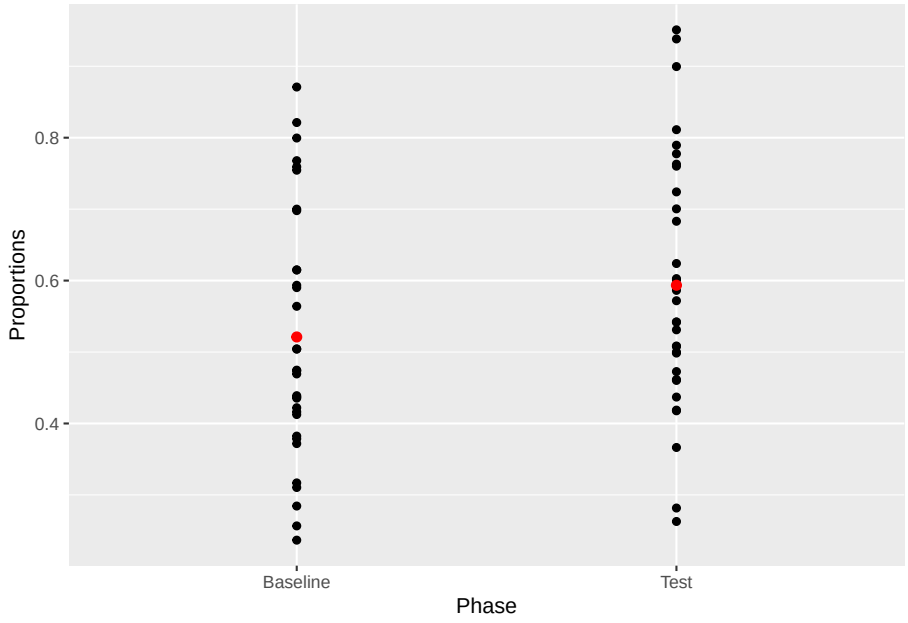
6.4.7.3 Dot plot with means and raw scores

Question: What kinds of inferences about the role of chance in producing the difference between the means can we make from this graph? What is missing?

`ggplot2` is great because it let's us add different layers on top of an existing plot. It would be good to see where the mean values for each sample lie on top of the sample scores. We can do this. But, to do it, we need to supply ggplot with another data frame, one that contains the means for each phase in long form. There are are only two phases, and two means, so we will make a rather small data.frame. It will have two columns, a Phase column, and Mean_value column. There will only be two rows in the data frame, one for the mean for each phase.

To make the smaller data frame for the means we will use the `aggregate` function. This allows us to find the means for each phase from the plot_df data frame. It also automatically returns the data frame we are looking for.

```
mean_df <- aggregate(Proportions ~ Phase, plot_df, mean)

ggplot(plot_df, aes(x=Phase, y=Proportions))+
  geom_point()+
  geom_point(data=mean_df, color="Red", size=2)
```



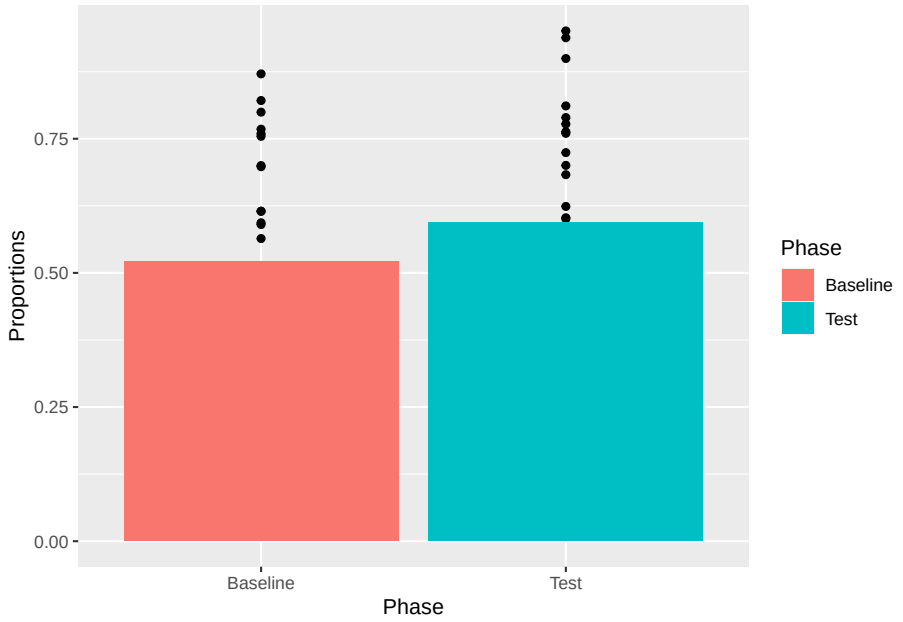
6.4.7.4 Bar plot

It's very common to use bars in graphs. We can easily do this by using `geom_bar`, rather than `geom_point`. Also, we can plot bars for the means, and keep showing the dots like this…(note this will be messed up, but I want to show you why).

Also look for these changes.

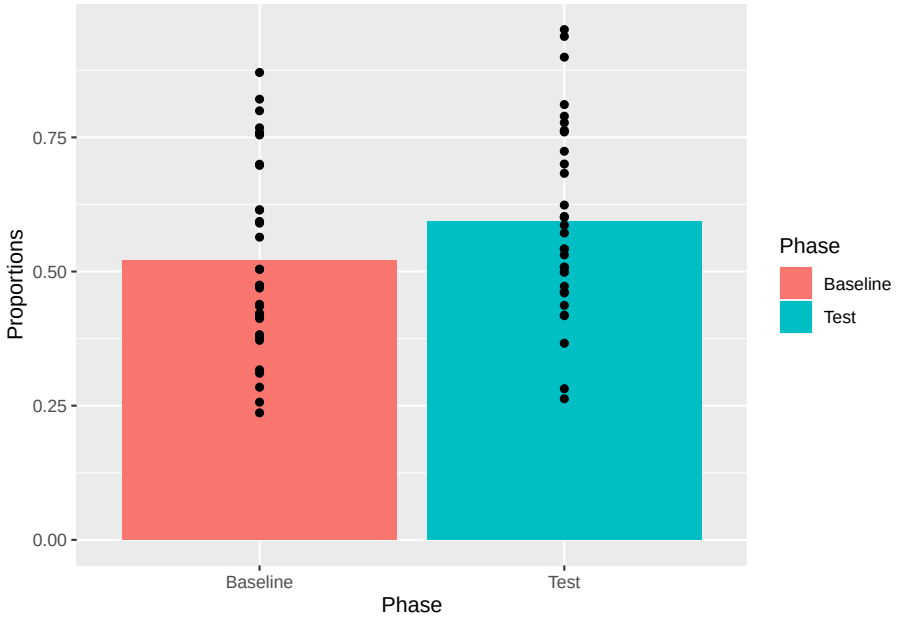
1. added `stat="identity"` Necessary for bar plot to show specific numbers
2. added `aes(fill=Phase)` Makes each bar a different color, depending on which phase it comes from

```
ggplot(plot_df, aes(x=Phase, y=Proportions))+
  geom_point()+
  geom_bar(data=mean_df, stat="identity",aes(fill=Phase))
```



OK, we see the bars and some of the dots, but not all of them. What is going on? Remember, ggplot2 works in layers. Whatever layer you add first will be printed first in the graph, whatever layer you add second will be printed on top of the first. We put the bars on top of the dots. Let's change the order of the layers so the dot's go on top of the bars.

```
ggplot(plot_df, aes(x=Phase, y=Proportions))+
  geom_bar(data=mean_df, stat="identity",aes(fill=Phase))+
  geom_point()
```



6.4.7.5 Bar plot with error bars

So far we have only plotted the means and individual sample scores. These are useful, but neither of them give us clear visual information about our statistical test. Our paired sample t-test suggested that the mean difference between Baseline and Test was not very likely by chance. It could have happened, but wouldn't happen very often.

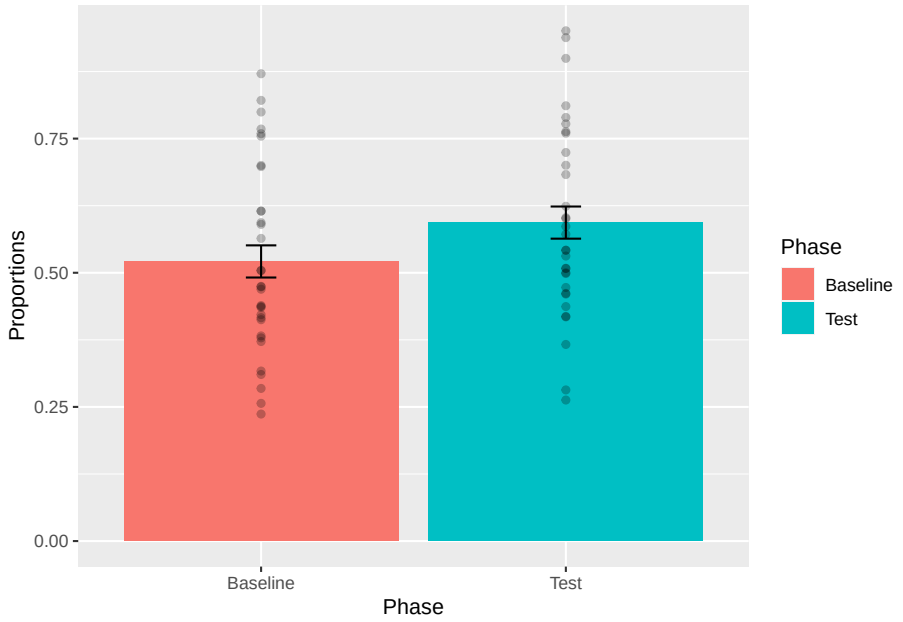
Question: Why would the standard deviation of each mean, or the standard error of each mean be inappropriate to use in this case?

Question: How would error bars based on the standard error of the mean differences aid in visual inference about the role of chance in producing the difference?

Error bars are commonly used as an aid for visual inference. The use of error bars can be a subtle nuanced issue. This is because there a different kinds of error bars that can be plotted, and each one supports different kinds of inference. In general, the error bar is supposed to represent some aspect of the variability associated with each mean. We could plot little bars that are +1 or -1 standard deviations of each mean, or we would do +1 or -1 standard errors of each mean. In the case of paired samples, neither or these error bars would be appropriate, they wouldn't reflect the variability associated with mean we are interested in. In a paired samples t-test, we are interested in the variability of the mean of the difference scores. Let's calculate the standard error of the mean (SEM) for

the difference scores between Baseline and Test, and then add error bars to the plot.

```
difference_scores <- baseline-test_phase #calculate difference scores
standard_error <- sd(difference_scores)/sqrt(length(difference_scores)) #calculate SEM


ggplot(plot_df, aes(x=Phase, y=Proportions))+
  geom_bar(data=mean_df, stat="identity",aes(fill=Phase))+
  geom_errorbar(data=mean_df, aes(ymin=Proportions-standard_error,
                                  ymax=Proportions+standard_error), width=.1) +
  geom_point(alpha=.25)
```

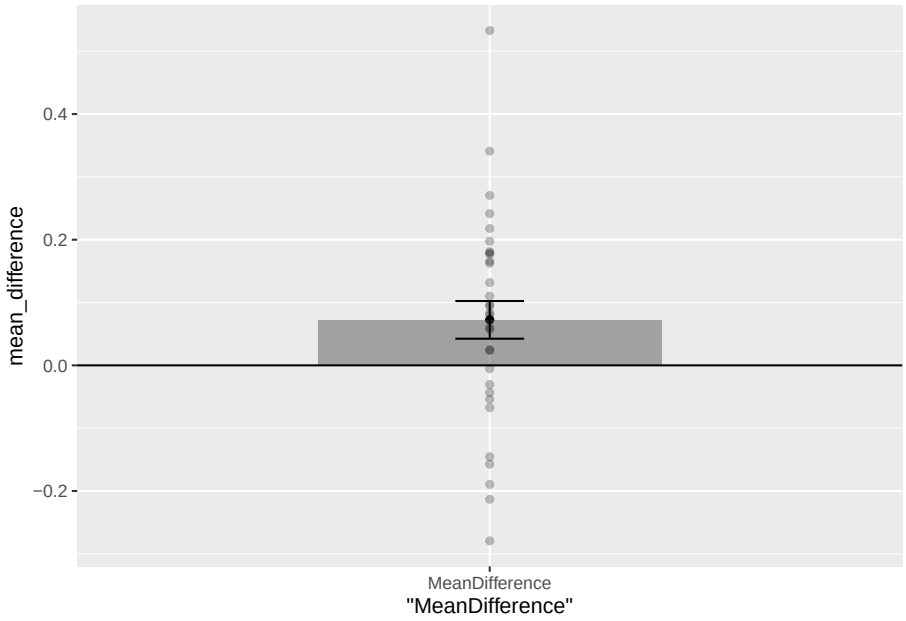


Question: What is one reason why these error bars (standard error of the mean difference between Baseline and Test) are appropriate to use. What is one reason they are not appropriate to use?

We have done something that is useful for visual inference. From the textbook, we learned that differences of about 2 standard errors of the mean are near the point where we would claim that chance is unlikely to have produced the difference. This is a rough estimate. But, we can see that the top of the error bar for Baseline is lower than the bottom of the error bar for Test, resulting in a difference greater than 2 standard error bars. So, based on this graph, we might expect the difference between conditions to be significant. We can also complain about what we have done here, we are placing the same error bars from the mean difference scores onto the means for each condition. In some

sense this is misleading. The error bars are not for the depicted sample means, they are for the hidden single set of difference scores. To make this more clear, we will make a bar plot with a single bar only for the differences scores.

```
difference_scores <- test_phase-baseline #calculate difference scores
standard_error <- sd(difference_scores)/sqrt(length(difference_scores)) #calculate SEM
mean_difference <- mean(difference_scores)

qplot(x="MeanDifference", y=mean_difference)+
  geom_bar(stat="identity", width=.5, alpha=.5)+
  geom_hline(yintercept=0)+
  geom_point(aes(y=difference_scores), alpha=.25)+
  geom_errorbar(aes(ymin=mean_difference-standard_error,
                                    ymax=mean_difference+standard_error), width=.1)
```



Question: Why is is it more appropriate to put the standard error of the difference on this bar graph? What important aspects of the original results shown in the previous graph are missing from this graph?

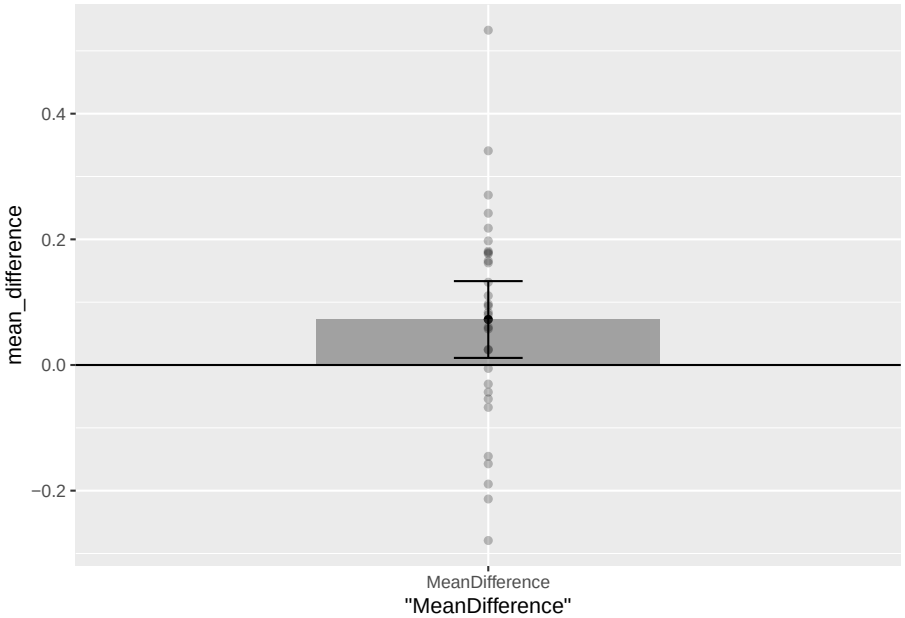
This plot is very useful too, it gives us some new information. We can see that the mean difference (test - baseline) was greater than 0. And, we are plotting the standard error of the mean differences, which are the error bars that more formally belong to this graph. Still, we are in a position to make some guesses for visual inference. The lower error bar represents only 1 SEM. It does not cross 0, but the fact that 1 SEM does not cross zero isn't important. For SEMs it's usually closer to 2. We can sort of visually guesstimate that that 2 SEMs

would not cross zero, which would suggest we would obtain a small p-value. We also see each of the mean difference scores. It's very clear that they are all over the place. This means that not every infant showed a looking time preference toward the singer of the familiar song. Finally, this single bar plot misses something. It doesn't tell us what the values of the original means were.

6.4.7.6 Bar plot with confidence intervals

Confidence intervals are also often used for error bars, rather than the standard error (or other measure of variance). If we use 95% confidence intervals, then our error bars can be even more helpful for visual inference. Running the `t.test` function produces confidence interval estimates, and we can pull them out and use them for error bars.

```
t_test_results <- t.test(difference_scores)
lower_interval<- t_test_results$conf.int[1]
upper_interval<- t_test_results$conf.int[2]

qplot(x="MeanDifference", y=mean_difference)+
  geom_bar(stat="identity", width=.5, alpha=.5)+
  geom_hline(yintercept=0)+
  geom_point(aes(y=difference_scores), alpha=.25)+
  geom_errorbar(aes(ymin=lower_interval,
                                    ymax=upper_interval), width=.1)
```

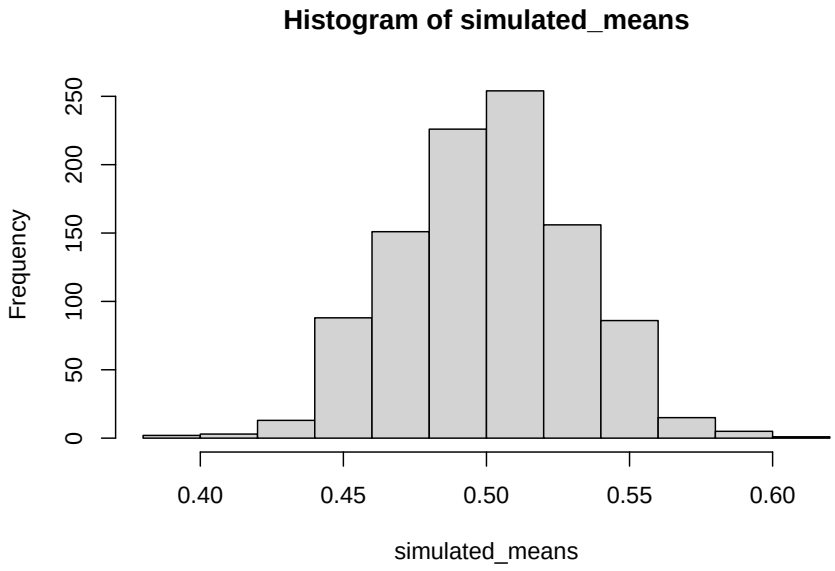


Notice that the 95% confidence intervals around the mean are wider than the SEM error bars from the previous graph. These new confidence intervals tell us that 95% of the time our sample mean will fall between the two lines. The bottom line is slightly above 0, so we can now visually see support for our statistical inference that chance was unlikely to produce the result. If chance was likely to produce the result, the horizontal line indicating 0, would be well inside the confidence interval. We can also notice that the mean difference was just barely different from chance, that lower bar is almost touching 0.

6.4.8 Data-simulation

We can do a little bit of data simulation to get a better feel for this kind of data. For example, we saw that the dots in our plots were quite variable. We might wonder about what chance can do in the current experiment. One way to do this is to estimate the standard deviation of the looking time proportions. Perhaps the best way to do that would be to an average of the standard deviation in the baseline and test_phase conditions. Then, we could simulate 32 scores from a normal distribution with mean = .5, and standard deviation equaling our mean standard deviation. We could calculate the mean of our simulated sample. And, we could do this many times, say 1000 times. Then, we could look at a histogram of our means. This will show the range of sample means we would expect just by chance. This is another way to tell whether the observed difference in this experiment in the testing phase was close or not close from being produced by chance. Take a look at the histogram. What do you think?

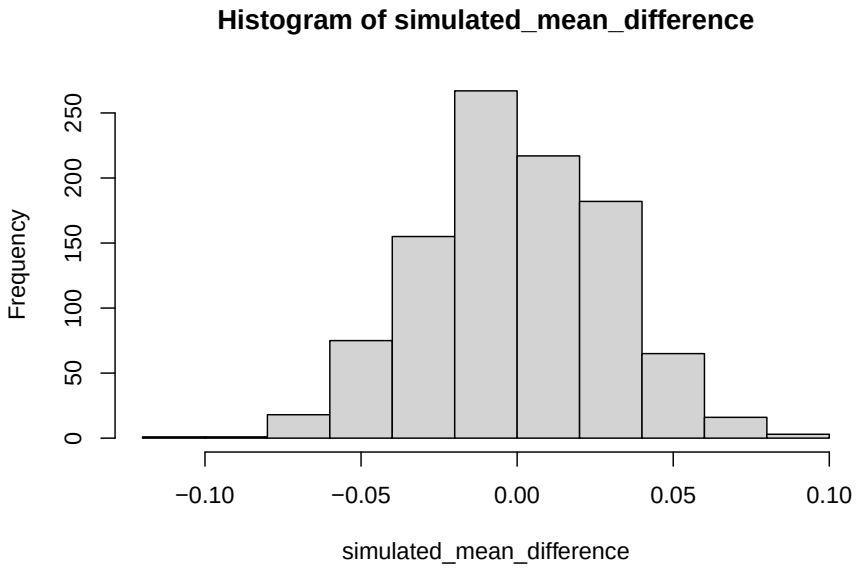
```
sample_sd   <- (sd(baseline)+sd(test_phase))/2

simulated_means <- length(1000)
for(i in 1:1000){
 simulated_means[i] <- mean(rnorm(32,.5, sample_sd))
}

hist(simulated_means)
```



6.4.8.1 Simulating the mean differences

We can do the simulation slightly differently to give us a different look at chance. Above we simulated the sample means from a normal distribution centered on .5. The experimental question of interest was whether the mean difference between the baseline and test_phase condition was different. So, we should do a simulation of the difference scores. First, we estimate the standard deviation of the difference scores, and then run the simulation with a normal distribution centered on 0 (an expected mean difference of 0). This shows roughly how often we might expect mean differences of various sizes to occur. One major limitation is that we likely had only a rough estimate of the true standard deviation of these mean differences, after all there were only 32 of them, so we should take this with a grain of salt. Nevertheless, the pattern in the simulation fits well with the observations in that we already made from the data.

```
sample_sd   <- sd(baseline-test_phase)

simulated_mean_difference <- length(1000)
for(i in 1:1000){
 simulated_mean_difference[i] <- mean(rnorm(32,0, sample_sd))
}

hist(simulated_mean_difference)
```



6.4.9 Generalization Exercise

(1 point - Pass/Fail)

The following code creates two variables with simulated means for each of 20 subjects in two conditions (A and B). Each sample comes from a normal distribution with mean = 100, and standard deviation = 25.

```
Condition_A <- rnorm(20,100,25)
Condition_B <- rnorm(20,100,25)
```

1. Conduct a paired samples t-test on sample data stored in the variables `Condition_A`, and `Condition_B`. Report the results of the t-test, and the mean difference between conditions

2. The above code assumes no difference in the means between Condition A and Condition B. Both samples come from the same normal distribution. Change the mean for one of the distributions. Make the change large enough so that you find a significant p-value ($p < 0.05$) when you conduct the t-test on the new simulated data. Report the t-test and the means for each condition

6.4.10 Writing assignment

(2 points - Graded)

Complete the writing assignment described in your R Markdown document for this lab. When you have finished everything. Knit the document and hand in your stuff (you can submit your .RMD file to blackboard if it does not knit.)

1. Answer the following questions

a. Explain the general concept of a t value, and how it is different from a mean and the standard error. (.33 points)

b. Imagine you obtained a t-value with an associated p-value of .25. Explain what this means. (.33 points)

c. Imagine the critical t value for a particular test was 2.6. What does the critical t-value mean (assuming alpha = 0.05 and the test is two-tailed) (.33 points)

d. Explain the differences between a one-sample and paired-sample t-test (1 point)

General grading.

- You will receive 0 points for missing answers
- You must write in complete sentences. Point form sentences will be given 0 points.
- Completely incorrect answers will receive 0 points.
- If your answer is generally correct but very difficult to understand and unclear you may receive half points for the question

6.4.11 Practice Problems

---

1. Use the data file from this lab tutorial to test whether the number of frames the baby spent gazing at the familiar song is significantly different than the number of frames spent gazing at the unfamiliar song (use alpha = .05). Report your results in proper statistical reporting format.

2. Graph this result (including 1 SEM error bars) as a bar graph.

3. Compute a new variable representing the difference in number of frames the baby spent gazing between the familiar and unfamiliar song conditions. Test this difference score against a mean of 0 (use alpha=.05). Report your results in proper statistical reporting format.

Chapter 7

Lab 7: t-test (Independent Sample)

I think he [Gosset] was really the big influence in statistics… he asked the questions and Pearson and Fisher put them into statistical language, and then Neyman came to work with the mathematics. But I think most of it came from Gosset. —F. N. David

This lab is modified and extended from Open Stats Labs. Thanks to Open Stats Labs (Dr. Kevin P. McIntyre) for their fantastic work.

7.1 Do you come across as smarter when people read what you say or hear what you say?

7.1.1 STUDY DESCRIPTION

Imagine you were a job candidate trying to pitch your skills to a potential employer. Would you be more likely to get the job after giving a short speech describing your skills, or after writing a short speech and having a potential employer read those words? That was the question raised by Schroeder and Epley (2015).The authors predicted that a person's speech (i.e., vocal tone, cadence, and pitch) communicates information about their intellect better than their written words (even if they are the same words as in the speech).

To examine this possibility, the authors randomly assigned 39 professional recruiters for Fortune 500 companies to one of two conditions. In the audio condition, participants listened to audio recordings of a job candidate's spoken job pitch. In the transcript condition, participants read a transcription of the job candidate's pitch. After hearing or reading the pitch, the participants rated

the job candidates on three dimensions: intelligence, competence, and thoughtfulness. These ratings were then averaged to create a single measure of the job candidate's intellect, with higher scores indicating the recruiters rated the candidates as higher in intellect. The participants also rated their overall impression of the job candidate (a composite of two items measuring positive and negative impressions). Finally, the participants indicated how likely they would be to recommend hiring the job candidate (0 - not at all likely, 10 - extremely likely).

What happened? Did the recruiters think job applicants were smarter when they read the transcripts, or when the heard the applicants speak? We have the data, we can find out.

7.2 Lab skills learned

1. Conduct independent samples t-tests
2. Generate figures
3. Discuss the results and implications

7.3 Important Stuff

- citation: Schroeder, J., & Epley, N. (2015). The sound of intellect: Speech reveals a thoughtful mind, increasing a job candidate's appeal. Psychological Science, 26, 877-891.
- Link to .pdf of article
- Data in .csv format
- Data in SPSS format

7.4 R

7.4.1 Load the data

Remember that any line with a # makes a comment and the code does not run. Below is how to load the .csv data from the online repository, or from a local file (you need to change the file path to where the local file is, if you downloaded it). The data contains all of the measures and conditions from Experiment 4.

```
library(data.table)
# load from github repo
#all_data <- fread("https://raw.githubusercontent.com/CrumpLab/statisticsLab/master/da

all_data <- fread("data/SchroederEpley2015data.csv") # load from file on computer
```

7.4.2 Inspect data frame

This will give you a big picture of the data frame. Click the button to view it in your browser, then take a look to see what is in it.

```
library(summarytools)
view(dfSummary(all_data))
```

7.4.3 Find the data you need

This time the data comes pre-filtered for us. The authors ran lots of experiments, but we only have the data from Experiment 4. This is great, we don't need to subset the data frame to find all of the data that we need. But, we do still need to understand what data we want to analyze. Let's start with identify the column that codes the experimental conditions for whether or not the evaluator read a transcript or heard the interview.

7.4.3.1 Condition variable

Lucky for us, the condition variable is called `CONDITION`! Let's take a look. We printed it out just by writing down `all_data$CONDITION`. There 0s and 1s for each condition (audio vs. transcript). But which one is which? This isn't clear from the data, and it isn't clear from the paper, or from the repository. We have to do some guess work. I went ahead and computed the means for the Intellect_rating between each condition, and then compared those to the graph in the paper for E4. It looks like 1 = audio condition, and 0 = transcript condition.

```
all_data$CONDITION
```

```
##  [1] 1 1 1 0 0 0 1 0 1 0 0 1 1 0 0 1 1 1 0 0 0 0 0 1 1 1 0 1 1 1 0 0 1 1 0 1 0 1
## [39] 1
```

```
aggregate(Intellect_Rating~CONDITION,all_data,mean)
```

```
##   CONDITION Intellect_Rating
## 1         0         3.648148
## 2         1         5.634921
```

Let's use words instead of 0s and 1s to refer to our experimental conditions. To do this, we will chance the values of 0 and 1, to the words `transcript` and `audio`. We can do this in two steps. First we convert the CONDITION column

to a factor. This will automatically turn the 0s and 1s into strings (not numbers, text). Factors have an internal variable for the names of the levels, which will be 0 and 1. We can simply change the level names to transcript and audio.

```
all_data$CONDITION <- as.factor(all_data$CONDITION)
levels(all_data$CONDITION) <- c("transcript","audio")
```

Now if you look at the `all_data` variable, you will see the words transcript and audio, where 0s and 1s used to be.

7.4.3.2 Dependent Measures

Next it's time to find the dependent measure columns. The graph from the paper shows three different measures in each condition. These included `Intellect`, `General Impression`, and `Hiring Likelihood`. Every evaluator (either given a transcript or audio recording of the interview) gave ratings on a scale of 1 to 10 for each of those concepts. It's not immediately clear which columns in `all_data` correspond to those three measures. There are lots of different measures that could be the ones they reported. It turns out the relevant ones are called

1. `Intellect_Rating`
2. `Impression_Rating`
3. `Hire_Rating`

In this tutorial we are going to walk through doing an independent samples t-test for the first measure, `Intellect_Rating`. You can follow these same steps to complete the same kind of t-test for the other two variables.

7.4.4 Look at the dependent variable.

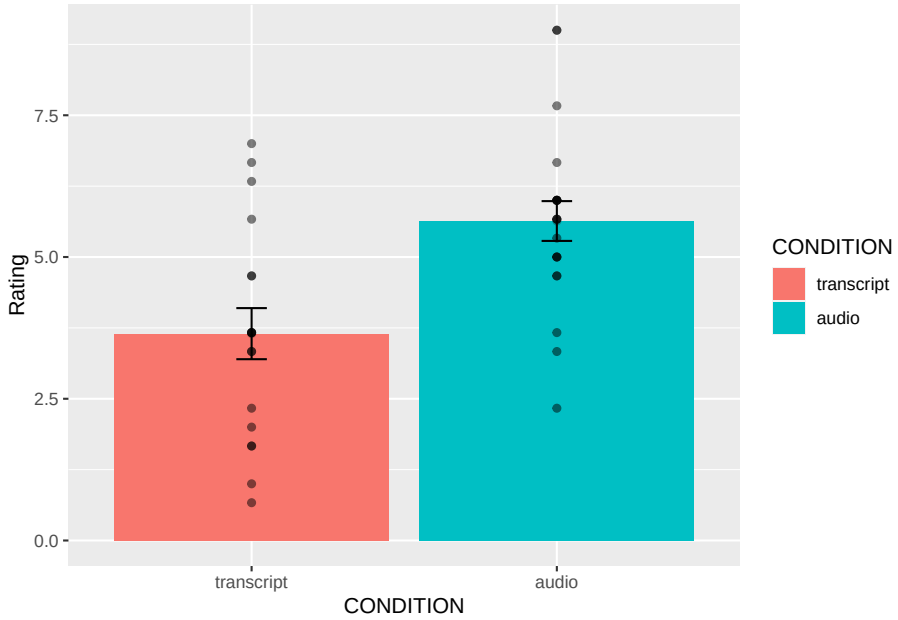
Question: Why do we always want to look at the data?

What is the first thing we do before even considering an inferential test? Look at the data. Always look at the data. We could make a dot plot or histogram of the data from the `Intellect_ratings`. But, from our last lab we already learned how to make graphs showing most of the information we would want to look at. For example, we could make a bar graph that has the means for each condition (transcript vs. audio), standard errors of the mean and the actual scores as little dots. This would be great to look at it. Not only will it tell us if there are really weird numbers in the data (who knows maybe the data file is corrupted, you need to look), it will also give us strong intuitions about what to expect for the t-test.

We can plot each score as a dot using the `all_data` data frame. If we want to add on a layer for the sample means, and for the sample standard errors, we have to compute those and put them in a new data frame first. Then we use both data frames with ggplot to plot all of the information.

We will use `dplyr` to quickly get the means and the standard errors and put them in a new data frame called `decriptive_df`.

```
library(dplyr)
library(ggplot2)

# get means and SEs
descriptive_df <- all_data %>%
                    group_by(CONDITION) %>%
                    summarise(means= mean(Intellect_Rating),
                              SEs = sd(Intellect_Rating)/sqrt(length(Intellect_Rating)))

# Make the plot
ggplot(descriptive_df, aes(x=CONDITION, y=means))+
  geom_bar(stat="identity", aes(fill=CONDITION))+ # add means
  geom_errorbar(aes(ymin=means-SEs,               # add error bars
                    ymax=means+SEs), width=.1) +
  geom_point(data=all_data, aes(x=CONDITION, y=Intellect_Rating), alpha=.5)+
  geom_point(alpha=.25)+
  ylab("Rating")
```



This plot is very useful. First, we can see the numbers in our dependent measure are behaving sensibly. We know that the numbers have to be between 1-10, because those were the only options in the scale. If we found numbers bigger or smaller, we would know something was wrong. Checking for things that are obviously wrong in the data is one reason why we always look at first. We are checking for obvious errors. There are other ways to check to, but looking is fast and easy.

Question: Why are the standard errors of each sample an appropriate thing to use for error bars?

Now that you can see the patterns in the data, you should form an intuition about how the independent samples t-test will turn out. You can see how big the error bars (+1/-1 standard error of each sample man). The t-test will tell us whether the observed difference (or greater) is likely due to chance. Should we find a big t-value or a small t-value? Should we find a big p-value or a small t-value. If you understand how t-values and p-values work, the answer should be very clear from the graph. You should already know how the t-test will turn out before you run it. Running it will confirm what you already suspect to be true.

7.4.5 Conduct Independent samples t-test

Question: Why are we conducting an independent samples t-test, and not a one-sample or paired samples t-test?

We use the very same `t.test` function that we used last time to conduct a t-test. The only difference is that we don't tell the R to use a paired sample t-test. We leave the `paired=TRUE` statement out, and R automatically knows we want to do an independent samples t-test. Remember to set the `var.equal=TRUE`, otherwise R will compute a different version of the t-test.

You can use different syntax to run the t-test. Because our data is already in a data frame we can use this syntax.

```
t.test(Intellect_Rating~CONDITION, data=all_data, var.equal=TRUE)
```

```
##
##  Two Sample t-test
##
## data:  Intellect_Rating by CONDITION
## t = -3.5259, df = 37, p-value = 0.001144
## alternative hypothesis: true difference in means between group transcript and group
## 95 percent confidence interval:
##  -3.1284798 -0.8450652
## sample estimates:
```

```
## mean in group transcript      mean in group audio
##                 3.648148                 5.634921
```

The `t.test` function also will work on two variables, not in a data frame. For example, the following does the same thing. But, it's harder to read, and the means are described in terms of X and Y, not terms of `transcript` and `audio`, like the report above.

```
t.test(all_data[all_data$CONDITION=='transcript',]$Intellect_Rating,
       all_data[all_data$CONDITION=='audio',]$Intellect_Rating,
       var.equal=T)
```

```
##
##  Two Sample t-test
##
## data:  all_data[all_data$CONDITION == "transcript", ]$Intellect_Rating and all_data[all_data$C
## t = -3.5259, df = 37, p-value = 0.001144
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -3.1284798 -0.8450652
## sample estimates:
## mean of x mean of y
##  3.648148  5.634921
```

Question: What conclusions do we draw from the t-test? Based on these results, if you were being evaluated for a job interview, would you rather have the evaluator read a transcript of your interview or listen to an audio recording?

So, now we have the t-test. It shows the t-value, the p-value, and the means for each group. You can double-check with the paper to see if we found the same results as reported by the authors.

7.4.6 Remaining ratings

Now, you should use what you have learned to analyse the last two ratings for the dependent variables `Impression_Rating`, and `Hire_Rating`. This is your task for the generalization exercise. Remember to plot the data for each, and conduct a t-test for each. Then compare what you found to the original article. What did you find, and what do the results mean?

7.4.7 Reconstructing the graph from the paper

The results from Experiment 4 in the paper plot the means and error bars (+1 / -1 SEM) for all three dependent measures, for both experimental conditions.

We can do this in ggplot using the data. We will have to make a couple changes to the data frame. But, it won't be too hard. What we need to do is make a fully long form data frame. Remember a long form data frame has one row per dependent measure.

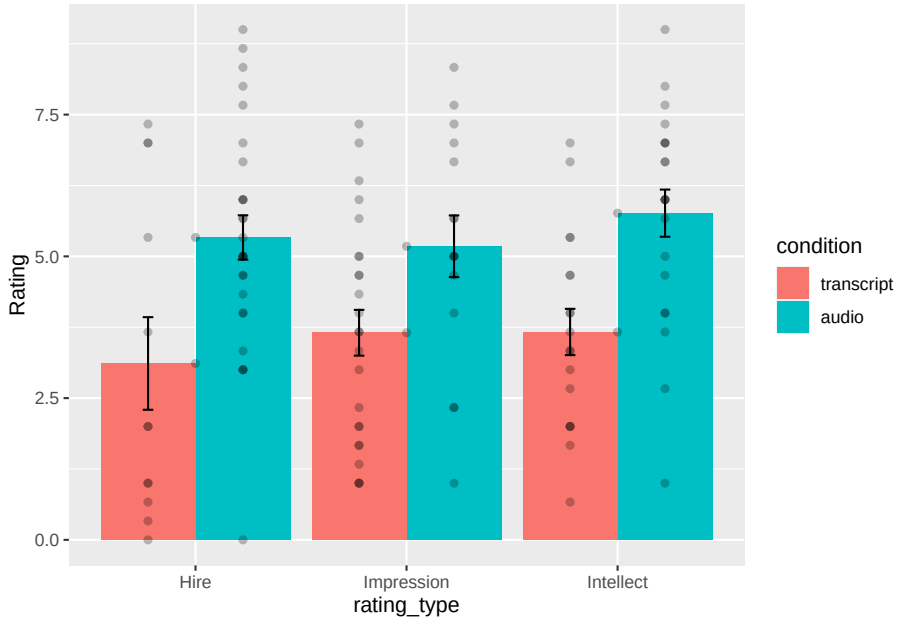
The `all_data` frame is partly long and partly wide. If we are only interested in one dependent measure, then it is a long data frame for that measure. For example, example if we are only interested in plotting `Intellect_Rating`, then we already have one observation of that dependent measure for each row. But, in the other columns, the dependent measures for `Impression_Rating` and `Hire_Rating` are in the same rows.

Before continuing, it is very much worth mentioning that this part of data analysis happens a lot, and it is kind of annoying. I call it the rubix cube problem, because we need to "rotate" and transform the format of the data to accomplish different kinds of analysis goals. It's good to be able to know how to do this. This problem occurs all of the time, and can occur for any software package. It's a good thing you are learning R, because we can do these things easily in R. They are not often so easy to do without a computer programming language like R. The worst thing to do is transform the data by hand. That really sucks. Believe me you don't want to do it. Why? Because you will make mistakes, and you will mess up the data, then you will mess up your analysis. And, you won't be able to find your mistakes, and it will take you ages to correct them. That sucks.

There's more than one way to transform data in R. For example the `cast` and `melt` functions do this kind of thing. You can look those up. In this example we will not use those functions. Instead we will show some steps to build the required data frame one step at a time.

```
# repeat CONDITION column three times

condition <- rep(all_data$CONDITION,3)

# make a ratings variable with all three ratings in one variable

ratings <- c(all_data$Intellect_Rating,
             all_data$Impression_Rating,
             all_data$Hire_Rating)

# make a new factor variable with the names of the ratings
# need to repeat each level name the appropriate number of times

num_to_repeat <- length(all_data$CONDITION)

rating_type <- rep(c("Intellect","Impression","Hire"),num_to_repeat)
```

```
# put the new variables into a data frame

plot_all <- data.frame(condition,rating_type,ratings)

# Get the means and standard errors for each rating by condition

descriptive_all <- plot_all %>%
                     group_by(condition,rating_type) %>%
                     summarise(means= mean(ratings),
                               SEs = sd(ratings)/sqrt(length(ratings)))

# Make the plot

ggplot(descriptive_all, aes(x=rating_type, y=means, group=condition))+
  geom_bar(stat="identity", aes(fill=condition), position='dodge')+
  geom_errorbar(aes(ymin=means-SEs,
                    ymax=means+SEs),
                width=.1,
                position = position_dodge(width=.9)) +
  geom_point(data=plot_all, aes(x=rating_type,
                                y=ratings,
                                group=condition),
             alpha=.25,
             position = position_dodge(width=.9))+
  geom_point(alpha=.25)+
  ylab("Rating")
```



Well, we didn't make the exact graph. We have the bars, the error bars, and we added the individual scores because they are useful to look at. Otherwise, it's the same graph (except the the ordering of bars is determined alphabetically here. We change that in ggplot, but we won't do that today.)

7.4.8 Generalization Exercise

(1 point - Pass/Fail)

Complete the generalization exercise described in your R Markdown document for this lab.

Now, you should use what you have learned to analyse the last two ratings for the dependent variables `Impression_Rating`, and `Hire_Rating`. Report the t-tests and means for each.

7.4.9 Writing assignment

(2 points - Graded)

Complete the writing assignment described in your R Markdown document for this lab. When you have finished everything. Knit the document and hand in your stuff (you can submit your .RMD file to blackboard if it does not knit.)

1. Answer the following questions

a. Explain the difference between a paired-samples t-test and an independent samples t-test. (1 point)

b. Imagine you were to conduct a between-subjects experiment with two groups, where the manipulation had no effect whatsoever. If you repeated this experiment (that doesn't work) 100 times and computed a t-test each time, approximately how many of the experiments out of 100 would you expect find the associated p-value is .05 or smaller? Explain (1 point)

General grading.

- You will receive 0 points for missing answers
- You must write in complete sentences. Point form sentences will be given 0 points.
- Completely incorrect answers will receive 0 points.
- If your answer is generally correct but very difficult to understand and unclear you may receive half points for the question

7.4.10 Practice Problems

---

1. Use the same data file from this lab's tutorial to test whether intelligence ratings were different between genders (use alpha = .05). Who was rated as more intelligent, males or females? Report your result in proper statistical reporting format.

2. Graph this result (including 1 SEM error bars) as a bar graph.

Chapter 8

Lab 8 One-way ANOVA

The analysis of variance is not a mathematical theorem, but rather a convenient method of arranging the arithmetic. —R. A. Fisher

This lab is modified and extended from Open Stats Labs. Thanks to Open Stats Labs (Dr. Kevin P. McIntyre) for their fantastic work.

8.1 How to not think about bad memories by playing Tetris

This lab activity uses the open data from Experiment 2 of James et al. (2015) to teach one-way ANOVA with planned comparisons. Results of the activity provided below should exactly reproduce the results described in the paper.

8.1.1 STUDY DESCRIPTION

Following traumatic experiences, some people have flashbacks, which are also called "intrusive memories"" and are characterized by involuntary images of aspects of the traumatic event. Although people often try to simply forget traumatic memories, this approach is not very effective. Instead, previous research suggests that a better approach may be to try to change aspects of the memory after it is formed. For example, some research shows that traumatic memories can be altered and weakened to the point that they are no longer intrusive.

Because intrusive memories of trauma are often visual in nature, James and colleagues (2015) sought to explore whether completing a visuospatial task (e.g., Tetris) after a memory was formed would interfere with the storage of that memory, and thereby reduce the frequency of subsequent intrusions. They

hypothesized that only participants who complete a visuo-spatial task after reactivation of the traumatic memories would experience a reduction in intrusive memories. In comparison, simply completing a visuo-spatial task (without reactivation) or reactivation (without a visuo-spatial task), would not reduce the occurrence intrusive memories.

In other words, if you play Tetris shortly after you were remembering bad memories, playing Tetris might weaken those memories, which could cause you experience those kinds of intrusive memories less often in the future.

8.1.2 Study Methods

To test their hypothesis, the authors conducted an experiment (N = 72, n = 18 per condition). The procedure is summarized as follows:

Trauma Film: All participants viewed a series of video clips of graphic violence (e.g., a person getting hit by a van while using his phone as he crosses the road) as a way to create memories that should become intrusive memories. Participants then went home and recorded the number of intrusive memories they experienced over the next 24 hours. Because this is before the experimental manipulations, all groups were predicted to have an equal occurrence of intrusive memories during the first 24-hours (called Day 0).

Experimental Task: After this 24-hour period, the participants returned to the lab and completed the experimental task. The experimenters randomly assigned participants to ONE of the following conditions:

1. No-task control: These participants completed a 10-minute music filler task.
2. Reactivation + Tetris: These participants were shown a series of images from the trauma film to reactivate the traumatic memories (i.e., reactivation task). After a 10-minute music filler task, participants played the video game Tetris for 12 minutes.
3. Tetris Only: These participants played Tetris for 12 minutes, but did not complete the reactivation task.
4. Reactivation Only: These participants completed the reactivation task, but did not play Tetris.

Intrusive Memories: All participants were asked to record the number of intrusive memories that they experienced over the next seven days (Days 1 to 7).

After the seven days had passed, participants completed an Intrusion-Provocation Task, in which they were shown blurred images from the trauma film and asked to indicate whether the blurred image triggered an intrusive memory.

8.2 Lab Skills Learned

8.3 Important Stuff

- citation: James, E. L., Bonsall, M. B., Hoppitt, L., Tunbridge, E. M., Geddes, J. R., Milton, A. L., & Holmes, E. A. (2015). Computer game play reduces intrusive memories of experimental trauma via re-consolidation-update mechanisms. Psychological Science, 26, 1201-1215.
- Link to .pdf of article
- Data in .csv format
- Data in SPSS format

8.4 R

8.4.1 Load the data

Remember that any line with a # makes a comment and the code does not run. Below is how to load the .csv data from the online repository, or from a local file (you need to change the file path to where the local file is, if you downloaded it). The data contains all of the measures and conditions from Experiment 2 in the paper.

```
library(data.table)
#fread("https://raw.githubusercontent.com/CrumpLab/statisticsLab/master/data/Jamesetal2015Experim
all_data <- fread("data/Jamesetal2015Experiment2.csv")
```

8.4.2 Inspect the dataframe

This will give you a big picture of the data frame. Click the button to view it in your browser, then take a look to see what is in it.

```
library(summarytools)
view(dfSummary(all_data))
```

8.4.3 Get the data you need

Again we have only the data from Experiment 2, so we don't need to get rid of any rows of the data. But we do need look at the columns to see how the independent variable and dependent variables were coded.

8.4.3.1 The independent variable

There was one important independent variable, and it had four levels. The first column in the data frame is called condition, and it has four levels. The levels are 1, 2, 3, and 4 in the data-frame. These will correspond to the four levels in shown in figure:

- No-task control
- Reactivation Plus Tetris
- Tetris only
- Reactivation only

Each of these refer to what subjects did after they watched the traumatic film. But, which of these correspond to the numbers 1 to 4 in the data-frame? It turns out the are in the right order, and 1 to 4 refer to:

1. No-task control
2. Reactivation Plus Tetris
3. Tetris only
4. Reactivation only

Let's do ourselves a favor and rename the levels of the `Condition` column with words so we know what they refer to. First, convert the `Condition` column to a factor, then rename the levels. Then.

```
all_data$Condition <- as.factor(all_data$Condition)
levels(all_data$Condition) <- c("Control",
                                "Reactivation+Tetris",
                                "Tetris_only",
                                "Reactivation_only")
```

8.4.3.2 The dependent variable

The authors showed two figures, one where they analysed intrusive memory frequency as the mean for the week, and the other where the used intrusive memory frequency on Day 7. In this tutorial, we will do the steps to run an ANOVA on the mean for the week data, and you will do follow these steps to run another ANOVA on the Day 7 data.

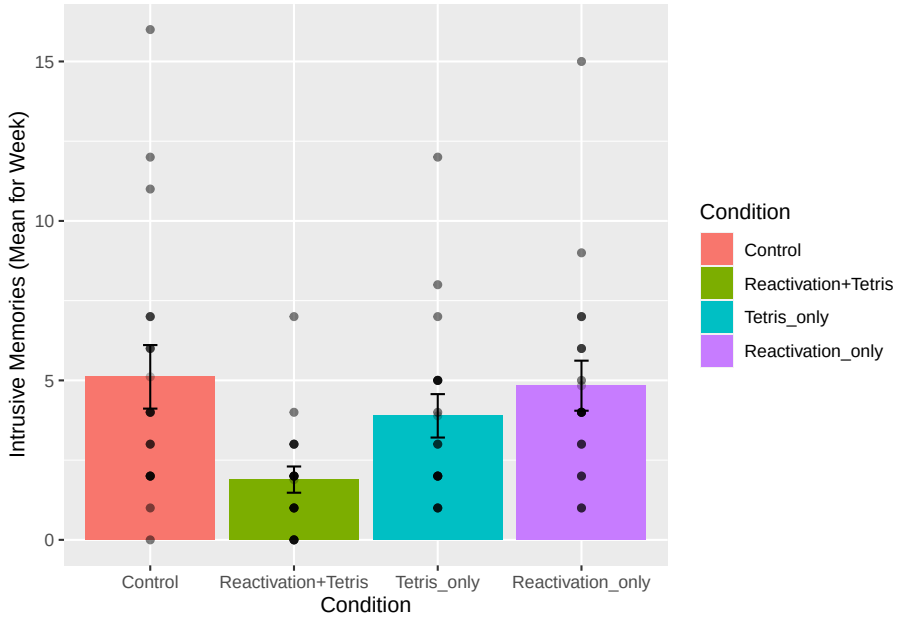
The mean for the week data for each subject is apparently coded in the column `Days_One_to_Seven_Number_of_Intrusions`.

8.4.4 Look at the data

Remember before we do any analysis, we always want to "look" at the data. This first pass let's us know if the data "look right". For example, the data file could be messed up and maybe there aren't any numbers there, or maybe the numbers are just too weird.

In the last two labs, we saw how to show all the data we are interested in looking at in one go. We can do the same things here. For example, in one little piece of code, we can display the means in each condition, the standard errors of the mean, and the individual scores for each subject in each condition. This is a lot to look at, but it's everything we want to look at for starters all in the same place. Looking at the data this way will also give us intuitions about what our ANOVA will tell us before we run the ANOVA. This is helpful for determining whether the results of your ANOVA are accurate or not. Let's do it...also notice that the code is very similar to what we did for the independent t-test. In fact, all I did was copy and paste that code right here, and edited it a little bit. This is really fast, and shows the efficiency of doing things this way.

```
library(dplyr)

library(ggplot2)

# get means and SEs
descriptive_df <- all_data %>%
                    group_by(Condition) %>%
                    summarise(means= mean(Days_One_to_Seven_Number_of_Intrusions),
                              SEs = sd(Days_One_to_Seven_Number_of_Intrusions)/sqrt(length(Days_O

# Make the plot
ggplot(descriptive_df, aes(x=Condition, y=means))+
  geom_bar(stat="identity", aes(fill=Condition))+ # add means
  geom_errorbar(aes(ymin=means-SEs,               # add error bars
                    ymax=means+SEs), width=.1) +
  geom_point(data=all_data, aes(x=Condition, y=Days_One_to_Seven_Number_of_Intrusions), alpha=.5)
  geom_point(alpha=.25)+
  ylab("Intrusive Memories (Mean for Week)")
```



There we have it. A nice graph showing us everything. We can see there was a lot of differences at the level of individual subjects. Some subjects had a mean of 15 intrusive memories for the week. Some had 0. Lots of differences.

And, to be completely honest, this data seems a bit weird to me. It might not be weird, but it might be. The wording in the manuscript is that this data is the mean frequency of intrusive memories over the week. For the people who had 15, this means that every day they had on average 15 intrusive memories. Some people had on average 0 per day. This could be the data. But, it also seems like the data might just be frequency counts and not means at all. For example, the data could be that some people had a total of 15 intrusive over the week. The data might make more sense if these were frequency counts. Otherwise the differences between people are truly very large. For example the person who had an average of 15 intrusive memories per week, must have had 15*7 = 105 intrusive memories, which is a lot more than zero. In any case, this kind of wondering about the data is what happens when you start to notice how numbers work. It's useful develop your data sense.

Let's move on to the ANOVA. By looking at the above graph do you have an intuition about what the ANOVA will tell us? I do, it should easily tell us that we are going to get an F-value that is bigger than one, and a p-value that is probably smaller than .05? How do I know this? I looked at the error bars, which represent the standard errors of the mean. If we look across conditions we can see that that the error bars don't always overlap. This suggests there are differences in the data that don't happen very often by chance. So, we expect a smallish p-value. Why do you think I expect the F-value to be greater than

1? If you can answer this question with a justification and explanation of how F works, pat yourself on the back!

8.4.5 Conduct the ANOVA

Conducting an ANOVA in R is pretty easy. It's one line of code, just like the t-test.

It's worth knowing that there are a few different packages out there to do an ANOVA, for example Mike Lawrence's `ezANOVA` package is pretty popular.

For this tutorial we'll show you how to run the ANOVA using the `aov` function from base R (comes pre-installed). This is pretty "easy" too. I put easy in quotes because the first time I saw this, it was not easy for me. Here's a brief digression for me to tell you that I feel your pain. I was first introduced to R by Patrick Bennett (a professor at McMaster University, where I attended graduate school). Pat, like I am doing know, forced us to use R in his statistics class. I remember having zero clue about so many things, and was often very frustrated. So, I imagine some of you are quite frustrated too. I was luck, like some of you, to have had some previous experience with other programming languages, so I was familiar with what R might be doing. What I was most frustrated with, was learning how to tell R what to do. In other words, I didn't know how to write the commands properly. I didn't understand what we call the **syntax** of R.

This was back many years ago now, well before there was so many helpful examples on Google with working code, showing you how the syntax works. All we had was the R help files, which were a total mystery to me. If you want to see the help file for `aov`, just type `?aov()` into the console, and press enter. You will see an "explanation" of how the `aov` function is supposed to work. You can use the same trick for any R function, like this `?name_of_function()`. To be clear, you have to replace the letters `name_of_function`, with the name of the function. Some of you think that might be super obvious, but that is the kind of thing I did not think was obvious. So, when I read the help file for how to use the `aov` function, that is to learn what to put where, I didn't feel like it was showing me what I needed to do. Usually, at the bottom of the help file, there are some examples, and these are helpful, but sometimes they are missing the example you need, and you are expected to generalize your knowledge of how `aov` works, to make it work for your problem. This is a catch-22 because if you don't know how it works, you can't generalize. IMO, you need a lot of examples of things that work.

So, with that digression, I'm going to explain the syntax for the aov function. It looks like this:

```
aov(DV ~ IV, dataframe)
```

That probably looks really foreign. Let me explain. First you need write `aov()`. `aov` is the name of the function, followed by the brackets. The brackets are a sandwich. Sandwiches have a top and a bottom, and they enclose the things you put in the sandwich. We then put things inside the `()`, in specific ways to make the `aov` sandwich. The `DV` stands for the name of the dependent variable in the data frame. For us, this will be `Days_One_to_Seven_Number_of_Intrusions`. So, when we add that, our function will look like:

```
aov(Days_One_to_Seven_Number_of_Intrusions ~ IV, dataframe)
```

Next, the `~` (tilda) stands for the word 'by'. We are saying we want to analyse the Dependent variable **by** the conditions of the independent variable.

The `IV` stands for the name of the column that is your independent variable. Our's is called `Condition`. Adding that in, our formula looks like:

```
aov(Days_One_to_Seven_Number_of_Intrusions ~ Condition, dataframe)
```

Finally, the last part is the name of the data-frame we are using. The `aov` function only works on long-form data, where each score on the dependent variable has it's own row. Our's is already set up this way! The name of our data-frame is `all_data`. We add that in, and it looks like:

```
aov(Days_One_to_Seven_Number_of_Intrusions ~ Condition, all_data)
```

In English, this means, do an ANOVA on the dependent variable as a function of the independent variable, and use the data in my data frame.

This is it for now. The `aov` function is very flexible because you can define different kinds of formulas (the `DV ~ IV` part). We'll see other examples in later chapters. For now, this is all we need. Also, what's cool, is that this will work for any single IV with any number of levels (conditions) 2 or greater. Fun. Let's see it in action.

```
aov(Days_One_to_Seven_Number_of_Intrusions ~ Condition, all_data)
```

```
## Call:
##    aov(formula = Days_One_to_Seven_Number_of_Intrusions ~ Condition,
##     data = all_data)
##
## Terms:
##                 Condition Residuals
## Sum of Squares   114.8194  685.8333
## Deg. of Freedom         3        68
##
## Residual standard error: 3.175812
## Estimated effects may be unbalanced
```

What is this garbage? I don't see an ANOVA table, what is this? You are seeing the raw print out of the aov function. Clearly, this is not helpful, it's not what we want to see.

Fortunately, R comes with another function called `summary`. What it does is summarize the results of functions like `aov`, and prints them out in a nicer way. Let's see the summary function do it's thing:

```
summary(aov(Days_One_to_Seven_Number_of_Intrusions ~ Condition, all_data))
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## Condition    3  114.8   38.27   3.795 0.0141 *
## Residuals   68  685.8   10.09
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Alright, now we have an ANOVA table we can look at. However, it still looks ugly, at least to me. When you are working inside an R Markdown document, you have some more options to make it look nice. We can use the `kable` and `xtable` function together, like this.

```
library(xtable)
aov_out<-aov(Days_One_to_Seven_Number_of_Intrusions ~ Condition, all_data)
summary_out<-summary(aov_out)

knitr::kable(xtable(summary_out))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Condition	3	114.8194	38.27315	3.794762	0.0140858
Residuals	68	685.8333	10.08578	NA	NA

Now we see a nicer print out. Especially if we `knit` the document into a webpage.

8.4.6 Reporting the ANOVA results

Refer tot the textbook on ANOVAs for a deeper discussion of all the things in the ANOVA table. We'll remind about some of those things here.

First, let's look at how we might report the results. There are three very important parts to this.

1. Saying what test you did to what data
2. Reporting the inferential statistics
3. Reporting the pattern in the means

Here is part 1, we need to say what data we used, and what kind of test we used on that data:

> We submitted the mean intrusive memories for the week from each subject in each condition to a one-factor betwee-subjects ANOVA, with Intervention type (No-task control, Reactivation Plus tetris, Tetris only, Reactivation only) as the sole independent variable.

Part 2 is saying what the results of the test were. Specifically, we report the values from the inferential test (see the textbook for why these values). Also, you should be able to answer this question: why do we report the values that we do?

> We found a main effect of Intervention type, $F(3, 68) = 3.79$, $MSE = 10.09$, $p = 0.014$.

Part 3 is saying what the pattern was in the means. Remember, that in the ANOVA, a significant effect refers to the global variation among the means. In other words, we can say that there are some differences between the means, but we can't specifically say which pairs of means are different, or which groups of means are different from one another. How can we report this, where are the means? In fact, we already found them when we plotted the data earlier. So, we can copy paste that code, and print out the means, rather than the figure:

```
# get means and SEs
descriptive_df <- all_data %>%
                    group_by(Condition) %>%
                    summarise(means= mean(Days_One_to_Seven_Number_of_Intrusions),
                              SEs = sd(Days_One_to_Seven_Number_of_Intrusions)/sqrt(le

knitr::kable(descriptive_df)
```

Condition	means	SEs
Control	5.111111	0.9963623
Reactivation+Tetris	1.888889	0.4113495
Tetris_only	3.888889	0.6806806
Reactivation_only	4.833333	0.7848650

No we have to use a sentence to describe these means.

> Refer to table 1 for the means and standard errors of the mean in each condition

or,

> Mean intrusive memories per week were 5.11 (SE = .99); 1.89 (SE = .41); 3.89 (SE = .68); and 4.83 (SE= .78), in the Control, Reaction plus Tetris, Tetris Only, and Reactivation only conditions, respectively

Ugh, what a mouthful. Be mindful of how you write results. The above is not helpful because you see a list of numbers, and then a list of conditions, and the reader has to do a lot of work to keep everything straight. I like the table option.

I also like this other kind of option:

> Mean intrusive memories were significantly different between the Control (M = 5.11, SE = .99), Reactivation plus Tetris (M = 3.89, SE = .68), Tetris only (M= 3.89, SE = .68), and Reactivation only (M = 4.83, .78) conditions.

That's a little bit better. Let's put it all in one place to see what it look like:

> We submitted the mean intrusive memories for the week from each subject in each condition to a one-factor betwee-subjects ANOVA, with Intervention type (No-task control, Reactivation Plus tetris, Tetris only, Reactivation only) as the sole independent variable. We found a main effect of Intervention type, F(3, 68) = 3.79, MSE = 10.09, p = 0.014. Mean intrusive memories were significantly different between the Control (M = 5.11, SE = .99), Reactivation plus Tetris (M = 3.89, SE = .68), Tetris only (M= 3.89, SE = .68), and Reactivation only (M = 4.83, .78) conditions.

8.4.7 Individual comparisons

This next part is complicated, so we intentionally simplify it. There are these things (remember from the textbook), called comparisons. We use them to compare differences between specific conditions of interest. That part isn't very complicated. You just pick the things you want to compare, and compare them.

What is complicated is exactly what you "should" do to make the comparison. It turns out there are lots of recommendations and disagreements about what you should do. There are also lots of tests that you can do, so you have a lot of options. We are not going to show you here all of the tests. This is beyond the scope of what we are trying to teach you. Instead, we will use tests that you already know, the t-test for independent samples from the last lab. It will do the job for this data.

We think that before you can make good decisions about the kind of comparison test you want to use, you have to have a solid understanding of **what you are**

comparing and **what you are not comparing** when you use different tests. We think this understanding is more important than what test you use. More important, is that you know what means you want to compare. In this case, we will talk about what means we want to compare, and then just do a t-test.

8.4.7.1 What did the ANOVA tell us

Remember, the ANOVA we conducted is termed the **omnibus** test in the textbook. What means was it comparing? It wasn't comparing specific means. It was asking a kind of blind and very general question: Are any of these means different. Our answer was yes. Our next question is: What means were different from what other means? The ANOVA doesn't know the answer to this question. It just says I don't know…

8.4.7.2 Comparing specific means and the experimental question

Notice there are 4 means to compare. So, there are (4-1)! = 3! = 3x2x1 = 6 total different comparisons. The ! stands for factorial. What's more important is recognizing that when you have more than two conditions (where you can only make one comparison, A vs. B), you get increasingly more comparisons. For four conditions, A, B, C, D, you get six comparisons, they are:

`AB, AC, AD, BC, BD, and CD` where each letter pair refers to A compared to B (AB), A compared to C (AC), and so on.

Do we actually care about all of these comparisons? Perhaps. What was the point of the experiment? Remember, the experiment was asking a questions, that's why they set-up the condition necessary to produce these means. What question were they asking? What did they want to know?

They wanted to find out if various interventions after watching the scary movie, would change how many bad intrusive memories people would experience in the week following the movie. They discuss the idea that a memory can become malleable when it is re-activated. They want to "Re-activate" the bad memories, and then while they were changeable, do something to them to make them less likely to be intrusive later on. The big idea was that doing a bit of "re-activation" AND then playing Tetris (which takes up visual cognitive bandwidth) could cause changes to the re-activated memories, that would decrease the number of intrusive memories later on. With that reminder, let's go through some different comparisons that we can make, and talk about what they might mean.

8.4.7.3 Control vs. Reactivation_only

There was a control group that did not do anything special after watching the traumatic movie. The mean number of intrusive memories for the control

group, gives some idea of the amount of intrusive memories we would expect to measure, when you do nothing to change that number.

Comparing to the control group is a very sensible thing do to for each of the other groups. If one of the manipulations worked, it should show a different mean (something changed) than the control group.

So, did the Reaction_only group have less intrusive memories over the control group? First we use the `filter` function from `dplyr` to select only the rows from the data frame that have the Control and Reactivation_only conditions. Then we run a t-test

```
comparison_df <- all_data %>%
                  filter(Condition %in% c('Control','Reactivation_only')==TRUE)

t.test(Days_One_to_Seven_Number_of_Intrusions ~ Condition,
       comparison_df,
       var.equal=TRUE)
```

```
##
##  Two Sample t-test
##
## data:  Days_One_to_Seven_Number_of_Intrusions by Condition
## t = 0.219, df = 34, p-value = 0.828
## alternative hypothesis: true difference in means between group Control and group Reactivation_
## 95 percent confidence interval:
##  -2.299851  2.855406
## sample estimates:
##           mean in group Control mean in group Reactivation_only
##                        5.111111                        4.833333
```

The means are both basically 5, not a big difference!. The p-value is large, suggesting that change could easily have produced the tiny differences between the means. In other words, it doesn't look like the "re-activation" phase did anything to suppress the amount of intrusive memories that people would have over one week, compared to control.

Notice, this was a comparison we could make. But, was it an informative one about the goal of the study? Not really.

8.4.7.4 Control vs. Reactivation+Tetris

What we really want to know is if Reactivation+Tetris cause fewer intrusive memories...but compared to what? Well, if it did something, it should have a smaller mean than the Control group. So, let's do that comparison:

Note: we just change the one level name to the level we want `Reactivation+Tetris`.

```
comparison_df <- all_data %>%
                  filter(Condition %in% c('Control','Reactivation+Tetris')==TRUE)

t.test(Days_One_to_Seven_Number_of_Intrusions ~ Condition,
       comparison_df,
       var.equal=TRUE)
```

```
##
##  Two Sample t-test
##
## data:  Days_One_to_Seven_Number_of_Intrusions by Condition
## t = 2.9893, df = 34, p-value = 0.005167
## alternative hypothesis: true difference in means between group Control and group Rea
## 95 percent confidence interval:
##  1.031592 5.412852
## sample estimates:
##             mean in group Control mean in group Reactivation+Tetris
##                          5.111111                          1.888889
```

There is a bigger difference now, roughly 5.1 intrusive memories for control, and 1.9 for Reactivation+Tetris. The p-value is quite small, indicating this difference was not likely produced by chance. Now, we have some evidence that Reactivation+Tetris caused something to change, that condition produced fewer intrusive memories than control.

8.4.7.5 Control vs. Tetris_only

Now we can really start wondering what caused the difference. Was it just playing Tetris? It wasn't just doing the reactivation, we already found out that didn't do anything. Does just playing Tetris reduce the number of intrusive memories during the week? Let's compare that to control:

```
comparison_df <- all_data %>%
                  filter(Condition %in% c('Control','Tetris_only')==TRUE)

t.test(Days_One_to_Seven_Number_of_Intrusions ~ Condition,
       comparison_df,
       var.equal=TRUE)
```

```
##
##  Two Sample t-test
##
## data:  Days_One_to_Seven_Number_of_Intrusions by Condition
```

```
## t = 1.0129, df = 34, p-value = 0.3183
## alternative hypothesis: true difference in means between group Control and group Tetris_only i
## 95 percent confidence interval:
##  -1.230036  3.674480
## sample estimates:
##     mean in group Control mean in group Tetris_only
##                  5.111111                  3.888889
```

There's mean difference of about 1, but the p-value isn't very small. This suggests chance produces a difference of this size fairly often. If we claimed that just playing Tetris caused a difference based on this data, we could easily be making a type I error (claiming the result is real when it is not, a false-positive). Still, the difference was in the right direction wasn't it.

8.4.7.6 Tetris_only vs. Reactivation + Tetris

Finally, we might ask if the Reactivation+Tetris group had fewer unwanted memories than the Tetris_only group. Did putting the two things together (reactivation AND Tetris) really do something special here, beyond just playing Tetris.

```
comparison_df <- all_data %>%
                  filter(Condition %in% c('Tetris_only','Reactivation+Tetris')==TRUE)

t.test(Days_One_to_Seven_Number_of_Intrusions ~ Condition,
       comparison_df,
       var.equal=TRUE)
```

```
##
##  Two Sample t-test
##
## data:  Days_One_to_Seven_Number_of_Intrusions by Condition
## t = -2.5147, df = 34, p-value = 0.01681
## alternative hypothesis: true difference in means between group Reactivation+Tetris and group T
## 95 percent confidence interval:
##  -3.6162855 -0.3837145
## sample estimates:
## mean in group Reactivation+Tetris         mean in group Tetris_only
##                          1.888889                          3.888889
```

Well, according to the t-test, the p-value is again fairly small. Suggesting that the difference between Reactivation+Tetris (M=1.89) and Tetris_only (3.89), was not likely to be produced by chance. So, on the basis of this, there is some evidence that Reactivation+Tetris, really does cause fewer intrusive memories.

8.4.8 Writing it all up.

Because we have spent so much time on individual comparisons, we won't do a full write up of the results. A full write-up would include telling the reader what data was used, what test was conducted, the results of the test, and the pattern of the means, AND then, the results of specific comparisons of interest. You can read the paper to see how the authors did it.

8.4.9 Food for thought

Think about what we did here. We almost blindly just downloaded the data and ran the same analysis as the authors did. Sure, we looked at the data first, and then did the analysis. But, did we really look? Did you notice anything about what you looked at? What did we not look closely at that might make you skeptical of the conclusions from the research…

Here's a hint. Sample-size. We know that is important. Let's ask the question, was there an equal number of participants in each of the 4 conditions. We can use `dplyr` again to do this. We'll add the `length` function, which counts the number of subjects in each condition:

```
descriptive_df <- all_data %>%
                    group_by(Condition) %>%
                    summarise(means= mean(Days_One_to_Seven_Number_of_Intrusions),
                              SEs = sd(Days_One_to_Seven_Number_of_Intrusions)/sqrt(le
                              count = length(Days_One_to_Seven_Number_of_Intrusions))

knitr::kable(descriptive_df)
```

Condition	means	SEs	count
Control	5.111111	0.9963623	18
Reactivation+Tetris	1.888889	0.4113495	18
Tetris_only	3.888889	0.6806806	18
Reactivation_only	4.833333	0.7848650	18

The answer is YES, there were an equal number of subjects. That's good. We should have checked that before. Lesson for next time. For example, if there were only 9 subjects in the Reactivation+Tetris group, we might be suspicious that they got lucky, and accidentally (by chance) assigned people to that group who are unlikely to report having intrusive memories. After all, different people are different, and not everybody is as susceptible to intrusive memories.

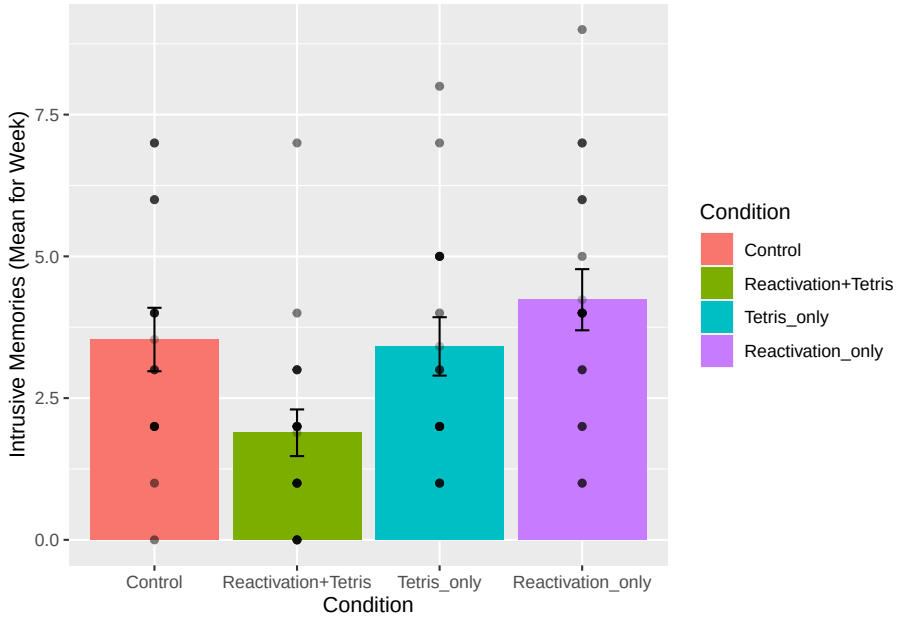
Let's do one more thing for fun, and to see everything in action all in one place. Let's consider the role of outliers. Looking at the first graph we can see that most people in all the groups had fewer than 10 intrusive memories (mean we assume) per week. It looks like 5 people had more than that, and they just

happened to be in the other groups. Maybe Reactivation+Tetris made those people have way less intrusive memories (which is why no one is above 10), or maybe the researchers got a little bit unlucky, and accidentally didn't get any "outliers" (people with extreme values on the measure) in that group.

Let's re-run the analysis, but remove anybody with a mean higher than 10. This will only remove 5 subjects, so we will still have a lot left. What happens?

Before we find out, let me point out again the beauty of R. All we need to do is copy and paste our previous code. Then, just filter the data once to remove the outliers, then voila, we redo everything all in one go. It's much more complicated and time consuming to do this in many other software programs. You are lucky to be learning R.

```
# get rid out of outliers

all_data  <- all_data %>%
             filter(Days_One_to_Seven_Number_of_Intrusions < 10)

# get means and SEs

descriptive_df <- all_data %>%
                    group_by(Condition) %>%
                    summarise(means= mean(Days_One_to_Seven_Number_of_Intrusions),
                              SEs = sd(Days_One_to_Seven_Number_of_Intrusions)/sqrt(length(Days_O

# Make the plot

ggplot(descriptive_df, aes(x=Condition, y=means))+
  geom_bar(stat="identity", aes(fill=Condition))+ # add means
  geom_errorbar(aes(ymin=means-SEs,               # add error bars
                    ymax=means+SEs), width=.1) +
  geom_point(data=all_data, aes(x=Condition, y=Days_One_to_Seven_Number_of_Intrusions), alpha=.5)
  geom_point(alpha=.25)+
  ylab("Intrusive Memories (Mean for Week)")
```




```
# run and report the ANOVA

aov_out<-aov(Days_One_to_Seven_Number_of_Intrusions ~ Condition, all_data)
summary_out<-summary(aov_out)

knitr::kable(xtable(summary_out))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Condition	3	51.49152	17.163841	4.024458	0.0110347
Residuals	63	268.68758	4.264882	NA	NA

```
# conduct critical comparisons

## control vs reactivation+Tetris

comparison_df <- all_data %>%
                 filter(Condition %in% c('Control','Reactivation+Tetris')==TRUE)

t.test(Days_One_to_Seven_Number_of_Intrusions ~ Condition,
       comparison_df,
       var.equal=TRUE)


##
##  Two Sample t-test
```

```
##
## data:  Days_One_to_Seven_Number_of_Intrusions by Condition
## t = 2.4159, df = 31, p-value = 0.02178
## alternative hypothesis: true difference in means between group Control and group Reactivation+
## 95 percent confidence interval:
##  0.2562181 3.0326708
## sample estimates:
##             mean in group Control mean in group Reactivation+Tetris
##                          3.533333                          1.888889
```

```
## Tetris_only vs reactivation+Tetris

comparison_df <- all_data %>%
                  filter(Condition %in% c('Tetris_only','Reactivation+Tetris')==TRUE)

t.test(Days_One_to_Seven_Number_of_Intrusions ~ Condition,
       comparison_df,
       var.equal=TRUE)
```

```
##
##  Two Sample t-test
##
## data:  Days_One_to_Seven_Number_of_Intrusions by Condition
## t = -2.3239, df = 33, p-value = 0.02643
## alternative hypothesis: true difference in means between group Reactivation+Tetris and group T
## 95 percent confidence interval:
##  -2.8561054 -0.1896463
## sample estimates:
## mean in group Reactivation+Tetris         mean in group Tetris_only
##                          1.888889                          3.411765
```

The take home is that yes, even after removing outliers, the same basic pattern in the data is observed. Overall, this is a small n study, and ideally the basic findings should be replicated in another lab before we really have full confidence in them. But, I'd say the trends here look promising.

That's ANOVA. Come back next week for another ANOVA tutorial, this time using within-subject data. It's called a repeated measures ANOVA, and it's what's happening next week.

8.4.10 Generalization Exercise

Your task is to conduct the ANOVA using `Day_Zero_Number_of_Intrusions` as the dependent variable. Report the ANOVA table, a figure to show the means, and a short write-up of the results.

8.4.11 Writing assignment

(2 points - Graded)

Answer the following questions:

1. Explain why the ANOVA is called an omnibus test, and how the omnibus test is different from comparing specific means with t-tests. (1 point)
2. Explain the general similarity between the ratios that are used to calculate the F value and the t-value (1 point)

General grading.

- You will receive 0 points for missing answers
- You must write in complete sentences. Point form sentences will be given 0 points.
- Completely incorrect answers will receive 0 points.
- If your answer is generally correct but very difficult to understand and unclear you may receive half points for the question

8.4.12 Practice Problems

Using this lab's data set, think about the following question: What if participants' intrusive memories were not actually affected by the manipulation (tetris and reactivation), but rather the group with the most intrusive memories just happened to react more strongly to the disturbing films? What if there were differences in "level of disturbance" (hint hint: post-film distress rating) among the 4 groups?

1. Test this hypothesis using an alpha level of .05. Report your result in proper statistical reporting format. What do you conclude?
2. Do the same type of analysis to determine whether the amount of attention paid to the film differed between the 4 groups. Report your result in proper statistical reporting format. What do you conclude?

Chapter 9

Lab 9 Repeated Measures ANOVA

However, perhaps the main point is that you are under no obligation to analyse variance into its parts if it does not come apart easily, and its unwillingness to do so naturally indicates that one's line of approach is not very fruitful. —R. A. Fisher

9.1 Betcha can't type JHDBZKCO very fast on your first try

This lab activity uses the data from Behmer & Crump (2017) to teach one-factor repeated measures ANOVA with-up follow comparisons

9.1.1 STUDY DESCRIPTION

Behmer & Crump (2017) used the everyday task of typing on a computer keyboard to ask questions about how people learn to put sequences of actions together. Whenever you type a series of letters on the keyboard, you are putting a sequence of actions together, so typing is task that could be used to measure skilled sequencing. Typing also happens to be a convenient task for measuring sequencing. For example, every time a person types a letter, the timing of the button press and the letter pressed can be measured and stored for later analysis.

Behmer & Crump were interested in asking a few different questions, however, we will simplify everything and talk about replication. First we describe an

interesting finding from previous research. Behmer & Crump repeated an experiment that should also produce this same finding. If they succeed in doing this, it means the finding can be replicated, and that it happens in more than one lab.

Finding from previous resaearch: Prior research showed that typists do something funny. Skilled typists can type normal words very fast. This suggests they know how to locate all of the letters on the keyboard, and can press each letter very quickly to type words. That part isn't particularly funny. However, if you take really skilled typists and make them type random letters like this: kwitb dhhgjtryq xkldpt mazhyffdt, guess what happens? They slow down a lot. It's kind of weird that a typist would slow down, after all they can type letters really fast when they appear in words, but not when they appear in random orders…what gives? Last, it turns out that typists are kind of in the middle in terms of speed, if you ask them to type non-words that have similar properties to words, such as: quenp hamlke phwempy.

To summarize, prior research showed that typing speed changes as a function of the structure of the text, roughly in this order from fastest to slowest.

(FASTEST) Normal Words < Word-like Non-words < Random strings (SLOWEST)

Replication question: Behmer & Crump also measured typists while they typed words, non-words that were English-like, and random strings. They had some additional things they were interested in, but for us, we are interested in whether they would show the same effect. Would they replicate the pattern: Normal words (Fastest) < Word-like Non-words (medium) <- Random strings (Slowest)?

9.1.2 Study Methods

The authors conducted a repeated measures experiment. A total of 38 subjects were used for the analysis.

Independent Variable: The IV Stimulus or typing material had three levels: Normal, Bigrams, and Random. Normal refers to normal 5 letter English words (like truck, or plant). Bigrams refers to non-words that have properties similar to words (e.g., phemt quilp). Random refers to 5 letter strings whose letters were totally random (qmklt gdrzn lprni).

Dependent Variables: There were three dependent variables, that all measured different aspects of typing performance. Reaction times (RTs) were defined as the temporal interval between seeing a stimulus (to type), and then starting to type it (first key press). Inter-keystroke intervals (IKSIs) are the times between each key-press. Last, accuracy was also measured (correct or incorrect key-presses)

The task: Participants (who happened to also be students from Brooklyn College) sat in front a computer. They were presented with one stimulus (word, bigrams, or random) at a time. As soon as they saw the string of letters, they typed it as quickly and accurately as they could, then they moved on to the next trial.

Reminder, this is a repeated measures design because each participant typed letter strings from the word, bigrams, and random conditions.

9.2 Lab Skills Learned

- Conducting a one-factor repeated measures ANOVA
- Conducting follow-up comparisons

9.3 Important Stuff

- citation: Behmer, Lawrence P., Crump, M. J. C. (2017). Spatial Knowledge during Skilled Action Sequencing: Hierarchical versus Non-Hierarchical Representations. Attention, Perception & Psychophysics, 79, 2435-2448.
- Link to .pdf of article
- Data in .csv format

9.4 R

9.4.1 Load the data

Remember that any line with a # makes a comment and the code does not run. Below is how to load the .csv data from the online repository, or from a local file (you need to change the file path to where the local file is, if you downloaded it). The data contains all of the measures and conditions from Experiment 1 in the paper.

```
library(data.table)
#all_data <- fread("https://github.com/CrumpLab/statisticsLab/raw/master/data/exp1_BehmerCrumpAPP
all_data <- fread("data/exp1_BehmerCrumpAPP.csv")
```

9.4.2 Inspect the dataframe

This will give you a big picture of the data frame. Click the button to view it in your browser, then take a look to see what is in it.

```
library(summarytools)
view(dfSummary(all_data[,c(1:7,10:20)]))
```

Note, there is some weird stuff in code above. Normally, we would just write `view(dfSummary(all_data))`, why we add this: `all_data[,c(1:7,10:20)]`? It turns out the dfSummary function didn't like some of the data. In particular it didn't like the data in columns 8 an 9 (notice those numbers are missing, the range inside c is 1 to 7 and 10 to 20). It doesn't mean the data isn't there, just that it didn't want to display it in the viewer.

9.4.3 Get the data you need

This data file contains all of the data from Experiment 1 in the paper. So, we don't need to get rid of any rows.

There are numerous columns, some of them we don't need for the analysis. But, we'll just ignore these later when we use `dplyr` to group by the columns we want.

The structure of this data a file is in long form. Every row described a measurement for a single key-press. For example, the first 5 rows, have data for the timing of the first 5 key-presses, that the first subject made to type the first string of letters they saw. In total there were 85,410 key-presses made. That's quite a lot.

9.4.3.1 The independent variable

The important independent variable is in the column `Stimulus`.

- Normal (5 letter English words)
- Bigrams (5 letter strings that kind of looked like words)
- Random (5 letter strings that were random)

It is also important to know that the `Order` column codes the position for each letter, from 1 to 5.

Note: there was another independent variable in the study as well. We talk about this later. The second IV is coded in the `Block` column.

- Baseline (normal typing, keyboard is visible while typing)
- Manipulation (occluded typing, keyboard is covered while typing)

9.4.3.2 The dependent variables

1. `TimeFromOnset` : This column records the temporal interval in milliseconds between the onset of the word and each key-press. When order is 1 (first keystroke), the number here is the reaction time to start typing.
2. `PureRTs` : This column contains keystroke intervals. The first interval is between the onset of the word and the first key-press (order 1), the second interval is between the first and second key-press (order 2), and so on. `PureRTs` for orders 2 to 5, represent the inter-keystroke intervals reported in paper.
3. `AllCorrect` : 0 means incorrect (wrong letter was typed), 1 means correct (correct letter was typed)

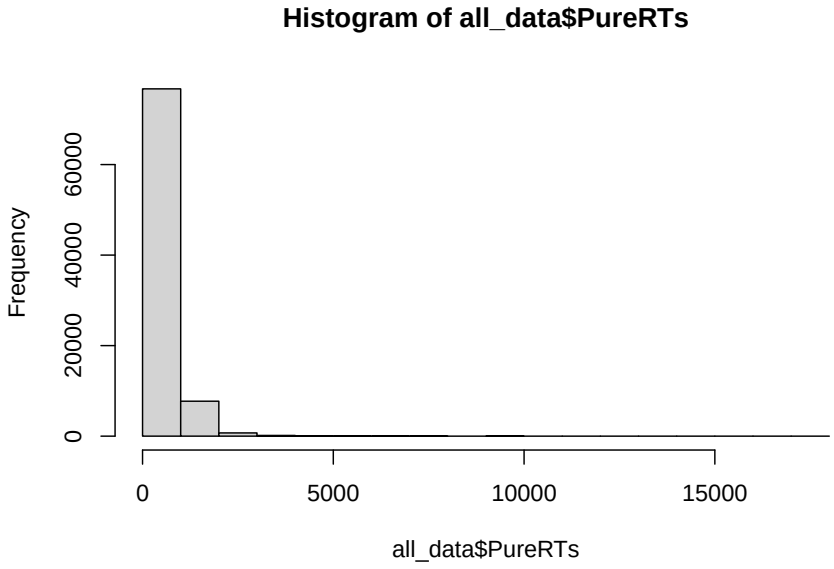
9.4.4 Look at the data

Remember before we do any analysis, we always want to "look" at the data. This first pass let's us know if the data "look right". For example, the data file could be messed up and maybe there aren't any numbers there, or maybe the numbers are just too weird.

For example, this study involves reaction times: the time between seeing something and responding to it. If you had done a study like this before, you would know that it usually doesn't take people that long to start responding. Most reaction times will be under a second (or 1000 milliseconds). But, sometime people are little slow, and sometimes they do funny things like check their phone in the middle of an experiment.

Before I analyze reaction time data, I often make a histogram of all of the RT data, like this:

```
hist(all_data$PureRTs)
```



We can see that almost all of the reaction times are well below 5000 milliseconds (5 seconds), which is good. Most of the time people were paying attention and not "checking their phone". Notice, the range of the histogram goes out to 15,000 milliseconds. You can't see any bars out there (too small to notice), but there must be at least a few trials where somebody took 15 seconds to start responding. These are called outliers. We will remove them before we conduct our analysis

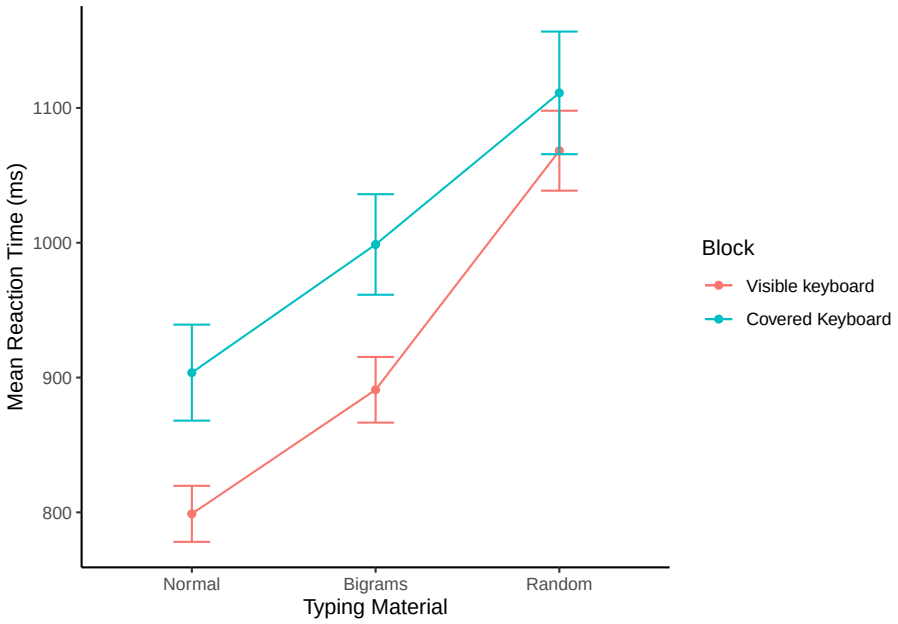
9.4.5 Look at the means

As part of looking at the data, we might as well make a figure that shows the mean reaction times in each condition, and some error bars to look at the spread in each condition. The following code takes three important steps:

1. Get the means for each subject in each condition. These are put into the data frame called `subject_means`.
2. Get the means for each condition, by averaging over the means for each subject. These are put into the data frame called `plot_means`.
3. Make a graph with the `plot_means` data frame using ggplot2.

```
library(dplyr)
library(ggplot2)

all_data$Block<-as.factor(all_data$Block)
```

```r
levels(all_data$Block) <- c("Visible keyboard","Covered Keyboard")

## get subject mean RTs

subject_means <- all_data %>%
                 filter(Order==1, Correct==1, PureRTs<5000) %>%
                 group_by(Subject, Block, Stimulus) %>%
                 summarise(mean_rt = mean(PureRTs))

subject_means$Subject<-as.factor(subject_means$Subject)
subject_means$Block<-as.factor(subject_means$Block)
subject_means$Stimulus<-as.factor(subject_means$Stimulus)

## get condition mean RTs

plot_means <- subject_means %>%
              group_by(Block, Stimulus) %>%
              summarise(means = mean(mean_rt),
                        SEs = sd(mean_rt)/sqrt(length(mean_rt)))

## plot the condition means

# re-order stimulus factor for plotting
plot_means$Stimulus <- factor(plot_means$Stimulus, levels = c("Normal", "Bigrams", "Random"))

ggplot(plot_means, aes(x=Stimulus, y=means, group=Block, color=Block))+
  geom_point()+
  geom_line()+
  geom_errorbar(aes(ymin=means-SEs, ymax=means+SEs), width=.2)+
  theme_classic()+
  ylab("Mean Reaction Time (ms)")+
  xlab("Typing Material")
```



Alright, we made things a little bit more complicated than they need to be. Our primary question is whether reaction times followed this pattern: Normal < Bigrams < Random. We can see the means do follow this pattern. However, shouldn't we only be looking at three means, why are their six means, and two lines?

The above code included the second independent variable `Block`. As a result, you are seeing the means for Typing material when subjects could see the keyboard, and when the couldn't see the keyboard. We will come back to this later. For now, let's ignore the Block condition, and find the means for the Typing Material IV by averaging over the Block conditions. We run the same code as above, by take out `Block`, in the `group_by` function. We also take `Block` out the ggplot function.

VERY IMPORTANT: We did something in the above code that we didn't point out. We filtered the data before we found the means. For most of the data sets in other labs, we given you data that is more or less ready to analyse. More often than not data needs to be pre-processed, or filtered before you analyze it. We can use the `filter` function in `dplyr` to do our filtering. `filter` filters the rows for us, so we will only include the rows that we want.

1. We want to analyze the time between the onset of the stimulus and the first keystroke. The reaction times for this value are in the `PureRTs` column, but this column contains other RTs that we do not want to analyse. For example, the `Order` column codes for the letter position in the string. We only want to analyze the rows that contain a `1`, for the first position. So,

that is why we add `Order==1` to the filter function below.

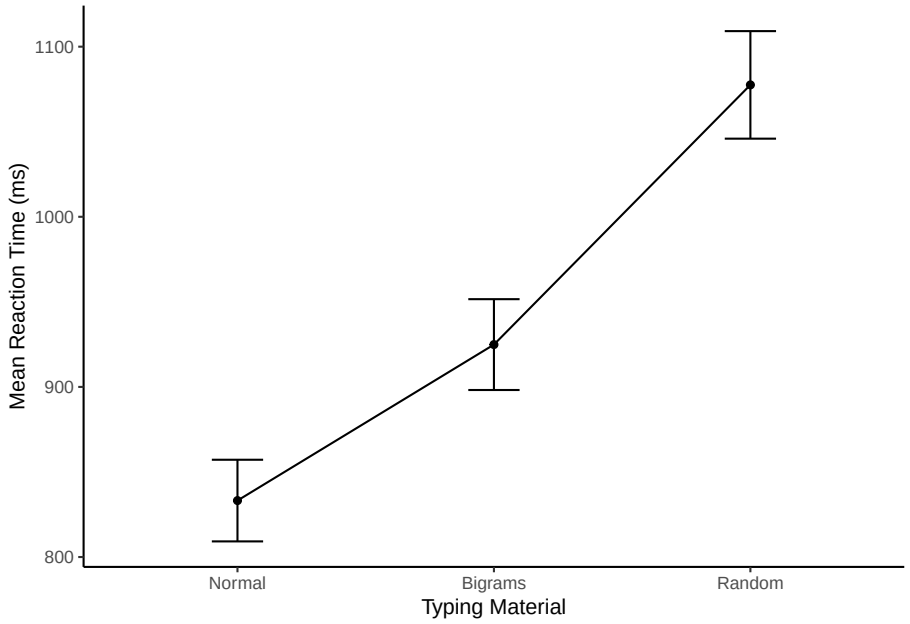
2. We want to analyze only the reaction times that are correct. That is, when the subject typed the first letter correctly, and did not make a typo. Accuracy is coded in the `Correct` column, with 1 = correct, and 0 = incorrect. We add `Correct==1` to the filtering function.

Note the use of `==`, that is two equal signs in a row. In R, two equal signs in a row has a special meaning. It means conduct a `logic` test to determine if one thing is the same as another.

3. We want to analyze only reaction times that are "sensible" to analyze. What does sensible mean? We don't want to analyze data that is clearly garbage data. For example, if someone fell asleep at the computer and didn't respond for 15 seconds, that kind of data is not what we want to analyze. If we were to filter the data, and exclude these kinds of `outliers`, we would be conducting an outlier elimination procedure. Behmer & Crump (2017) did this, and it is commonly done in many different kinds of studies. We skip an extended discussion of outlier elimination for this lab. But, we do introduce the idea of doing it. We want to keep as much of the data as possible. So, what we do is keep all of the RTs that are less than 5000 ms (that's 5 seconds). To do this, we add `PureRTs<5000` to the filter function.

```
## get subject mean RTs

subject_means <- all_data %>%
                 filter(Order==1, Correct==1, PureRTs<5000) %>%
                 group_by(Subject, Stimulus) %>%
                 summarise(mean_rt = mean(PureRTs))

subject_means$Subject<-as.factor(subject_means$Subject)
subject_means$Stimulus<-as.factor(subject_means$Stimulus)

## get condition mean RTs

plot_means <- subject_means %>%
              group_by(Stimulus) %>%
              summarise(means = mean(mean_rt),
                        SEs = sd(mean_rt)/sqrt(length(mean_rt)))

## plot the condition means

# re-order stimulus factor for plotting
plot_means$Stimulus <- factor(plot_means$Stimulus, levels = c("Normal", "Bigrams", "Random"))
```

```
ggplot(plot_means, aes(x=Stimulus, y=means, group=1))+
  geom_point()+
  geom_line(stat="identity")+
  geom_errorbar(aes(ymin=means-SEs, ymax=means+SEs), width=.2)+
  theme_classic()+
  ylab("Mean Reaction Time (ms)")+
  xlab("Typing Material")
```



9.4.6 Conduct the repeated Measures ANOVA

We use the same `aov` function as we used last time. The only difference is that we add in a new part to the formula. Remember the formula for a one-factor between subjects ANOVA looked like this:

`aov( DV ~ IV , dataframe)`, where DV is the name of the column with your independent variable, IV is the name of the column with your independent variable, and `dataframe` is the name of your data frame containing the means in each condition.

The formula for a repeated-measures ANOVA looks like this:

`aov( DV ~ IV + Error(Subject/IV), dataframe)`. We have added `+ Error(Subject/IV)`. This tells R to use the appropriate error term for the repeated measures ANOVA. In the formula, `Subject` refers to the name of the

column coding your subjects (make sure this is a factor in R), and `IV` is the name of the column for your independent variable.

The formula for our data would be: `aov( mean_rt ~ Stimulus + Error(Subject/Stimulus), subject_means)`.

Here is the code below. Just as reminder, the raw data codes every single key press on each row. We don't want to submit this as the data frame to the `aov` function. Instead, we need to calculate the data frame for the subject means in each condition. We did that above as a step toward making the graphs. We do it again here to remind you that you need to do this.

```
# get subject means

subject_means <- all_data %>%
                 filter(Order==1, Correct==1, PureRTs<5000) %>%
                 group_by(Subject, Stimulus) %>%
                 summarise(mean_rt = mean(PureRTs))

# Make sure IV and Subject are coded as factors
subject_means$Subject  <- as.factor(subject_means$Subject)
subject_means$Stimulus <- as.factor(subject_means$Stimulus)

# Conduct the anova

aov_out <- aov( mean_rt ~ Stimulus + Error(Subject/Stimulus), subject_means)
summary_out <- summary(aov_out)

library(xtable)
knitr::kable(xtable(summary_out))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Residuals	37	3030779.9	81912.970	NA	NA
Stimulus	2	1157965.2	578982.606	230.5806	0
Residuals1	74	185812.3	2510.977	NA	NA

Great, we have conducted the ANOVA. We could write up the results of the ANOVA like this:

> For each subject we computed mean reactions for correct keystrokes in each condition of the Stimulus factor. These means were submitted to a one-factor repeated-measures ANOVA, with Stimulus (Normal, Bigrams, and Random) as the sole factor. The effect of Stimulus was signficant, $F(2, 74) = 230.58$, $MSE = 2510.98$, $p < 0.001$.

Note, the p-value shows up as a zero, that's because it is so small that R doesn't want to print the actual number 0.000000000000000…1.

What does this tell us?

1. The F value we obtained (230.58) almost never occurs by chance. More specifically, the sampling distribution of F from the distribution of no differences virtually never produces a huge F like 230.58
2. It is super-duper unlikely that chance (sampling error) could have produced the difference we observed.
3. We reject the idea that chance caused the differences, and are very confident that the manipulation (changing the kinds of letters that people have to type), has a causal influence on reaction time in typing.

9.4.6.1 Report the means too

Remember, the important goal when conducting analyses, and then writing about them, is to tell people what you did and what you found. This involves more than one step. For this example, we might do three basic things. 1) make a figure to show the means, 2) report the ANOVA so people know if there is support for the inference that the differences between the means are not caused by chance, and 3) report descriptives for the means, so people know what the numbers are (the figure doesn't show the exact values).

We've already made the figure and done the ANOVA, let's report the condition means. To do this, we need to find the means for each condition, collapsing over the means for each subject in each condition. Note that, we already did this to make the figure. Here's the code again:

```
## get subject mean RTs

subject_means <- all_data %>%
                 filter(Order==1, Correct==1, PureRTs<5000) %>%
                 group_by(Subject, Stimulus) %>%
                 summarise(mean_rt = mean(PureRTs))

subject_means$Subject<-as.factor(subject_means$Subject)
subject_means$Stimulus<-as.factor(subject_means$Stimulus)

## get condition mean RTs

plot_means <- subject_means %>%
              group_by(Stimulus) %>%
              summarise(means = mean(mean_rt),
                        SEs = sd(mean_rt)/sqrt(length(mean_rt)))

knitr::kable(plot_means)
```

Stimulus	means	SEs
Bigrams	924.8764	26.69375
Normal	833.1872	24.00055
Random	1077.5361	31.60979

Now, our full write-up of the results would look like this.

> For each subject we computed mean reactions for correct keystrokes in each condition of the Stimulus factor. These means were submitted to a one-factor repeated-measures ANOVA, with Stimulus (Normal, Bigrams, and Random) as the sole factor. The effect of Stimulus was signficant, $F(2, 74) = 230.58$, $MSE = 2510.98$, $p < 0.001$. The mean reaction time was fastest in the Normal condition ($M = 833$ ms, $SE = 24$ ms), followed by the Bigram condition, ($M = 924$ ms, $SE = 27$ ms) and slowest in the Random Condition ($M = 1078$ ms, $SE = 32$ ms).

9.4.7 Follow-up comparisons

The ANOVA tells us that the differences between the means are unlikely to be due to chance. But, remember, this is an omnibus test. It does not tell us if specific pairs of means are different from one another. To determine whether the difference between two specific means is not likely due to chance, we need to conduct follow-up tests.

Because this is a repeated-measures design, we can use the paired-samples t-test for follow-up tests. Let's do two follow-up tests to confirm that the RTs for Normal words were indeed faster than the RTs for the Bigram condition (word-like non-words); and then, let's confirm that the RTs for the Bigram condition were indeed faster than the RTs for the Random condition.

9.4.7.1 Normal vs Bigrams

We use the `subject_means` data frame. But, we want to rid of all the rows containing the means from the Random condition. We use filter to do that, then we conduct the paired-samples t-test.

```
comparison_df <- subject_means %>%
                  filter(Stimulus != "Random")

t.test(mean_rt~Stimulus,
       paired=TRUE,
       var.equal=TRUE,
       data = comparison_df)
```

```
##
##  Paired t-test
##
## data:  mean_rt by Stimulus
## t = 12.14, df = 37, p-value = 1.807e-14
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##   76.38601 106.99253
## sample estimates:
## mean difference
##        91.68927
```

9.4.7.2 Bigrams vs Random

We use the `subject_means` data frame. But, we want to rid of all the rows containing the means from the Normal condition. We use filter to do that, then we conduct the paired-samples t-test.

```
comparison_df <- subject_means %>%
                  filter(Stimulus != "Normal")

t.test(mean_rt~Stimulus,
       paired=TRUE,
       var.equal=TRUE,
       data = comparison_df)
```

```
##
##  Paired t-test
##
## data:  mean_rt by Stimulus
## t = -14.212, df = 37, p-value < 2.2e-16
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -174.4245 -130.8949
## sample estimates:
## mean difference
##       -152.6597
```

9.4.8 Reporting everything

Now we can look at some write-ups that report everything we did, and everything we want to know. I'll show you two ways to do it.

9.4.8.1 First way

In the first way, we embed the results of the t-test into the description of the mean reaction times.

For each subject we computed mean reactions for correct keystrokes in each condition of the Stimulus factor. These means were submitted to a one-factor repeated-measures ANOVA, with Stimulus (Normal, Bigrams, and Random) as the sole factor. The effect of Stimulus was significant, $F(2, 74) = 230.58$, MSE $= 2510.98$, $p < 0.001$. The mean reaction time was significantly faster in the Normal condition (M = 833 ms, SE = 24 ms), compared to the Bigram condition, (M = 924 ms, SE = 27 ms), $t(37) = 12.14$, $p<0.001$. Additionally, mean reactions in the Bigram condition were significantly faster than the Random Condition (M = 1078 ms, SE = 32 ms), $t(37) = 14.21$, $p < 0.001$.

9.4.8.2 Second way

In the second way, we first report the means as we did the very first time, and then after that we report the t-test results to highlight the size the of the differences between each comparison.

For each subject we computed mean reactions for correct keystrokes in each condition of the Stimulus factor. These means were submitted to a one-factor repeated-measures ANOVA, with Stimulus (Normal, Bigrams, and Random) as the sole factor. The effect of Stimulus was significant, $F(2, 74) = 230.58$, MSE $= 2510.98$, $p < 0.001$. The mean reaction time was fastest in the Normal condition (M = 833 ms, SE = 24 ms), followed by the Bigram condition, (M = 924 ms, SE = 27 ms) and slowest in the Random Condition (M = 1078 ms, SE = 32 ms). Mean reaction times were significantly faster (M = 91 ms) in the Normal than Bigrams condition, $t(37) = 12.14$, $p < 0.001$. And, mean reaction times were significantly faster (M = 152 ms) in the Bigrams than Random condition, $t(37) = 14.21$, $p < 0.01$.

There are other ways to write-up statistical results. These are just some example recipes. The important thing is to:

1. Say what the numbers were that you are analyzing
2. Say what the statistical test was
3. Say the results of the statistical test
4. Say what the patterns of means were
5. Say what the follow-up tests were when you test differences between specific means.
6. Add a table or figure so it is easier to "see" the results.

9.4.9 Generalization Exercise

Your task is to conduct another repeated-measures ANOVA. Rather than using the reaction time for the first-keystroke as the dependent measure, you will use the reaction times between all of the keystrokes in each word, these are called interkeystroke intervals. The `Order` variable is used to code keystroke position (1 to 5). You will want to analyze only the `PureRTs` that have an `Order` greater than 1. For example, you could use the following code to get the subject_means for the mean interkeystroke intervals.

```
subject_means <- all_data %>%
                 filter(Order > 1, Correct==1, PureRTs<5000) %>%
                 group_by(Subject, Stimulus) %>%
                 summarise(mean_rt = mean(PureRTs))
```

A. Make a figure for the new DV B. Report the ANOVA table for the new repeated measures ANOVA C. Discuss whether the general pattern is the same as before.

9.4.10 Writing assignment

(2 points - Graded)

1. Explain the concept of SS_{Total} (.5 points)
2. Explain the concept of partitioning SS_Total into smaller pieces. What is the goal of the spitting? (.5 points)
3. Explain the major difference between a between-subjects ANOVA and repeated-measures ANOVA in terms of what is being partioned. (1 point)

General grading.

- You will receive 0 points for missing answers
- You must write in complete sentences. Point form sentences will be given 0 points.
- Completely incorrect answers will receive 0 points.
- If your answer is generally correct but very difficult to understand and unclear you may receive half points for the question

9.4.11 Practice Problems

1. Run the same analysis as illustrated in this lab tutorial but with accuracy (correct) as the dependent variable. Use an alpha level of .05. Remember to calculate means per subject and stimulus first. This will generate a table, whose values you can enter into a new SPSS spreadsheet file.

2. Is there an effect of stimulus on error rate? If so, conduct the appropriate planned comparisons.

3. Graph the means using a bar graph; include +/-1 SEM Error bars.

Chapter 10

Lab 10: Factorial ANOVA

Simplicity is complex. It's never simple to keep things simple. Simple solutions require the most advanced thinking. —Richie Norton

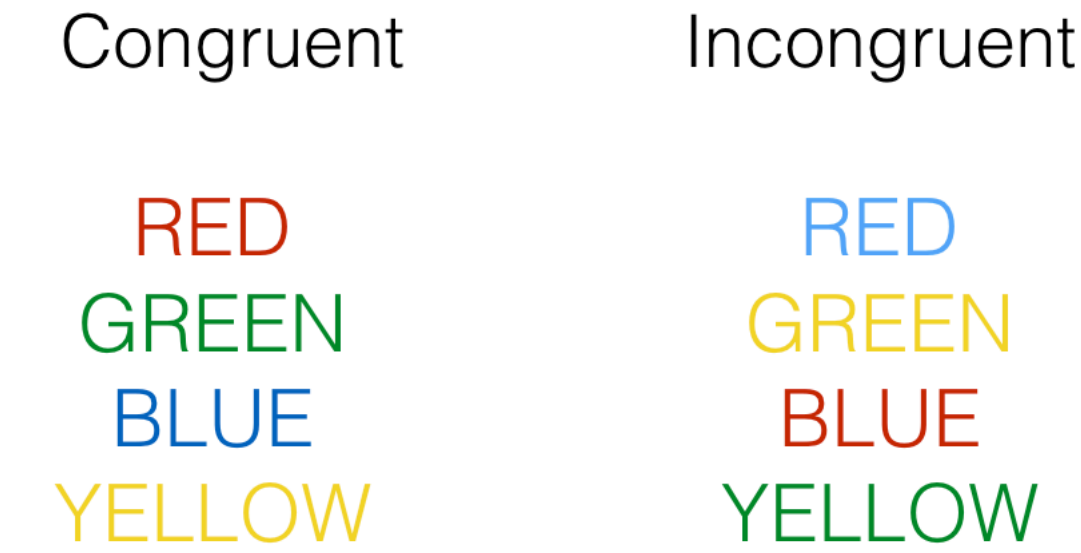
10.1 Does standing up make you focus more?

This lab activity uses the data from "Stand by your Stroop: Standing up enhances selective attention and cognitive control" (Rosenbaum, Mama, Algom, 2017) to teach the analysis of a 2x2 design using ANOVA. Although the research design is a 2x2 repeated meaures design, we treat the design both as repeated measures, and as a between-subjects design to illustrate how to conduct either type of ANOVA in software.

10.1.1 STUDY DESCRIPTION

Do you pay more attention when you are sitting or standing? We analyse the data from "Stand by your Stroop: Standing up enhances selective attention and cognitive control" (Rosenbaum, Mama, Algom, 2017). This paper asked whether sitting versus standing would influence a measure of selective attention, the ability to ignore distracting information.

They used a classic test of selective attention, called the Stroop effect. In a typical Stroop experiment, subjects name the color of words as fast as they can. The trick is that sometimes the color of the word is the same as the name of the word, and sometimes it is not. Here are some examples:



Congruent trials occur when the color and word match. So, the correct answers for each of the congruent stimuli shown would be to say, red, green, blue and yello. Incongruent trials occur when the color and word mismatch. The correct answers for each of the incongruent stimuli would be: blue, yellow, red, green.

The Stroop effect is an example of a well-known phenomena. What happens is that people are faster to name the color of the congruent items compared to the color of the incongruent items. This difference (incongruent reaction time - congruent reaction time) is called the Stroop effect.

Many researchers argue that the Stroop effect measures something about selective attention, the ability to ignore distracting information. In this case, the target information that you need to pay attention to is the color, not the word. For each item, the word is potentially distracting, it is not information that you are supposed to respond to. However, it seems that most people can't help but notice the word, and their performance in the color-naming task is subsequently influenced by the presence of the distracting word.

People who are good at ignoring the distracting words should have small Stroop effects. They will ignore the word, and it won't influence them very much for either congruent or incongruent trials. As a result, the difference in performance (the Stroop effect) should be fairly small (if you have "good" selective attention in this task). People who are bad at ignoring the distracting words should have big Stroop effects. They will not ignore the words, causing them to be relatively fast when the word helps, and relatively slow when the word mismatches. As a

result, they will show a difference in performance between the incongruent and congruent conditions.

If we take the size of the Stroop effect as a measure of selective attention, we can then start wondering what sorts of things improve selective attention (e.g., that make the Stroop effect smaller), and what kinds of things impair selective attention (e.g., make the Stroop effect bigger).

The research question of this study was to ask whether standing up improves selective attention compared to sitting down. They predicted smaller Stroop effects when people were standing up and doing the task, compared to when they were sitting down and doing the task.

10.1.2 Study Methods

The design of the study was a 2x2 repeated-measures design. The first IV was congruency (congruent vs incongruent). The second IV was posture (sitting vs. standing). The DV was reaction time to name the word. There were 50 participants in the study.

10.2 Lab Skills Learned

- Conducting a 2x2 between-subjects ANOVA
- Conducting a 2x2 repeated-measures ANOVA

10.3 Important Stuff

- citation: Rosenbaum, D., Mama, Y., & Algom, D. (2017). Stand by Your Stroop: Standing Up Enhances Selective Attention and Cognitive Control. Psychological science, 28(12), 1864-1867.
- Link to .pdf of article
- Data in .csv format

10.4 R

10.4.1 Load the data

Remember that any line with a # makes a comment and the code does not run. Below is how to load the .csv data from the online repository, or from a local file (you need to change the file path to where the local file is, if you downloaded it). The data contains all of the measures and conditions from Experiment 1 in the paper.

```
library(data.table)
#all_data <- fread("https://github.com/CrumpLab/statisticsLab/raw/master/stroop_stand.
all_data <- fread("data/stroop_stand.csv")
```

10.4.2 Inspect the dataframe

This will give you a big picture of the data frame. Click the button to view it in your browser, then take a look to see what is in it.

```
library(summarytools)
view(dfSummary(all_data))
```

We see there are four columns of numbers. The column names tell us whether the data is for a congruent or incongruent condition, and whether the participant was sitting or standing. Note, this data is in wide-format, not long-format. Each subject has 4 measures per row. We will need to change this to work with the data in R.

10.4.3 Get the data you need

This data file contains all of the data from Experiment 1 in the paper. So, we don't need to get rid of any rows.

10.4.4 Get the data into the format you want

As mentioned before we need to convert the data from wide to long format. What we want at the end of this conversion is:

1. A column for the subject variable
2. A column for the congruency variable
3. A column for the posture (sit vs. stand) variable
4. A column for the DV (mean reaction times)

We look at two ways to do the transformation from wide to long. The first way is to "do it by hand", which refers to creating every variable individually, and then putting them together in a single data frame. This next bit of code does this, and you can check out `stroop_df` to see the result.

```
RTs <- c(as.numeric(unlist(all_data[,1])),
         as.numeric(unlist(all_data[,2])),
         as.numeric(unlist(all_data[,3])),
```

```
         as.numeric(unlist(all_data[,4]))
         )

Congruency <- rep(rep(c("Congruent","Incongruent"),each=50),2)
Posture <- rep(c("Stand","Sit"),each=100)
Subject <- rep(1:50,4)

stroop_df <- data.frame(Subject,Congruency,Posture,RTs)
```

Another way to transform between long and wide is to use R functions that were designed to do this job. For example there are the `spread` and `gather` functions from the `tidyr` package, and the `melt` and `cast` functions, which also do some data frame transforming. The transformation from wide to long can be complicated depending on the structure of the data, and you may often find it helpful to google these functions to look for more examples of their use.

Let's use the `tidyr gather` function to change our data from wide to long

```
library(tidyr)

stroop_long<- gather(all_data, key=Condition, value=RTs,
                     congruent_stand, incongruent_stand,
                     congruent_sit, incongruent_sit)
```

Take a moment to look at `stroop_long`. It is almost what we need. It is certainly in long format. There is a column for Subjects, and a column for the RTs, but there is only one column for both IVs, that's no good. There are two IVs, we need two columns. Fortunately, the levels in the new Condition column are coded with a specific and consistent structure:

1. congruent_stand
2. incongruent_stand
3. congruent_sit
4. incongruent_sit

If only we could split these by the "_" (underscore), then we would have two columns for the congruency and the posture variable. We can do this using `tstrsplit` from the `data.table` package

```
new_columns <- tstrsplit(stroop_long$Condition, "_", names=c("Congruency","Posture"))
```

You can look inside `new_columns` to see that we succesfully made the split. Now, we just need to add them on to the `stroop_long data` frame.

```
stroop_long <- cbind(stroop_long,new_columns)
```

Look at the `stroop_long` data frame and you will find that we have added two new columns, one that codes for Congruency, and the other that codes for posture.

Using this method we still haven't added a column for subjects. We can do that like this:

```
stroop_long <- cbind(stroop_long,Subject=rep(1:50,4))
```

10.4.4.1 The independent variables

After all of this data transformation you should be familiar with the IVs.

1. Congruency: congruent vs. incongruent
2. Posture: stand vs. sit

10.4.4.2 The dependent variables

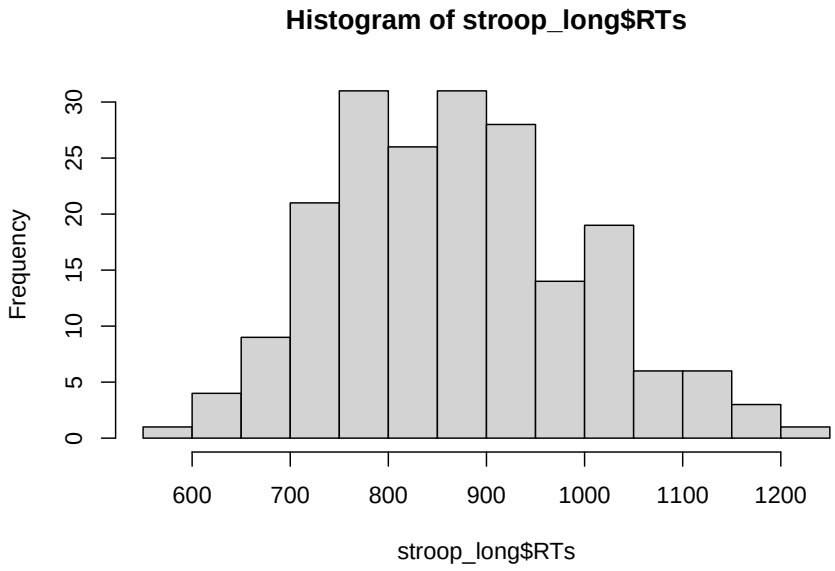
There is only one DV that we look at, that is the mean reaction time to name the color.

10.4.5 Look at the data

Remember before we do any analysis, we always want to "look" at the data. This first pass let's us know if the data "look right". For example, the data file could be messed up and maybe there aren't any numbers there, or maybe the numbers are just too weird.

Let's make a quick histogram of all of the RT data, like this:

```
hist(stroop_long$RTs)
```



This looks pretty good, there are no super huge numbers here.

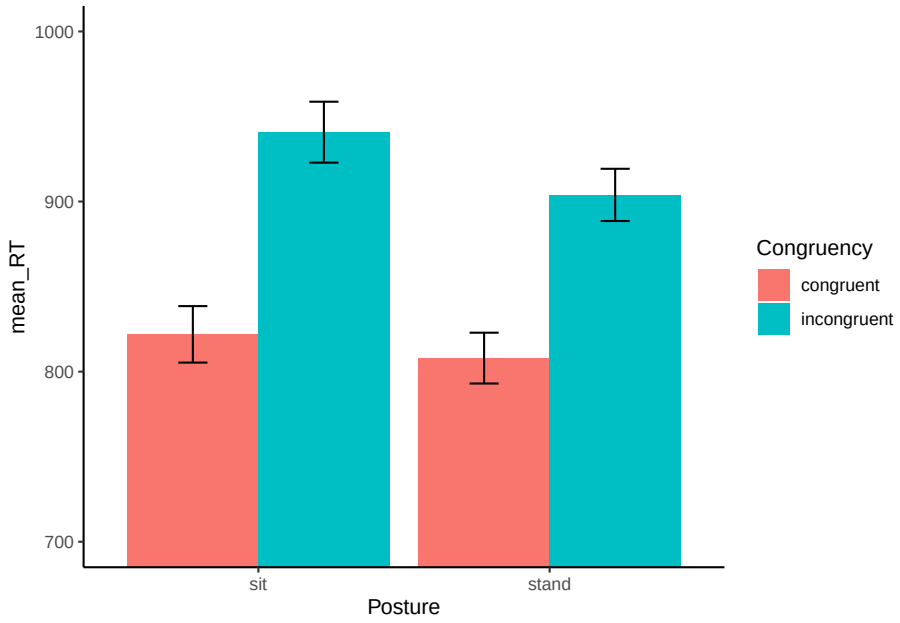
10.4.6 Look at the means

As part of looking at the data, we might as well make a figure that shows the mean reaction times in each condition, and some error bars to look at the spread in each condition. The following code takes two important steps:

1. Get the means for each condition, by averaging over the means for each subject. These are put into the data frame called `plot_means`.
2. Make a graph with the `plot_means` data frame using ggplot2.

```
library(dplyr)
library(ggplot2)

plot_means <- stroop_long %>%
            group_by(Congruency,Posture) %>%
            summarise(mean_RT = mean(RTs),
                      SEM = sd(RTs)/sqrt(length(RTs)))

ggplot(plot_means, aes(x=Posture, y=mean_RT, group=Congruency, fill=Congruency))+
  geom_bar(stat="identity", position="dodge")+
  geom_errorbar(aes(ymin=mean_RT-SEM, ymax=mean_RT+SEM),
```

```
                position=position_dodge(width=0.9),
                width=.2)+
theme_classic()+
coord_cartesian(ylim=c(700,1000))
```



10.4.7 Conduct the ANOVA

In this lab we will show you how to conduct ANOVAs for factorial designs that are for:

1. fully between-subjects designs (both IVs are between-subjects IVs)
2. fully repeated measures designs (both IVs are repeated measures)

The data we are looking at right now is fully repeated measures.

However, in this lab we are first going to pretend that the experiment was not repeated measures. We are going to pretend it was fully between-subjects. Then we are going to conduct a between-subjects ANOVA. After that, we will conduct a repeated-measures ANOVA, which is what would be most appropriate for this data set. The overall point is to show you how to both of them, and the discuss how to interpret them and write them both up.

10.4.8 Between Subjects ANOVA

We can always conduct a between-subjects version of the ANOVA on repeated-measures data if we wanted to. In this case we wouldn't really want to do this. But, we will do this for educational purposes to show you how to do it in R.

The syntax is very similar to what we do for one-way ANOVAs, remember the syntax was:

`aov(DV ~ IV, dataframe)`

If you want to add another IV, all you need to do is insert another one into the formula, like this:

`aov(DV ~ IV1*IV2, dataframe)`

Just, switch DV to the name of your dependent measure, and IV1 and IV2 to the names of your independent variables. Finally, put the name of your dataframe. Your dataframe must be in long format with one observation of the DV per row.

Our formula will look like this:

`aov(RTs ~ Congruency*Posture, stroop_long)`

In plain language, this formula means, analyze RTs by the Congruency and Posture Variables. R will automatically produce the main effects for Congruency and Posture, as well as the interaction (Congruency X Posture). Also, remember, that in the following code, we use a few other functions so that we can print out the results nicely.

```
library(xtable)

aov_out<-aov(RTs ~ Congruency*Posture, stroop_long)
summary_out<-summary(aov_out)

library(xtable)
knitr::kable(xtable(summary_out))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Congruency	1	576821.635	576821.635	43.7344419	0.0000000
Posture	1	32303.453	32303.453	2.4492381	0.1191950
Congruency:Posture	1	6560.339	6560.339	0.4974029	0.4814808
Residuals	196	2585080.215	13189.185	NA	NA

We can also have R print out the Grand Mean, the means for each level of each main effect, and the means for the interaction term. This is the same print out you would get in the console for R. It is admittedly not very pretty. There's probably a way to make the means provided by `model.tables()` more pretty. If we find a way we will update this section, if you find a way, please let us know.

```
print(model.tables(aov_out,"means"), format="markdown")
```

```
## Tables of means
## Grand mean
##
## 868.6454
##
##  Congruency
## Congruency
##   congruent incongruent
##       814.9       922.3
##
##  Posture
## Posture
##   sit stand
## 881.4 855.9
##
##  Congruency:Posture
##              Posture
## Congruency    sit   stand
##   congruent   821.9 808.0
##   incongruent 940.8 903.9
```

10.4.8.1 ANOVA write-up

Here are the steps for writing up the results of an ANOVA:

1. Say what means you analyzed
2. Say what test you performed
3. Say the inferential statisic for each of the effects (main effects and interaction)
4. Say the pattern of results for each effect.

A short example of the whole write-up is below:

Example write-up

We submitted the mean reaction times for each group to a 2 (Congruency: congrueny vs. incongruent) x 2 (Posture: Standing vs. Sitting) between-subjects ANOVA.

There was a main effect of Congruency, F (1, 196) = 43.73, MSE = 13189.185, p < 0.001. Mean reaction times were slower for incongruent (922 ms) than congruent groups (815 ms).

There main effect of Posture was not significant, F (1, 196) = 2.45, MSE = 13189.185, p =.119. Mean reaction times were slower for sitting (881 ms) than standing groups (855 ms).

The two-way interaction between Congruency and Posture was not significant, F (1, 196) = .497, MSE = 13189.185, p < 0.481.

For every F-value, we report F (df1, df2) = F-value, MSE = MSE for the error term, and p = x.xxx.

In R, the df1, for the df in the numerator is always listed beside the name for a particular effect. For example, Congruency has 1 degree of freedom (there are two condition, and 2-1 =1). Similarly, the relevant F and p-value are listed in the same row as the effect of interest.

However, the error term used to calculate the F-value is listed at the bottom, in R this is called "Residuals". Df2, the df for the denominator is listed beside "Residuals", in our case it was 196. The important bit is the MSE, which was 13189.185. Notice, that in the write up for each main effect and interaction we always reported the same MSE. That's because in this between-subjects version of the ANOVA, we divide by same very same error term. Also notice that we don't report the sums of squares of the MSE for the effect.

Why not? The main reason why not is that you can reconstruct those missing numbers just by knowing the dfs, the MSE for the error, and the f-value.

For example, you can get the MSE for the effect by multiplying the F-value by the MSE for the error. Now you have both MSEs. You can get both Sums of Squares by multiplying by their associated dfs. That's just working backwards from the F-value.

You can always check if you are reporting the correct MSE for the error term. If the MSE for your effect (numerator) divided by the MSE you are using for the error term does not equal the F-value, then you must be using the wrong terms!

10.4.9 Repeated measures ANOVA

Of course, the design for this experiment was not between-subjects, it was fully within-subjects. Every participant completed both congruent and incongruent trials, while they were standing or sitting. For this reason, we should conduct a repeated measures ANOVA. This way we will be able capitilize on the major

benefit provided by the repeated measures design. We can remove the variance due to individual subjects from the error terms we use to calculate F-values for each main effect and interaction.

Rember the formula for the one-factor repeated-measures ANOVA, we'll remind you:

```
aov( DV ~ IV + Error(Subject/IV), dataframe)
```

To do the same for a design with more than one IV we put in another IV to the formula, like this:

```
aov( DV ~ IV1*IV2 + Error( Subject/(IV1*IV2) ), dataframe)
```

- DV = name of dependent variable
- IV1 = name of first independent variable
- IV2 = name of second indpendent variable
- Subject = name of the subject variable, coding the means for each subject in each condition
- dataframe = name of the long-format data frame

Here is what our formula will look like:

```
aov(RTs ~ Congruency*Posture + Error(Subject/(Congruency*Posture)),
stroop_long)
```

The main thing you need to watch out for when running this analysis in R, is that all your factors need to be `factors` in R. Often times people will use numbers rather than words or letters to code the levels for specific factors. This can be very often done for the subjects factor, using number 1 for subject one, and number 2 for subject 2. If you want your column variable to be treated as a factor, then you may need to convert it to a factor. We do this below for the Subject variable, which happens to be coded as numbers. If we do not do this, the repeated-measures ANOVA will return incorrect results.

For example, if you look at the `stroop_long` data frame, and click the little circle with an arrow on in it in the environment panel, you should see that Subject is an `int`. That stands for integer. You should also see that Congruency and Posture are `Factor`, that's good. We need to turn Subject into `Factor`.

```
stroop_long$Subject <- as.factor(stroop_long$Subject) #convert subject to factor

summary_out<-aov(RTs ~ Congruency*Posture + Error(Subject/(Congruency*Posture)), stroo

library(xtable)
knitr::kable(xtable(summary_out))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Residuals	49	2250738.636	45933.4416	NA	NA
Congruency	1	576821.635	576821.6349	342.452244	0.0000000
Residuals	49	82534.895	1684.3856	NA	NA
Posture	1	32303.453	32303.4534	7.329876	0.0093104
Residuals1	49	215947.614	4407.0942	NA	NA
Congruency:Posture	1	6560.339	6560.3389	8.964444	0.0043060
Residuals	49	35859.069	731.8177	NA	NA

```
print(model.tables(aov_out,"means"), format="markdown")
```

```
## Tables of means
## Grand mean
##
## 868.6454
##
##  Congruency
## Congruency
##   congruent incongruent
##       814.9       922.3
##
##  Posture
## Posture
##   sit stand
## 881.4 855.9
##
##  Congruency:Posture
##              Posture
## Congruency    sit   stand
##   congruent   821.9 808.0
##   incongruent 940.8 903.9
```

What's different here? Are any of the means different now that we have conducted a repeated-meaures version of the ANOVA, instead of the between-subjects ANOVA? NO! The grand mean is still the grand mean. The means for the congruency conditions are still the same, the means for the Posture conditions are still the same, and the means for the interaction effect are still the same. The only thing that has changed is the ANOVA table. Now that we have removed the variance associated with individual subjects, our F-values are different, and so are the-pvalues. Using an alpha of 0.05, all of the effects are "statistically significant".

Each main effect and the one interaction all have their own error term. In the table below, R lists each effect in one row, and then immediately below lists the error term for that effect.

10.4.9.1 ANOVA write-up

Here is what a write-up would look like.

Example write-up

We submitted the mean reaction times for each subject in each condition to a 2 (Congruency: congrueny vs. incongruent) x 2 (Posture: Standing vs. Sitting) repeated measures ANOVA.

There was a main effect of Congruency, F (1, 49) = 342.45, MSE = 1684.39, $p < 0.001$. Mean reaction times were slower for incongruent (922 ms) than congruent groups (815 ms).

There main effect of Posture was significant, F (1, 49) = 7.33, MSE = 4407.09, p =.009. Mean reaction times were slower for sitting (881 ms) than standing groups (855 ms).

The two-way interaction between Congruency and Posture was significant, F (1, 49) = 8.96, MSE = 731.82, $p < 0.004$. The Stroop effect was 23 ms smaller in the standing than sitting conditions.

10.4.10 Follow-up comparisons

In a 2x2 ANOVA there are some follow-up comparisons you may be interested in making that are not done for you with the ANOVA. If an IV only have 2 levels, then you do not have to do any follow-up tests for the main effects of those IVs (that's what the main effect from the ANOVA tells you). So, we don't have to do follow-up comparisons for the main effects of congruency or posture. What about the interaction?

Notice the interaction is composed of four means. The mean RT for congruent and incongruent for both sitting and standing.

Also notice that we only got one F-value and one p-value from the ANOVA for the interaction term. So, what comparison was the ANOVA making? And what comparisons was it not making? It has already made one comparison, so you do not need a follow-up test for that…which one is it?

If you remember back to the textbook, we should you how to analyze a 2x2 design with paired-samples t-tests. We analyzed the interaction term as the comparison of difference scores. Here, we would find the differences scores between incongruent and congruent for each level of the posture variable. In other words, we compute the Stroop effect for each subjet when they were sitting and

standing, then compare the two Stroop effects. This comparison is looking at the difference between two differences scores, and that is the comparison that the ANOVA does for the interaction. To be more precise the comparison is:

$(sit : incongruent - sit : congruent) - (stand : incongruent - stand : congruent)$

What comparisons are not made, what are the other ones we could do? Here are some:

1. sit:congruent vs sit:incongruent
2. stand:congruent vs stand:incongruent
3. sit:congruent vs stand:incongruent
4. stand:congruent vs sit:incongruent

We could add a few more. These kinds of comparisons are often called **simple effects**, apparently referring to the fact they are just comparing means in a straight forward way. There are a few different comparisons we could do. Should we do any of them?

Whether or not you compare means usually depends on the research question you are asking. Some comparisons make sense within context of the research question, and others may not. We will do two follow-up comparisons. Our question will be about the size of the Stroop effect in the Sitting and Standing conditions. We already know that the size of the effect was smaller in the Standing condition. But, we don't know if it got so small that it went away (at least statistically speaking). Now, we can ask:

1. Was the Stroop effect only for the sitting condition statistically signficant. In other words, was the difference in mean RT between the incongruent and congruent conditions unlikely under the null (or unlikely to be produced by chance)

2. Was the Stroop effect only for the standing condition statistically signficant. In other words, was the difference in mean RT between the incongruent and congruent conditions unlikely under the null (or unlikely to be produced by chance)

We can answer both of the questions using paired sample t-tests comparing the means in question

10.4.10.1 Sitting Stroop

```
means_to_compare <- stroop_long %>%
                      filter(Posture=="sit")

t.test(RTs~Congruency, paired=TRUE, var.equal=TRUE, data=means_to_compare)
```

```
##
##  Paired t-test
##
## data:  RTs by Congruency
## t = -16.516, df = 49, p-value < 2.2e-16
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -133.3250 -104.3997
## sample estimates:
## mean difference
##       -118.8623
```

10.4.10.2 Standing Stroop

```
means_to_compare <- stroop_long %>%
                      filter(Posture=="stand")

t.test(RTs~Congruency, paired=TRUE, var.equal=TRUE, data=means_to_compare)
```

```
##
##  Paired t-test
##
## data:  RTs by Congruency
## t = -14.327, df = 49, p-value < 2.2e-16
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -109.41185  -82.49462
## sample estimates:
## mean difference
##       -95.95323
```

10.4.11 Generalization Exercise

Here are some means for four conditions in a 2x2 Design:

		IV1	
		Level 1	Level 2
IV 2	Level 1	100	200
	Level 2	200	500

Your task is to:

A. Compute the mean difference for the main effect of IV1

B. Compute the mean difference for the main effect of IV2

C. Compute the mean difference for the interaction

10.4.12 Writing asignment

(2 points - Graded)

Factorial designs have main effects and interactions.

1. Explain the concept of a main effect. (1 point)
2. Explain the concept of an interaction. (1 point)

General grading.

- You will receive 0 points for missing answers
- You must write in complete sentences. Point form sentences will be given 0 points.
- Completely incorrect answers will receive 0 points.
- If your answer is generally correct but very difficult to understand and unclear you may receive half points for the question

10.4.13 Practice Problems

Below is fictitious data representing the number of milliimeters a plant has grown under several water/sunlight combinations:

Water & Sunlight	NoWater & Sunlight	Water & NoSunlight	NoWater & NoSunlight
1.2	2.4	3.1	2.5
3.0	1.1	2.2	3.4

Water & Sunlight	NoWater & Sunlight	Water & NoSunlight	NoWater & NoSunlight
2.5	1.2	2.5	4.2
1.6	2.4	4.3	2.1

1. Enter this data into SPSS as appropriate for a Two-Factor Between-Subjects ANOVA (N=16). Perform the ANOVA and report all results in standard statistical reporting format (use alpha=.05). Include a plot of means.

2. Enter this data into SPSS as appropriate for a Two-Factor Repeated-Measures ANOVA (N=4). Perform the ANOVA and report all results in standard statistical reporting format (use alpha=.05). Include a plot of means.

Chapter 11

Lab 11: Mixed Factorial ANOVA

No amount of experimentation can ever prove me right; a single experiment can prove me wrong —Albert Einstein

11.1 Do you remember things better when you take pictures of them?

People take pictures of things all the time on their phones. Barasch et al. (2017) asked whether taking pictures of things had consequences for later memory of those experiences.

11.1.1 Study description

In Experiment 1, participants visited a museum exhibit. Half of the participants were allowed to take photographs (with camera, at least 10 pictures) and the other half were not (no camera). They freely looked at anything in the exhibit, and were allowed to take pictures of anything they wanted (if they were in the camera condition). Additionally, while visiting the exhibit, participants listened to audio guides about the things the were looking at.

After participants were done with the exhibit the returned to the sign-in desk. At this point they were given two memory tests for the things they saw and heard in the exhibit. They were given a visual recognition test containing pictures of objects, and were asked to identify which objects they remembered seeing. They were also given an auditory recognition test containing statements that could

have been on the audio guide, and they had to identify which ones they had heard before.

This is a 2x2 mixed design. IV 1 was a between-subjects manipulation involving picture-taking (camera vs. no camera). IV2 was a within-subject manipulation of memory test (visual vs. audio). The dependent measure was performance on the memory test.

An overarching question was whether or not participants would have better visual memory for exhibit objects when they took pictures, compared to when they didn't. Additionally, taking pictures or not, may have no influence on memory for the statements in the audio guide.

11.2 Lab Skills Learned

- Conducting a 2x2 mixed design ANOVA

11.3 Important Stuff

- citation: Barasch, A., Diehl, K., Silverman, J., & Zauberman, G. (2017). Photographic memory: The effects of volitional photo taking on memory for visual and auditory aspects of an experience. Psychological science, 28(8), 1056-1066.
- Link to .pdf of article
- Data in .csv format

11.4 R

11.4.1 Load the data

Remember that any line with a # makes a comment and the code does not run. Below is how to load the .csv data from the online repository, or from a local file (you need to change the file path to where the local file is, if you downloaded it). The data contains all of the measures and conditions from Experiment 1 in the paper.

```
library(data.table)
#all_data <- fread("https://github.com/CrumpLab/statisticsLab/raw/master/stroop_stand.
all_data <- fread("data/study1_data_photo.csv")
```

11.4.2 Inspect the dataframe

This will give you a big picture of the data frame. Click the button to view it in your browser, then take a look to see what is in it.

```
library(summarytools)
view(dfSummary(all_data))
```

11.4.3 Get the data you need

This data file contains all of the data from Experiment 1 in the paper.

11.4.4 Get the data into the format you want

The data is sort of in long-format, we will see that we need to do some transformation after looking more closely at the independent and dependent variables

11.4.4.1 The independent variables

1. Photo vs. No photo is coded in the `condition` column
2. Memory task (visual vs. audio). There are no column variables describing which memory task people performed. Instead, the percent correct for the visual memory task is coded in the `vpercent` column, and the percent correct for the audio memory task is coded in the `apercent` column. We will need to transform the data, we do that after describing the DV

11.4.4.2 The dependent variable

In a sense there are two dependent variables, `vpercent` and `apercent`. However, we will treat them as a single memory performance variable.

11.4.4.3 Transforming the data

There were 297 participants. You can check that we have data for each participant by looking at the `labID` column.

```
length(unique(all_data$labID))
```

```
## [1] 297
```

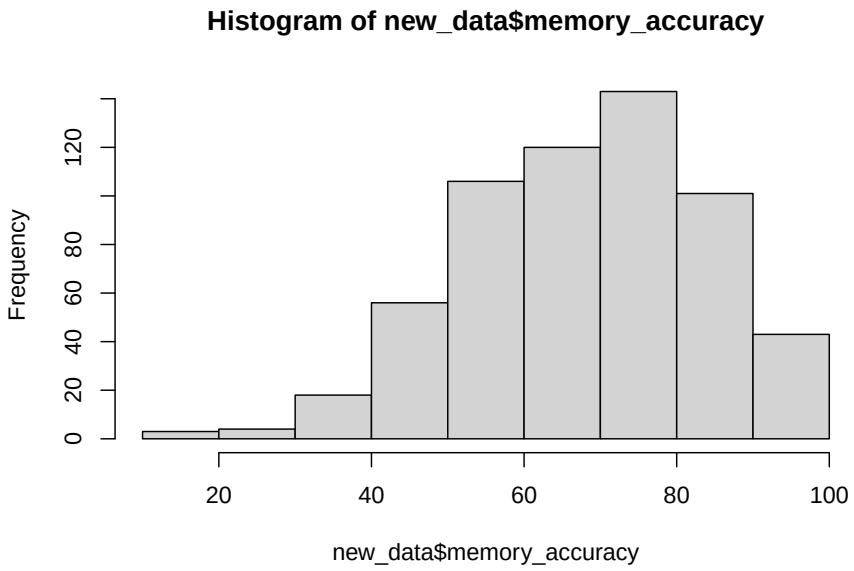
There are 297 rows of data, each corresponding to a single subject. Let's build a data frame we can use for analysis

```
subjects <- as.factor(c(all_data$labID,all_data$labID))
memory_accuracy <- c(all_data$vpercent,all_data$apercent)
memory_task<-as.factor(rep(c("visual","audio"), each=297))
camera <- as.factor(c(all_data$condition,all_data$condition))

new_data <- data.frame(subjects,
                       memory_accuracy,
                       memory_task,
                       camera)
```

11.4.5 Look at the data

Remember before we do any analysis, we always want to "look" at the data. This first pass let's us know if the data "look right". For example, the data file could be messed up and maybe there aren't any numbers there, or maybe the numbers are just too weird. For example, the memory performance DV is a percent, so it should range between 0 and 100, if we find numbers that are negative or greater than 100, then we know something is wrong.

```
hist(new_data$memory_accuracy)
```



```
range(new_data$memory_accuracy)
```

```
## [1]  11.11111 100.00000
```

Great, the numbers check out, they are all inside the range of 0 to 100.

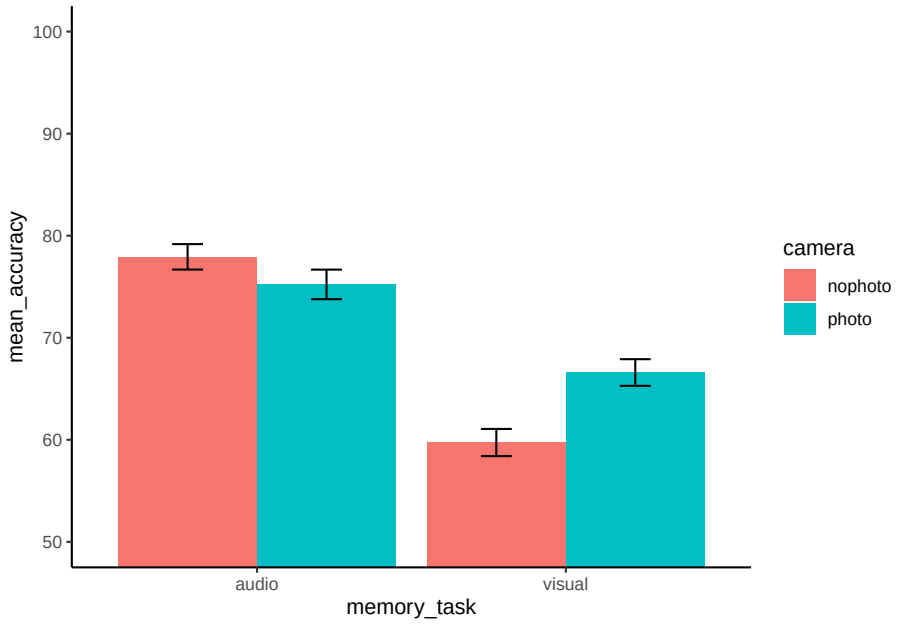
11.4.6 Look at the means

As part of looking at the data, let's graph the means in each condition.

1. Get the means for each condition, by averaging over the means for each subject. These are put into the data frame called `plot_means`.

2. Make a graph with the `plot_means` data frame using ggplot2.

```
library(dplyr)
library(ggplot2)

plot_means <- new_data %>%
            group_by(memory_task,camera) %>%
            summarise(mean_accuracy = mean(memory_accuracy),
                      SEM = sd(memory_accuracy)/sqrt(length(memory_accuracy)))

ggplot(plot_means, aes(x=memory_task, y=mean_accuracy, group=camera, fill=camera))+
  geom_bar(stat="identity", position="dodge")+
  geom_errorbar(aes(ymin=mean_accuracy-SEM, ymax=mean_accuracy+SEM),
                position=position_dodge(width=0.9),
                width=.2)+
  theme_classic()+
  coord_cartesian(ylim=c(50,100))
```



11.4.7 Conduct the ANOVA

This is a 2x2 mixed design. So, we need to run a mixed design ANOVA. The formula for running a mixed design ANOVA is very similar what we have seen before. The only difference is that we specify which IV is within-subjects by placing it in the error term:

```
aov(DV ~ IVB * IVW + Error(Subjects/IVW, data)
```

```
library(xtable)

aov_out<-aov(memory_accuracy ~ camera*memory_task + Error(subjects/memory_task), new_da
summary_out<-summary(aov_out)

knitr::kable(xtable(summary_out))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
camera	1	641.9545	641.9545	2.26222	0.1336337
Residuals	295	83712.7032	283.7719	NA	NA
memory_task	1	26786.5902	26786.5902	108.84808	0.0000000
camera:memory_task	1	3394.1862	3394.1862	13.79237	0.0002441
Residuals	295	72597.0014	246.0915	NA	NA

Let's also print out the means for the main effects and interaction:

```
print(model.tables(aov_out,"means"), format="markdown")
```

```
## Tables of means
## Grand mean
##
## 69.86532
##
##  camera
##     nophoto  photo
##       68.83  70.91
## rep  298.00 296.00
##
##  memory_task
##      audio visual
##      76.58  63.15
## rep 297.00 297.00
##
##  camera:memory_task
##          memory_task
## camera    audio  visual
##   nophoto  77.93  59.73
##   rep     149.00 149.00
##   photo    75.23  66.59
##   rep     148.00 148.00
```

11.4.8 Generalization Exercise

The generalization exercise is the writing assignment for this lab.

11.4.9 Writing assignment

Your writing assignment is to write up the results of the ANOVA that you just conducted. You can follow the general recipe from the ANOVA write-up from the previous lab on factorial designs. Your write up will be in two parts

(3 points total)

Part 1

1. Say what the numbers were that you are analyzing
2. Say what the statistical test was
3. Say the results of the statistical test for each main effect and interaction
4. For each effect, say what the patterns of the means were.

Part 2

Conduct follow-up t-tests.

A. Determine whether memory accuracy is better in the camera vs no camera condition for the visual memory task. Report the t-test and the pattern of means.

B. Determine whether memory accuracy is better in the camera vs. no camera condition for the audio memory task. Report the t-test and the pattern of means.

11.4.10 Practice Problems

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1. Using the same data file we used for this lab's tutorial, run a Mixed-Factorial ANOVA using test type (audio and visual) and Gender (Male, Female). Use an alpha level of .05. Report your results in standard statistical reporting format.

2. Produce a plot of means.