R Programming for Research

Colorado State University, ERHS 535

Brooke Anderson and Rachel Severson

2016-09-25

To ...

Contents

Online course book, ERHS 535 **v**

Course information **vii**

0.1 Course overview vii

0.2 Time and place vii

0.3 Detailed schedule vii

0.4 Grading viii

0.5 Weekly in-course group exercises ix

0.6 Course set-up xi

0.7 Helpful books for learning R xi

I Part I: Preliminaries **xiii**

R Preliminaries **xv**

0.8 R and R Studio xv

0.9 The "package" system xvii

0.10 Basic code conventions of R xxii

0.11 R's most basic object types xxv

0.12 Using R functions xxx

0.13 In-course Exercise xxxiii

II Part II: Basics **xli**

Entering and cleaning data #1 **xliii**

0.14 R scripts . . . xliii

0.15 Directories and pathnames . . . xlvi

0.16 Diversion: `paste` . . . lii

0.17 Reading data into R . . . liii

0.18 Data cleaning . . . lx

0.19 Dates in R . . . lxviii

0.20 In-course Exercise . . . lxxii

Exploring data #1 **lxxxix**

0.21 Data from a package . . . lxxxix

0.22 Plots to explore data . . . xc

0.23 Simple statistics functions . . . ciii

0.24 Logical vectors . . . cvii

0.25 Regression models . . . cx

0.26 In-course exercise . . . cxx

Reporting data results #1 **cxlvii**

0.27 Guidelines for good plots . . . cxlvii

0.28 High data density . . . cxlviii

0.29 References . . . clii

0.30 Highlighting . . . cliv

0.31 Order . . . clvi

0.32 Small multiples . . . clvii

0.33 Advanced customization . . . clx

0.34 To find out more . . . clxvi

0.35 In-course exercise . . . clxvi

Reproducible research #1 **clxxxv**

0.36 What is reproducible research? . . . clxxxv
0.37 Markdown . . . clxxxvi
0.38 Literate programming in R . . . clxxxviii
0.39 Style guidelines . . . cxcii
0.40 More with knitr . . . cxcv
0.41 Saving graphics files . . . cxcviii
0.42 In-course exercise . . . cxcix

Appendix A: Vocabulary **cciii**

.1 Week 1 (Quiz 1) . . . cciii
.2 Week 2 (Quiz 2) . . . cciv
.3 Week 3 (Quiz 3) . . . ccv
.4 Week 4 (Quiz 4) . . . ccvi
.5 Week 5 (Quiz 5) . . . ccvii
.6 Week 6 (Quiz 6) . . . ccvii
.7 Week 7 (Quiz 7) . . . ccviii
.8 Week 8 (Quiz 8) . . . ccviii

Appendix B: Homework **ccix**

.9 Homework #1 . . . ccix
.10 Homework #2 . . . ccxi
.11 Homework #3 . . . ccxiii
.12 Homework #4 . . . ccxiii
.13 Homework #5 . . . ccxiii
.14 Homework #6 . . . ccxiii

Online course book, ERHS 535

This is the online book for Colorado State University's ERHS 535 *R Programming for Research* course. This book includes course information, course notes, links to download pdfs of lecture slides, in-course exercises, homework assignments, and vocabulary lists for quizzes for this course. Because this is my first semester teaching the course with this online book, it will be evolving throughout the semester, as we get to new material.

Course information

Download a pdf of the lecture slides covering this topic.

0.1 Course overview

This document provides the course notes for Colorado State University's ERHS 535 course for Fall 2016. The course offers in-depth instruction on data collection, data management, programming, and visualization, using data examples relevant to academic research.

0.2 Time and place

This course meets in Room 120 of the Environmental Health Building on Mondays and Wednesdays, 10:00 am–12:00 pm. Exceptions to these meeting times are:

- There will be no meeting on Wednesday, Aug. 31.
- There will be no meeting on Labor Day (Monday, Sept. 5).
- To make up for missing class on Aug. 31, we will have a supplemental class on Friday, Sept. 9, 10:00 am–12:00 pm. You **will not** lose attendance points if you cannot attend this class, but **will** be responsible for the material covered.
- There are no course meetings the week of Thanksgiving.

0.3 Detailed schedule

Here is a more detailed view of the schedule for this course for Fall 2016:

Dates	Level	Lecture content	Graded items
Aug. 22, 24	Preliminary	R Preliminaries	
Aug. 29	Basic	Entering and cleaning data	
Sept. 7, Sept. 9*	Basic	Exploring data	Quiz (W)
Sept. 12, 14	Basic	Reporting data results	Quiz (M), HW #1 (W)
Sept. 19, 21	Basic	Reproducible Research	Quiz (M)
Sept. 26, 28	Intermediate	Entering and cleaning data	Quiz (M), HW #2 (W)
Oct. 3, 5	Intermediate	Exploring data	Quiz (M)
Oct. 10, 12	Intermediate	Reporting data results	Quiz (M), HW #3 (W)
Oct. 17, 19	Intermediate	Reproducible Research	Quiz (M)
Oct. 24, 26	Advanced	Entering and cleaning data	Quiz (M), HW #4 (W)
Oct. 31, Nov. 2	Advanced	Exploring data	Project proposal (M)
Nov. 7, 9	Advanced	Reporting data results	HW #5 (W)
Nov. 14, 16	Advanced	Mapping in R	
Nov. 28, 30	Advanced	Package development 1	HW #6 (W)
Dec. 5, 7	Advanced	Package development 2	Project draft (M)
Week of Dec. 12		Group presentations	Final project (M)

0.4 Grading

Course grades will be determined by the following five components:

Assessment component	Percent of grade
Final group project	30
Weekly in-class quizzes, weeks 3-10	25
Homework	25
Attendance and class participation	10
Weekly in-course group exercises	10

0.4.1 Attendance and class participation

Because so much of the learning for this class is through interactive work in class, it is critical that you come to class. Out of a possible 10 points for class attendance, you will get:

- **10 points** if you attend all classes
- **8 points** if you miss one class
- **6 points** if you miss two classes
- **4 points** if you miss three classes
- **2 points** if you miss four classes
- **0 points** if you miss five or more classes

You can get two extra credit attendance points (i.e., make up for a missed class) by attending either the seminar that Yihui Xie will give on Sept. 23 at 4:00 pm

for the Statistics Department in Weber 237 to the short course he will give at 10:00-11:00 am in Weber 223H. (You are welcome to attend both, but can only get a maximum of two extra credit attendance points.)

0.5 Weekly in-course group exercises

Part of each class will be spent doing in-course group exercises. Ten points of your final grade will be based on your participation in these exercises. As long as you are in class and participate in these exercises, you will get full credit for this component. If you miss a class, to get credit towards this component of your grade, you will need to turn in a one-page document describing what you learned from doing the in-course exercise on your own time. All in-class exercises are included in the online course book at the end of the chapter on the associated material.

0.5.1 In-class quizzes

You will have eight total in-class quizzes. You will have one for each of the Week 2–10 class meetings. There will be *at least* 10 questions per quiz. You will get 1/3 point for each correct answer. If you do the math, you can get full credit for this if you get at least 75% of your answers right. You can not get more than the maximum of 25 points for this component– once you reach 25 points on quizzes, you will have achieved full credit for the quiz component of the course grade.

All quiz questions will be multiple choice, matching, or some other form of "close-answered" question (i.e., no open-response-style questions). You can not make up a quiz for a class period you missed. You can still get full credit on your total possible quiz points if you miss a class, but it means you will have to work harder and get more questions right for days you are in class.

Because grading format for these quizzes allows for you to miss some questions and still get the full quiz credit for the course, I will not ever re-consider the score you got on a previous quiz, give points back for a wrong answer on a poorly-worded question, etc. However, if a lot of people got a particular question wrong, I will be sure to cover it in the next class period. Also, especially if a question was poorly worded and caused confusion, I will work a similar question into a future quiz– in addition to the 10 guaranteed questions for that quiz– so every student will have the chance to get an extra 1/3 point of credit for the question.

The "Vocabulary" appendix of our online book has the list of material for which you will be responsible for this quiz. Most of the functions and concepts will have been covered in class, but some may not. You are responsible for going through the list and, if there are things you don't know or remember from class, learning

them. To do this, you can use help functions in R, Google, StackOverflow, books on R, ask a friend, and any other resource you can find.

In general, using R frequently in your research or other coursework will help you to prepare and do well on these quizzes.

0.5.2 Homework

There will be six homework assignments, starting a few weeks into the course and then due approximately every two weeks (see the detailed schedule in the online course book for exact due dates).

Homeworks should be done individually. You will get many chances to work with others during in-course exercises and your final group project, but these homeworks should be a chance to assess how well you understand and can use the course material on your own.

Homeworks will be graded for correctness, but some partial credit will be given for questions you try but fail to answer correctly. If you can't completely do a required task, be sure to show and explain what you tried to do to complete it.

Homework is due by the start of class on the due date. Your grade will be reduced by 10 points for each day it is late, and will receive no credit if it is late by over a week.

0.5.3 Final group project

You will do the final group project in groups of 2–3. The final product will be a statistical blog post-style article of 1,500 words or less and an accompanying Shiny web application. Come up with an interesting question you'd love to get the answer to that you think you can find data to help you answer. You will need to use the data you find, and R, to write your article. The final product will be a Word document created from an RMarkdown file and an accompanying Shiny web application.

Here are some articles to give you an idea of the style and content for this project:

- Does Christmas come earlier each year?
- Hilary: the most poisoned baby name in US history
- Every Guest Jon Stewart Ever Had On "The Daily Show"
- Should Travelers Avoid Flying Airlines That Have Had Crashes in the Past?
- Billion-Dollar Billy Beane

You will have in-class group work time during weeks 10–15 to work on this. This project will also require some work with your group outside of class. You

will be able to get feedback from me through weekly informal written reports in these weeks. I will also provide feedback and help during the in-class group work time.

The final group project will be graded with A through F, with the following point values (out of 30 possible):

- **30 points** for an A
- **25 points** for a B
- **20 points** for a C
- **15 points** for a D
- **10 points** for an F

If you turn nothing in, you will get **0 points**.

We will discuss expectations for this project, create groups, etc. around the middle of the semester. The focus for this will be on finding, cleaning, and using good data to answer an interesting question, and on presenting, summarizing, and explaining the data well.

0.6 Course set-up

Please be sure you have the latest version of R and RStudio installed. Also, be sure to sign up for a free GitHub account.

0.7 Helpful books for learning R

There are three publishers that are leaders in good books for learning R:

- O'Reilly
- No Starch Press
- Springer

Some particular books you might want to check out:

- R for Data Science
- R for Dummies
- R in a Nutshell
- R Cookbook
- R Graphics Cookbook
- A Beginner's Guide to R
- Roger Peng's Leanpub books

Books that other students have found useful include:

- Introductory R by Robert J. Knell

Part I

Part I: Preliminaries

R Preliminaries

Download a pdf of the lecture slides covering this topic.

0.8 R and R Studio

0.8.1 What is R?

R in an open-source programming language that evolved from the S language. The S language was developed at Bell Labs in the 1970s, which is the same place (and about the same time) that the C programming language was developed.

R itself was developed in the 1990s–2000s at the University of Auckland. It is open-source software, freely and openly distributed under the GNU General License. The base version of R that you download when you install R on your computer includes the critical code for running R, but you can also install and run "packages" that people all over the world have developed to extend R.

With new developments, R is becoming more and more useful for a variety of programming tasks. However, where it really shines is in working with data and doing statistical analysis. R is currently popular in a number of fields, including:

- Statistics
- Machine learning
- Data journalism / data analysis

R has some of the same strengths (quick and easy to code, interfaces well with other languages, easy to work interactively) and weaknesses (slower than compiled languages) as Python. For data-related tasks, R and Python are fairly neck-and-neck. However, R is still the first choice of statisticians in most fields, so I would argue that R has a an advantage if you want to have access to cutting-edge statistical methods.

> "The best thing about R is that it was developed by statisticians. The worst thing about R is that… it was developed by statisticians."
> -Bo Cowgill, Google, at the Bay Area R Users Group

0.8.2 Open-source software

R is open-source software. Many other popular statistical programming languages, conversely, are proprietary. It's useful to know what it means for software to be "open-source", both conceptually and in terms of how you will be able to use and add to R in your own work.

R is free, and it's tempting to think of open-source software just as "free software". Things, however, are a little more subtle than that. It helps to consider some different meanings of the word "free". "Free" can mean:

- *Gratis*: Free as in beer
- *Libre*: Free as in speech

Open-source software software is the *libre* type of free. This means that, with software that is open-source, you can:

- Access all of the code that makes up the software
- Change the code as you'd like for your own applications
- Build on the code with your own extensions
- Share the software and its code, as well as your extensions, with others

In practice, this means that, once you are familiar with the software, you can dig deeply into the code to figure out exactly how it's performing certain tasks. This can be useful for finding bugs and eliminating bugs, and also can help researchers figure out if there are any limitations in how the code works for their specific research.

It also means that you can build your own software on top of existing R software and its extensions. I explain a bit more about R packages a bit later, but this open-source nature of R (and other languages, including Python) has created a large community of people worldwide who develop and share extensions to R. As a result, you can pull in packages that let you do all kinds of things in R, like visualizing Tweets, cleaning up accelerometer data, analyzing complex surveys, fitting maching learning models, and a wealth of other cool things.

0.8.3 What is RStudio?

To get the R software, you'll download R from the R Project for Statistical Computing. This is enough for you to use R on your own computer. However, I would suggest one additional, free piece of software to improve your experience while working with R, RStudio.

RStudio is an integrated development environment (IDE) for R. This basically means that it provides you an interface for running R and coding in R, with a lot of nice extras that will make your life easier.

You download RStudio separately from R– you'll want to download and install R itself first, and then you can download RStudio. You want the Desktop version with the free license.

The company that develops this IDE is a fantastic contributer to the global R community. RStudio currently:

- Develops and freely provides the RStudio IDE
- Provides excellent resources for learning and using R (cheatsheets,)
- Is producing some of the most-used R packages
- Employs some of the top people in R development

R has been advancing by leaps in bounds in terms of what it can do and the elegance with which it does it, in large part because of the enormous contributions of people involved with RStudio.

0.8.4 Setting up

If do not already have them, you will need to download and install both R and RStudio.

- Go to CRAN and download the latest version of R for your system. Install.
- Go to the RStudio download page and download the latest version of RStudio for your system. Install.

Defaults should be fine for everything when you install both R and RStudio. You will want the latest stable version, rather than the development version, for this course.

0.9 The "package" system

0.9.1 R packages

Your original download of R is only a starting point. To me, this is a bit like the toy train set that my son was obsessed with for a while. You first buy a very basic set that looks something like Figure 1.

To take full advantage of R, you'll want to add on packages. In the case of the train set, at this point, a doting grandparent adds on extensively through birthday presents, so you end up with something that looks like Figure 2.

The main source for installing packages for R remains the Comprehensive R Archive Network, or CRAN. However, GitHub is growing in popularity, especially for packages that are still in development. You can also create and share packages among your collaborators or co-workers, without ever posting them publicly.

Figure 1: The toy version of base R.

Figure 2: The toy version of what your R set-up will look like once you find cool packages to use for your research.

Figure 3: Telephone keypad with letters corresponding to each number.

0.9.2 Installing from CRAN

The most popular place from which to get packages is currently CRAN. You can install packages from CRAN using R code. For example, telephone keypads include letters for each number (Figure 3), which allow companies to have "named" phone numbers that are easier for people to remember, like 1-800-GO-FEDEX and 1-800-FLOWERS.

The `phonenumber` package is a cool little package that will convert between numbers and letters based on the telephone keypad. Since this package is on CRAN, you can install the package to your computer using the `install.packages` function:

```
install.packages("phonenumber")
```

This downloads the package from CRAN and saves it in a special location on your computer where R can load it when you're ready to use it.

0.9.3 Loading an installed package

Once you have installed a package, it will be saved to your computer, but you won't be able to access it's functions until you load it in your R session. You can

load a package in an R session using the `library` function, with the package name inside the parentheses.

```
library(phonenumber)
```

One thing that people often find confusing when they start using R is knowing when to use and not use quotation marks. The general rule is that you use quotation marks when you want to refer to a character string literally, but no quotation marks when you want to refer to the value in a previously-defined object. For example, if you saved the string `"Anderson"` as the object `my_name` (`my_name <- "Anderson"`), then in later code, if you type `my_name` (no quotation marks), you'll get `"Anderson"`, while if you type out `"my_name"` (with quotation marks), you'll get `"my_name"` (what you typed, literally).

One thing that makes this rule confusing is that there are a few cases in R where you really should (by this rule) use quotation marks, but the function is coded to let you be lazy and get away without them. One example is the `library` function. In the above code, you want to literally load the package "phonenumber", rather than load whatever character string is saved in the object named `phonenumber`. However, `library` is one of the functions where you can be lazy and skip the quotation marks, and it will still load "phonenumber" for you (although, if you want, this function also works if you follow the rule and call `library("phonenumber")` instead).

Once a package is loaded, you can use all its exported (i.e., public) functions by calling them directly. For example, the `phonenumber` has a function called `letterToNumber` that converts a character string to a number. Once you've loaded `phonenumber` using `library`, you can use this function in your R session:

```
fedex_number <- "GoFedEx"
letterToNumber(fedex_number)
```

```
## [1] "4633339"
```

R vectors can have several different *classes*. One common class is the character class, which is the class of the character string we're using here ("GoFedEx"). You'll always put character strings in quotation marks. Another key class is numeric (numbers). Later in the course, we'll introduce other classes that vectors can have, including factors and dates.

0.10 Basic code conventions of R

0.10.1 R's MVP: The *gets arrow*

The *gets arrow*, `<-`, is R's assignment operator. It takes whatever you've created on the right hand side of the `<-` and saves it as an object with the name you put on the left hand side of the `<-`. The basic structure of a call with a gets arrow looks like this:

```
## Note: Generic code
[name of object] <- [thing I want to save]
```

Sometimes, we'll show "generic" code in a code block, that doesn't actually work if you put it in R, but instead shows the generic structure of an R call. We'll try to always include a comment with any generic code, so you'll know not to try to run it in R.

For example, if I just type `"GoFedEx"` at the R prompt, R will print that string back to me, but won't save it anywhere for me to use later:

```
"GoFedEx"
```

```
## [1] "GoFedEx"
```

However, if I assign `"GoFedEx"` to an object using a gets arrow, I can print it out or use it later by typing ("referencing") that object name:

```
fedex_number <- "GoFedEx"
fedex_number
```

```
## [1] "GoFedEx"
```

```
letterToNumber(fedex_number)
```

```
## [1] "4633339"
```

0.10.2 Assignment operator wars: <- vs. =

You can make assignments in R using either the gets arrow (`<-`) or `=`. When you read other people's code, you'll see both. R gurus advise using `<-` rather than `=` when coding in R, and as you move to doing more complex things, some subtle problems might crop up if you use `=`. I have heard from someone in the know that you can tell the age of a programmer by whether he or she uses the gets arrow or `=`, with `=` more common among the young and hip. For this course, however, I am asking you to code according to Hadley Wickham's R style guide, which specifies using the gets arrow for assignment.

While you will be coding with the gets arrow exclusively in this course, it will be helpful for you to know that the two assignment arrows do pretty much the same thing:

```
one_to_ten <- 1:10
one_to_ten
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10
```

```
one_to_ten = 1:10
one_to_ten
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10
```

0.10.3 Naming objects

When you assign objects, you will need to choose names for them. This object name is what you will type later in your code to reference the object and use it in functions, figures, etc. For example, with the following code, I am assigning the character string "GoFedEx" to an object that I am naming `fedex_number`:

```
fedex_number <- "GoFedEx"
```

There are only two fixed rules for naming objects in R:

- Use only letters, numbers, and underscores
- Don't start with anything but a letter

In addition to these fixed rules, there are also some guidelines for naming objects that you should adopt now, since they will make your life easier as you advance to writing more complex code in R. The following three guidelines for naming objects are from Hadley Wickham's R style guide:

- Use lower case for variable names (`fedex_number`, not `FedExNumber`)
- Use an underscore as a separator (`fedex_number`, not `fedex.number` or `fedexNumber`)
- Avoid using names that are already defined in R (e.g., don't name an object `mean`, because a function named `mean` already exists)

Another good practice is to name objects after nouns (e.g., `fedex_number`) and later, when you start writing functions, name those after verbs (e.g., `call_fedex`). You'll want your object names to be short enough that they don't take forever to type as you're coding, but not so short that you can't remember what they stand for.

Sometimes, you'll want to create an object that you won't want to keep for very long. For example, you might want to create a small object to test some code, but you plan to not need the object again once you've done that. You may want to come up with some short, generic object names that you use for these kinds of objects, so that you'll know that you can delete them without problems when you want to clean up your R session.

There are all kinds of traditions for these placeholder variable names in computer science. `foo` and `bar` are two popular choices, as are, evidently, `xyzzy`, `spam`, `ham`, and `norf`. There are different placeholder names in different languages: for example, `toto`, `truc`, and `azerty` (French); and `pippo`, `pluto`, `paperino` (Disney character names; Italian). See the Wikipedia page on metasyntactic variables to find out more.

0.10.4 Commenting code

Sometimes, you'll want to include notes in your code. You can do this in all programming languages by using a *comment character* to start the line with your comment. In R, the comment character is the hash symbol, `#`. R will skip any line that starts with `#` in a script. For example, if you run the following code:

```
# Don't print this.
"But print this"
```

```
## [1] "But print this"
```

R will only print the second, uncommented line.

You can also use a comment in the middle of a line, to add a note on what you're doing in that line of the code. R will skip any part of the code from the hash symbol on. For example:

```
"Print this" ## But not this, it's a comment.
```

```
## [1] "Print this"
```

0.11 R's most basic object types

An R *object* stores some type of data that you want to use later in your R code, without fully recreating it. The content of R objects can vary from very simple (the `"GoFedEx"` string in the example code above) to very complex objects with lots of elements (for example, a machine learning model).

There are a variety of different object types in R, shaped to fit different types of objects ranging from the simple to complex. In this section, we'll start by describing two object types that you will use most often in basic data analysis, **vectors** (1-dimensional objects) and **dataframes** (2-dimensional objects).

0.11.1 Vectors

To get an initial grasp of the *vector* object type in R, think of it as a 1-dimensional object, or a string of values. All values in a vector must be of the same class (i.e., all numbers, all characters, all dates). If you try to create a vector with elements from different classes (like "FedEx", which is a character, and 3, a number), R will coerce all of the elements to the most generic class of any of the elements (i.e., "FedEx" and "3" will both become characters, since "3" can be changed to a character, but "FedEx" can't be changed to a number).

To create a vector from different elements, you'll use the concatenation function, `c` to join them together, with commas between the elements. For example, to create a vector with the first five elements of the Fibonacci sequence, you can run:

```
fibonacci <- c(1, 1, 2, 3, 5)
fibonacci
```

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

Here is an example of creating a vector using elements with the character class instead of numbers (note the quotation marks used around each element for character strings):

```
one_to_five <- c("one", "two", "three", "four", "five")
one_to_five
```

```
## [1] "one"   "two"   "three" "four"  "five"
```

If you mix classes when you create the vector, R will coerce all the elements to most generic of the elements' classes:

```
mixed_classes <- c(1, 3, "five")
mixed_classes
```

```
## [1] "1"    "3"    "five"
```

A vector's *length* is the number of elements in the vector. You can use the `length` function to determine a vector's length:

```
length(mixed_classes)
```

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

Once you create an object, you will often want to reference the whole object in future code. However, there will be some times when you'll want to reference just certain elements of the object (for example, the first three values). You can pull out certain values from a vector by using indexing with square brackets (`[...]`) to identify the locations of the elements you want to pull, with a numeric vector inside the brackets that lists the numbered positions of the elements you want to get:

```
fibonacci[2] # Get the second value
```

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

```
fibonacci[c(1, 5)] # Get first and fifth values
```

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

```
fibonacci[1:3] # Get the first three values
```

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

You can also use logic to pull out some values of a vector. For example, you might only want to pull out even values from the `fibonacci` vector. We'll cover using logical statements to index vectors later in the book.

0.11.2 Dataframes

A dataframe is a 2-dimensional object, and is made of one or more vectors of the same length stuck together side-by-side. It is the closest R has to an Excel spreadsheet-type structure. You can create dataframes using the `data.frame` function. However, most often you will create a dataframe by reading in data from a file, using something like `read.csv`.

To create a dataframe using `data.frame`, in this case by sticking together vectors you already have saved as R objects, you can run:

```
fibonacci_seq <- data.frame(num_in_seq = one_to_five,
                            fibonacci_num = fibonacci)
fibonacci_seq
```

```
##   num_in_seq fibonacci_num
## 1        one             1
## 2        two             1
## 3      three             2
## 4       four             3
## 5       five             5
```

Note that this call requires that the `one_to_five` and `fibonacci` vectors are the same length, although they don't have to be (and in this case aren't) the same class of objects (`one_to_five` is a character class, `fibonacci` is numeric).

You can also create a dataframe using `data.frame` even if you don't have the vectors for the columns saved as objects. Instead, in this case, you can put the vector assignment directly within the `data.frame` call:

```
fibonacci_seq <- data.frame(num_in_seq = c("one", "two", "three",
                                           "four", "five"),
                            fibonacci_num = c(1, 1, 2, 3, 5))
fibonacci_seq
```

```
##   num_in_seq fibonacci_num
## 1        one             1
## 2        two             1
## 3      three             2
## 4       four             3
## 5       five             5
```

You can put more than one function call in a single line of R code, as in this example (the `c` creates a vector, while the `data.frame` creates a dataframe, using the vectors created by the calls to `c`). When you use multiple functions within a single R call, R will evaluate starting from the inner-most parentheses out, much like the order of operations in a math equation with parentheses.

The general format for using `data.frame` is:

```
## Note: Generic code
[name of object] <- data.frame([1st column name] = [1st column content],
                               [2nd column name] = [2nd column content])
```

with an equals sign between the column name and column content for each column, and commas between each of the columns.

You can use square-bracket indexing (`[..., ...]`) for dataframes, too, but now they'll have two dimensions (rows, then columns). Put the rows you want before the comma, the columns after. If you want all of something (e.g., all rows in the dataframe), leave the designated spot blank. Here are two examples of using square-bracket indexing to pull a subset of the `fibonacci_seq` dataframe we created above:

```
fibonacci_seq[1:2, 2] # First two rows, second column
```

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

```
fibonacci_seq[5, ] # Last row, all columns
```

```
##   num_in_seq fibonacci_num
## 5       five             5
```

If you forget to put the comma in the indexing for a dataframe (e.g., `fibonacci_seq[1:2]`), you will index out the *columns* that fall at that position or positions. To avoid confusion, I suggest that you always use indexing with a comma when working with dataframes.

So far, we've only shown how to create dataframes from scratch within an R session. Usually, however, you'll create R dataframes instead by reading in data from an outside file using `read.csv` and related functions. For example, you might want to analyze data on all the guests that came on the *Daily Show*, *circa* Jon Stewart. If you have this data in a comma-separated (csv) file on your computer called "daily_show_guests.csv", you can read it into your R session with the following code:

```
daily_show <- read.csv("daily_show_guests.csv",
                       header = TRUE,
                       skip = 4)
```

In this code, the `read.csv` function is reading in the data from "daily_show_guests", while the gets arrow (`<-`) assigns that data to the object `daily_show`, which you can then reference in later code to explore and plot the data.

Once you've read in the data and saved the resulting dataframe as an object, you can use square-bracket indexing to look at the first two rows in the data:

```
daily_show[1:2, ]
```

```
##   YEAR GoogleKnowlege_Occupation    Show  Group  Raw_Guest_List
## 1 1999                    actor 1/11/99 Acting  Michael J. Fox
## 2 1999                 Comedian 1/12/99 Comedy Sandra Bernhard
```

You can use the functions `dim`, `nrow`, and `ncol` to figure out the dimensions (number of rows and columns) of a dataframe:

```
dim(daily_show)
```

```
## [1] 2693    5
```

```
nrow(daily_show)
```

```
## [1] 2693
```

```
ncol(daily_show)
```

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

0.12 Using R functions

0.12.1 Function structure

In general, functions in R take the following structure:

```
## Generic code
function.name(parameter 1 = argument 1, parameter 2 = argument 2,
              parameter 3 = argument 3)
```

The result of the function will be output to your R session, unless you choose to save the output in an object:

```
## Generic code
new_object <- function.name(parameter 1 = argument 1,
                            parameter 2 = argument 2,
                            parameter 3 = argument 3)
```

Here are some example function calls, to give you examples of this structure:

```
head(daily_show)
```

```
##   YEAR GoogleKnowlege_Occupation    Show  Group   Raw_Guest_List
## 1 1999                    actor 1/11/99 Acting   Michael J. Fox
## 2 1999                 Comedian 1/12/99 Comedy  Sandra Bernhard
## 3 1999        television actress 1/13/99 Acting    Tracey Ullman
## 4 1999              film actress 1/14/99 Acting Gillian Anderson
## 5 1999                    actor 1/18/99 Acting David Alan Grier
## 6 1999                    actor 1/19/99 Acting  William Baldwin
```

```
head(daily_show, n = 3)
```

```
##   YEAR GoogleKnowlege_Occupation    Show  Group  Raw_Guest_List
## 1 1999                    actor 1/11/99 Acting  Michael J. Fox
## 2 1999                 Comedian 1/12/99 Comedy Sandra Bernhard
## 3 1999        television actress 1/13/99 Acting   Tracey Ullman
```

```
daily_show <- read.csv("daily_show_guests.csv",
                       skip = 4,
                       header = TRUE)
```

Within the function call, *parameters* allow you to customize the function to run in a certain way (e.g., use a certain dataframe as an input, give output in a certain format). Some function parameters will have *default arguments*, which means that you don't have to put a value for that parameter for the function to run, but you can if you want the function to do something other than the default.

0.12.2 Function help files

You can find out more about a function, include what parameters it has and what the default values, if any, are by using `?` before the function name in the R console. For example, to find out more about the `read.csv` command, run:

```
?read.csv
```

From the "Usage" section of the help file, you can figure out that the only required parameter is `file`, the pathname of the file that you want to read in, since this is the only argument in the "Usage" example without an argument value:

```
read.csv(file, header = TRUE, sep = ",", quote = "\"",
         dec = ".", fill = TRUE, comment.char = "", ...)
```

You can also see from this "Usage" section that the default value of `header` is `TRUE`, the default value of `sep` is a comma, etc.

The "Arguments" section explains each of the parameters, and possible arguments that each can take. For example, here is the explanation of the `nrows` parameter in the `read.csv` function:

```
integer: the maximum number of rows to read in. Negative and other
    invalid values are ignored.
```

From this, you can determine that you should put in a whole number, 1 or higher, and the function will only read in that many lines of the dataframe when you run `read.csv`.

0.12.3 Function parameters

Each function parameter has a name (e.g., `nrows`, `header`, `file`). The safest way to call a function in R is to use the structure `parameter name = argument value` for every parameter, like this:

```
head(x = daily_show, n = 3)
```

However, you can also give argument values by position. For example, in the `head` function, the first parameter is `x`, the object you want to look at, and the second is `n`, the number of elements you want to include when you look at the object. If you know this, you can call `head` using the shorter call:

```
head(daily_show, 3)
```

If you use position alone, you will have problems if you don't include arguments in exactly the right order. However, if you use parameter names to set each argument, it doesn't matter what order you include arguments when calling a function:

```
# These two calls return the exact same object
head(x = daily_show, n = 3)
head(n = 3, x = daily_show)
```

Because code tends to be more robust to errors when you use parameter names to set arguments, we recommend against using position, rather than name, to give arguments when calling functions, at least while you're learning R. It's too easy to forget the exact order and get errors in your code. However, there is one exception– the first argument to a function is almost always required (i.e., there's not a default value), and you very quickly learn what the first parameter of most functions are as soon as you start using the function regularly. Therefore, it's fine to use position alone to specify the first argument in a function, but for now always use the parameter name to set any later arguments:

```
head(daily_show, n = 3)
```

Using the full parameter names for arguments can take a bit more time, since it requires more typing. However, RStudio helps you out with that by offering *code completion*. Once you start typing the first few letters of a parameter name within a function call, try pressing the tab key. All possible arguments that start with those letters should show up, and you can scroll through to pick the right one, or keep typing until the argument you want is atnthe top of the list of choices, and then press the tab key again.

0.13 In-course Exercise

0.13.1 About the dataset

For today's class, you'll be using a dataset of all the guests on Jon Stewart's *The Daily Show*. This data was originally collected by Nate Silver's website,

FiveThirtyEight and is available on FiveThirtyEight's GitHub page under the Creative Commons Attribution 4.0 International License. The only change made to the original file was to add (commented) attribution information at the start of the file.

First, check out a bit more about this data and its source:

- Check out the Creative Commons license. What are we allowed to do with this data? What restrictions are there on using the data?
- It's often helpful to use prior knowledge to help check out or validate your dataset. One thing we might want to know about this data is if it covers the whole time that Jon Stewart hosted *The Daily Show*. Find out the dates he started and finished as host.
- Briefly browse around FiveThirtyEight's GitHub data page. What are some other datasets available that you find interesting? You can scroll to the bottom of the page to get to the compiled README.md content, which gives the full titles and links to relevant datasets. You can also click on any dataset to get more information.
- Look at the GitHub page for this *Daily Show* data. How many columns will be in this dataset? What kind of information does the data include?

In this exercise, you're using data posted by FiveThirtyEight on GitHub. We'll be using a lot of data that's on GitHub this semester, and GitHub is being used behind-the-scenes for both this book and the course note slides. We'll talk more about GitHub later, but you might find it interesting to explore a bit now. It's a place where people can post, work on, and share code in a number of programming languages– it's been referred to as "Facebook for Nerds". You can search GitHub repositories and code specifically by programming language, so it can be a good way to find example R code from which to learn.

If you have extra time:

- Check out the related article on FiveThirtyEight. What are some specific questions they used this data to answer for this article?
- Who is Nate Silver?

0.13.2 Getting the data onto your computer

First, download the data from GitHub onto your computer. Make a directory (folder) on your computer specifically for this course (I strongly recommend that you put it somewhere where the file path will not have any spaces in it– for

example, putting it in your home directory, under the name "R_Prog_Course" would be great. Putting it in a directory called "R Prog Course" would not.). Put the *Daily Show* data in your directory for this course.

Take the following steps to get the data onto your computer

- If you do not yet have a directory (folder) just for this course, make one someplace straightforward like in your home directory. Do not use any spaces in the directory name.
- Download the file from GitHub. Right click on `Raw` and then choose "Download linked file". Put the file into the directory you created for this course.
- Find out what your home directory is in R. To do this, make sure R is set to your home directory using `setwd("~")`, and then get R to print that home directory path using `getwd()`.
- Outside of R, open Finder (or your system's equivalent). Go to your home directory (mine, for example, is `/Users/brookeanderson`). Figure out how to get from your home directory to the directory you created for this course. For example, from my home directory, I would go `RProgrammingForResearch` to `data`.
- Go back into R. Set R's working directory to your directory for this class using the `setwd` command, now that you know the pathname for the directory. For example, I would use `setwd("~/RProgrammingForResearch/data")`.
- Use the `list.files` command to make sure that the "daily_show_guests.csv" file is in your current working directory.

The full R code for this task might look something like:

```
setwd("~")
getwd()

setwd("~/RProgrammingForResearch/data")
getwd()

list.files()

"daily_show_guests.csv" %in% list.files()
```

If you have extra time:

- See if you can figure out the last line of code in the example R code.

0.13.3 Getting the data into R

Now that you have the dataset in your working directory, you can read it into R. This dataset is in a *.csv* (comma separated values) format. (We will talk more about different file formats next week.) You can read csv files into R using the `read.csv` function.

Read the data into your R session

- Use the `read.csv` function to read the data into R and save it as the object `daily_show`.
- Use the help file for the `read.csv` function to figure out how this function works. To pull that up, use `?read.csv`. Why are we using the option `header = TRUE`? Can you figure out why we're using the `skip` option, and why it's set to 4?
- Note that you need to put the file name in quotation marks.
- What would have happened if you'd used `read.csv` but hadn't saved the result as the object `daily_show`? (For example, you'd run the code `read.csv("daily_show_guests.csv")` rather than `daily_show <- read.csv("daily_show_guests.csv")`.)

Example R code:

```
daily_show <- read.csv("daily_show_guests.csv", header = TRUE, skip = 4)
```

If you have extra time:

- Say this was a really big dataset. You want to check out just the first 10 rows to make sure that you've got your code right before you take the time to pull in the whole dataset. Use the help file for `read.csv` to figure out how to only read in a few rows.
- Look through the help file for other options available for `read.csv`. Can you think of examples when some of these options would be useful?

Example R code:

```
daily_show_first10 <- read.csv("daily_show_guests.csv", header = TRUE,
                               skip = 4, nrows = 10)
daily_show_first10
```

0.13.4 Checking out the data

You now have the data available in the `daily_show` option. You'll want to check it out to make sure it read in correctly, and also to get a feel for the data. Throughout, you can use the help pages to figure out more about any of the functions being used (for example, `?dim`).

Take the following steps to check out the dataset

- Use indexing to look at the first two rows of the dataset. Based on this, what does each row "measure"? What information do you get for each "measurement"? As a reminder, indexing uses square brackets immediately after the object name. If the object has two dimensions, like a dataframe (rows and columns), you put the rows you want, then a comma, then the columns you want. If you want all rows (or columns), you leave that space blank. For example, if you wanted to get the first two rows and the first three columns, you'd use `daily_show[1:2, 1:3]`. If you wanted to get the first five rows and all the columns, you'd use `daily_show[1:5, ]`.
- Use the `dim` function to find out how many rows and columns this dataframe has. Based on what you found out about the data from the GitHub page, does it have the number of columns you expected? Based on what you know about the data (all the guests who came on The Daily Show with Jon Stewart), do you think it has about the right number of rows?
- Use the `head` function to look at the first few rows of the dataframe. Does it look like the rows go in order by date? What was the date of Jon Stewart's first show? Does it look like this dataset covers that first show?
- Use the `tail` function to look at the last few rows of the dataframe. What is the last show date covered by the dataframe? Who was the last guest?

Example R code:

```
daily_show[1:2, ]
dim(daily_show)
head(daily_show)
tail(daily_show)
```

If you have extra time:

- Say you wanted to look at the first ten rows of the dataframe, rather than the first six. How could you use an option with `head` to do this?

Example R code:

```
head(daily_show, n = 10)
```

0.13.5 Using the data to answer questions

Nate Silver was a guest on *The Daily Show*. Let's use this data to figure out how many times he was a guest and when he was on the show.

Find out more about Nate Silver on The Daily Show

- Use the `subset` function to create a new dataframe that only has the rows of `daily_show` when Nate Silve was a guest. Put it in the object `nate_silver`.
- Print out the full `nate_silver` dataframe by typing `nate_silver`. (You could just use this to answer both questions, but still try the next steps. They would be important with a bigger dataset.)
- To count the number of times Nate Silver was a guest, you'll need to count the number of rows in the new dataset. You can either use the `dim` function or the `nrow` function to do this. What additional information does the `dim` function give you?
- To get the dates when Nate Silver was a guest, you can print out just the `Show` column of the dataframe. There are a few ways you can do this using indexing: `nate_silver[ , 3]` (since `Show` is the third column), `nate_silver[ , "Show"]`, or `nate_silver$Show`. Try these.

Example R code:

```
nate_silver <- subset(daily_show,
                      Raw_Guest_List == "Nate Silver")
nate_silver
dim(nate_silver)
nrow(nate_silver)
nate_silver[ , 3]
nate_silver[ , "Show"]
```

If you have extra time:

- When you print out the `Show` column, why does it also print out something underneath about Levels? Hint: This has to do with the class that R has saved this column as. What class is it currently? What other classes might we want to consider converting it to as we continue working with the dataset? Check out the example code below to get some ideas.

- Was Nate Silver the only statistician to be a guest on the show?
- What were the occupations that were only represented by one guest visit? Since `GoogleKnowlege_Occupation` is a factor, you can use the `table` function to create a new vector with the number of times each value of `GoogleKnowlege_Occupation` shows up. You can put this information into a new vector and then pull out only the values that equal 1 (so, only had one guest). (Note that "Statistician" doesn't show up– there was only one person who was a guest, but he had three visits.) Pick your favorite "one-off" example and find out who the guest was for that occupation.

Example R code:

```
class(nate_silver$Show)
```

```
range(nate_silver$Show)
```

```
nate_silver$Show <- as.Date(nate_silver$Show,
                            format = "%m/%d/%y")
range(nate_silver$Show)
diff(range(nate_silver$Show)) # Time between Nate's first and last shows
```

```
statisticians <- subset(daily_show,
                        GoogleKnowlege_Occupation == "Statistician")
statisticians
```

```
num_visits <- table(daily_show[ , 2])
head(num_visits) # Note: This is a vector rather than a dataframe
names(num_visits[num_visits == 1])
subset(daily_show, GoogleKnowlege_Occupation == "chess player")
subset(daily_show, GoogleKnowlege_Occupation == "mathematician")
subset(daily_show, GoogleKnowlege_Occupation == "orca trainer")
subset(daily_show, GoogleKnowlege_Occupation == "Puzzle Creator")
subset(daily_show, GoogleKnowlege_Occupation == "Scholar")
```

Part II

Part II: Basics

Entering and cleaning data #1

Download a pdf of the lecture slides covering this topic.

There are four basic steps you will often repeat as you prepare to analyze data in R:

1. Identify where the data is (If it's on your computer, which directory? If it's online, what's the url?)
2. Read data into R (`read.csv`, `read.table`) using the file path you figured out in step 1
3. Check to make sure the data came in correctly (`dim`, `head`, `tail`, `str`)
4. Clean the data up

In this chapter, I'll go basics for each of these steps, as well as dive a bit deeper into some related topics you should learn now to make your life easier as you get started using R for research.

0.14 R scripts

This is a good point in learning R for you to start putting your work in R scripts, rather than entering commands at the console.

An R script is a plain text file where you can save a series of R commands. You can save the script and open it up later to see (or re-do) what you did earlier, just like you could with something like a Word document when you're writing a paper.

To open a new R script in RStudio, go to the menu bar and select "File" -> "New File" -> "R Script". Alternatively, you can use the keyboard shortcut Command-Shift-N. Figure 4 gives an example of an R script file opened in RStudio and points out some interesting elements.

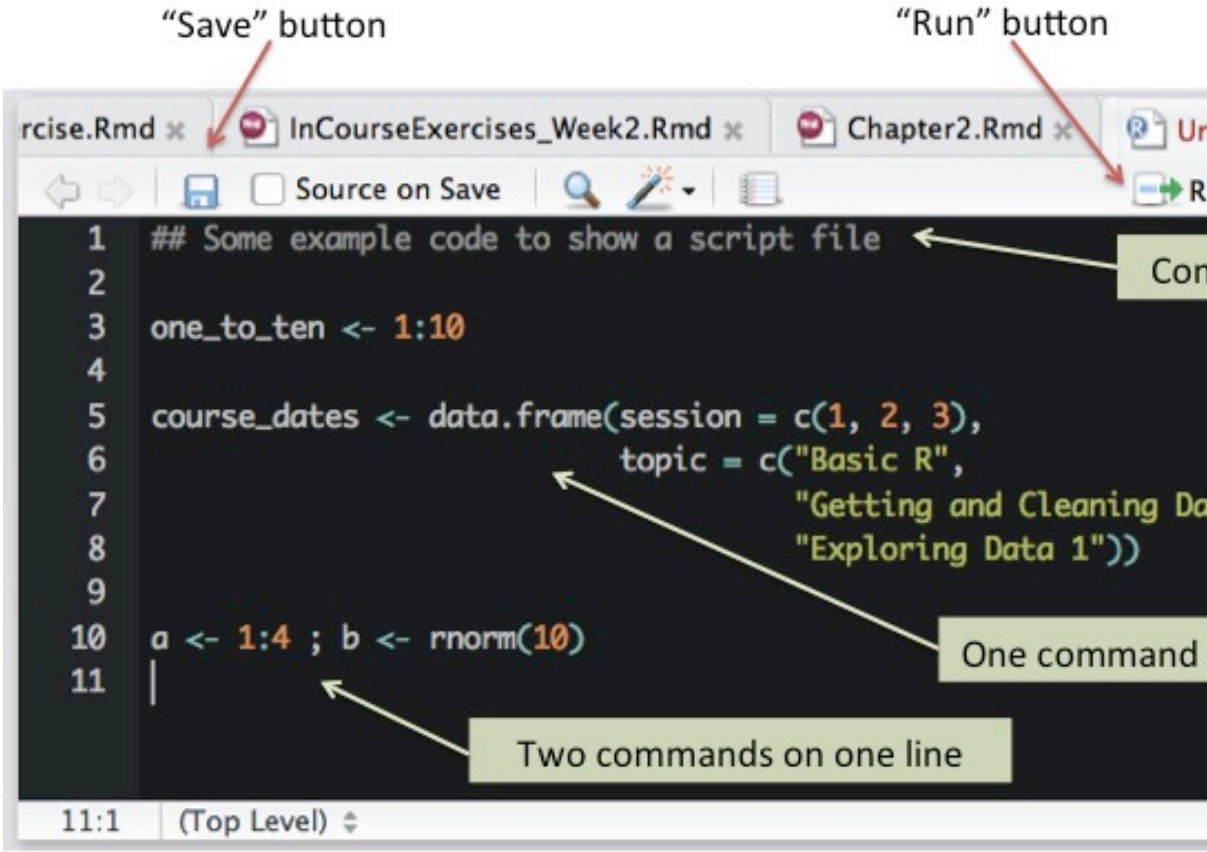


Figure 4: Example of an R script in RStudio.

To save a script you're working on, you can click on the "Save" button (which looks like a floppy disk) at the top of your R script window in RStudio or use the keyboard shortcut Command-S. You should save R scripts using a ".R" file extension.

Within the R script, you'll usually want to type your code so there's one command per line. If your command runs long, you can write a single call over multiple lines. It's unusual to put more than one command on a single line of a script file, but you can if you separate the commands with semicolons (`;`). These rules all correspond to how you can enter commands at the console.

Running R code from a script file is very easy in RStudio. You can use either the "Run" button or Command-Return, and any code that is selected (i.e., that you've highlighted with your cursor) will run at the console. You can use this functionality to run a single line of code, multiple lines of code, or even just part of a specific line of code. If no code is highlighted, then R will instead run all the code on the line with the cursor and then move the cursor down to the next line in the script.

You can also run all of the code in a script. To do this, use the "Source" button at the top of the script window. You can also run the entire script either from the console or from within another script by using the `source()` function, with the filename of the script you want to run as the argument. For example, to run all of the code in a file named "MyFile.R" that is saved in your current working directory, run:

```
source("MyFile.R")
```

You can add comments into an R script to let others know (and remind yourself) what you're doing and why. To do this, use R's comment character, `#`. Any line on a script line that starts with `#` will not be read by R. You can also take advantage of commenting to comment out certain parts of code that you don't want to run at the moment.

While it's generally best to write your R code in a script and run it from there rather than entering it interactively at the R console, there are some exceptions. A main example is when you're initially checking out a dataset, to make sure you've read it in correctly. It often makes more sense to run commands for this task, like `str()`, `head()`, `tail()`, and `summary()`, at the console. These are all examples of commands where you're trying to look at something about your data **right now**, rather than code that builds toward your analysis, or helps you read in or clean up your data.

0.15 Directories and pathnames

0.15.1 Directory structure

It seems a bit of a pain and a bit complex to have to think about computer directory structure in the "basics" part of this class, but this structure is not terribly complex once you get the idea of it. There are a couple of very good reasons why it's worth learning now.

First, many of the most frustrating errors you get when you start using R trace back to understanding directories and filepaths. For example, when you try to read a file into R using only the filename, and that file is not in your current working directory, you will get an error like:

```
Error in file(file, "rt") : cannot open the connection
In addition: Warning message:
In file(file, "rt") : cannot open file 'Ex.csv': No such file or directory
```

This error is especially frustrating when you're new to R because it happens at the very beginning of your analysis – you can't even get your data in. Also, if you don't understand a bit about working directories and how R looks for the file you're asking it to find, you'd have no idea where to start to fix this error.

Second, once you understand how to use pathnames, especially relative pathnames, to tell R how to find a file that is in a directory other than your working directory, you will be able to organize all of your files for a project in a much cleaner way. For example, you can create a directory for your project, then create one subdirectory to store all of your R scripts, and another to store all of your data, and so on. This can help you keep very complex projects more structured and easier to navigate. We'll talk about these ideas more in the course sections on Reproducible Research, but it's good to start learning how directory structures and filepaths work early.

Your computer organizes files through a collection of directories. Chances are, you are fairly used to working with these in your daily life already (although you may call them "folders" rather than "directories"). For example, you've probably created new directories to store data files and Word documents for a specific project.

Figure 5 illustrates the file directory structure on my computer. (Note that I have omitted many, many additional files and directories – this just shows an example of a few directories and files and how they are structured together). Directories are shown in blue, and files in green.

You can notice a few interesting things from Figure 5. First, you might notice the structure includes a few of the directories that you use a lot on your own computer, like `Desktop`, `Documents`, and `Downloads`. Next, the directory at the

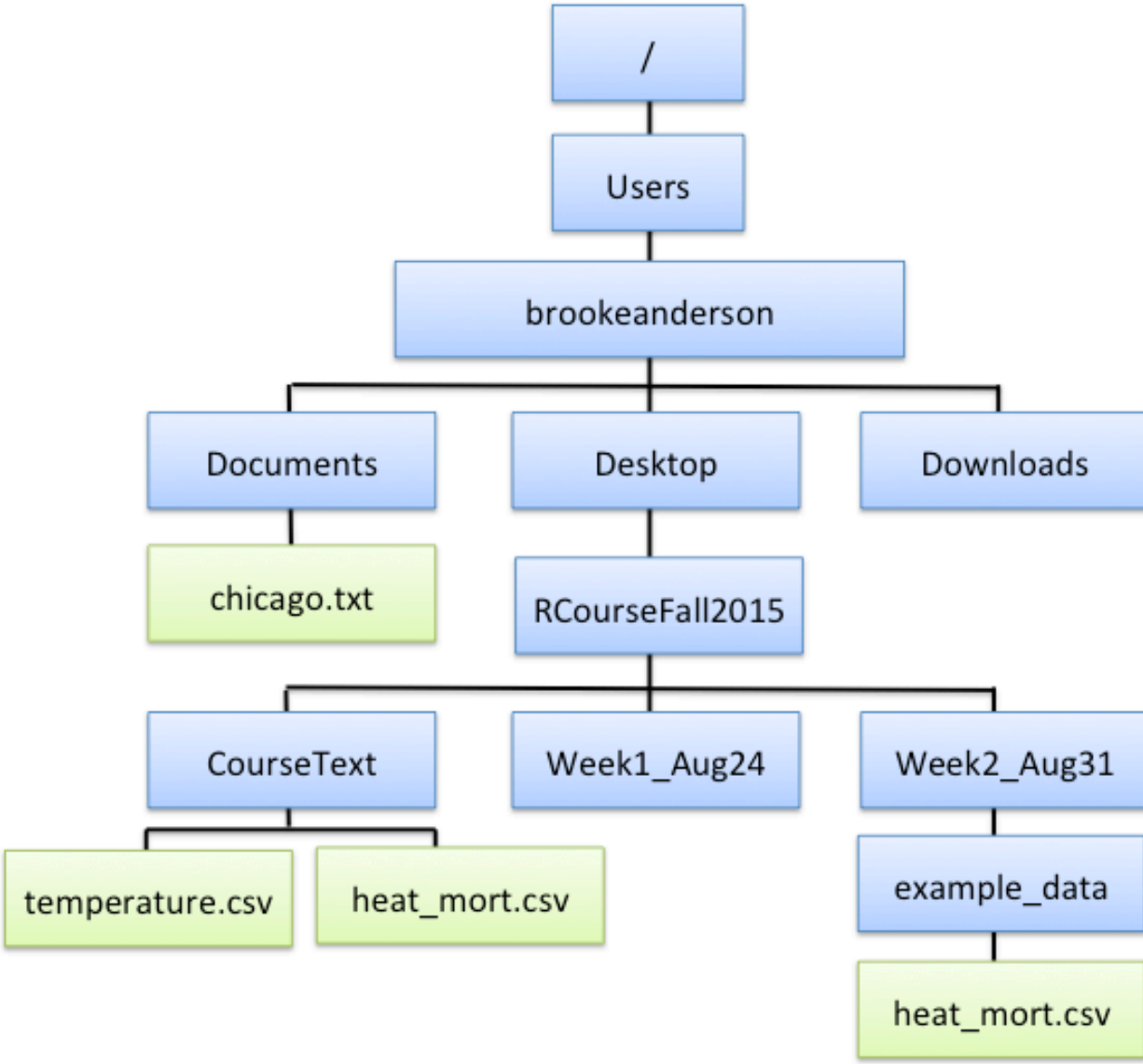


Figure 5: An example of file directory structure.

very top is the computer's root directory, `/`. For a PC, the root directory might something like `C:`; for Unix and Macs, it's usually `/`. Finally, if you look closely, you'll notice that it's possible to have different files in different locations of the directory structure with the same file name. For example, in the figure, there are files names `heat_mort.csv` in both the `CourseText` directory and in the `example_data` directory. These are two different files with different contents, but they can have the same name as long as they're in different directories. This fact – that you can have files with the same name in different places – should help you appreciate how useful it is that R requires you to give very clear directions to describe exactly which file you want R to read in, if you aren't reading in something in your current working directory.

You will have a home directory somewhere near the top of your structure, although it's likely not your root directory. My home directory is `/Users/brookeanderson`. I'll describe just a bit later how you can figure out what your own home directory is on your own computer.

0.15.2 Working directory

When you run R, it's always running from within some working directory, which will be one of the directories somewhere in your computer's directory structure. At any time, you can figure out which directory R is working in by running the command `getwd()` (short for "get working directory"). For example, my R session is currently running in the following directory:

```
getwd()
```

```
## [1] "/home/travis/build/geanders/RProgrammingForResearch"
```

This means that, for my current R session, R is working in the `RProgrammingForResearch` subdirectory of my `brookeanderson` directory (which is my home directory).

There are a few general rules for which working directory R will start in when you open an R session. These are not absolute rules, but they're generally true. If you have R closed, and you open it by double-clicking on an R script, then R will generally open with, as its working directory, the directory in which that script is stored. This is often a very convenient convention, because often any of the data you'll be reading in for that script is somewhere near where the script file is saved in the directory structure.

If you open R by double-clicking on the R icon in "Applications" (or something similar on a PC), R will start in its default working directory. You can find out what this is, or change it, in RStudio's "Preferences". I have never had a compelling reason to change this on my own computer, as I find it very easy to just

move around the directories and set a new working directory using pathnames and the `setwd()` function.

Finally, later in the course, we'll talk about using R Projects from within RStudio. If you open an R Project, R will start in that project's working dirctory (the directory in which the `.Rproj` file for the project is stored).

0.15.3 File and directory pathnames

Once you get a picture of how your directories and files are organized, you can use pathnames, either absolute or relative, to move around the directories, set a different working directory, and read in files from different directories than your current working directory. Pathnames are the directions for getting to a directory or file stored on your computer.

When you want to reference a directory or file, you can use one of two types of pathnames:

- *Relative pathname*: How to get to the file or directory from your current working directory
- *Absolute pathname*: How to get to the file or directory from anywhere on the computer

Absolute pathnames are a bit more straightforward conceptually, because they don't depend on your current working directory. However, they're also a lot longer to write, and they're much less convenient if you'll be sharing some of your code with other people who might run it on their own computers. I'll explain this second point a bit more later in this section.

Absolute pathnames give the full directions to a directory or file, starting all the way at the root directory. For example, the `heat_mort.csv` file in the `CourseText` directory has the absolute pathname:

```
"/Users/brookeanderson/Desktop/RCourseFall2015/CourseText/heat_mort.csv"
```

You can use this absolute pathname to read this file in using `read.csv`. This absolute pathname will *always* work, regardless of your current working directory, because it gives directions from the root – it will always be clear to R exactly what file you're talking about. Here's the code to use to read that file in using the `read.csv` function with the file's absolute pathname:

```
heat_mort <- read.csv("/Users/brookeanderson/Desktop/RCourseFall2015/CourseText/heat_mort.csv")
```

The *relative pathname*, on the other hand, gives R the directions for how to get to a directory or file from the current working directory. If the file or directory you're looking for is pretty close to your current working directory in your directory structure, then a relative pathname can be a much shorter way to tell R how to get to the file than an absolute pathname. However, the relative pathname depends on your current working directory – the relative pathname that works perfectly when you're working in one directory will not work at all once you move into a different working directory.

As an example of a relative pathname, say you're working in the directory `RCourseFall2015` within the file structure shown in Figure 5, and you want to read in the `heat_mort.csv` file in the `CourseText` directory. To get from `RCourseFall2015` to that file, you'd need to look in the subdirectory `CourseText`, where you could find `heat_mort.csv`. Therefore, the relative pathname from your working directory would be:

```
"CourseText/heat_mort.csv"
```

You can use this relative pathname to tell R where to find and read in the file:

```
heat_mort <- read.csv("CourseText/heat_mort.csv")
```

While this pathname is much shorter than the absolute pathname, it is important to remember that if you changed your working directory (for example, if you used `setwd("CourseText")` to move into the `CourseText` directory), this relative pathname would no longer work.

There are a few abbreviations that can be really useful for pathnames:

Shorthand	Meaning
'~'	Home directory
'.'	Current working directory
'..'	One directory up from current working directory
'../..'	Two directories up from current working directory

These can help you keep pathnames shorter and also help you move "up-and-over" to get to a file or directory that's not on the direct path below your current working directory.

For example, my home directory is `/Users/brookeanderson`. If I wanted to change my working directory to the `Downloads` directory, which is a direct subdirectory of my home directory, I could use:

```
setwd("~/Downloads")
```

As a second example, say I was working in the working directory `CourseText`, but I wanted to read in the `heat_mort.csv` file that's in the `example_data` directory, rather than the one in the `CourseText` directory. I can use the `..` abbreviation to tell R to look up one directory from the current working directory, and then down within a subdirectory of that. The relative pathname in this case is:

```
"../Week2_Aug31/example_data/heat_mort.csv"
```

This tells R to look one directory up from the working directory (`..`), which in this case is to `RCourseFall2015`, and then down within that directory to `Week2_Aug31`, then to `example_data`, and then to look there for the file `heat_mort.csv`.

The relative pathname to read this file while R is working in the `CourseTest` directory would be:

```
heat_mort <- read.csv("../Week2_Aug31/example_data/heat_mort.csv")
```

These relative pathnames would "break" as soon as you tried them from a different working directory – this fact might make it seem like you would never want to use relative pathnames, and would always want to use absolute ones instead, even if they're longer. If that were the only consideration (length of the pathname), then perhaps that would be true. However, as you do more and more in R, there will likely be many occasions when you want to use relative pathnames instead. They are particularly useful if you ever want to share a whole directory, with R scripts and data, with a collaborator. In that case, if you've used relative pathnames, all the code should work fine for the person you share with, even though they're running it on their own computer. Conversely, if you'd used absolute pathnames, none of them would work on another computer, because the "top" of the directory structure (i.e., for me, `/Users/brookeanderson/Desktop`) will almost definitely be different for your collaborator's computer than it is for yours.

You can use absolute or relative pathnames for a number of things:

- To set your working directory: `setwd("../Week2_Aug31")`, for example
- To read in files from a different directory (as shown in the previous examples)
- To list files in a different directory: for example, `list.files("..")` will list all files in the directory directly about your current working directory (the *parent directory* of your working directory)

If you're getting errors reading in files, and you think it's related to the relative pathname you're using, it's often helpful to use `list.files()` to make sure the file you're trying to load is in the directory that the relative pathname you're using is directing R to.

0.16 Diversion: `paste`

This is a good opportunity to explain how to use some functions that can be very helpful when you're using relative or absolute pathnames: `paste()` and `paste0()`.

As a bit of important background information, it's important that you understand that you can save a pathname (absolute or relative) as an R object, and then use that R object in calls to later functions like `list.files()` and `read.csv()`. For example, to use the absolute pathname to read the `heat_mort.csv` file in the `CourseText` directory, you could run:

```
my_file <- "/Users/brookeanderson/Desktop/RCourseFall2015/CourseText/heat_mort.csv"
heat_mort <- read.csv(my_file)
```

You'll notice from this code that the pathname to get to a directory or file can sometimes become ungainly and long. To keep your code cleaner, you can address this by using the `paste` or `paste0` functions. These functions come in handy in a lot of other applications, too, but this is a good place to introduce them.

The `paste()` function is very straightforward. It takes, as inputs, a series of different character strings you want to join together, and it pastes them together in a single character string. (As a note, this means that your result vector will only be one element long, for basic uses of `paste()`, while the inputs will be several different character stings.) You separate all the different things you want to paste together using with commas in the function call. For example:

```
paste("Sunday", "Monday", "Tuesday")
```

```
## [1] "Sunday Monday Tuesday"
```

```
length(c("Sunday", "Monday", "Tuesday"))
```

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

```
length(paste("Sunday", "Monday", "Tuesday"))
```

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

The `paste()` function has an option called `sep =`. This tells R what you want to use to separate the values you're pasting together in the output. The default is for R to use a space, as shown in the example above. To change the separator, you can change this option, and you can put in just about anything you want. For example, if you wanted to paste all the values together without spaces, you could use `sep = ""`:

```
paste("Sunday", "Monday", "Tuesday", sep = "")
```

```
## [1] "SundayMondayTuesday"
```

As a shortcut, instead of using the `sep = ""` option, you could achieve the same thing using the `paste0` function. This function is almost exacly like `paste`, but it defaults to `""` (i.e., no space) as the separator between values by default:

```
paste0("Sunday", "Monday", "Tuesday")
```

```
## [1] "SundayMondayTuesday"
```

With pathnames, you will usually not want spaces. Therefore, you could think about using `paste0()` to write an object with the pathname you want to ultimately use in commands like `list.files()` and `setwd()`. This will allow you to keep your code cleaner, since you can now divide long pathnames over multiple lines:

```
my_file <- paste0("/Users/brookeanderson/Desktop/",
                  "RCourseFall2015/CourseText/heat_mort.csv")
heat_mort <- read.csv(my_file)
```

You will end up using `paste()` and `paste0()` for many other applications, but this is a good example of how you can start using these functions to start to get a feel for them.

0.17 Reading data into R

Data comes in files of all shapes and sizes. R has the capability to read data in from many of these, even priorietary files for other software (e.g., Excel and SAS files). As a small sample, here are some of the types of data files that R can read and work with:

- Flat files (much more about these in just a minute)
- Files from other statistical packages (SAS, Excel, Stata, SPSS)
- Tables on webpages (e.g., the table on ebola outbreaks near the end of this Wikipedia page)
- Data in a database (e.g., MySQL, Oracle)
- Data in JSON and XML formats
- Really crazy data formats used in other disciplines (e.g., netCDF files from climate research, MRI data stored in Analyze, NIfTI, and DICOM formats)
- Geographic shapefiles
- Data through APIs

Often, it is possible to read in and clean up even incredibly messy data, by using functions like `scan` and `readLines` to read the data in a line at a time, and then using regular expressions (which I'll cover in the "Intermediate" section of the course) to clean up each line as it comes in. In over a decade of coding in R, I think the only time I've come across a data file I couldn't get into R was for proprietary precision agriculture data collected at harvest by a combine.

0.17.1 Reading local flat files

Much of the data that you will want to read in will be in flat files. Basically, these are files that you can open using a text editor; the most common type you'll work with are probably comma-separated files (often with a `.csv` or `.txt` file extension). Most flat files come in two general categories:

1. Fixed width files
2. Delimited files

- ".csv": Comma-separated values
- ".tab", ".tsv": Tab-separated values
- Other possible delimiters: colon, semicolon, pipe ("|")

Fixed width files are files where a column always has the same width, for all the rows in the column. These tend to look very neat and easy-to-read when you open them in a text editor. For example, the first few rows of a fixed-width file might look like this:

```
Course          Number          Day          Time
Intro to Epi    501             M/W/F        9:00-9:50
Advanced Epi    521             T/Th         1:00-2:15
```

Delimited files use some *delimiter* (for example, a column or a tab) to separate each column value within a row. The first few rows of a delimited file might look like this:

```
Course, Number, Day, Time
"Intro to Epi", 501, "M/W/F", "9:00-9:50"
"Advanced Epi", 521, "T/Th", "1:00-2:15"
```

These flat files can have a number of different file extensions. The most generic is `.txt`, but they will also have ones more specific to their format, like `.csv` for a comma-delimited file or `.fwf` for a fixed with file.

R can read in data from both fixed with and delimited flat files. The only catch is that you need to tell R a bit more about the format of the flat file, including whether it is fixed width or delimited. If the file is fixed width, you will usually have to tell R the width of each column. If the file is delimited, you'll need to tell R which delimiter is being used.

If the file is delimited, you can use the `read.table` family of functions to read it in. This family of functions includes several specialized functions. All members of the `read.table` family are doing the same basic thing. The only difference is what defaults each function has for the separator (`sep`) and the decimal point (`dec`). Members of the `read.table` family include:

Function	Separator	Decimial point
'read.table'	comma	period
'read.csv'	comma	period
'read.csv2'	semi-colon	comma
'read.delim'	tab	period
'read.delim2'	tab	period

You can use `read.table` to read in any delimited file, regardless of the separator and the value used for the decimal point. However, you will need to specify these values using the `sep` and `dec` parameters if they differ from the defaults for `read.table` (a space for the delimiter and period for the decimal). If you remember the more specialized function call, therefore, you can save yourself some typing. There are a few other default values besides `sep` and `dec` that differ between different functions in this family: `header`, for example, specifies whether the first row should be used as column names.

For example, to read in the Ebola data, which is comma-delimited, you could either use `read.table` with a `sep` argument specified or use `read.csv`, in which case you don't have to specify `sep`:

```
# These two calls do the same thing
ebola <- read.table("data/country_timeseries.csv", sep = ",",
```

```
                    header = TRUE)
ebola <- read.csv("data/country_timeseries.csv")
```

These functions have a number of different parameters to help you tell R how to read in data. For example, if the first few lines of the file aren't part of the tabular data, you can tell R how many rows of the file to skip before it starts reading in the data. If the data uses an unusual value for missing data (e.g., -999), you can specify that, as well. Some of the interesting parameters with the `read.table` family of functions are:

Option	Description
'sep'	What is the delimiter in the data?
'skip'	How many lines of the start of the file should you skip?
'header'	Does the first line you read give column names?
'as.is'	Should you bring in strings as characters, not factors?
'nrows'	How many rows do you want to read in?
'na.strings'	How are missing values coded?

Remember that you can always find out more about a function by looking at its help file. For example, check out `?read.table` and `?read.fwf`. You can also use the help files to determine the default values of arguments for each function.

0.17.2 The `read_*` functions

The `read.table` family of functions are part of base R. There is a newer package called `readr` that has a family of `read_*` functions. These functions are very similar, but have some more sensible defaults. Compared to the `read.table` family of functions, the `read_*` functions:

- Work better with large datasets: faster, includes progress bar
- Have more sensible defaults (e.g., characters default to characters, not factors)

Functions in the `read_*` family include:

- `read_csv`, `read_tsv` (specific delimiters)
- `read_delim`, `read_table` (generic)
- `read_fwf`
- `read_log`
- `read_lines`

These functions work very similarly to functions from the `read.table` family. For example, to read in the Daily Show guest data, you can call:

```
library(readr)
daily_show <- read_csv("data/daily_show_guests.csv", skip = 4)
```

```
## Parsed with column specification:
## cols(
##   YEAR = col_integer(),
##   GoogleKnowlege_Occupation = col_character(),
##   Show = col_character(),
##   Group = col_character(),
##   Raw_Guest_List = col_character()
## )
```

The message that R prints after this call ("Parsed with column specification:..") lets you know what classes R used for each column (this function tries to guess the appropriate function and, unlike the `readr` functions, will assign characters to a character rather than factor class – this is usually what you want).

The `readr` package is a member of the tidyverse of packages. The *tidyverse* describes an evolving collection of R packages with a common philosophy, and they are unquestionably changing the way people code in R. Most were developed in part or full by Hadley Wickham and others at RStudio. Many of these packages are only a few years old, but have been rapidly adapted by the R community. As a result, newer examples of R code will often look very different from the code in older R scripts, including examples in books that are more than a few years old. In this course, I'll focus on "tidyverse" functions when possible, but I do put in details about base R equivalent functions or processes at some points – this will help you interpret older code. You can use the `tidyverse` package to download all tidyverse packages at one.

0.17.3 Reading online flat files

So far, I've only shown you how to read in data from files that are saved to your computer. R can also read in data directly from the web. If a flat file is posted online, you can read it into R in almost exactly the same way that you would read in a local file. The only difference is that you will use the file's url instead of a local file path for the `file` argument.

With the `read_*` family of functions, you can do this both for flat files from a non-secure webpage (i.e., one that starts with `http`) and for files from a secure webpage (i.e., one that starts with `https`), including GitHub and Dropbox. With the `read.table` family of functions, you can read in online flat files from non-secure webpages, but not from secure ones.

For example, to read in the tab-separated file saved at this web address, which is non-secure, you can run:

```
url <- paste0("http://www2.unil.ch/comparativegenometrics",
              "/docs/NC_006368.txt")
ld_genetics <- read_tsv(url)
ld_genetics[1:5, 1:4]
```

```
## # A tibble: 5 × 4
##     pos    nA    nC    nG
##   <int> <int> <int> <int>
## 1   500   307   153   192
## 2  1500   310   169   207
## 3  2500   319   167   177
## 4  3500   373   164   168
## 5  4500   330   175   224
```

Similarly , to read in data from this GitHub repository of Ebola data, which is a secure website, you can run:

```
url <- paste0("https://raw.githubusercontent.com/cmrivers/",
              "ebola/master/country_timeseries.csv")
ebola <- read_csv(url)
ebola[1:3, 1:3]
```

```
## # A tibble: 3 × 3
##       Date   Day Cases_Guinea
##      <chr> <int>        <int>
## 1 1/5/2015   289         2776
## 2 1/4/2015   288         2775
## 3 1/3/2015   287         2769
```

0.17.4 Saving and loading R objects

You can save an R object you've created as an `.RData` file.

To save an R object in a `.RData` file, use the `save` function:

```
save(ebola, file = "Ebola.RData")
list.files()
```

```
##  [1] "_book"                           "_bookdown.yml"
##  [3] "_build.sh"                       "_deploy.sh"
##  [5] "_output.yml"                     "01-course_info.Rmd"
##  [7] "02-prelim.Rmd"                   "03-databasics.Rmd"
##  [9] "book.bib"                        "data"
## [11] "DESCRIPTION"                     "Ebola.RData"
## [13] "figures"                         "homework.Rmd"
## [15] "index.Rmd"                       "LICENSE"
## [17] "packages.bib"                    "preamble.tex"
## [19] "README.md"                       "references.Rmd"
## [21] "RProgrammingForResearch.Rmd"  "RProgrammingForResearch.Rproj"
## [23] "slides"                          "style.css"
## [25] "toc.css"                         "vocabulary.Rmd"
```

Notice that, once you save the object, a new file named "Ebola.RData" is listed in the files in your current working directory. The default is for R to save the R object in your current working directory; to save it elsewhere, use a full relative or absolute pathname for the `file` argument.

Once you've saved an R object, you can re-load it later using the `load` function with the object's file path. For example, since I've saved this R object, I can remove it from my current R workspace using the `rm` function, after which it will not show up when I run `ls`:

```
rm(ebola)
ls()
```

```
## [1] "ld_genetics" "my_dir"      "url"
```

Then I can use the `load` command to re-load the object, after which it will again show up as an object in my R workspace:

```
load("Ebola.RData")
ls()
```

```
## [1] "ebola"       "ld_genetics" "my_dir"      "url"
```

There is one caveat for saving R objects: some people suggest you avoid this if possible, to make your research more reproducible. Imagine someone wants to look at your data and code in 30 years. R might not work the same way, so you might not be able to read an `.RData` file. Notice that, if you try to open an `.RData` file in a text edit, it won't make any sense. However, you can open flat files (e.g., `.csv`, `.txt`) and R scripts (`.R`) in text editors – you should still be able to do this regardless of what happens to R. Some potential exceptions, when it might be useful to save an R object, include when:

- You have an object that you need to save that has a structure that won't work well in a flat file (a list rather than a dataframe, for example); or
- Your starting dataset is very large, and it would take a long time for you to read in your data fresh every time. In this case it may make sense to do some data cleaning and then save the cleaned R object as a `.RData` file, but be sure to also save the script you used to clean the raw data.

0.17.5 Reading other file types

Later in the course, we'll talk about how to open a variety of other file types in R. However, you might find it immediately useful to be able to read in files from other statistical programs.

There are two "tidyverse" packages – `readxl` and `haven` – that help with this. They allow you to read in files from the following formats:

File type	Function	Package
Excel	'read_excel'	'readxl'
SAS	'read_sas'	'haven'
SPSS	'read_spss'	'haven'
Stata	'read_stata	'haven'

0.18 Data cleaning

Once you have loaded data into R, you'll likely need to clean it up a little before you're ready to analyze it. Here, I'll go over the first steps of how to do that with functions from `dplyr`, another package in the tidyverse. Here are some of the most common data-cleaning tasks, along with the corresponding `dplyr` function for each:

Task	'dplyr' function
Renaming columns	'rename'
Filtering to certain rows	'filter'
Selecting certain columns	'select'
Adding or changing columns	'mutate'

In this section, I'll describe how to do each of these four tasks; in later sections of the course, we'll go much deeper into how to clean messier data.

For the examples in this section, I'll use example data listing guests to the Daily Show. To follow along with these examples, you'll want to load that data, as well as load the `dplyr` package (install it using `install.packages` if you have not already):

```
library(dplyr)
daily_show <- read_csv("data/daily_show_guests.csv", skip = 4)
```

I've used this data in previous examples, but as a reminder, here's what it looks like:

```
head(daily_show)
```

```
## # A tibble: 6 × 5
##    YEAR GoogleKnowlege_Occupation    Show  Group   Raw_Guest_List
##   <int>                     <chr>   <chr>  <chr>            <chr>
## 1  1999                   actor 1/11/99 Acting   Michael J. Fox
## 2  1999                Comedian 1/12/99 Comedy  Sandra Bernhard
## 3  1999       television actress 1/13/99 Acting    Tracey Ullman
## 4  1999             film actress 1/14/99 Acting Gillian Anderson
## 5  1999                   actor 1/18/99 Acting David Alan Grier
## 6  1999                   actor 1/19/99 Acting  William Baldwin
```

0.18.1 Renaming columns

A first step is often re-naming the columns of the dataframe. It can be hard to work with a column name that:

- is long
- includes spaces
- includes upper case

You can check out the column names for a dataframe using the `colnames` function, with the dataframe object as the argument. Several of the column names in `daily_show` have some of these issues:

```
colnames(daily_show)
```

```
## [1] "YEAR"                          "GoogleKnowlege_Occupation"
## [3] "Show"                          "Group"
## [5] "Raw_Guest_List"
```

To rename these columns, use `rename`. The basic syntax is:

```
## Generic code
rename(dataframe,
       new_column_name_1 = old_column_name_1,
       new_column_name_2 = old_column_name_2)
```

The first argument is the dataframe for which you'd like to rename columns. Then you list each pair of new versus old column names (in that order) for each of the columns you want to rename. To rename columns in the `daily_show` data using `rename`, for example, you would run:

```
daily_show <- rename(daily_show,
                     year = YEAR,
                     job = GoogleKnowlege_Occupation,
                     date = Show,
                     category = Group,
                     guest_name = Raw_Guest_List)
head(daily_show, 3)
```

```
## # A tibble: 3 × 5
##    year                job    date category      guest_name
##   <int>              <chr>   <chr>    <chr>           <chr>
## 1  1999              actor 1/11/99   Acting  Michael J. Fox
## 2  1999           Comedian 1/12/99   Comedy Sandra Bernhard
## 3  1999 television actress 1/13/99   Acting   Tracey Ullman
```

Many of the functions in tidyverse packages, including those in `dplyr`, provide exceptions to the general rule about when to use quotation marks versus when to leave them off. Unfortunately, this may make it a bit hard to learn when to use quotation marks versus when not to. One way to

think about this, which is a bit of an oversimplification but can help as you're learning, is to assume that anytime you're using a `dplyr` function, every column in the dataframe you're working with has been loaded to your R session as its own object.

0.18.2 Selecting columns

Next, you may want to select only some columns of the dataframe. You can use the `select` function from `dplyr` to subset the dataframe to certain columns. The basic structure of this command is:

```
## Generic code
select(dataframe, column_name_1, column_name_2, ...)
```

In this call, you first specify the dataframe to use and then list all of the column names to include in the output dataframe, with commas between each column name. For example, to select all columns in `daily_show` except `year` (since that information is already included in `date`), run:

```
select(daily_show, job, date, category, guest_name)
```

```
## # A tibble: 2,693 × 4
##                    job    date category       guest_name
##                  <chr>   <chr>    <chr>            <chr>
## 1                actor 1/11/99   Acting   Michael J. Fox
## 2            Comedian 1/12/99   Comedy  Sandra Bernhard
## 3  television actress 1/13/99   Acting    Tracey Ullman
## 4        film actress 1/14/99   Acting Gillian Anderson
## 5                actor 1/18/99   Acting David Alan Grier
## 6                actor 1/19/99   Acting  William Baldwin
## 7     Singer-lyricist 1/20/99 Musician    Michael Stipe
## 8                model 1/21/99    Media   Carmen Electra
## 9                actor 1/25/99   Acting  Matthew Lillard
## 10  stand-up comedian 1/26/99   Comedy      David Cross
## # ... with 2,683 more rows
```

Don't forget that, if you want to change column names in the saved object, you must reassign the object to be the output of `rename`. If you run one of these cleaning functions without reassigning the object, R will print out the result, but the object itself won't change. You can take advantage of this, as I've done in this example, to look at the result of applying a function to a dataframe without changing the original dataframe. This can be helpful as you're figuring out how to write your code.

The `select` function also provides some time-saving tools. For example, in the last example, we wanted all the columns except one. Instead of writing out all the columns we want, we can use `-` with the columns we don't want to save time:

```
daily_show <- select(daily_show, -year)
head(daily_show, 3)
```

```
## # A tibble: 3 × 4
##                   job    date category      guest_name
##                 <chr>   <chr>    <chr>           <chr>
## 1               actor 1/11/99   Acting  Michael J. Fox
## 2           Comedian 1/12/99   Comedy Sandra Bernhard
## 3 television actress 1/13/99   Acting   Tracey Ullman
```

0.18.3 Filtering to certain rows

Next, you might want to filter the dataset down so that it only includes certain rows. For example, you might want to get a dataset with only the guests from 2015, or only guests who are scientists.

You can use the `filter` function from `dplyr` to filter a dataframe down to a subset of rows. The syntax is:

```
## Generic code
filter(dataframe, logical statement)
```

The `logical statement` in this call gives the condition that a row must meet to be included in the output data frame. For example, if you want to create a data frame that only includes guests who were scientists, you can run:

```
scientists <- filter(daily_show, category == "Science")
head(scientists)
```

```
## # A tibble: 6 × 4
##              job    date category             guest_name
##            <chr>   <chr>    <chr>                  <chr>
## 1   neurosurgeon 4/28/03  Science        Dr Sanjay Gupta
## 2      scientist 1/13/04  Science        Catherine Weitz
## 3      physician 6/15/04  Science         Hassan Ibrahim
## 4         doctor  9/6/05  Science        Dr. Marc Siegel
## 5      astronaut 2/13/06  Science Astronaut Mike Mullane
## 6 Astrophysicist 1/30/07  Science    Neil deGrasse Tyson
```

To build a logical statment to use in `filter`, you'll need to know some of R's logical operators. Some of the most commonly used ones are:

Operator	Meaning	Example
`==`	equals	`category == "Acting"`
`!=`	does not equal	`category != "Comedy`
`%in%`	is in	`category %in% c("Academic", "Science")`
`is.na()`	is NA	`is.na(job)`
`!is.na()`	is not NA	`!is.na(job)`
`&`	and	`year == 2015 & category == "Academic"`
`|`	or	`year == 2015 | category == "Academic"`

We'll use these logical operators a lot more as the course continues, so they're worth learning by heart.

Two common errors with logical operators are: (1) Using `=` instead of `==` to check if two values are equal; and (2) Using `== NA` instead of `is.na` to check for missing observations.

0.18.4 Add or change columns

You can change a column or add a new column using the `mutate` function from the `dplyr` package. That function has the syntax:

```
# Generic code
mutate(dataframe,
       changed_column = function(changed_column),
       new_column = function(other arguments))
```

For example, the `job` column in `daily_show` sometimes uses upper case and sometimes does not (this call uses the `unique` function to list only unique values in this column):

```
head(unique(daily_show$job), 10)
```

```
##  [1] "actor"            "Comedian"         "television actress"
##  [4] "film actress"       "Singer-lyricist"    "model"
##  [7] "stand-up comedian"  "actress"            "comedian"
## [10] "Singer-songwriter"
```

To make all the observations in the `job` column lowercase, use the `tolower` function within a `mutate` function:

```
mutate(daily_show, job = tolower(job))
```

```
## # A tibble: 2,693 × 4
##                    job    date category       guest_name
##                  <chr>   <chr>    <chr>            <chr>
## 1              actor 1/11/99   Acting   Michael J. Fox
## 2            comedian 1/12/99   Comedy  Sandra Bernhard
## 3  television actress 1/13/99   Acting    Tracey Ullman
## 4        film actress 1/14/99   Acting Gillian Anderson
## 5              actor 1/18/99   Acting David Alan Grier
## 6              actor 1/19/99   Acting  William Baldwin
## 7     singer-lyricist 1/20/99 Musician    Michael Stipe
## 8              model 1/21/99    Media   Carmen Electra
## 9              actor 1/25/99   Acting  Matthew Lillard
## 10  stand-up comedian 1/26/99   Comedy      David Cross
## # ... with 2,683 more rows
```

0.18.5 Piping

So far, I've shown how to use these `dplyr` functions one at a time to clean up the data, reassigning the dataframe object at each step. However, there's a trick

called "piping" that will let you clean up your code a bit when you're writing a script to clean data.

If you look at the format of these `dplyr` functions, you'll notice that they all take a dataframe as their first argument:

```
# Generic code
rename(dataframe,
       new_column_name_1 = old_column_name_1,
       new_column_name_2 = old_column_name_2)
select(dataframe, column_name_1, column_name_2)
filter(dataframe, logical statement)
mutate(dataframe,
       changed_column = function(changed_column),
       new_column = function(other arguments))
```

Without piping, you have to reassign the dataframe object at each step of this cleaning if you want the changes saved in the object:

```
daily_show <-read_csv("data/daily_show_guests.csv",
                      skip = 4)
daily_show <- rename(daily_show,
                     job = GoogleKnowlege_Occupation,
                     date = Show,
                     category = Group,
                     guest_name = Raw_Guest_List)
daily_show <- select(daily_show, -YEAR)
daily_show <- mutate(daily_show, job = tolower(job))
daily_show <- filter(daily_show, category == "Science")
```

Piping lets you clean this code up a bit. It can be used with any function that inputs a dataframe as its first argument. It *pipes* the dataframe created right before the pipe (%>%) into the function right after the pipe. With piping, therefore, the same data cleaning looks like:

```
daily_show <-read_csv("data/daily_show_guests.csv",
                      skip = 4) %>%
  rename(job = GoogleKnowlege_Occupation,
         date = Show,
         category = Group,
         guest_name = Raw_Guest_List) %>%
```

```
  select(-YEAR) %>%
  mutate(job = tolower(job)) %>%
  filter(category == "Science")
```

Notice that, when piping, the first argument (the name of the dataframe) is excluded from all function calls that follow a pipe. This is because piping sends the dataframe from the last step into each of these functions as the dataframe argument.

0.18.6 Base R equivalents to `dplyr` functions

Just so you know, all of these `dplyr` functions have alternatives, either functions or processes, in base R:

‘dplyr‘	Base R equivalent
‘rename‘	Reassign ‘colnames‘
‘select‘	Square bracket indexing
‘filter‘	‘subset‘
‘mutate‘	Use ‘$‘ to change / create columns

You will see these alternatives used in older code examples.

0.19 Dates in R

As part of the data cleaning process, you may want to change the class of some of the columns in the dataframe. For example, you may want to change a column from a character to a date.

Here are some of the most common vector classes in R:

Class	Example
`character`	“Chemistry”, “Physics”, “Mathematics”
`numeric`	10, 20, 30, 40
`factor`	Male [underlying number: 1], Female [2]
`Date`	“2010-01-01” [underlying number: 14,610]
`logical`	TRUE, FALSE

To find out the class of a vector (including a column in a dataframe – remember each column can be thought of as a vector), you can use `class()`:

```
class(daily_show$date)
```

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

It is especially common to need to convert dates during the data cleaning process, since date columns will usually be read into R as characters or factors – you can do some interesting things with vectors that are in a Date class that you cannot do with a vector in a character class. To convert a vector to the `Date` class, you can use the `as.Date` function. For example, to convert the `date` column in the `daily_show` data into a Date class, you can run:

```
daily_show <- mutate(daily_show,
                     date = as.Date(date, format = "%m/%d/%y"))
head(daily_show, 3)
```

```
## # A tibble: 3 × 4
##            job       date category      guest_name
##          <chr>     <date>    <chr>           <chr>
## 1 neurosurgeon 2003-04-28  Science Dr Sanjay Gupta
## 2    scientist 2004-01-13  Science Catherine Weitz
## 3    physician 2004-06-15  Science  Hassan Ibrahim
```

```
class(daily_show$date)
```

```
## [1] "Date"
```

Once you have an object in the `Date` class, you can do things like plot by date, calculate the range of dates, and calculate the total number of days the dataset covers:

```
range(daily_show$date)
diff(range(daily_show$date))
```

You can convert dates expressed in a number of different ways into a Date class in R, as long as you can explain to R how to parse the format that the date is in before you convert it. The only tricky thing in converting objects into a Date class is learning the abbreviations for the `format` option of the `as.Date` function. Here are some common ones:

Abbreviation	Meaning
`%m`	Month as a number (e.g., 1, 05)
`%B`	Full month name (e.g., August)
`%b`	Abbreviated month name (e.g., Aug)
`%y`	Two-digit year (e.g., 99)
`%Y`	Four-digit year (e.g., 1999)
`%A`	Full weekday (e.g., Monday)
`%a`	Abberviated weekday (e.g., Mon)

Here are some examples of what you would specify for the `format` argument of `as.Date` for some different original formats of date columns:

Your date	`format`
10/23/2008	"%m/%d%Y"
08-10-23	"%y-%m-%d"
Oct. 23 2008	"%b. %d %Y"
October 23, 2008	"%B %d, %Y"
Thurs, 23 October 2008	"%a, %d %B %Y"

You must use the `format` argument to specify what your date column looks like **before** it's converted to a Date class, not how you'd like it to look after its converted. Once an objects is in a date class, it will always be printed out using a common format, unless you change it back into a character class. (Confusingly, there is a `format` function that you can use to convert from a Date class to a character class and, in that case, the `format` argument does specify how the final date will look. This is mainly useful as a last step in data analysis, when you're creating plot labels of table columns, for example.)

There is also a function in the tidyverse, called `lubridate`, that helps in parsing dates. In many cases you can use functions from this package to parse dates much more easily, without having to specify specific starting formats.

The `ymd` function from lubridate can be used to parse a column into a Date clase, regardless of the original format of the date, as long as the date elements are in the order: year, month, day. For example:

```
library(lubridate)
ymd("2008-10-13")
```

```
## [1] "2008-10-13"
```

```
ymd("'08 Oct 13")
```

```
## [1] "2008-10-13"
```

```
ymd("'08 Oct 13")
```

```
## [1] "2008-10-13"
```

The `lubridate` package has similar functions for other date orders or for date-times, including:

- dmy
- mdy
- ymd_h
- ymd_hm

We could have used these to transform the date in `daily_show`, using the following pipe chain:

```
daily_show <- read_csv("data/daily_show_guests.csv",
                       skip = 4) %>%
  rename(job = GoogleKnowlege_Occupation,
         date = Show,
         category = Group,
         guest_name = Raw_Guest_List) %>%
  select(-YEAR) %>%
  mutate(date = mdy(date)) %>%
  filter(category == "Science")
head(daily_show, 2)
```

```
## # A tibble: 2 × 4
##            job       date category      guest_name
##          <chr>     <date>    <chr>           <chr>
## 1 neurosurgeon 2003-04-28  Science Dr Sanjay Gupta
## 2    scientist 2004-01-13  Science Catherine Weitz
```

The `lubridate` package also includes functions to pull out certain elements of a date, including:

- `wday`
- `mday`
- `yday`
- `month`
- `quarter`
- `year`

For example, we could use `wday` to create a new column with the weekday of each show:

```
mutate(daily_show,
       show_day = wday(date, label = TRUE)) %>%
  select(date, show_day, guest_name) %>%
  slice(1:5)
```

```
## # A tibble: 5 × 3
##         date show_day             guest_name
##       <date>    <ord>                  <chr>
## 1 2003-04-28      Mon        Dr Sanjay Gupta
## 2 2004-01-13     Tues        Catherine Weitz
## 3 2004-06-15     Tues         Hassan Ibrahim
## 4 2005-09-06     Tues        Dr. Marc Siegel
## 5 2006-02-13      Mon Astronaut Mike Mullane
```

0.20 In-course Exercise

0.20.1 Checking out directory structures

Download the whole directory for this week from Github. Put the "data" directory as a subdirectory in your directory for this class. To do that, go the the GitHub page for the course and, in the top right, choose "Clone or Download" and then choose "Download ZIP". Then move the "data" subdirectory into your course directory and throw away rest of what you downloaded.

Unfortunately, while GitHub will let you download data files one at a time, it doesn't offer a straightforward way of downloading a whole subdirectory from a repository. For this task, where you're pulling all of the data in

the "data" subdirectory of the course repository, the quickest method is to download the entire directory, find and move the subdirectory that you need, and then delete the rest.

- Look through the structure of the "data" directory. What files are in the directory? What subdirectories? Sketch out the structure of this directory.
- Create a new R script to put all the code you use for this exercise. Create a subdirectory in your course directory called "R" and save this script there using a `.R` extension (e.g., "week_2.R").

0.20.2 Using relative and absolute file pathnames

Once you have the data, I'd like you to try using `setwd()` to move around the directories on your computer. For this section of the exercise, you'll try to open the same file from different working directories, to get practice using absolute and relative file pathnames.

Start by changing your working directory to the "data" subdirectory you just downloaded. For me, the absolute path to that is `/Users/brookeanderson/RProgrammingForResearch/data`, so to change my working directory to this one using an absolute file pathname, I would run:

```
setwd("/Users/brookeanderson/RProgrammingForResearch/data")
getwd()
```

The absolute pathname will be different for each person, based on the directories on his or her computer and where he or she saved this particular directory.

Since "~" is shorthand for my home directory ("/Users/brookeanderson"), I could also use the absolute pathname "~/RProgrammingForResearch/data" when setting this directory as my working directory.

Now, use the `list.files` function to make sure you have all the files that you just pulled in your current working directory:

```
list.files()
```

```
## [1] "country_timeseries.csv"  "daily_show_guests.csv"
## [3] "deaths-weather.csv"      "icd-10.xls"
## [5] "ICU_Data_Code_Sheet.pdf" "icu.sas7bdat"
## [7] "ld_genetics.txt"         "measles_data"
```

Try the following tasks:

- Read in the ebola data in `country_timeseries.csv`. Save it as the R object `ebola`. How many rows and columns does it have? What are the names of the columns?
- Now try moving up one directory from your current working directory (which should be the "data" directory), into the directory you created for this course. What happens if you use the same code as before to read in the file? What do you need to change to be able to read the file in from here? Try to read in the data from here using:
  - A relative pathname
  - An absolute pathname
- Now move down into the subdirectory of "data" called "measles_data". Try to read in the Ebola data from this working directory using:
  - A relative pathname
  - An absolute pathname
- Which method (absolute or relative pathnames) always used the same code, regardless of your current working directory? Which method used different code, depending on the starting working directory?

Example R code:

```
getwd()  ## Make sure you're in the "data" directory to start
```

```
## [1] "/Users/brookeanderson/RProgrammingForResearch/data"
```

```
ebola <- read.csv("country_timeseries.csv", header = TRUE)
```

```
ebola[1:5, 1:5]
```

```
##         Date Day Cases_Guinea Cases_Liberia Cases_SierraLeone
## 1   1/5/2015 289         2776            NA             10030
## 2   1/4/2015 288         2775            NA              9780
## 3   1/3/2015 287         2769          8166              9722
## 4   1/2/2015 286           NA          8157                NA
## 5 12/31/2014 284         2730          8115              9633
```

```
dim(ebola) # To figure out number of rows and columns
```

```
## [1] 122  18
```

```
colnames(ebola) # To figure out column names
```

```
##  [1] "Date"                 "Day"                  "Cases_Guinea"
##  [4] "Cases_Liberia"        "Cases_SierraLeone"    "Cases_Nigeria"
##  [7] "Cases_Senegal"        "Cases_UnitedStates"   "Cases_Spain"
## [10] "Cases_Mali"           "Deaths_Guinea"        "Deaths_Liberia"
## [13] "Deaths_SierraLeone"   "Deaths_Nigeria"       "Deaths_Senegal"
## [16] "Deaths_UnitedStates"  "Deaths_Spain"         "Deaths_Mali"
```

```
## Move up one directory
setwd("..")
getwd()

## Get the file using the relative pathname
ebola <- read.csv("data/country_timeseries.csv", header = TRUE)
```

```
ebola[1:5, 1:5]
```

```
##         Date Day Cases_Guinea Cases_Liberia Cases_SierraLeone
## 1   1/5/2015 289         2776            NA             10030
## 2   1/4/2015 288         2775            NA              9780
## 3   1/3/2015 287         2769          8166              9722
## 4   1/2/2015 286           NA          8157                NA
## 5 12/31/2014 284         2730          8115              9633
```

```
## Get the file using the absolute pathname
abs_path <- paste0("/Users/brookeanderson/RProgrammingForResearch/",
                   "data/country_timeseries.csv")
abs_path
```

```
## [1] "/Users/brookeanderson/RProgrammingForResearch/data/country_timeseries.csv"
```

```
ebola <- read.csv(abs_path, header = TRUE)
```

```
ebola[1:5, 1:5]
```

```
##         Date Day Cases_Guinea Cases_Liberia Cases_SierraLeone
## 1   1/5/2015 289         2776            NA             10030
## 2   1/4/2015 288         2775            NA              9780
## 3   1/3/2015 287         2769          8166              9722
## 4   1/2/2015 286           NA          8157                NA
## 5 12/31/2014 284         2730          8115              9633
```

```
## Reset your working directory as your directory for this course
## and then check that you're in the right place
getwd()
```

```
## [1] "/Users/brookeanderson/RProgrammingForResearch"
```

```
## Move into the measles_data subdirectory
setwd("data/measles_data")
getwd()
```

```
## [1] "/Users/brookeanderson/RProgrammingForResearch/data/measles_data"
```

```
## Get the file using the relative pathname
ebola <- read.csv("../country_timeseries.csv", header = TRUE)
```

```
ebola[1:5, 1:5]
```

```
##         Date Day Cases_Guinea Cases_Liberia Cases_SierraLeone
## 1   1/5/2015 289         2776            NA             10030
## 2   1/4/2015 288         2775            NA              9780
## 3   1/3/2015 287         2769          8166              9722
## 4   1/2/2015 286           NA          8157                NA
## 5 12/31/2014 284         2730          8115              9633
```

```
# Get the file using the absolute pathname (note: we've already assigned
# the absolute pathname in the `abs_path` object, so we can just use that
# object in the `read.csv` call here, rather than typing out the full
# absolute pathname again.)
ebola <- read.csv(abs_path, header = TRUE)
```

```
ebola[1:5, 1:5]
```

```
##         Date Day Cases_Guinea Cases_Liberia Cases_SierraLeone
## 1   1/5/2015 289         2776            NA             10030
## 2   1/4/2015 288         2775            NA              9780
## 3   1/3/2015 287         2769          8166              9722
## 4   1/2/2015 286           NA          8157                NA
## 5 12/31/2014 284         2730          8115              9633
```

If you have extra time:

- Find out some more about this Ebola dataset by checking out Caitlin Rivers' Ebola data GitHub repository. Who is Caitlin Rivers? How did she put this dataset together?
- Search for R code related to Ebola research on GitHub. Go to the GitHub home page and use the search bar to search for "ebola". On the results page, scroll down and use the "Language" sidebar on the left to choose repositories with R code. Did you find any interesting projects?
- When you `list.files()` when your working directory is the "data" directory, almost everything listed has a file extension, like `.csv`, `.xls`, `.sas7bdat`. One thing does not. Which one? Why does this listing not have a file extension?

0.20.3 Reading in different types of files

First, make sure your reset your working directory to your course directory:

```
setwd("~/RProgrammingForResearch/")
```

Now you'll try reading in data from a variety of types of file formats. All of these files are stored in the "data" subdirectory of your current working directory, so you'll use filenames throughout that start with "data/".

Try the following tasks:

- What type of flat file do you think the "ld_genetics.txt" file is? See if you can read it in and save it as the R object `ld_genetics`. Use the `summary` function to check out basic statistics on the data.
- Check out the file "measles_data/02-09-2015.txt". What type of flat file do you think it is? Stay in the "data" directory and use a relative pathname to read the file in and save it as the R object `ca_measles`. Use the `col.names` option to name the columns "city" and "count". What would the default column names be if you didn't use this option?
- Read in the Excel file "icd-10.xls" and assign it to the object name `idc10`. Use the `readxl` package to do that (examples are at the bottom of the linked page).
- Read in the SAS file `icu.sas7bdat`. To do this, use the `haven` package. Read the file into the R object `icu`.

Example R code:

```
ld_genetics <- read.delim("data/ld_genetics.txt", header = TRUE)
summary(ld_genetics)
```

```
##       pos                nA            nC              nG
##  Min.   :    500   Min.   :185   Min.   :120.0   Min.   : 85.0
##  1st Qu.: 876000   1st Qu.:288   1st Qu.:173.0   1st Qu.:172.0
##  Median :1751500   Median :308   Median :190.0   Median :189.0
##  Mean   :1751500   Mean   :309   Mean   :191.9   Mean   :191.8
##  3rd Qu.:2627000   3rd Qu.:329   3rd Qu.:209.0   3rd Qu.:208.0
##  Max.   :3502500   Max.   :463   Max.   :321.0   Max.   :326.0
##        nT             GCsk              TAsk             cGCsk
##  Min.   :188.0   Min.   :-189.0000   Min.   :-254.000   Min.   : -453
##  1st Qu.:286.0   1st Qu.: -30.0000   1st Qu.: -36.000   1st Qu.:10796
##  Median :306.0   Median :   0.0000   Median :  -2.000   Median :23543
```

```
##  Mean   :307.2   Mean   :  -0.1293   Mean   :  -1.736   Mean   :22889
##  3rd Qu.:328.0   3rd Qu.:  29.0000   3rd Qu.:  32.500   3rd Qu.:34940
##  Max.   :444.0   Max.   : 134.0000   Max.   : 205.000   Max.   :46085
##       cTAsk
##  Min.   :-6247
##  1st Qu.: 1817
##  Median : 7656
##  Mean   : 7855
##  3rd Qu.:15036
##  Max.   :19049
```

```
ca_measles <- read.delim("data/measles_data/02-09-2015.txt",
                         header = FALSE, col.names = c("city", "count"))
head(ca_measles)
```

```
##                  city count
## 1             ALAMEDA     6
## 2         LOS ANGELES    20
## 3 City of Long Beach     2
## 4   City of Pasadena     4
## 5              MARIN     2
## 6             ORANGE    34
```

```
library(readxl)
icd10 <- read_excel("data/icd-10.xls")
```

```
## DEFINEDNAME: 20 00 00 01 0b 00 00 00 01 00 00 00 00 00 00 06 3b 00 00 00 00 51 2b 00 00 0a 00
## DEFINEDNAME: 20 00 00 01 0b 00 00 00 01 00 00 00 00 00 00 06 3b 00 00 00 00 51 2b 00 00 0a 00
## DEFINEDNAME: 20 00 00 01 0b 00 00 00 01 00 00 00 00 00 00 06 3b 00 00 00 00 51 2b 00 00 0a 00
## DEFINEDNAME: 20 00 00 01 0b 00 00 00 01 00 00 00 00 00 00 06 3b 00 00 00 00 51 2b 00 00 0a 00
```

```
head(icd10)
```

```
## # A tibble: 6 × 2
##      Code                                          `ICD Title`
##     <chr>                                               <chr>
## 1 A00-B99       I. Certain infectious and parasitic diseases
## 2 A00-A09                     Intestinal infectious diseases
```

```
## 3     A00                                                Cholera
## 4   A00.0 Cholera due to Vibrio cholerae 01, biovar cholerae
## 5   A00.1    Cholera due to Vibrio cholerae 01, biovar eltor
## 6   A00.9                                Cholera, unspecified
```

```
library(haven)
icu <- read_sas("data/icu.sas7bdat")
icu[1:5, 1:5]
```

```
## # A tibble: 5 × 5
##       ID   STA   AGE GENDER  RACE
##    <dbl> <dbl> <dbl>  <dbl> <dbl>
## 1     4     1    87      1     1
## 2     8     0    27      1     1
## 3    12     0    59      0     1
## 4    14     0    77      0     1
## 5    27     1    76      1     1
```

If you have extra time:

- Is there a way to read the "ld_genetics.txt" file in using `read.table()` and specific options? If so, try to read the data in using that function. Why can you use both `read.delim` and `read.table` to read in this file?

Example R code:

```
## Using the read.table function
ld_genetics <- read.table("data/ld_genetics.txt", header = TRUE,
                          sep = "\t")
ld_genetics[1:5, 1:5]
```

```
##    pos  nA  nC  nG  nT
## 1  500 307 153 192 348
## 2 1500 310 169 207 314
## 3 2500 319 167 177 337
## 4 3500 373 164 168 295
## 5 4500 330 175 224 271
```

0.20.4 Cleaning up data

Try out the following tasks:

- You now have an R object called `ebola`. Create an object called `ebola_liberia` that only has the columns with the Date and cases and deaths in Liberia. How many observations do you have?
- Change the column names to `date`, `cases`, and `deaths`.
- What class is the `date` column currently in? Convert it to a Date object. If it's currently a factor, you will need to first convert it to a character (do you know why)? What are the starting and ending dates of this data?
- This data has earliest dates last and latest dates first. Often, we want our data in chronological order. Change the dataset so it's in chronological order. *Hint: You can use row indices to do this, if you use row indices to list the data from last row to first. For example, what do you get if you do `3:1`? What about if you do `ebola[3:1, ]`? Think of how you can extend this, along with `nrow()` do this task. There are a number of different ways to do this step, and we'll talk about more ways later in the course.*

Example R code:

```
library(dplyr)
## Create a subset with just the Liberia columns and Date
ebola_liberia <- select(ebola, Date, Cases_Liberia, Deaths_Liberia)
head(ebola_liberia)
```

```
##         Date Cases_Liberia Deaths_Liberia
## 1   1/5/2015            NA             NA
## 2   1/4/2015            NA             NA
## 3   1/3/2015          8166           3496
## 4   1/2/2015          8157           3496
## 5 12/31/2014          8115           3471
## 6 12/28/2014          8018           3423
```

```
## How many rows does the whole dataset have?
nrow(ebola_liberia)
```

```
## [1] 122
```

```
## Rename the columns
ebola_liberia <- rename(ebola_liberia,
                        date = Date,
                        cases = Cases_Liberia,
                        deaths = Deaths_Liberia)
ebola_liberia[1:3, ]
```

```
##       date cases deaths
## 1 1/5/2015    NA     NA
## 2 1/4/2015    NA     NA
## 3 1/3/2015  8166   3496
```

```
## What class is the `date` column?
class(ebola_liberia$date)
```

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

```
## Use the `mdy` from `lubridate` to convert to Date class
library(lubridate)
ebola_liberia <- mutate(ebola_liberia,
                        date = mdy(date))
head(ebola_liberia$date)
```

```
## [1] "2015-01-05" "2015-01-04" "2015-01-03" "2015-01-02" "2014-12-31"
## [6] "2014-12-28"
```

```
## What are the starting and ending dates?
range(ebola_liberia$date)
```

```
## [1] "2014-03-22" "2015-01-05"
```

```
## Re-order the dataset from last to first
ebola_liberia <- ebola_liberia[nrow(ebola_liberia):1, ]
ebola_liberia[1:3, ]
```

```
##           date cases deaths
## 122 2014-03-22    NA     NA
## 121 2014-03-24    NA     NA
## 120 2014-03-25    NA     NA
```

If you have extra time:

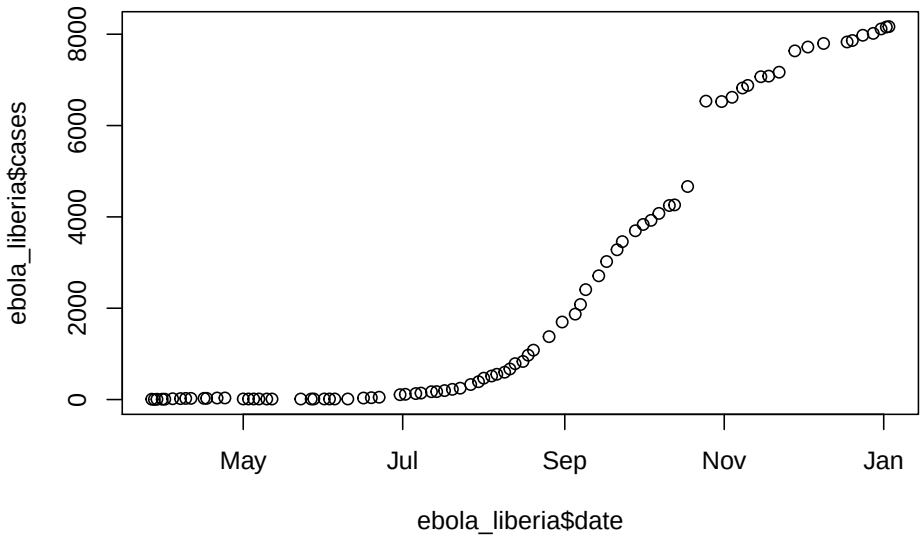
- Limit the `ebola_liberia` dataset just to the days with non-missing case data. How many observations do you have now?
- Write a pipe chain for the full data cleaning process for creating `ebola_liberia` up to this point. *Hint: Try using the* ***`arrange`*** *function from* ***`dplyr`*** *to re-order the data by dates in this pipe.*
- Try using the basic plotting function, `plot()`, to plot the number of cases over time. Do you think that the `cases` variable is measuring the count of cases for that day, or the cumulative number of cases up to that day? See if you can figure out more on Caitlin Rivers' GitHub documentation. Do you notice any potential data quality issues in this data? *Hint: The* ***`plot()`*** *function takes, as required arguments, the vector you want to plot on the x-axis and then the vector you want to plot on the y-axis, like* ***`plot([x vector], [y vector])`****. If you are pulling the vectors from a dataset, you will need to use indexing to pull out the column you want as a vector, like* ***`plot([dataframe name]$[column name for x], [dataframe]$[column name for y])`****.*

Example R code:

```
## Remove observations with missing cases
ebola_liberia <- filter(ebola_liberia, !is.na(cases))
nrow(ebola_liberia)
```

```
## [1] 83
```

```
## Rewrite the data cleaning for `ebola_liberia` using a pipe chain
ebola_liberia <- ebola %>%
  select(Date, Cases_Liberia, Deaths_Liberia) %>%
  rename(date = Date, cases = Cases_Liberia, deaths = Deaths_Liberia) %>%
  mutate(date = mdy(date)) %>%
  arrange(date) %>%
  filter(!is.na(cases))

## Plot the data
plot(ebola_liberia$date, ebola_liberia$cases)
```



0.20.5 A taste of what's to come...

Here's an example to give you a feel for why it's worth learning all these different things about directories, `list.files`, and pathnames.

The `measles_data` subdirectory includes counts of measles made at different times in different cities in California. Say that we wanted to read them all in and make put them into one long dataframe with the variables `city`, `count`, and `date`. You can put together the things you've learned so far, along with a few new ideas (including doing a loop), to do this very easily.

We'll talk more later about using loops and functions to make your programming more efficient, but for right now just look through this code and see if you can get a feel for how it's working (make sure your directory for this course is your working directory):

```
## Create a vector of all the file names in the `measles_data` subdirectory
measles_files <- list.files("data/measles_data")
measles_files
```

```
##  [1] "02-09-2015.txt" "02-11-2015.txt" "02-13-2015.txt" "02-18-2015.txt"
##  [5] "02-20-2015.txt" "02-23-2015.txt" "02-25-2015.txt" "02-27-2015.txt"
##  [9] "03-02-2015.txt" "03-06-2015.txt" "03-13-2015.txt" "03-20-2015.txt"
## [13] "03-27-2015.txt" "04-03-2015.txt" "04-10-2015.txt" "04-17-2015.txt"
```

```
## Create a vector of all the dates for files by taking the
## `.txt` off each of these file names and change it into
## a date
measles_dates <- sub(".txt", "", measles_files)
measles_dates
```

```
##  [1] "02-09-2015" "02-11-2015" "02-13-2015" "02-18-2015" "02-20-2015"
##  [6] "02-23-2015" "02-25-2015" "02-27-2015" "03-02-2015" "03-06-2015"
## [11] "03-13-2015" "03-20-2015" "03-27-2015" "04-03-2015" "04-10-2015"
## [16] "04-17-2015"
```

```
class(measles_dates)
```

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

```
measles_dates <- mdy(measles_dates)
measles_dates
```

```
##  [1] "2015-02-09" "2015-02-11" "2015-02-13" "2015-02-18" "2015-02-20"
##  [6] "2015-02-23" "2015-02-25" "2015-02-27" "2015-03-02" "2015-03-06"
## [11] "2015-03-13" "2015-03-20" "2015-03-27" "2015-04-03" "2015-04-10"
## [16] "2015-04-17"
```

```
## Before I show the loop, let me talk you through some
## of the parts of it:
i <- 1 # I'm setting the index to 1

## Now I'll use `paste0` to create the first file name
## I want to read.
file_name <- paste0("data/measles_data/", measles_files[i])
file_name
```

```
## [1] "data/measles_data/02-09-2015.txt"
```

```
## Now I'll read in that tab-delimited file
df <- read_tsv(file_name, col_names = c("city", "count"))
head(df)
```

```
## # A tibble: 6 × 2
##                 city count
##                <chr> <int>
## 1            ALAMEDA     6
## 2        LOS ANGELES    20
## 3 City of Long Beach     2
## 4   City of Pasadena     4
## 5              MARIN     2
## 6             ORANGE    34
```

```
## Now I'll add on a column with the date for all the
## values from that file. Notice that I'm using `i` to
## index this, as well

df <- mutate(df, date = measles_dates[i])
head(df)
```

```
## # A tibble: 6 × 3
##                 city count       date
##                <chr> <int>     <date>
## 1            ALAMEDA     6 2015-02-09
## 2        LOS ANGELES    20 2015-02-09
## 3 City of Long Beach     2 2015-02-09
## 4   City of Pasadena     4 2015-02-09
## 5              MARIN     2 2015-02-09
## 6             ORANGE    34 2015-02-09
```

```
## Loop through and read in files. After the first file,
## add on the new information to the data that's already
## been read in. Note that you can use `rbind` to add on
## new rows to a dataframe as long as the new and old rows
## have the same number of columns and the same column names.
for(i in 1:length(measles_files)){
        file_name <- paste0("data/measles_data/", measles_files[i])
        df <- read.delim(file_name, header = FALSE,
```

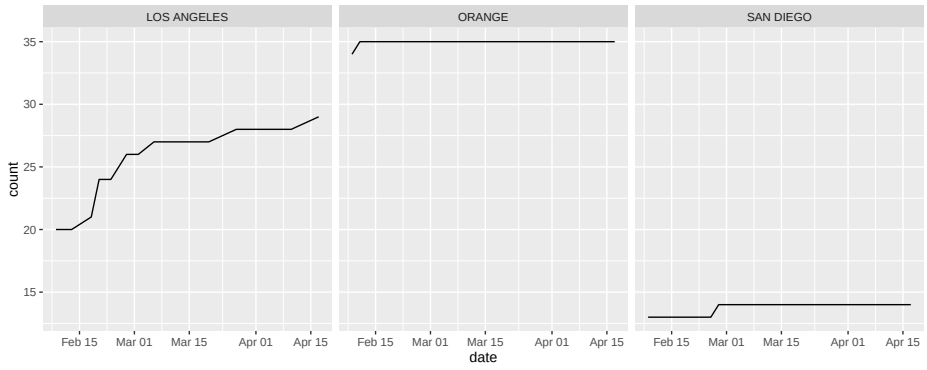
```
                        col.names = c("city", "count"))
        df <- mutate(df, date = measles_dates[i])
        if(i == 1){
                ca_measles <- df
        } else {
                 ca_measles <- rbind(ca_measles, df)
                }
}

dim(ca_measles)
```

```
## [1] 232   3
```

```
summary(ca_measles)
```

```
##                  city         count             date
##  ALAMEDA           : 16   Min.   : 1.000   Min.   :2015-02-09
##  City of Long Beach: 16   1st Qu.: 2.000   1st Qu.:2015-02-20
##  City of Pasadena  : 16   Median : 4.000   Median :2015-03-02
##  LOS ANGELES       : 16   Mean   : 8.698   Mean   :2015-03-07
##  MARIN             : 16   3rd Qu.:12.000   3rd Qu.:2015-03-27
##  ORANGE            : 16   Max.   :35.000   Max.   :2015-04-17
##  (Other)           :136
```

```
library(ggplot2)
ggplot(subset(ca_measles, city %in% c("LOS ANGELES", "SAN DIEGO", "ORANGE")),
       aes(x = date, y = count)) +
        geom_line()  +
        facet_grid(. ~ city)
```



Exploring data #1

Download a pdf of the lecture slides covering this topic.

0.21 Data from a package

So far we've covered three ways to get data into R:

1. From flat files (either on your computer or online)
2. From files like SAS and Excel
3. From R objects (i.e., using `load()`)

Many R packages come with their own data, which is very easy to load and use. For example, the `faraway` package, which complements Julian Faraway's book *Linear Models with R* (available as an ebook from the CSU library), has a dataset called `worldcup` that I'll use for some examples and that you'll use for part of this week's in-course exercise. To load this dataset, first load the package with the data (`faraway`) and then use the `data()` function with the dataset name ("worldcup") as the argument to the `data` function:

```
library(faraway)
data("worldcup")
```

Unlike most data objects you'll work with, datasets that are part of an R package will often have their own help files. You can access this help file for a dataset using the `?` operator with the dataset's name:

```
?worldcup
```

This helpful will usually include information about the size of the dataset, as well as definitions for each of the columns.

To get a list of all of the datasets that are available in the packages you currently have loaded, run `data()` without an option inside the parentheses:

```
data()
```

If you run the `library` function without any arguments (`library()`), it works in a similar way– R will open a list of all the R packages that you have installed on your computer and can open with a `library` call.

0.22 Plots to explore data

Exploratory data analysis is a key step in data analysis, and plotting your data in different ways is an important part of this process. In this section, I will focus on the basics of `ggplot2` plotting, to get you started creating some plots to explore your data. This section will focus on making **useful**, rather than **attractive** graphs, since at this stage we are focusing on exploring data for yourself rather than presenting results to others. Next week, I will explain more about how you can customize ggplot objects, to help you make plots to communicate with others.

All of the plots we'll make today will use the `ggplot2` package (another member of the tidyverse!). If you don't already have that installed, you'll need to install it. You then need to load the package in your current session of R:

```
# install.packages("ggplot2")  ## Uncomment and run if you don't have `ggplot2` instal
library(ggplot2)
```

The process of creating a plot using `ggplot2` follows conventions that are a bit different than most of the code you've seen so far in R (although it is somewhat similar to the idea of piping I introduced in the last chapter). The basic steps behind creating a plot with `ggplot2` are:

1. Create an object of the `ggplot` class, typically specifying the **data** and some or all of the **aesthetics**;
2. Add on **geoms** and other elements to create and customize the plot, using `+`.

You can add on one or many geoms and other elements to create plots that range from very simple to very customized. This week, we'll focus on simple geoms and added elements, and then explore more detailed customization next week.

If R gets to the end of a line and there is not some indication that the call is not over (e.g., `%>%` for piping or `+` for `ggplot2` plots), R interprets that as a message to run the call without reading in further code. A common error when writing `ggplot2` code is to put the `+` to add a geom or element at the beginning of a line rather than the end of a previous line– in this case, R will try to execute the call too soon. To avoid errors, be sure to end lines with `+`, don't start lines with it.

0.22.1 Initializing a ggplot object

The first step in creating a plot using `ggplot2` is to create a ggplot object. This object will not, by itself, create a plot with anything in it. Instead, it typically specifies the data frame you want to use and which aesthetics will be mapped to certain columns of that data frame (aesthetics are explained more in the next subsection).

Use the following conventions to initialize a ggplot object:

```
## Generic code
object <- ggplot(dataframe, aes(x = column_1, y = column_2))
```

The data frame is the first parameter in a `ggplot` call and, if you like, you can use the parameter definition with that call (e.g., `data = dataframe`). Aesthetics are defined within an `aes` function call that typically is used within the `ggplot` call.

While the `ggplot` call is the place where you will most often see an `aes` call, `aes` can also be used within the calls to add specific geoms. This can be particularly useful if you want to map aesthetics differently for different geoms in your plot. We'll see some examples of this use of `aes` more in later sections, when we talk about customizing plots. The `data` parameter can also be used in geom calls, to use a different data frame from the one defined when creating the original ggplot object, although this tends to be less common.

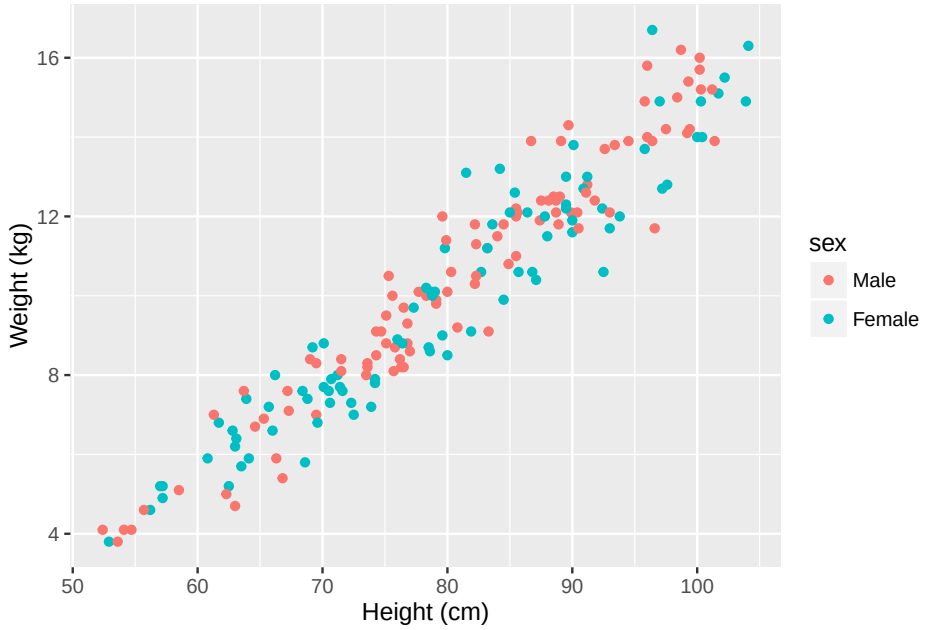


Figure 6: Example of how different properties of a plot can show different elements to the data. Here, color indicates gender, position along the x-axis shows height, and position along the y-axis shows weight. This example is a subset of data from the 'nepali' dataset in the 'faraway' package.

0.22.2 Plot aesthetics

Aesthetics are properties of the plot that can show certain elements of the data. For example, in Figure 6, color shows (is mapped to) gender, x-position shows height, and y-position shows weight in a sample data set of measurements of children in Nepal.

Any of these aesthetics could also be given a constant value, instead of being mapped to an element of the data. For example, all the points could be red, instead of showing gender.

Which aesthetics are required for a plot depend on which geoms (more on those in a second) you're adding to the plot. You can find out the aesthetics you can use for a geom in the "Aesthetics" section of the geom's help file (e.g., `?geom_point`). Required aesthetics are in bold in this section of the help file and optional ones are not. Common plot aesthetics you might want to specify include:

Code	Description
‘x‘	Position on x-axis
‘y‘	Position on y-axis
‘shape‘	Shape
‘color‘	Color of border of elements
‘fill‘	Color of inside of elements
‘size‘	Size
‘alpha‘	Transparency (1: opaque; 0: transparent)
‘linetype‘	Type of line (e.g., solid, dashed)

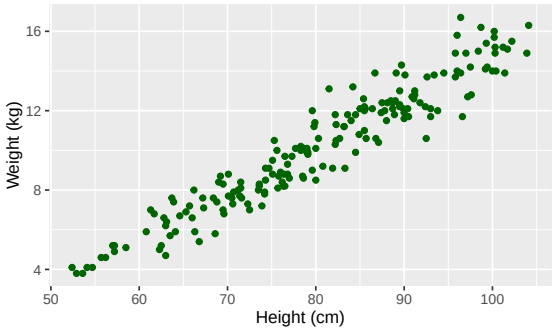
0.22.3 Adding geoms

Next, you'll want to add one or more `geoms` to create the plot. You can add these with `+` after the `ggplot` statement to initialize the ggplot object. Some of the most common geoms are:

Plot type	ggplot2 function
Histogram (1 numeric variable)	‘geom_histogram‘
Scatterplot (2 numeric variables)	‘geom_point‘
Boxplot (1 numeric variable, possibly 1 factor variable)	‘geom_boxplot‘
Line graph (2 numeric variables)	‘geom_line‘

0.22.4 Constant aesthetics

Instead of mapping an aesthetic to an element of your data, you can use a constant value for it. For example, you may want to make all the points green, rather than having color map to gender:



In this case, you'll define that aesthetic when you add the geom, outside of an `aes` statement. In R, you can specify the shape of points with a number. Figure 7 shows the shapes that correspond to the numbers 1 to 25 in the `shape` aesthetic. This figure also provides an example of the difference between color

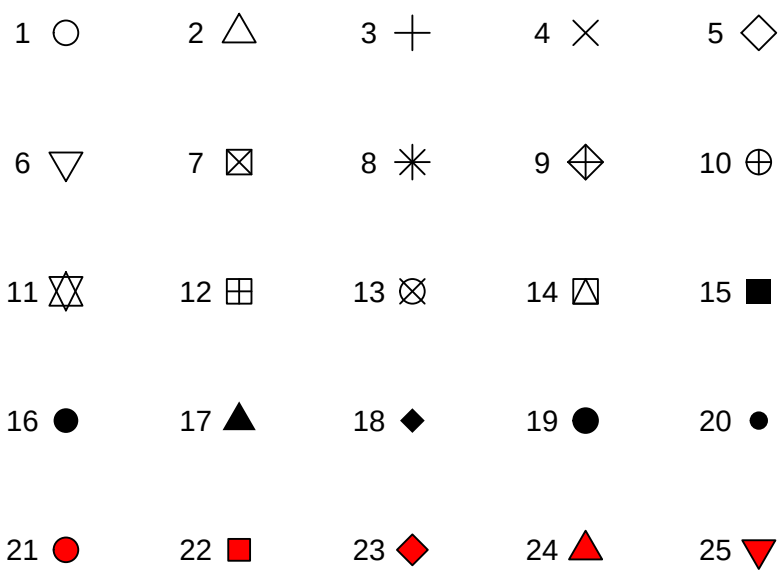


Figure 7: Examples of the shapes corresponding to different numeric choices for the 'shape' aesthetic. For all examples, 'color' is set to black and 'fill' to red.

(black for all these example points) and fill (red for these examples). You can see that some point shapes include a fill (21 for example), while some are either empty (1) or solid (19).

If you want to set color to be a constant value, you can do that in R using character strings for different colors. Figure 8 gives an example of some of the different blues available in R. To find links to listings of different R colors, google "R colors" and search by "Images".

0.22.5 Useful plot additions

There are also a number of elements that you can add onto a `ggplot` object using `+`. A few that are used very frequently are:

Element	Description
'ggtitle'	Plot title
'xlab', 'ylab'	x- and y-axis labels
'xlim', 'ylim'	Limits of x- and y-axis

0.22.6 Example dataset

For the example plots, I'll use a dataset in the `faraway` package called `nepali`. This gives data from a study of the health of a group of Nepalese children.

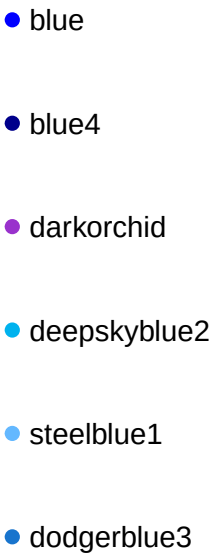


Figure 8: Example of available shades of blue in R.

```
library(faraway)
data(nepali)
```

I'll be using functions from `dplyr` and `ggplot2`, so those need to be loaded:

```
library(dplyr)
library(ggplot2)
```

Each observation is a single measurement for a child; there can be multiple observations per child. I used the following code to select only the columns for child id, sex, weight, height, and age. I also used `distinct` to limit the dataset to only include one measurement for each chile, the child's first measurement in the dataset.

```
nepali <- nepali %>%
  select(id, sex, wt, ht, age) %>%
  mutate(id = factor(id),
         sex = factor(sex, levels = c(1, 2),
                      labels = c("Male", "Female"))) %>%
  distinct(id, .keep_all = TRUE)
```

After this cleaning, the data looks like this:

```
head(nepali)
```

```
##       id    sex   wt    ht age
## 1 120011   Male 12.8  91.2  41
## 2 120012 Female 14.9 103.9  57
## 3 120021 Female  7.7  70.1   8
## 4 120022 Female 12.1  86.4  35
## 5 120023   Male 14.2  99.4  49
## 6 120031   Male 13.9  96.4  46
```

0.22.7 Histograms

Histograms show the distribution of a single variable. Therefore, `geom_histogram()` requires only one main aesthetic, `x`, the (numeric) vector for which you want to create a histogram. For example, to create a histogram of children's heights for the Nepali dataset (Figure 9), run:

```
ggplot(nepali, aes(x = ht)) +
  geom_histogram()
```

If you run the code with no arguments for `binwidth` or `bins` in `geom_histogram`, you will get a message saying "`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.". This message is just saying that a default number of bins was used to create the histogram. You can use arguments to change the number of bins used, but often this default is fine. You may also get a message that observations with missing values were removed.

You can add some elements to the histogram now to customize it a bit. For example (Figure @ref()), you can add a figure title (`ggtitle`) and clearer labels for the x-axis (`xlab`). You can also change the range of values shown by the x-axis (`xlim`).

```
ggplot(nepali, aes(x = ht)) +
  geom_histogram(fill = "lightblue", color = "black") +
  ggtitle("Height of children") +
  xlab("Height (cm)") + xlim(c(0, 120))
```

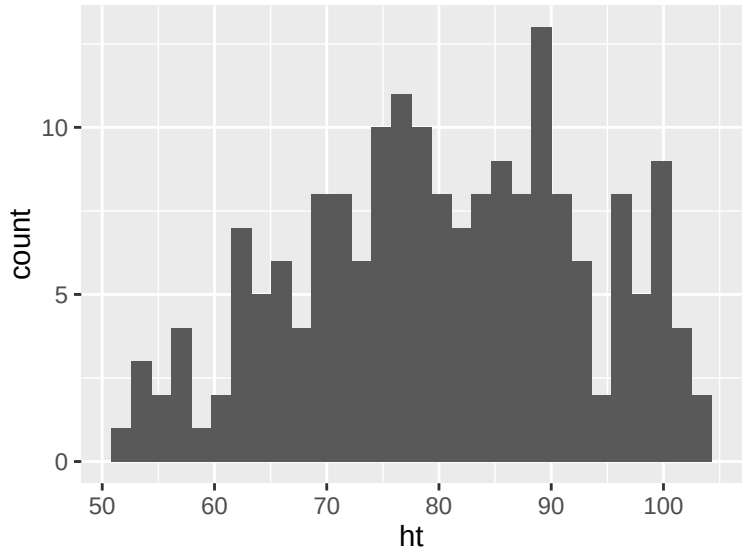


Figure 9: Basic example of plotting a histogram with 'ggplot2'. This histogram shows the distribution of heights for the first recorded measurements of each child in the 'nepali' dataset.

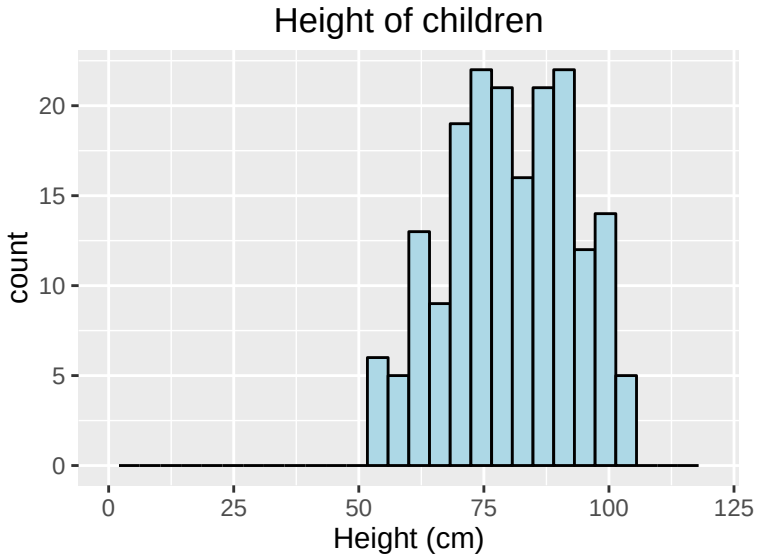


Figure 10: Example of adding ggplot elements to customize a histogram.

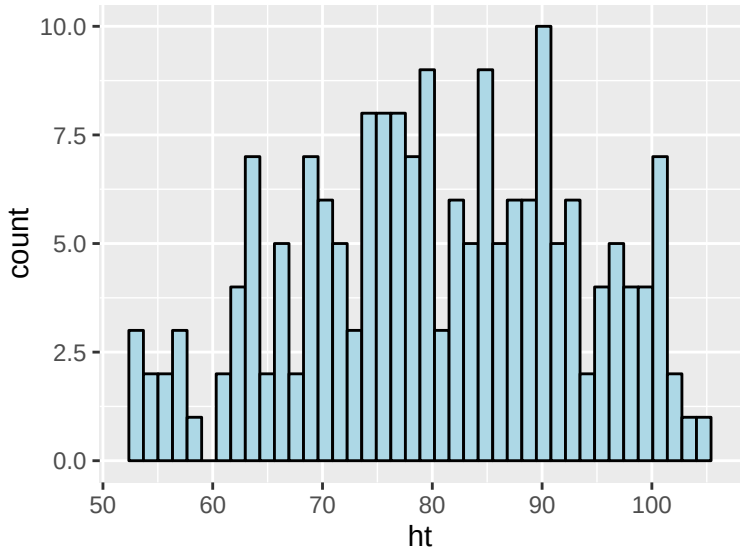


Figure 11: Example of using the 'bins' argument to change the number of bins used in a histogram.

The geom `geom_histogram` also has special argument for setting the number of width of the bins used in the histogram. Figure **??** shows an example of how you can use the `bins` argument to change the number of bins that are used to make the histogram of height for the `nepali` dataset.

```
ggplot(nepali, aes(x = ht)) +
  geom_histogram(fill = "lightblue", color = "black",
                 bins = 40)
```

Similarly, the `binwidth` argument can be used to set the width of bins. Figure 12 shows an example of using this function to create a histogram of the Nepali children's heights with binwidths of 10 centimeters (note that this argument is set in the same units as the x variable).

```
ggplot(nepali, aes(x = ht)) +
  geom_histogram(fill = "lightblue", color = "black",
                 binwidth = 10)
```

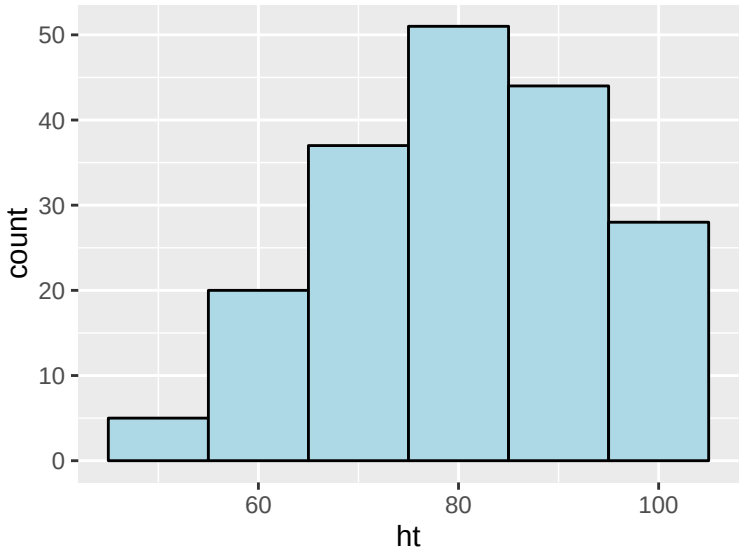


Figure 12: Example of using the 'binwidth' argument to set the width of each bin used in a histogram.

0.22.8 Scatterplots

A scatterplot shows how one variable changes as another changes. You can use the `geom_point` geom to create a scatterplot. For example, to create a scatterplot of height versus age for the Nepali data (Figure 13), you can run the following code:

```
ggplot(nepali, aes(x = ht, y = wt)) +
  geom_point()
```

Again, you can use some of the options and additions to change the plot appearance. For example, to add a title, change the x- and y-axis labels, and change the color and size of the points on the scatterplot (Figure 14), you can run:

```
ggplot(nepali, aes(x = ht, y = wt)) +
  geom_point(color = "blue", size = 0.5) +
  ggtitle("Weight versus Height") +
  xlab("Height (cm)") + ylab("Weight (kg)")
```

You can also try mapping another variable in the dataset to the `color` aesthetic. For example, to use color to show the sex of each child in the scatterplot (Figure 15), you can run:

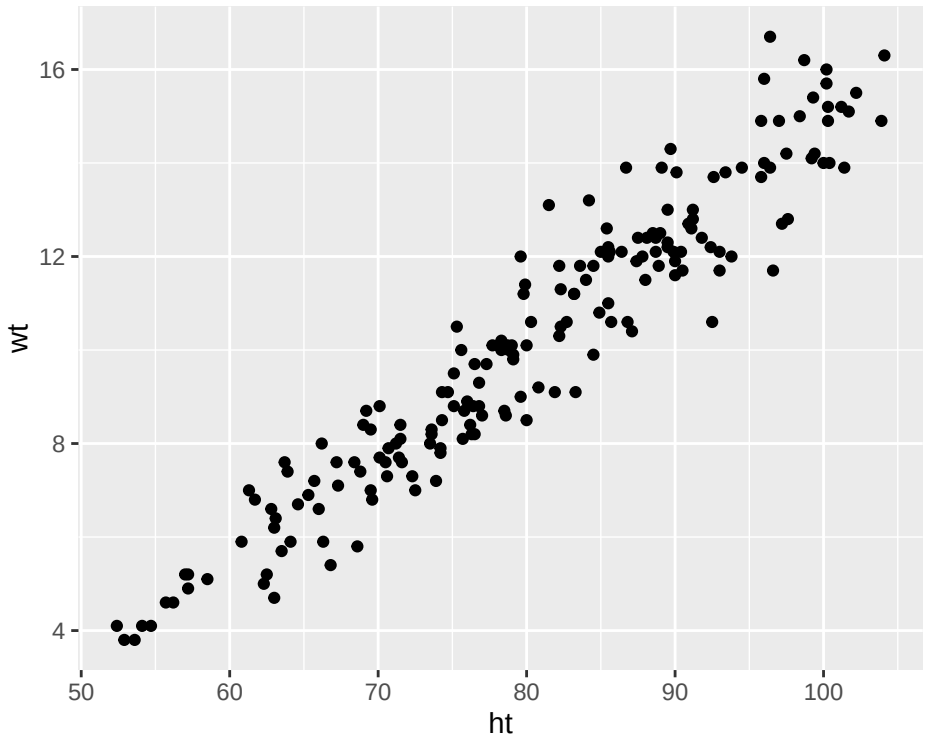


Figure 13: Example of creating a scatterplot. This scatterplot shows the relationship between children's heights and weights within the nepali dataset.

```
ggplot(nepali, aes(x = ht, y = wt, color = sex)) +
  geom_point(size = 0.5) +
  ggtitle("Weight versus Height") +
  xlab("Height (cm)") + ylab("Weight (kg)")
```

0.22.9 Boxplots

Boxplots can be used to show the distribution of a continuous variable. To create a boxplot, you can use the `geom_boxplot` geom. To plot a boxplot for a single, continuous variable, you can map that variable to `y` in the `aes` call, and map `x` to the constant `1`. For example, to create a boxplot of the heights of children in the Nepali dataset (Figure 16), you can run:

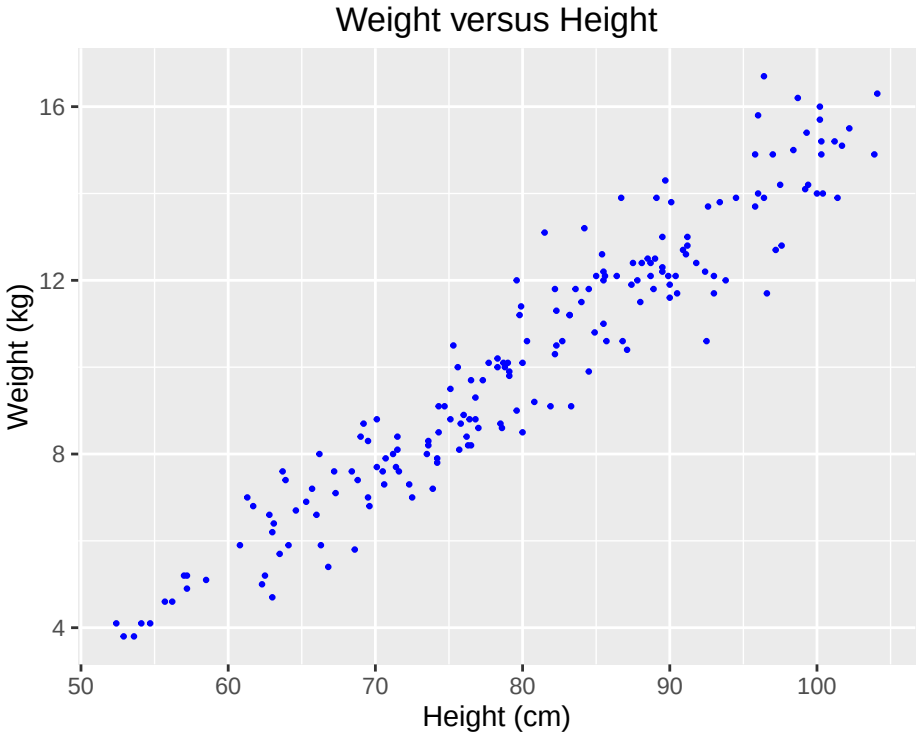


Figure 14: Example of adding ggplot elements to customize a scatterplot.

```
ggplot(nepali, aes(x = 1, y = ht)) +
  geom_boxplot() +
  xlab("")+ ylab("Height (cm)")
```

You can also create separate boxplots, one for each level of a factor (Figure 17). In this case, you'll need to include two aesthetics (`x` and `y`) when you initialize the ggplot object The `y` variable is the variable for which the distribution will be shown, and the `x` variable should be a discrete (categorical or TRUE/FALSE) variable, and will be used to group the variable. This `x` variable should also be specified as the grouping variable, using `group` within the aesthetic call.

```
ggplot(nepali, aes(x = sex, y = ht, group = sex)) +
  geom_boxplot() +
  xlab("Sex")+ ylab("Height (cm)")
```

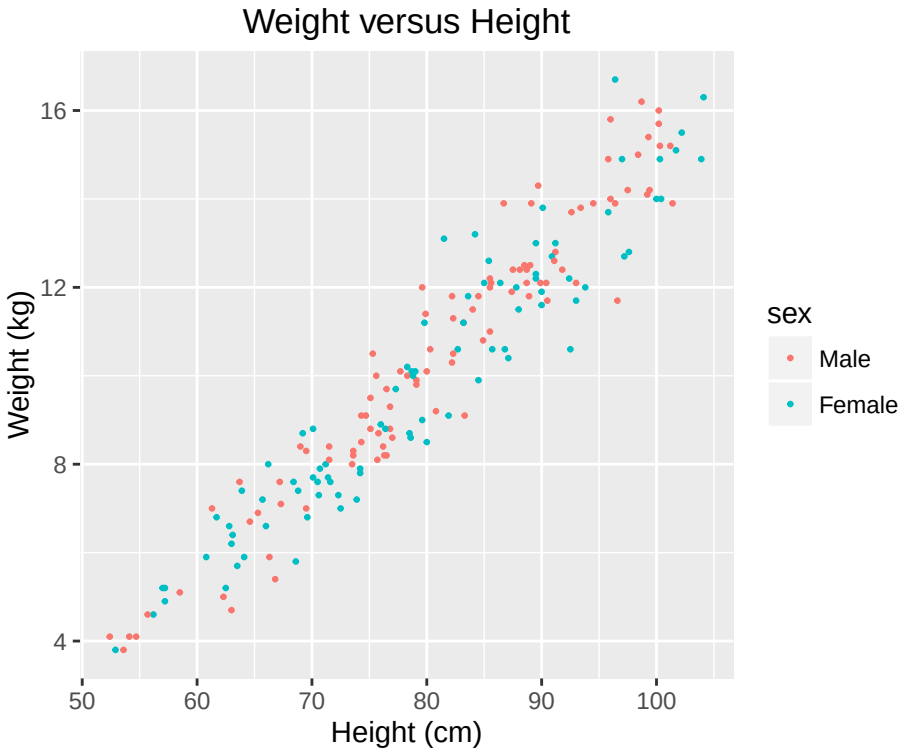


Figure 15: Example of mapping color to an element of the data in a scatterplot.

0.22.10 Extensions of `ggplot2`

There are lots of R extensions for creating other interesting plots. For example, you can use the `ggpairs` function from the `GGally` package to plot all pairs of scatterplots for several variables (Figure 18).

```
library(GGally)
ggpairs(nepali %>% select(sex, wt, ht, age))
```

Notice how this output shows continuous and binary variables differently. For example, the center diagonal shows density plots for continuous variables, but a bar chart for the categorical variable.

See `https://www.ggplot2-exts.org` to find more `ggplot2` extensions.

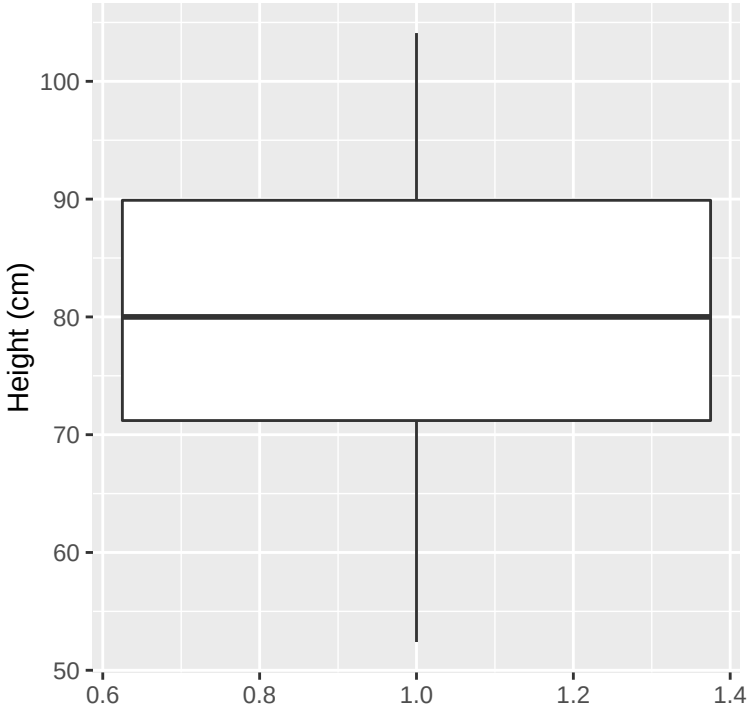


Figure 16: Example of creating a boxplot. The example shows the distribution of height data for children in the nepali dataset.

0.23 Simple statistics functions

0.23.1 Summary statistics

To explore your data, you'll need to be able to calculate some simple statistics for vectors, including calculating the mean and range of continuous variables and counting the number of values in each category of a factor or logical vector.

Here are some simple statistics functions you will likely use often:

Function	Description
`range()`	Range (minimum and maximum) of vector
`min()`, `max()`	Minimum or maximum of vector
`mean()`, `median()`	Mean or median of vector
`sd()`	Standard deviation of vector
`table()`	Number of observations per level for a factor vector
`cor()`	Determine correlation(s) between two or more vectors
`summary()`	Summary statistics, depends on class

All of these functions take, as the main argument, the vector or vectors for which you want the statistic. If there are missing values in the vector, you'll typically need to add an argument to say what to do with the missing values. The parameter name for this varies by function, but for many of these functions it's `na.rm = TRUE` or `use="complete.obs"`.

```
mean(nepali$wt, na.rm = TRUE)
```

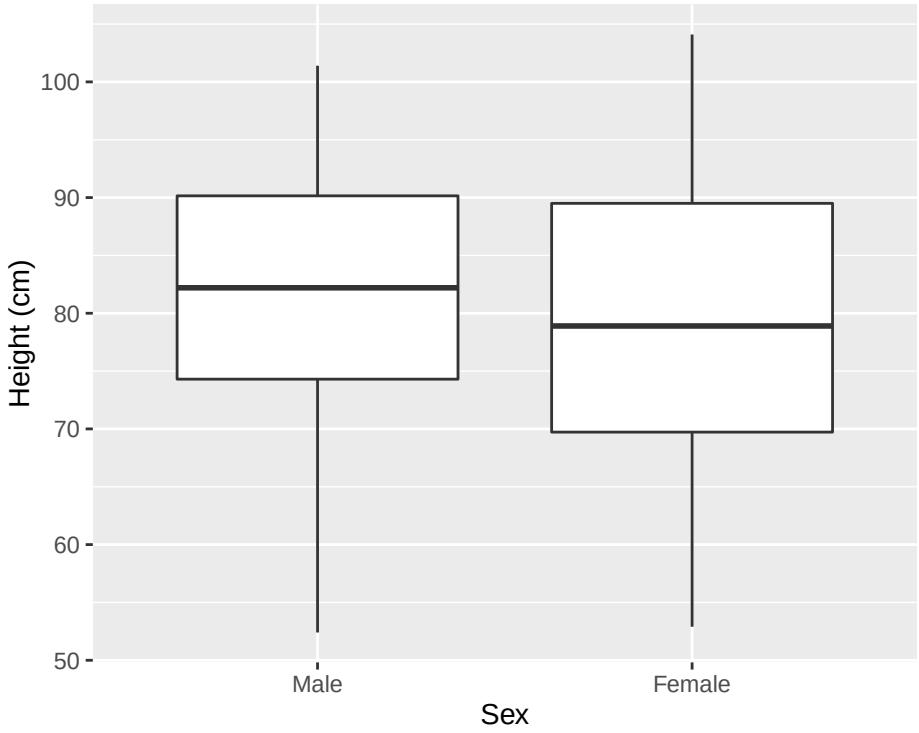


Figure 17: Example of creating separate boxplots, divided by a categorical grouping variable in the data.

```
table(nepali$sex)
```

```
##
##   Male Female
##    107     93
```

Most of these functions take a single vector as the input. The `cor` function, however, calculates the correlation between vectors and so takes two or more vectors. If you give it multiple values, it will give the correlation matrix for all the vectors.

```
cor(nepali$wt, nepali$ht, use = "complete.obs")
```

```
## [1] 0.9571535
```

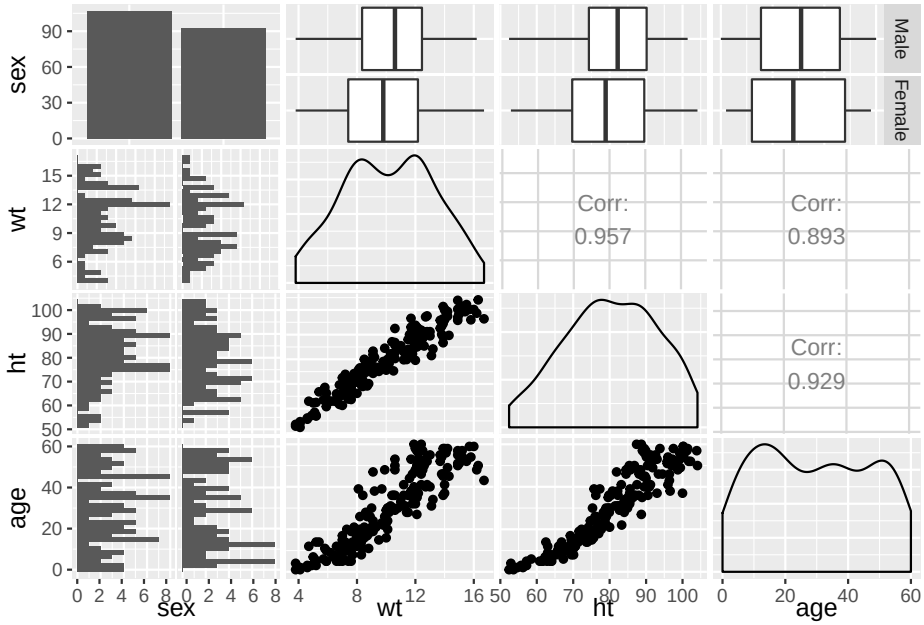


Figure 18: Example of using ggpairs from the GGally package for exploratory data analysis.

```
cor((nepali %>% select(wt, ht, age)), use = "complete.obs")
```

```
##            wt        ht       age
## wt  1.0000000 0.9571535 0.8931195
## ht  0.9571535 1.0000000 0.9287129
## age 0.8931195 0.9287129 1.0000000
```

R supports object-oriented programming. Your first taste of this shows up with the `summary` function. For the `summary` function, R does not run the same code every time. Instead, R first checks what type of object was input to `summary`, and then it runs a function (*method*) specific to that type of object. For example, if you input a continuous vector, like the `ht` column in `nepali`, to `summary`, the function will return the mean, median, range, and 25th and 75th percentile values:

```
summary(nepali$wt)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's
##    3.80    7.90   10.10   10.18   12.40   16.70      15
```

However, if you submit a factor vector, like the `sex` column in `nepali`, the `summary` function will return a count of how many elements of the vector are in each factor level (as a note, you could do the same thing with the `table` function):

```
summary(nepali$sex)
```

```
##   Male Female
##    107     93
```

The `summary` function can also input other data structures, including dataframes, lists, and special object types, like regression model objects. In each case, it performs different actions specific to the object type. Later in this section, we'll cover regression models, and see what the `summary` function returns when it is used with regression model objects.

0.23.2 `summarize` function

You will often want to use these functions in conjunction with the `summarize` function in `dplyr`. For example, to create a new dataframe with the mean weight of children in the `nepali` dataset, you can use `mean` inside a `summarize` function:

```
nepali %>%
  summarize(mean_wt = mean(wt, na.rm = TRUE))
```

```
##    mean_wt
## 1 10.18432
```

There are also some special functions that you can use with `summarize`. For example, the `n` function will calculate the number of observations and the `first` function will return the first value of a column:

```
nepali %>%
  summarize(n_children =n(),
            first_id = first(id))
```

```
##   n_children first_id
## 1        200   120011
```

See the "summary function" section of the the RStudio Data Wrangling cheatsheet for more examples of these special functions.

Often, you will be more interested in summaries within certain groupings of your data, rather than overall summaries. For example, you may be interested in mean height and weight by sex, rather than across all children, for the `nepali` data. It is very easy to calculate these grouped summaries using `dplyr`– you just need to group data using the `group_by` function (also a `dplyr` function) before you run the `summarize` function:

```
nepali %>%
  group_by(sex) %>%
  summarize(mean_wt = mean(wt, na.rm = TRUE),
            n_children =n(),
            first_id = first(id))
```

```
## # A tibble: 2 × 4
##      sex   mean_wt n_children first_id
##   <fctr>     <dbl>      <int>   <fctr>
## 1   Male 10.497980        107   120011
## 2 Female  9.823256         93   120012
```

Don't forget that you need to save the output to a new object if you want to use it later. The above code, which creates a dataframe with summaries for Nepali children by sex, will only be printed out to your console if run as-is. If you'd like to save this output as an object to use later (for example, for a plot or table), you need to assign it to an R object.

0.24 Logical vectors

Last week, you learned a lot about logical statements and how to use them with the `filter` function. You can also use logical vectors, created with these logical statements, for a lot of other things. For example, you can use them directly in the square bracket indexing (`[..., ...]`) to pull out just the rows of a dataframe that meet a certain condition.

When you run a logical statement on a vector, you create a logical vector the same length as the original vector:

```
is_male <- nepali$sex == "Male"
length(nepali$sex)
```

```
## [1] 200
```

```
length(is_male)
```

```
## [1] 200
```

The logical vector (`is_male` in this example) will have the value `TRUE` at any position where the original vector (`nepali$sex` in this example) met the logical condition you tested, and `FALSE` anywhere else:

```
head(nepali$sex)
```

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

```
head(is_male)
```

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

You can "flip" this logical vector (i.e., change every `TRUE` to `FALSE` and vice-versa) using the *bang operator*, `!`:

```
head(is_male)
```

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

```
head(!is_male)
```

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

The bang operator turns out to be very useful. You will often find cases where it's difficult to write a logical vector to get what you want, but fairly easy to write the inverse (find everything you don't want). One example is filtering down to non-missing values– the `is.na` function will return `TRUE` for any value that is `NA`, so you can use `!is.na()` to identify any non-missing values.

You can do a few cool things with a logical vector. For example, you can use it with indexing to pull out just the rows of a dataframe where `is_male` is `TRUE`:

```
head(nepali[is_male, ])
```

```
##        id  sex   wt   ht age
## 1  120011 Male 12.8 91.2  41
## 5  120023 Male 14.2 99.4  49
## 6  120031 Male 13.9 96.4  46
## 7  120051 Male  8.3 69.5   8
## 9  120053 Male 15.8 96.0  54
## 11 120062 Male 12.1 89.9  57
```

Or, with `!`, just the rows where `is_male` is `FALSE`:

```
head(nepali[!is_male, ])
```

```
##        id    sex   wt    ht age
## 2  120012 Female 14.9 103.9  57
## 3  120021 Female  7.7  70.1   8
## 4  120022 Female 12.1  86.4  35
## 8  120052 Female 11.8  83.6  32
## 10 120061 Female  8.7  78.5  26
## 15 120082 Female 11.2  79.8  36
```

For these cases, the length of the logical vector and the number of rows in the dataframe will match.

You can also use `sum()` and `table()` with a logical vector to find out how many of the values in the vector are `TRUE` AND `FALSE`. In the example, you can use these functions to find out how many males and females are in the dataset:

```
sum(is_male)
```

```
## [1] 107
```

```
sum(!is_male)
```

```
## [1] 93
```

```
table(is_male)
```

```
## is_male
## FALSE  TRUE
##    93   107
```

Note that you could also achieve the same thing with `dplyr` functions. For example, you could use `mutate` with a logical statement to create an `is_male` column in the `nepali` dataframe, then group by the new `is_male` column and summarize, using the `n` function to count the number of observations in each group:

```
nepali %>%
  mutate(is_male = sex == "Male") %>%
  group_by(is_male) %>%
  summarize(n_children = n())
```

```
## # A tibble: 2 × 2
##   is_male n_children
##     <lgl>      <int>
## 1   FALSE         93
## 2    TRUE        107
```

0.25 Regression models

0.25.1 Formula structure

Regression models can be used to estimate how the expected value of a *dependent variable* changes as *independent variables* change.

In R, regression formulas take this structure:

```
## Generic code
[response variable] ~ [indep. var. 1] +  [indep. var. 2] + ...
```

Notice that a tilde, `~`, is used to separate the independent and dependent variables and that a plus sign, `+`, is used to join independent variables. This format mimics the statistical notation:

$$Y_i \sim X_1 + X_2 + X_3$$

You will use this type of structure in R fo a lot of different function calls, including those for linear models (fit with the `lm` function) and generalized linear models (fit with the `glm` function).

There are some conventions that can be used in R formulas. Common ones include:

Convention	Meaning
`I()`	evaluate the formula inside `I()` before fitting (e.g., `I(x1 + x2)`)
`:`	fit the interaction between `x1` and `x2` variables
`*`	fit the main effects and interaction for both variables (e.g., `x1*x2` equals `x1 + x2 + x1:x2`)
`.`	include as independent variables all variables other than the response (e.g., `y ~ .`)
`1`	intercept (e.g., `y ~ 1` for an intercept-only model)
`-`	do not include a variable in the dataframe as an independent variables (e.g., `y ~ . - x1`); usually used in conjunction with `.` or `1`

0.25.2 Linear models

To fit a linear model, you can use the function `lm()`. This function is part of the `stats` package, which comes installed with base R. In this function, you can use the `data` option to specify the dataframe from which to get the vectors.

```
mod_a <- lm(wt ~ ht, data = nepali)
```

This previous call fits the model:

$$Y_i = \beta_0 + \beta_1 X_{1,i} + \epsilon_i$$

where:

- Y_i : weight of child i
- $X_{1,i}$: height of child i

If you run the `lm` function without saving it as an object, R will fit the regression and print out the function call and the estimated model coefficients:

```
lm(wt ~ ht, data = nepali)
```

```
##
## Call:
## lm(formula = wt ~ ht, data = nepali)
##
## Coefficients:
## (Intercept)           ht
##     -8.6948       0.2351
```

However, to be able to use the model later for things like predictions and model assessments, you should save the output of the function as an R object:

```
mod_a <- lm(wt ~ ht, data = nepali)
```

This object has a special class, `lm`:

```
class(mod_a)
```

```
## [1] "lm"
```

This class is a special type of list object. If you use `is.list` to check, you can confirm that this object is a list:

```
is.list(mod_a)
```

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

There are a number of functions that you can apply to an `lm` object. These include:

Function	Description
`summary`	Get a variety of information on the model, including coefficients and p-values for the coefficients
`coefficients`	Pull out just the coefficients for a model
`fitted`	Get the fitted values from the model (for the data used to fit the model)
`plot`	Create plots to help assess model assumptions
`residuals`	Get the model residuals

For example, you can get the coefficients from the model by running:

```
coefficients(mod_a)
```

```
## (Intercept)          ht
##   -8.694768    0.235050
```

The estimated coefficient for the intercept is always given under the name "(Intercept)". Estimated coefficients for independent variables are given based on their column names in the original data ("ht" here, for β_1, or the estimated increase in expected weight for a one unit increase in height).

You can use the output from a `coefficients` call to plot a regression line based on the model fit on top of points showing the original data (Figure 19).

```
mod_coef <- coefficients(mod_a)
ggplot(nepali, aes(x = ht, y = wt)) +
  geom_point(size = 0.2) +
  xlab("Height (cm)") + ylab("Weight (kg)") +
  geom_abline(aes(intercept = mod_coef[1],
                  slope = mod_coef[2]), col = "blue")
```

You can also add a linear regression line to a scatterplot by adding the geom `geom_smooth` using the argument `method = "lm"`.

You can use the function `residuals` on an `lm` object to pull out the residuals from the model fit:

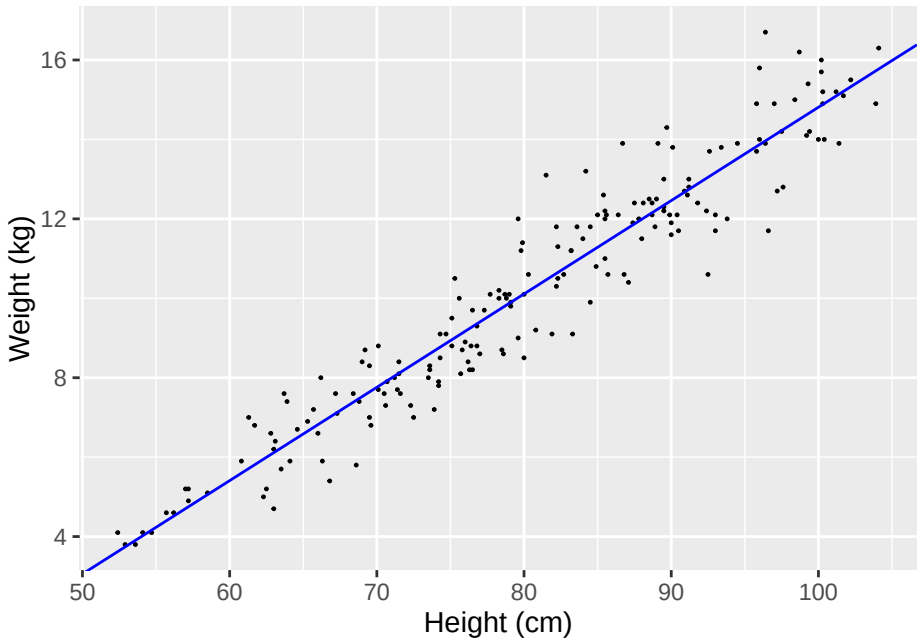


Figure 19: Example of using the output from a coefficients call to add a regression line to a scatterplot.

```
head(residuals(mod_a))
```

```
##          1          2          3          4          5          6
##  0.05820415 -0.82693141 -0.08223993  0.48644436 -0.46920621 -0.06405608
```

The result of a `residuals` call is a vector with one element for each of the non-missing observations (rows) in the dataframe you used to fit the model. Each value gives the different between the model fitted value and the observed value for each of these observations, in the same order the observations show up in the dataframe. The residuals are in the same order as the observations in the original dataframe.

You can also use the shorter function `coef` as an alternative to `coefficients` and the shorter function `resid` as an alternative to `residuals`.

As noted in the subsection on simple statistics functions, the `summary` function returns different output depending on the type of object that is input to the

function. If you input a regression model object to `summary`, the function gives you a lot of information about the model. For example, here is the output returned by running `summary` for the linear regression model object we just created:

```
summary(mod_a)
```

```
##
## Call:
## lm(formula = wt ~ ht, data = nepali)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.44736 -0.55708  0.01925  0.49941  2.73594
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -8.694768   0.427398  -20.34   <2e-16 ***
## ht           0.235050   0.005257   44.71   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9017 on 183 degrees of freedom
##   (15 observations deleted due to missingness)
## Multiple R-squared:  0.9161, Adjusted R-squared:  0.9157
## F-statistic:  1999 on 1 and 183 DF,  p-value: < 2.2e-16
```

This output includes a lot of useful elements, including (1) basic summary statistics for the residuals (to meet model assumptions, the median should be around zero and the absolute values fairly similar for the first and third quantiles), (2) coefficient estimates, standard errors, and p-values, and (3) some model summary statistics, including residual standard error, degrees of freedom, number of missing observations, and F-statistic.

The object returned by the `summary()` function when it is applied to an `lm` object is a list, which you can confirm using the `is.list` function:

```
is.list(summary(mod_a))
```

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

With any list, you can use the `names` function to get the names of all of the different elements of the object:

```
names(summary(mod_a))
```

```
##  [1] "call"         "terms"        "residuals"    "coefficients"
##  [5] "aliased"      "sigma"        "df"           "r.squared"
##  [9] "adj.r.squared" "fstatistic"   "cov.unscaled"  "na.action"
```

You can use the `$` operator to pull out any element of the list. For example, to pull out the table with information on the estimated model coefficients, you can run:

```
summary(mod_a)$coefficients
```

```
##              Estimate  Std. Error   t value      Pr(>|t|)
## (Intercept) -8.694768 0.427397843 -20.34350  7.424640e-49
## ht           0.235050 0.005256822  44.71334 1.962647e-100
```

The `plot` function, like the `summary` function, will give different output depending on the class of the object that you input. For an `lm` object, you can use the `plot` function to get a number of useful diagnostic plots that will help you check regression assumptions (Figure 20):

```
plot(mod_a)
```

You can also use binary variables or factors as independent variables in regression models. For example, in the `nepali` dataset, `sex` is a factor variable with the levels "Male" and "Female". You can fit a linear model of weight regressed on sex for this data with the call:

```
mod_b <- lm(wt ~ sex, data = nepali)
```

This call fits the model:

$$Y_i = \beta_0 + \beta_1 X_{1,i} + \epsilon_i$$

where $X_{1,i}$: sex of child i, where 0 = male and 1 = female.

Here are the estimated coefficients from fitting this model:

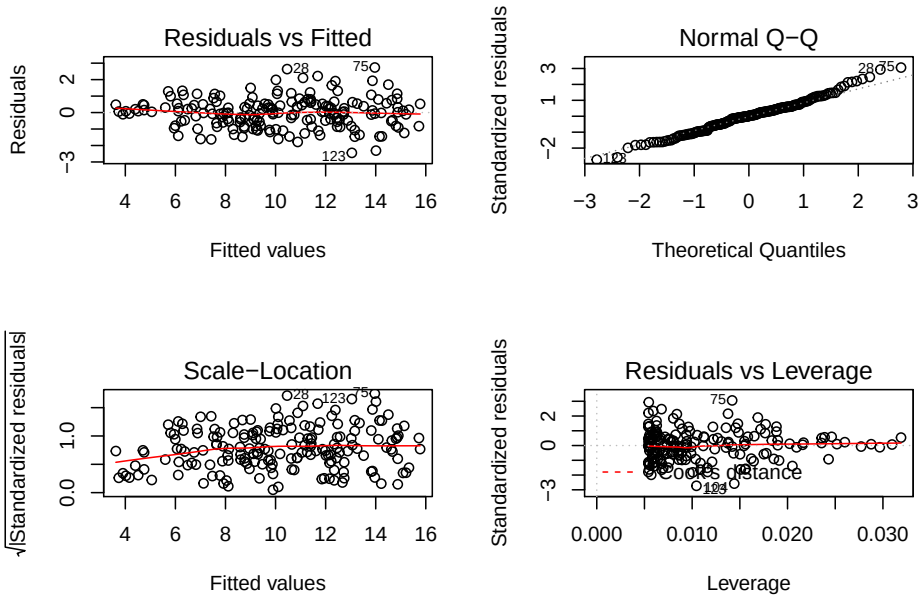


Figure 20: Example output from running the plot function with an lm object as the input.

```
summary(mod_b)$coefficients
```

```
##              Estimate Std. Error   t value     Pr(>|t|)
## (Intercept) 10.497980  0.3110957 33.745177 1.704550e-80
## sexFemale   -0.674724  0.4562792 -1.478752 1.409257e-01
```

You'll notice that, in addition to an estimated intercept (`(Intercept)`), the other estimated coefficient is `sexFemale` rather than just `sex`, although the column name in the dataframe input to `lm` for this variable is `sex`.

This is because, when a factor or binary variable is input as an independent variable in a linear regression model, R will fit an estimated coefficient for all levels of factors *except* the first factor level. By default, this first factor level is used as the baseline level, and so its estimated mean is given by the estimated intercept, while the other model coefficients give the estimated *difference* from this baseline.

For example, the model fit above tells us that the estimated mean weight of males is 10.5, while the estimated mean weight of females is 10.5 + -0.7 = 9.8.

If you would prefer that a different level of the factor be the baseline (for example, "Female" rather than "Male" for the previous regression), you can do that by

using the `levels` argument in the `factor` function to reset factor levels. For example:

```
nepali_reset <- nepali %>%
  mutate(sex = factor(sex, levels = c("Female", "Male")))
mod_b_reset <- lm(wt ~ sex, data = nepali_reset)
summary(mod_b_reset)$coef
```

```
##             Estimate Std. Error   t value     Pr(>|t|)
## (Intercept) 9.823256  0.3337816 29.430189 2.626719e-71
## sexMale     0.674724  0.4562792  1.478752 1.409257e-01
```

Now, `(Intercept)` gives the estimated mean weight for females, while the second estimated coefficient gives the estimated mean difference for males compared to the expected value for females.

0.25.3 Generalized linear models (GLMs)

You can fit a variety of models, including linear models, logistic models, and Poisson models, using generalized linear models (GLMs).

For linear models, the only difference between `lm` and `glm` are the mechanics of how they estimate the model coefficients (`lm` uses least squares while `glm` uses maximum likelihood). You will (almost always) get exactly the same estimated coefficients regardless of whether you use `glm` or `lm` to fit a linear regression.

For example, here is the code to fit a linear regression model for weight regressed on height from the `nepali` dataset:

```
mod_c <- glm(wt ~ ht, data = nepali)
```

This call fits the same regression model I fit earlier with the `lm` function and saved as `mod_a`. You can see that the two methods give exactly the same coefficient estimates:

```
coef(mod_c)
```

```
## (Intercept)          ht
##   -8.694768    0.235050
```

```
coef(mod_a)
```

```
## (Intercept)          ht
##   -8.694768    0.235050
```

Unlike the `lm` function, however, the `glm` function also allows you to fit other model types, including logistic and Poisson models. You can specify the model type using the `family` argument to the `glm` call:

Model type	'family' argument
Linear	'family = gaussian(link = 'identity')'
Logistic	'family = binomial(link = 'logit')'
Poisson	'family = poisson(link = 'log')'

For example, say we wanted to fit a logistic regression for the `nepali` data of whether the probability of a child weighing more than 13 kg is associated with the child's sex.

First, create a binary variable in the `nepali` dataset, `wt_over_13`, that is `TRUE` if a child weighed more than 13 kilograms and FALSE otherwise. You can use the `mutate` function from `dplyr` to add this new column (which, as a note, is a logical vector):

```
nepali <- nepali %>%
  mutate(wt_over_13 = wt > 13)
head(nepali)
```

```
##       id    sex   wt    ht age wt_over_13
## 1 120011   Male 12.8  91.2  41      FALSE
## 2 120012 Female 14.9 103.9  57       TRUE
## 3 120021 Female  7.7  70.1   8      FALSE
## 4 120022 Female 12.1  86.4  35      FALSE
## 5 120023   Male 14.2  99.4  49       TRUE
## 6 120031   Male 13.9  96.4  46       TRUE
```

Now you can fit a logistic regression of `wt_over_13` regressed on sex, using a logistic model:

```
mod_d <- glm(wt_over_13 ~ sex, data = nepali,
             family = binomial(link = "logit"))
```

Elements of a GLM can be pulled out in the same way that we looked at elements from the linear model fit with `lm`. For example, to see a table of estimated model coefficients, you can run:

```
summary(mod_d)$coef
```

```
##               Estimate Std. Error   z value     Pr(>|z|)
## (Intercept) -1.3121864  0.2458445 -5.337465 9.425485e-08
## sexFemale   -0.4133237  0.3886659 -1.063442 2.875815e-01
```

Because this model was a logistic model, fit with a log link, here the model coefficient estimate for `sexFemale` gives an estimate of the **log odds** of weight higher than 13 kg associated with females versus males. The p-value for this estimate (`Pr(>|z|)` = 0.29) isn't very small, suggesting that the difference between male and female children in the odds of weighing more than 13 kg is not statistically significant.

0.25.4 References– statistics in R

One great (and free online for CSU students through our library) book to find out more about using R for basic statistics is:

- Introductory Statistics with R

If you want all the details about fitting linear models and GLMs in R, Julian Faraway's books are fantastic. He has one on linear models and one on extensions including logistic and Poisson models:

- Linear Models with R (also free online through the CSU library)
- Extending the Linear Model with R

0.26 In-course exercise

0.26.1 Loading data from an R package

The data we'll be using today is from a dataset called `worldcup` in the package `faraway`. Load that data so you can use it on your computer (note: you will need to load and install the `faraway` package to do this). Use the help file for the data to find out more about the dataset. Use some basic functions, like `head`, `tail`, `colnames`, `str`, and `summary` to check out the data a bit. See if you can figure out:

- What variables are included in this dataset? (Check the column names.)
- What class is each column currently? In particular, which are numbers and which are factors?

0.26.1.1 Example R code:

Load the `faraway` package using `load()` and then load the data using `data()`:

```
## Uncomment the next line if you need to install the package
# install.packages("faraway")
library(faraway)
data("worldcup")
```

Check out the help file for the `worldcup` dataset to find out more about the data. (Note: Only datasets that are parts of packages will have help files.)

```
?worldcup
```

Check out the data a bit:

```
str(worldcup)
```

```
## 'data.frame':    595 obs. of  7 variables:
## $ Team    : Factor w/ 32 levels "Algeria","Argentina",..: 1 16 9 9 5 32 11 11 18 20 ...
## $ Position: Factor w/ 4 levels "Defender","Forward",..: 4 4 1 4 2 2 1 2 4 1 ...
##  $ Time    : int  16 351 180 270 46 72 138 33 21 103 ...
##  $ Shots   : int  0 0 0 1 2 0 0 0 5 0 ...
##  $ Passes  : int  6 101 91 111 16 15 51 9 22 38 ...
##  $ Tackles : int  0 14 6 5 0 0 2 0 0 1 ...
##  $ Saves   : int  0 0 0 0 0 0 0 0 0 0 ...
```

```
head(worldcup)
```

```
##                Team   Position Time Shots Passes Tackles Saves
## Abdoun      Algeria Midfielder   16     0      6       0     0
## Abe           Japan Midfielder  351     0    101      14     0
## Abidal       France   Defender  180     0     91       6     0
## Abou Diaby   France Midfielder  270     1    111       5     0
## Aboubakar  Cameroon    Forward   46     2     16       0     0
## Abreu       Uruguay    Forward   72     0     15       0     0
```

```
tail(worldcup)
```

```
##                    Team   Position Time Shots Passes Tackles Saves
## van Bommel     Netherlands Midfielder  540    2    307     31     0
## van Bronckhorst Netherlands   Defender  540    1    271     10     0
## van Persie      Netherlands    Forward  479   14    108      1     0
## von Bergen      Switzerland   Defender  234    0     79      3     0
## Alvaro Pereira     Uruguay Midfielder  409    6    140     17     0
## Ozil              Germany Midfielder  497    7    266      3     0
```

```
colnames(worldcup)
```

```
## [1] "Team"    "Position" "Time"    "Shots"   "Passes"  "Tackles"
## [7] "Saves"
```

```
summary(worldcup)
```

```
##         Team           Position        Time           Shots
##  Slovakia : 21   Defender  :188   Min.   :  1.0   Min.   : 0.000
##  Uruguay  : 21   Forward   :143   1st Qu.: 88.0   1st Qu.: 0.000
##  Argentina: 20   Goalkeeper: 36   Median :191.0   Median : 1.000
##  Cameroon : 20   Midfielder:228   Mean   :208.9   Mean   : 2.304
##  Chile    : 20                    3rd Qu.:270.0   3rd Qu.: 3.000
##  Paraguay : 20                    Max.   :570.0   Max.   :27.000
##  (Other)  :473
##      Passes          Tackles          Saves
##  Min.   :  0.00   Min.   : 0.000   Min.   : 0.0000
##  1st Qu.: 29.00   1st Qu.: 1.000   1st Qu.: 0.0000
##  Median : 61.00   Median : 3.000   Median : 0.0000
##  Mean   : 84.52   Mean   : 4.192   Mean   : 0.6672
##  3rd Qu.:115.50   3rd Qu.: 6.000   3rd Qu.: 0.0000
##  Max.   :563.00   Max.   :34.000   Max.   :20.0000
##
```

0.26.2 Basic plots of the data

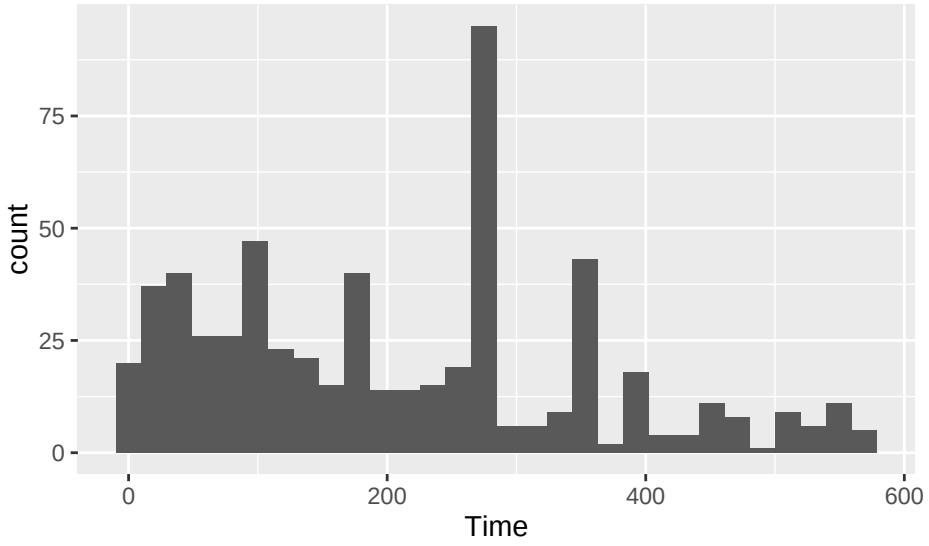
Use some basic plots to check out this data. Try the following:

- Plot histograms of all the numeric variables (`Time`, `Shot`, `Passes`, `Tackles`, `Saves`)
- Plot scatterplots of different combinations of numeric variables (e.g., `Time` vs. `Shots`). Try doing this using the `geom_point()` geom from `ggplot2`. Also try doing it using the `ggpairs()` function from the `GGally` package, to plot several of these at the same time. Try using different constant or mapped values with the `color` aesthetic.
- Create boxplots of `Time`, `Shots`, `Passes` and `Saves` by position.
- Go online and find out which teams were the top four teams in this World Cup (i.e., first through fourth places). Create a `top_teams` subset with just these teams. Plot boxplots of `Shots` and `Saves` by team for just these teams.
- Did you notice any interesting features of the data when you did any of the graphs in this section?

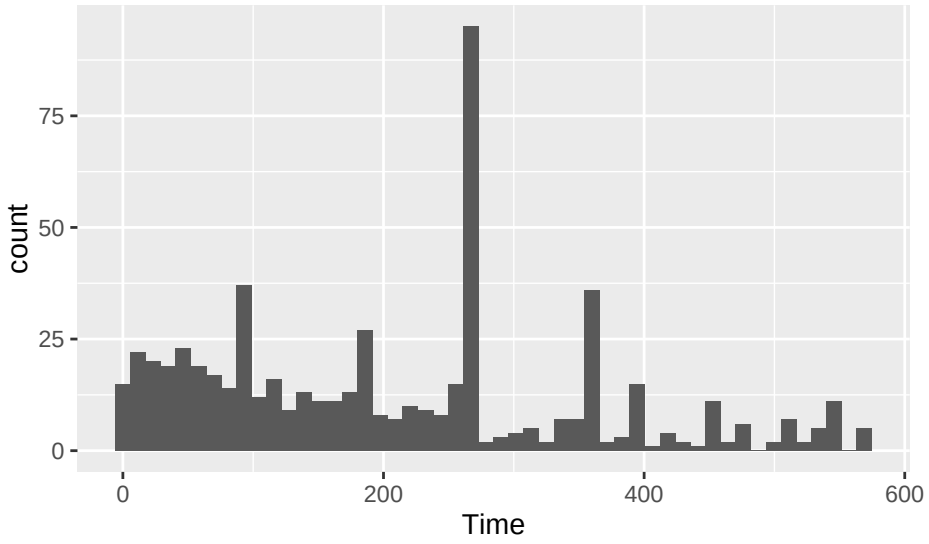
0.26.2.1 Example R code:

Use histograms to explore the distribution of different variables. If you want to change the number of bins in the histogram, try playing around with the `bins` and `binwidth` arguments. You can use the `bins` argument to say how many bins you want (e.g., `bins = 50`). You can use the `binwidth` argument to say how wide you want the bins to be (e.g., `binwidth = 10` if you wanted bins to be 10 units wide, in the units of the variable mapped to the `x` aesthetic. Try using `fill` and `color` to change the appearance of the plot. Google "R colors" and search the images to find links to listings of different R colors.

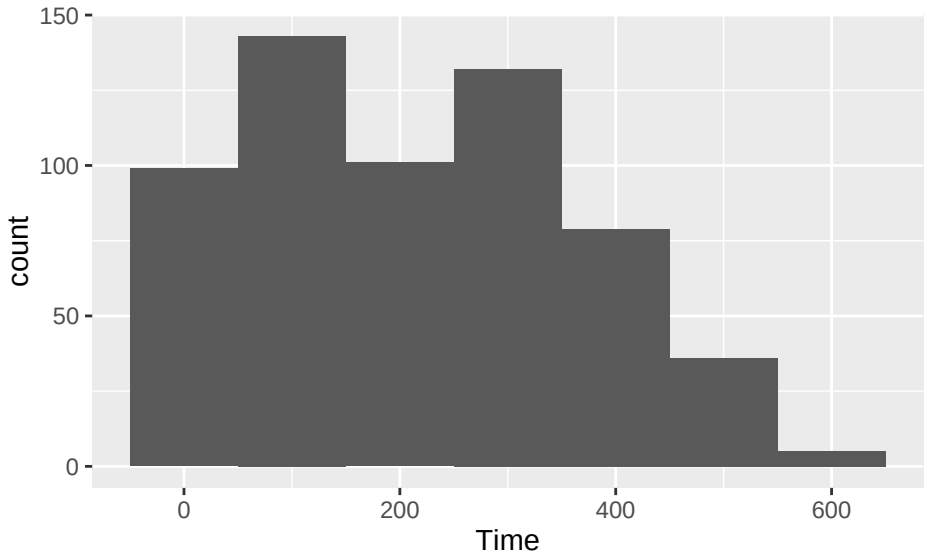
```
library(ggplot2)
ggplot(worldcup, aes(x = Time)) +
  geom_histogram()
```



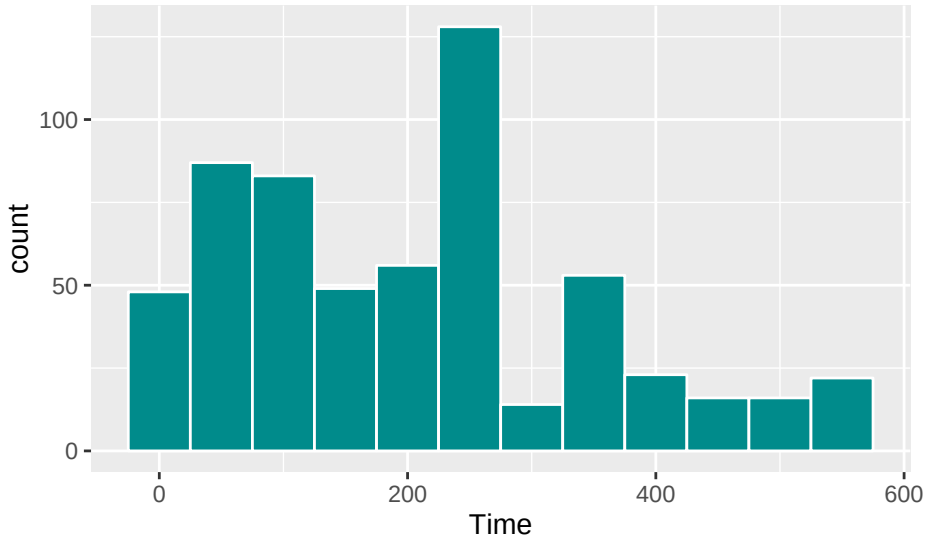

```
ggplot(worldcup, aes(x = Time)) +
  geom_histogram(bins = 50)
```



```
ggplot(worldcup, aes(x = Time)) +
  geom_histogram(binwidth = 100)
```

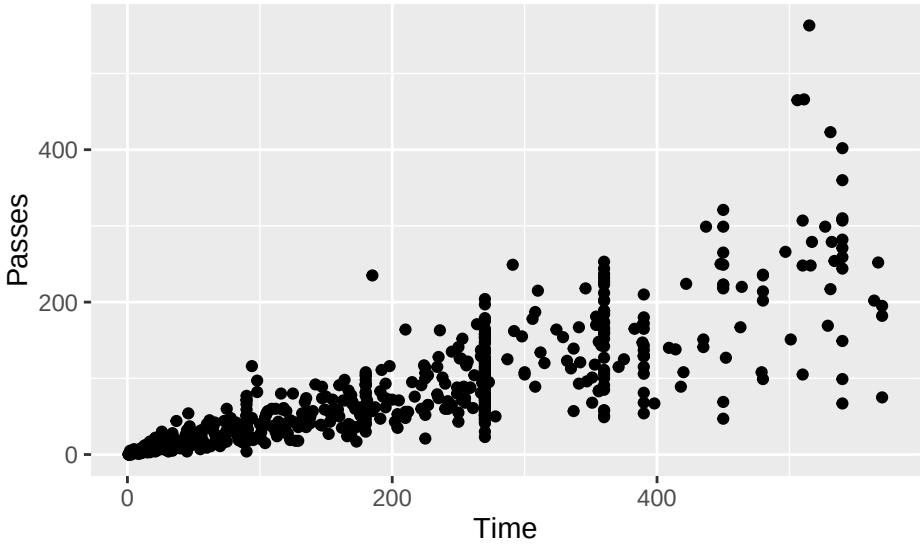



```
ggplot(worldcup, aes(x = Time)) +
  geom_histogram(binwidth = 50, color = "white", fill = "cyan4")
```

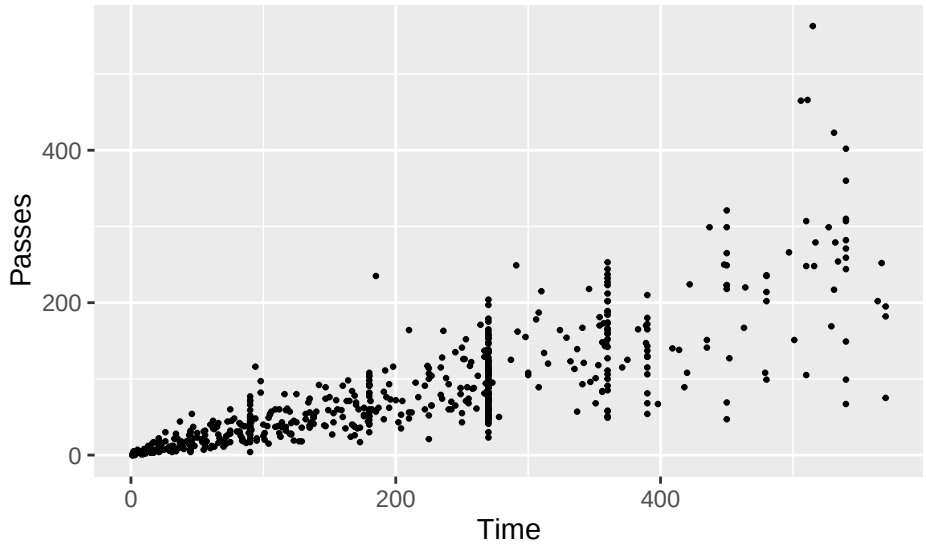


Create a scatterplot of `Time` versus `Passes`. To change the size of the points, use the `size` argument (use a number lower than 1 for smaller points, higher than 1 for larger points). Try changing the color and transparency of the points using the aesthetics `color` and `alpha`. Try using color to show each player's position by mapping `Position` to the `color` aesthetic.

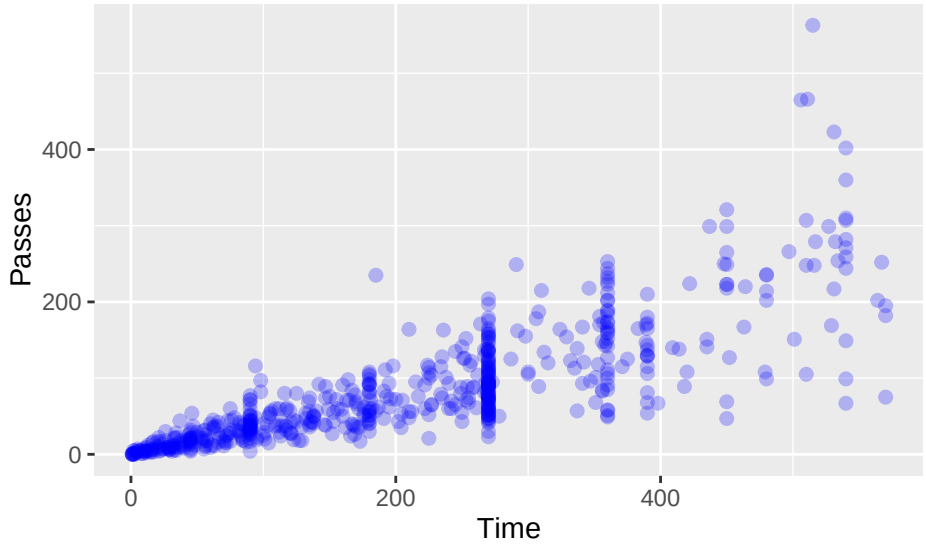
```
ggplot(worldcup, aes(x = Time, y = Passes)) +
  geom_point()
```



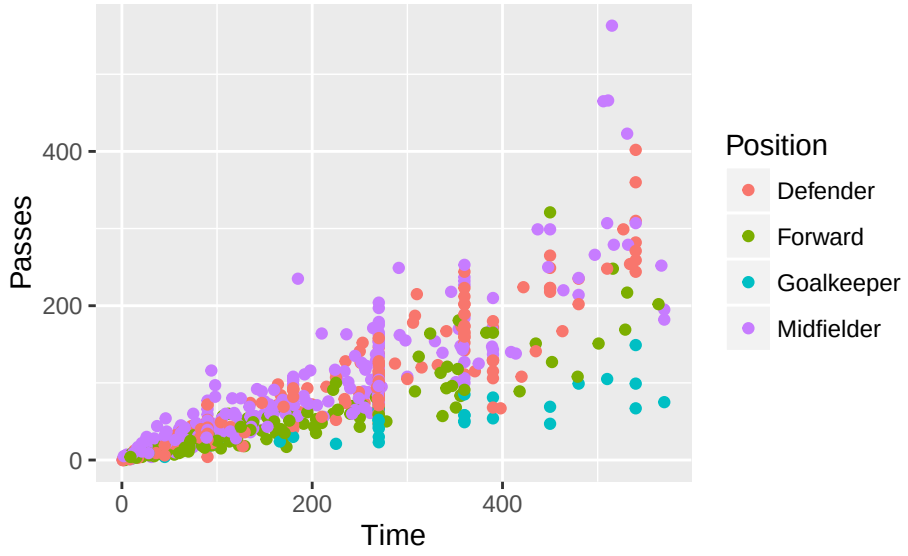

```
ggplot(worldcup, aes(x = Time, y = Passes)) +
  geom_point(size = 0.5)
```




```
ggplot(worldcup, aes(x = Time, y = Passes)) +
  geom_point(size = 2, color = "blue", alpha = 0.25)
```

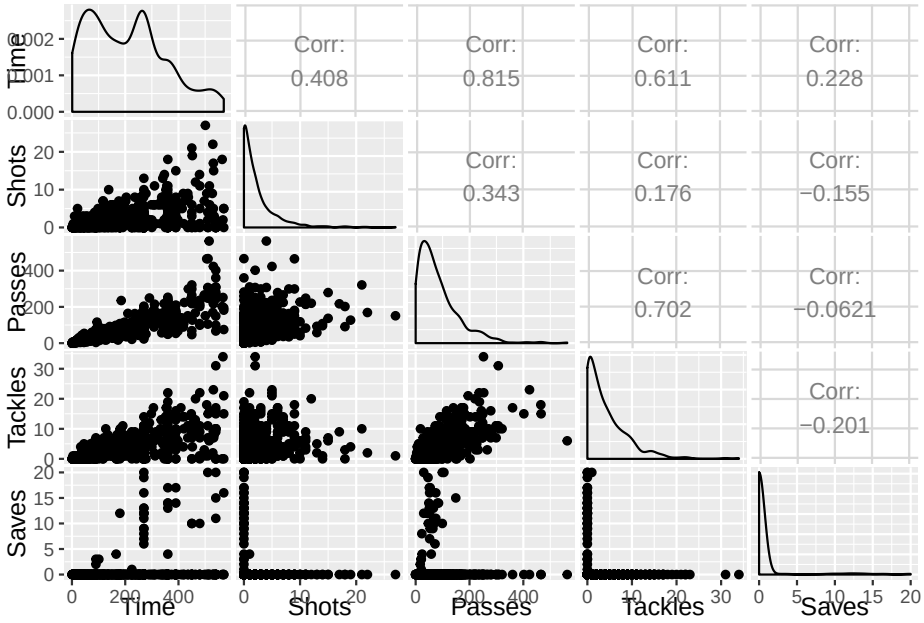


```
ggplot(worldcup, aes(x = Time, y = Passes, color = Position)) +
  geom_point()
```



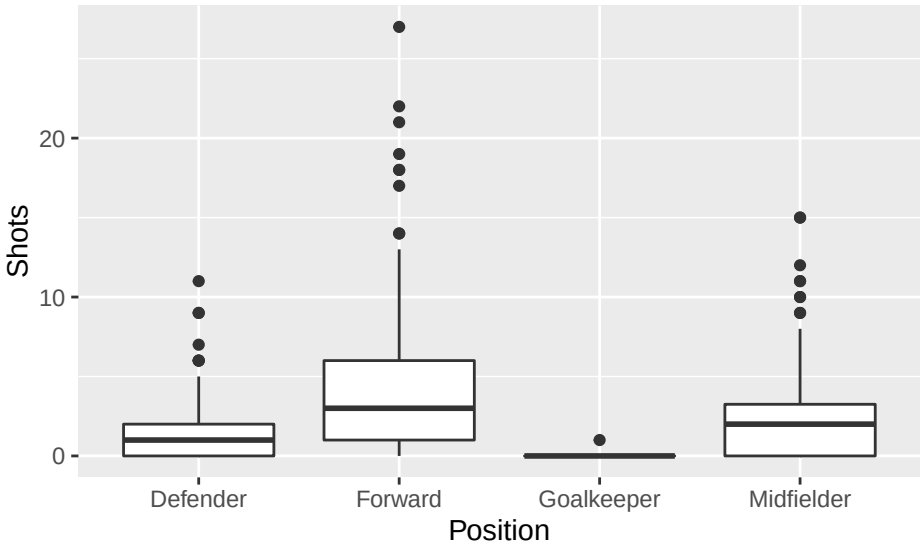
Use the `ggpairs` function from the `GGally` package to plot scatterplots of all combinations of several numeric variables.

```
library(GGally)
library(dplyr)
ggpairs(select(worldcup, Time, Shots, Passes, Tackles, Saves))
```



To create a boxplot of `Shots` by `Position`, you can use `geom_boxplot`:

```
ggplot(worldcup, aes(x = Position, y = Shots)) +
  geom_boxplot()
```



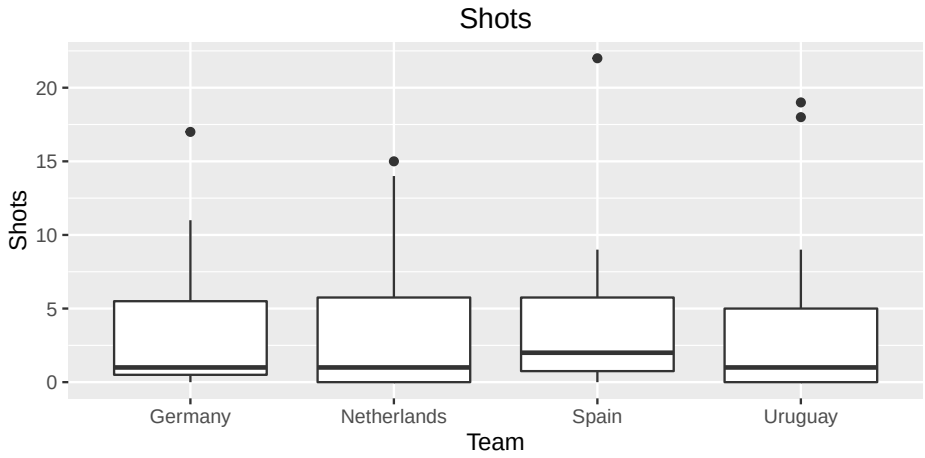
The top four teams in this World Cup were Spain, the Netherlands, Germany, and Uruguay. Create a subset with just the data for these four teams:

```
top_teams <- worldcup %>%
  filter(Team %in% c("Spain", "Netherlands", "Germany", "Uruguay")) %>%
  mutate(Team = factor(Team))
```

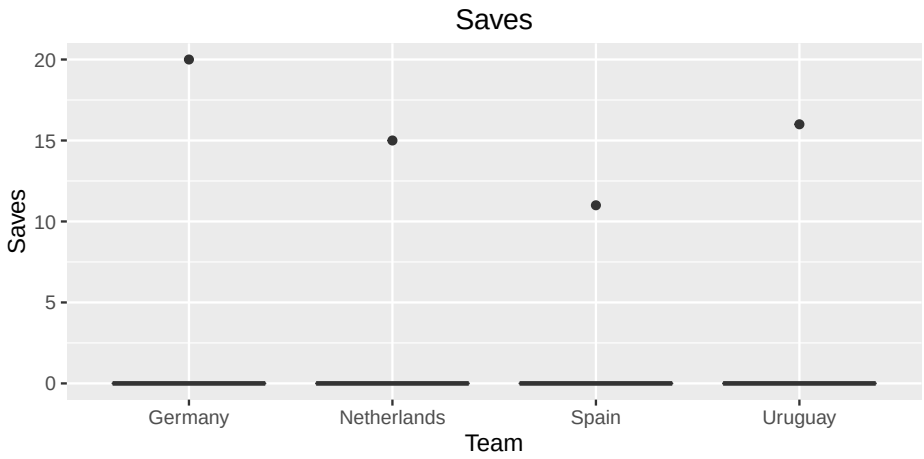
This dataset will still have all the levels saved for the `Team` factor, even though it isn't using them all. You can re-set this by resetting `Team` as a factor, which is what I've done with the `mutate` line. When R creates a factor from a vector, its default is to only use as levels the values that show up in the vector.

Now, you can plot the boxplots, mapping `Team` to the `x` aesthetic and `Shots` or `Saves` to the `y` aesthetic:

```
ggplot(top_teams, aes(x = Team, y = Shots)) +
  geom_boxplot() +
  ggtitle("Shots")
```



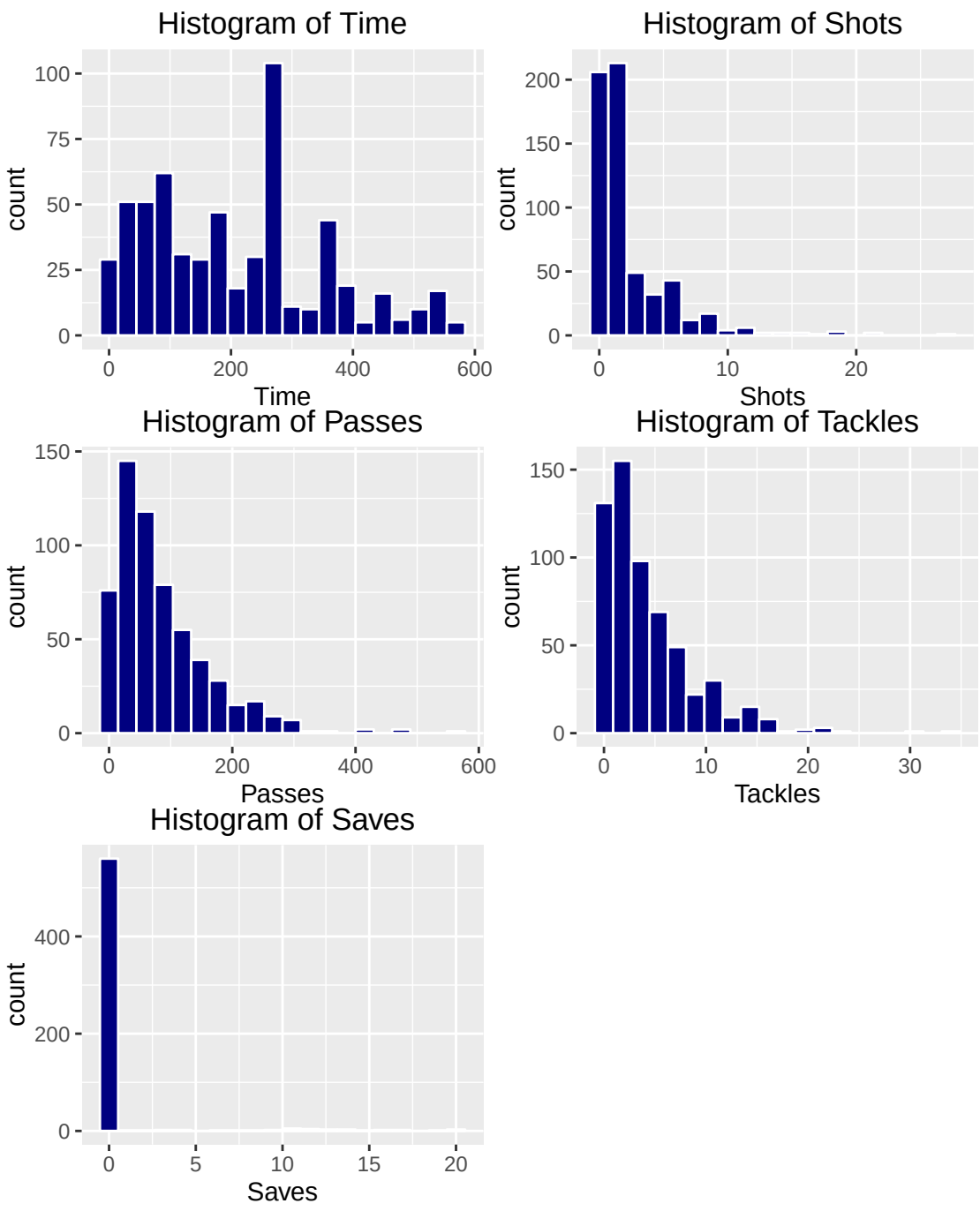

```
ggplot(top_teams, aes(x = Team, y = Saves)) +
  geom_boxplot() +
  ggtitle("Saves")
```



0.26.2.2 If you have extra time:

If you wanted to do the same plot for several different variables, you could loop through your code (we'll be covering more about loops in a few weeks). For example, you could create histograms for all of the numeric variables (if you do this in RStudio, you'll need to use the arrows on the plot window to move through and see all the different plots once you've created them):

```
## Create an object with the column names for all of the numeric variables
my_vars <- colnames(worldcup)[3:7]

## Loop through all of those variables. Print out a histogram with the
## variable, and have it print on the plot, as the main title, the
## column name for that variable
for(var in my_vars){
  worldcup$to_plot <- worldcup[ , var]
  a <- ggplot(worldcup, aes(x = to_plot)) +
    geom_histogram(bins = 20, color = "white", fill = "navy") +
    xlab(var) +
    ggtitle(paste("Histogram of", var))
  plot(a)
}
```



A few things to note in this example:

- To map an element of the data to an aesthetic, it's easiest if that element

is saved in a column in the dataframe. Within this loop, I'm making an extra column called `to_plot`, where I'm copying the column of the variable I want to plot each time the loop runs. That way, I can always use `x = to_plot` in the aesthetic mapping for the ggplot object.
- If you run code to create a ggplot object within a loop, it won't automatically print. Instead, you need to use `print` to get the object to print out. One way to do that is to save the final ggplot object as an R object (here I'm saving it to `a`) and then use the `print` function to print that object.
- Next week, we'll talk some about faceting, which can create multiple plots by variable like this in a lot less code. However, it's useful at this point to start thinking about how to extend code to use in loops, to save yourself time when you need to repeat something similar many times.

0.26.3 Exploring the data using simple statistics and logical statements

Next, try checking out the data using some basic commands for simple statistics, like `mean()`, `range()`, `max()`, and `min()`. Use these, along with some logical statements, to help you answer the following questions:

- What is the range of time that players spent in the game? Who played the most World Cup time in this World Cup? For the minimum of the range of `Time`, how many players played this amount of time?
- What is the mean number of saves that players made? What is the mean number of saves just among the goalkeepers? How many of the players are goalkeepers? Did any non-goalkeeper make a save?

0.26.3.1 Example R code:

Use `range()` to find out the range of time these players played in the World Cup.

```
range(worldcup$Time)
```

```
## [1]   1 570
```

To figure out who played the most time, you need to subset out the rows of the dataset where the `Time` variable equals the maximum of the `Time` variable for the whole dataset. There are a few ways to do that. Here I'm showing two: (1) using logic within the "square-bracket indexing", to pull out just rows where it is TRUE that the `Time` for that row equals `max(worldcup$Time)` and (2) using

`filter` from the `dplyr` package to filter down to rows where where it is TRUE that the `Time` for that row equals `max(Time)` for the whole dataset.

```
max(worldcup$Time)
```

```
## [1] 570
```

```
head(worldcup$Time == max(worldcup$Time))
```

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

```
worldcup[worldcup$Time == max(worldcup$Time), ]
```

```
##            Team   Position Time Shots Passes Tackles Saves to_plot
## Arevalo Rios Uruguay Midfielder  570     5    195      21     0       0
## Maxi Pereira Uruguay Midfielder  570     5    182      15     0       0
## Muslera     Uruguay Goalkeeper  570     0     75       0    16      16
```

```
worldcup %>%
  filter(Time == max(Time))
```

```
##      Team   Position Time Shots Passes Tackles Saves to_plot
## 1 Uruguay Midfielder  570     5    195      21     0       0
## 2 Uruguay Midfielder  570     5    182      15     0       0
## 3 Uruguay Goalkeeper  570     0     75       0    16      16
```

Note: You may have noticed that you lost the players names when you did this using the `dplyr` pipechain. That's because `dplyr` functions convert the data to a dataframe format that does not include rownames. If you want to keep players' names, use `mutate` to move those names from the rownames of the data into a column in the dataframe:

```
worldcup %>%
  mutate(Name = rownames(worldcup)) %>%
  filter(Time == max(Time))
```

```
##    Team   Position Time Shots Passes Tackles Saves to_plot      Name
## 1 Uruguay Midfielder  570    5   195     21    0     0 Arevalo Rios
## 2 Uruguay Midfielder  570    5   182     15    0     0 Maxi Pereira
## 3 Uruguay Goalkeeper  570    0    75      0   16     16     Muslera
```

To calculate the mean number of saves among all the players, use the `mean` function, either by itself or within a `summarize` call:

```
mean(worldcup$Saves)
```

```
## [1] 0.6672269
```

```
worldcup %>%
  summarize(mean_saves = mean(Saves))
```

```
##   mean_saves
## 1  0.6672269
```

For the next parts of the question, it will be convenient to have a logical vector for whether each player is a goalkeeper, so here's how you would create that:

```
goalie <- worldcup$Position == "Goalkeeper"
```

This new object, `goalie`, is a vector the same length as `worldcup$Position`. Each element of `goalie` says whether it is TRUE or FALSE that `worldcup$Position` is equal to "Goalkeeper" at that spot on the `worldcup$Position` vector.

```
head(goalie)
```

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

The `summary()` function will count up the total number of times that `goalie` is TRUE and FALSE.

```
summary(goalie)
```

```
##    Mode   FALSE    TRUE    NA's
## logical     559      36       0
```

There are a few ways to use this vector to figure out how many players were goalkeepers. First, you could use `summary` (which I just showed) or `table`, and just read how many times this vector has the value `TRUE`. Second, since R saves logical vectors with `TRUE` as 1 and `FALSE` as 0, you could just the `sum` function to add up the vector to find out how often it's `TRUE` (`sum` adds up every value in the vector).

```
table(goalie)
```

```
## goalie
## FALSE  TRUE
##   559    36
```

```
sum(goalie)
```

```
## [1] 36
```

You could also answer this question by using `summarize` from `dplyr`. You need to `group_by` player position and then you can use the `n` function in `summarize` to count up the total number of observations in each group:

```
worldcup %>%
  group_by(Position) %>%
  summarize(n_players = n())
```

```
## # A tibble: 4 × 2
##     Position n_players
##       <fctr>     <int>
## 1   Defender       188
## 2    Forward       143
## 3 Goalkeeper        36
## 4 Midfielder       228
```

Now, you can answer the questions about mean saves for goalies and max saves for non-goalies. First, try doing that using the `goalie` logical vector you created. If you put `goalie` in the square bracket indexing for the dataframe as the rows value (i.e., the index before the comma), R will subset out just the rows where `goalie` is equal to TRUE. If you put `!goalie` in the square bracket indexing as the rows value, R will just subset out the rows where `goalie` is equal to FALSE. You can use this index subsetting to figure out the mean number of saves per goalie and also whether any non-goalie made a save (by checking the maximum value or range of saves for non-goalies).

```
head(worldcup[goalie, ])
```

```
##            Team  Position Time Shots Passes Tackles Saves to_plot
## Barry    Ivory Coast Goalkeeper  270     0     23      0     8       8
## Benaglio Switzerland Goalkeeper  270     0     75      0    11      11
## Bravo         Chile Goalkeeper  360     0     58      0     4       4
## Buffon        Italy Goalkeeper   45     0      4      0     0       0
## Casillas      Spain Goalkeeper  540     0     67      0    11      11
## Chaouchi    Algeria Goalkeeper   90     0     17      0     2       2
```

```
mean(worldcup[goalie, "Saves"])
```

```
## [1] 11.02778
```

```
range(worldcup[!goalie, "Saves"])
```

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

You could also answer this quesiton using a `dplyr` pipe chain to summarize the data after grouping it by position:

```
worldcup %>%
  group_by(Position) %>%
  summarize(number_players = n(),
            mean_saves = mean(Saves),
            max_saves = max(Saves))
```

```
## # A tibble: 4 × 4
##     Position number_players mean_saves max_saves
##       <fctr>          <int>      <dbl>     <int>
## 1   Defender            188    0.00000         0
## 2    Forward            143    0.00000         0
## 3 Goalkeeper             36   11.02778        20
## 4 Midfielder            228    0.00000         0
```

0.26.4 Using regression models to explore data

For this part of the exercise, you'll use a dataset on weather, air pollution, and mortality counts in Chicago, IL. This dataset is called `chicagoNMMAPS` and is part of the `dlnm` package. Change the name of the dataframe to something shorter, like `chic`. Check out the data a bit to see what variables you have, and then perform the following tasks:

- Write out (on paper, not in R) the regression equation for regressing dewpoint temperature on temperature.
- Try fitting a linear regression of dew point temperature (`dptp`) on temperature (`temp`). (Bonus points: Notice anything that seems unusual about these two variables in this dataset? You can find out with `summary`, but it helps if you know a bit about what dewpoint temperature measures.) Save this model as the object `mod_1`.
- Based on this regression, does there seem to be a relationship between temperature and dewpoint temperature in Chicago? (Hint: Try using `summary()` on the model object to get more information about the model you fit.) What is the p-value for the coefficient for temperature?
- Plot temperature (x-axis) versus dewpoint temperature (y-axis) for Chicago. Add in the regression line from the model you fit.
- Use `plot()` on the model object to check if some of the assumptions for the regression model seem appropriate.
- Try fitting the regression as a GLM, using `glm()`. Are your coefficients different?
- Does PM_{10} vary by day of the week? (Hint: The `dow` variable is a factor that gives day of the week. You can do an ANOVA analysis by fitting a linear model using this variable as the independent variable, and then run `anova()` on that model, and R will compare it to an intercept-only model.) What day of the week is PM10 generally highest? (Check the model coefficients to figure this out.) Try to write out (on paper) the regression equation for the model you're fitting.
- Try using `glm()` to run a Poisson regression of respiratory deaths (`resp`) on temperature during summer days. Start by creating a subset with just summer days called `summer`. (Hint: Use the `month` variable to do this– just pull out the subset where the month is 6, 7, or 8, for June, July, and

August.) Try to write out the regression equation for the model you're fitting.

- The coefficient for the temperature variable in this model is our best estimate (based on this model) of the **log relative risk** for a one degree Celcius increase in temperature. What is the **relative risk** associated with a one degree Celsius increase?

0.26.4.1 Example R code:

Install and load the `dlnm` package and then load the `chicagoNMMAPS` data. Change the name of the dataframe to `chic`, so it will be shorter to call for the rest of your work.

```
# install.packages("dlnm")
library(dlnm)
data("chicagoNMMAPS")
chic <- chicagoNMMAPS
```

Fit a linear regression of `dptp` on `temp` and save as the object `mod_1`:

```
mod_1 <- lm(dptp ~ temp, data = chic)
mod_1
```

```
##
## Call:
## lm(formula = dptp ~ temp, data = chic)
##
## Coefficients:
## (Intercept)         temp
##      24.025        1.621
```

Use `summary()` to check out a bit more about the model you fit.

```
summary(mod_1)
```

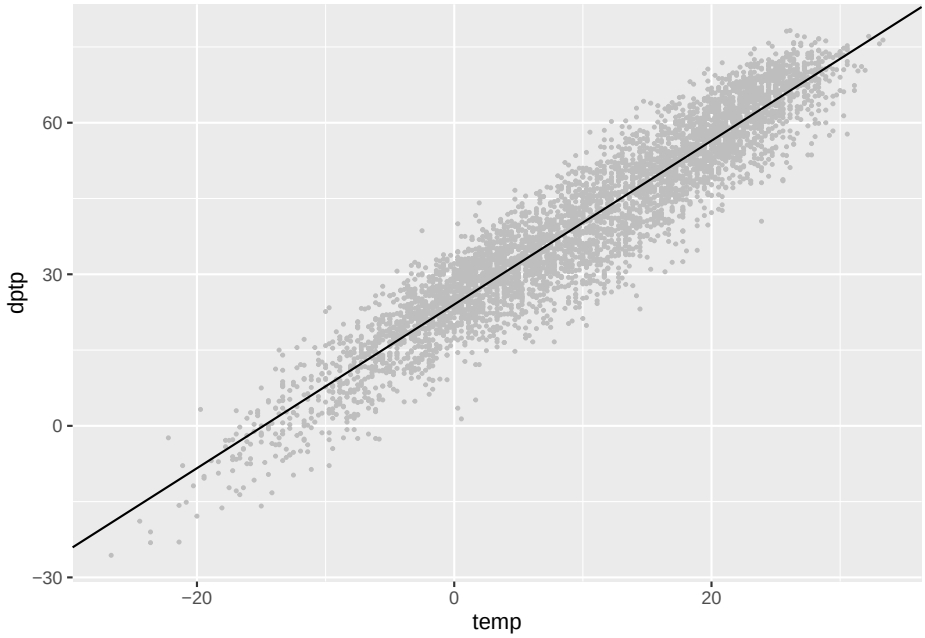
```
##
## Call:
## lm(formula = dptp ~ temp, data = chic)
##
```

```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -24.3093  -3.7470   0.4687   4.0738  18.6518
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 24.024869   0.112933   212.7   <2e-16 ***
## temp         1.620650   0.007631   212.4   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.899 on 5112 degrees of freedom
## Multiple R-squared:  0.8982, Adjusted R-squared:  0.8982
## F-statistic: 4.511e+04 on 1 and 5112 DF,  p-value: < 2.2e-16
```

There does seem to be an association between temperature and dewpoint temperature: a unit increase in temperature is associated with a 1.6 unit increase in dewpoint temperature. The p-value for the temperature coefficient is <2e-16. This is far below 0.05, which suggests we would be very unlikely to see such a strong association by chance if the null hypothesis, that the two variables are not associated, were true.

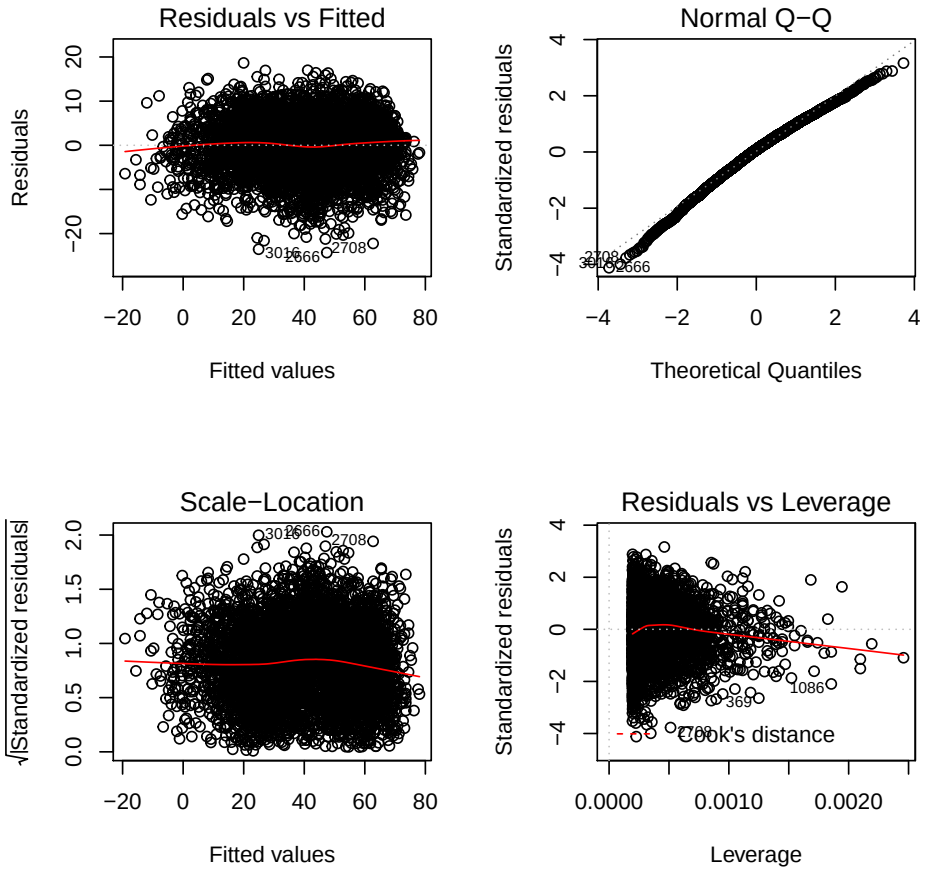
Plot these two variables and add in the regression line from the model (note: I've used the `color` option to make the color of the points gray). Use the values from `coef` with a `geom_abline` to add the regression line for the model you fit.

```
mod_coefs <- coef(mod_1)
ggplot(chic, aes(x = temp, y = dptp)) +
  geom_point(size = 0.5, col = "gray") +
  geom_abline(aes(intercept = mod_coefs[1], slope = mod_coefs[2]))
```



Plot some plots to check model assumptions for the model you fit using the `plot()` function on your model object:

```
par(mfrow = c(2, 2)) # Set to four plots per panel -- 2 rows, 2 columns
plot(mod_1)
```




```
par(mfrow = c(1, 1)) # Reset to one plot per panel
```

Try fitting the model using `glm()`. Call it `mod_1a`. Compare the coefficients for the two models. You can use the `coef()` function on an `lm` or `glm` object to pull out just the model coefficients.

```
mod_1a <- glm(dptp ~ temp, data = chic)

coef(mod_1)
```

```
## (Intercept)        temp
##    24.02487     1.62065
```

```
coef(mod_1a)
```

```
## (Intercept)        temp
##    24.02487     1.62065
```

The results from the two models are identical.

Fit a model of PM_{10} regressed on day of week, where day of week is a factor.

```
mod_2 <- lm(pm10 ~ dow, data = chic)
summary(mod_2)
```

```
##
## Call:
## lm(formula = pm10 ~ dow, data = chic)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -39.05 -12.55  -3.34   8.80 328.66
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   27.5217     0.7303  37.684  < 2e-16 ***
## dowMonday      6.1322     1.0340   5.931 3.22e-09 ***
## dowTuesday     6.7954     1.0269   6.617 4.05e-11 ***
## dowWednesday   8.4768     1.0262   8.261  < 2e-16 ***
## dowThursday    8.8047     1.0240   8.598  < 2e-16 ***
## dowFriday      9.4816     1.0262   9.240  < 2e-16 ***
## dowSaturday    3.6602     1.0269   3.564 0.000368 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 19.07 on 4856 degrees of freedom
##   (251 observations deleted due to missingness)
## Multiple R-squared:  0.02588,    Adjusted R-squared:  0.02467
## F-statistic:  21.5 on 6 and 4856 DF,  p-value: < 2.2e-16
```

Use the `anova()` command to compare this model to a model with only an intercept (i.e., one that only fits a global mean and uses that as the expected value for all of the observations).

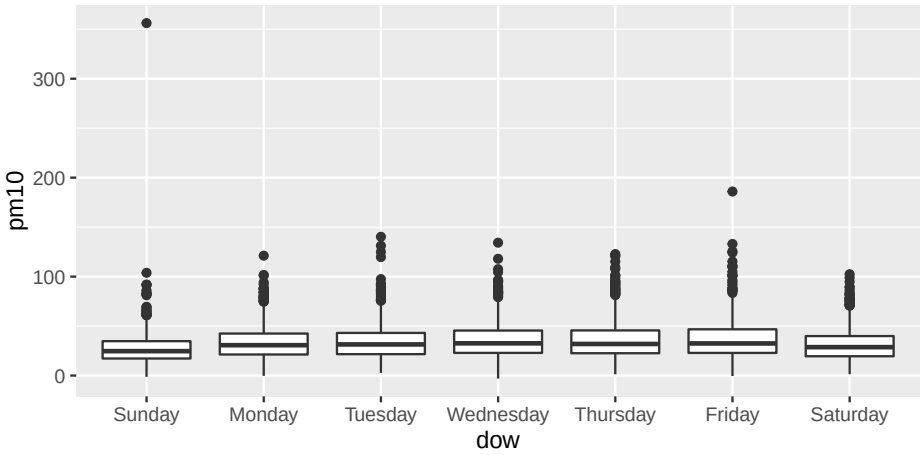
```
anova(mod_2)
```

```
## Analysis of Variance Table
##
## Response: pm10
##             Df  Sum Sq Mean Sq F value    Pr(>F)
## dow          6   46924  7820.6    21.5 < 2.2e-16 ***
## Residuals 4856 1766407   363.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The p-value for an ANOVA of the model with day-of-week coefficients versus the model that just has an intercept is < 2.2e-16. This is well below 0.05, which suggests that day-of-week is associated with PM10 concentration, as a model that includes day-of-week does a much better job of explaining variation in PM10 than a model without it does. (Note, too, that the F value and Pr(>F) for the `anova()` call are identical to the F-statistic information given in the `summary()` of the model object. This will always be true when you're using `anova()` to compare a model to a model with just an intercept.)

Use a boxplot to visually compare PM10 by day of week.

```
ggplot(chic, aes(x = dow, y = pm10)) +
  geom_boxplot()
```

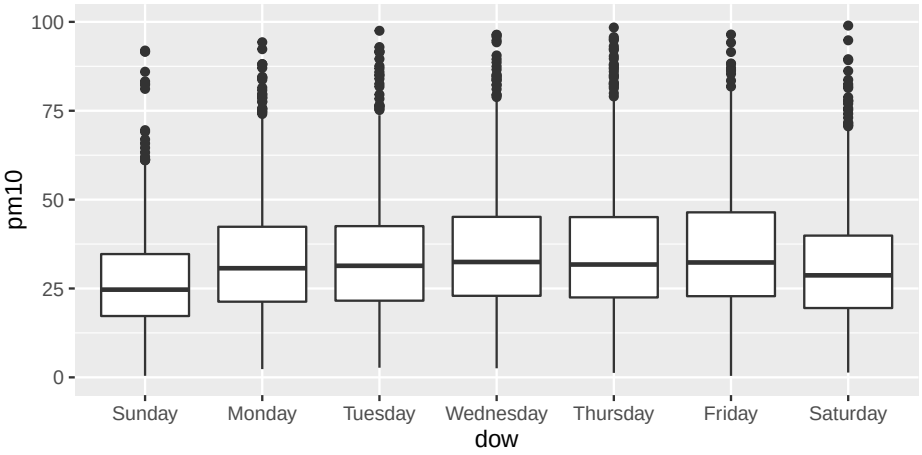


Now try the same plot, but try using the `ylim =` option to change the limits on the y-axis for the graph, so you can get a better idea of the pattern by day of

week (some of the extreme values are very high, which makes it hard to compare by eye when the y-axis extends to include them all).

```
ggplot(chic, aes(x = dow, y = pm10)) +
  geom_boxplot() +
  ylim(c(0, 100))
```

```
## Warning: Removed 292 rows containing non-finite values (stat_boxplot).
```



Create a subset called `summer` with just the summer days:

```
summer <- chic %>%
  filter(month %in% 6:8)
```

Use `glm()` to fit a Poisson model of respiratory deaths regressed on temperature. Since you want to fit a Poisson model, use the option `family = poisson(link = "log")`.

```
mod_3 <- glm(resp ~ temp, data = summer,
             family = poisson(link = "log"))
summary(mod_3)
```

```
##
## Call:
## glm(formula = resp ~ temp, family = poisson(link = "log"), data = summer)
```

```
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -3.9755  -0.7162  -0.1807   0.6927   3.6555
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 1.910317   0.058373  32.726   <2e-16 ***
## temp        0.006137   0.002581   2.378   0.0174 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 1499.4  on 1287  degrees of freedom
## Residual deviance: 1493.8  on 1286  degrees of freedom
## AIC: 6425.4
##
## Number of Fisher Scoring iterations: 4
```

Use the fitted model coefficient to determine the relative risk for a one degree Celcius increase in temperature. First, remember that you can use the `coef()` function to read out the model coefficients. The second of these is the value for the temperature coefficient. That means that you can use indexing (`[2]`) to get just that value. That's the log relative risk; take the exponent to get the relative risk.

```
coef(mod_3)
```

```
## (Intercept)        temp
## 1.910316958 0.006136743
```

```
coef(mod_3)[2]
```

```
##        temp
## 0.006136743
```

```
exp(coef(mod_3)[2])
```

```
##     temp
## 1.006156
```

Reporting data results #1

Download a pdf of the lecture slides covering this topic.

0.27 Guidelines for good plots

There are a number of very thoughtful books and articles about creating graphics that effectively communicate information. Some of the authors I highly recommend (and from whose work I've pulled the guidelines for good graphics we'll talk about this week) are:

- Edward Tufte
- Howard Wainer
- Stephen Few
- Nathan Yau

You should plan, in particular, to read *The Visual Display of Quantitative Information* by Edward Tufte before you graduate.

This week, we'll focus on six guidelines for good graphics, based on the writings of these and other specialists in data display. The guidelines are:

1. Aim for high data density.
2. Use clear, meaningful labels.
3. Provide useful references.
4. Highlight interesting aspects of the data.
5. Make order meaningful.
6. When possible, use small multiples.

For the examples, I'll use `dplyr` for data cleaning and, for plotting, the packages `ggplot2`, `gridExtra`, and `ggthemes`.

```
library(tidyverse) ## Loads `dplyr` and `ggplot2`
library(gridExtra)
library(ggthemes)
```

You can load the data for today's examples with the following code:

```
library(faraway)
data(nepali)
data(worldcup)

library(dlnm)
data(chicagoNMMAPS)
chic <- chicagoNMMAPS
chic_july <- chic %>%
  filter(month == 7 & year == 1995)
```

0.28 High data density

Guideline 1: **Aim for high data density.**

You should try to increase, as much as possible, the **data to ink ratio** in your graphs. This is the ratio of "ink" providing information to all ink used in the figure. One way to think about this is that the only graphs you make that use up a lot of your printer's ink should be packed with information.

The two graphs in Figure 21 show the same information, but use very different amounts of ink. Each shows the number of players in each of four positions in the `worldcup` dataset. Notice how, in the plot on the right, a single dot for each category shows the same information that a whole filled bar is showing on the left. Further, the plot on the right has removed the gridded background, removing even more "ink".

Figure 22 gives another example of two plots that show the same information but with very different data densities. This figure uses the `chicagoNMMAPS` data from the `dlnm` package, which includes daily mortality, weather, and air pollution data for Chicago, IL. Both plots show daily mortality counts during July 1995, when a very severe heat wave hit Chicago. Notice how many of the elements in the plot on the left, including the shading under the mortality time series and the colored background and grid lines, are unnecessary for interpreting the message from the data.

By increasing the data-to-ink ratio in a plot, you can help viewers see the message of the data more quickly. A cluttered plot is harder to interpret. Further,

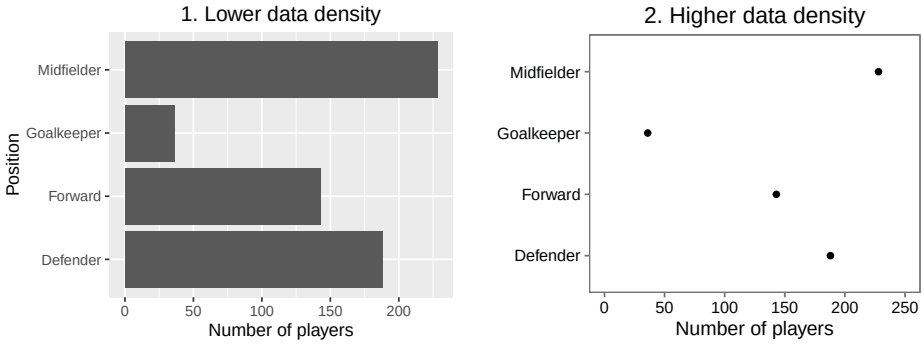


Figure 21: Example of plots with lower (left) and higher (right) data-to-ink ratios. Each plot shows the number of players in each position in the worldcup dataset from the faraway package.

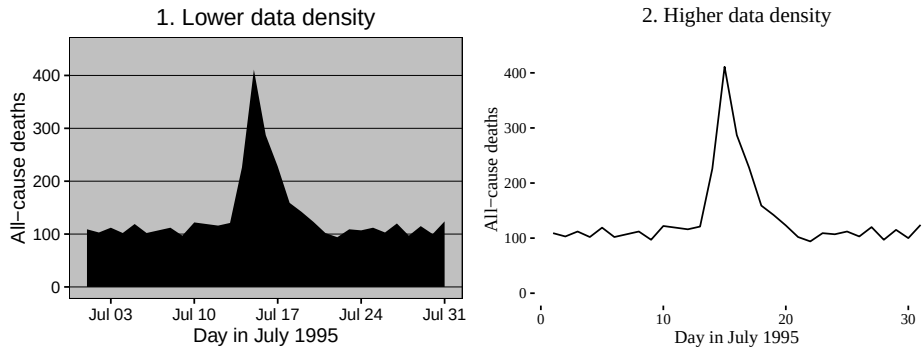


Figure 22: Example of plots with lower (left) and higher (right) data-to-ink ratios. Each plot shows daily mortality in Chicago, IL, in July 1995 using the chicagoNMMAPS data from the dlnm package.

you leave room to add some of the other elements I'll talk about, including highlighting interesting data and adding useful references. Notice how the plots on the left in Figures 21 and 22 are already cluttered and leave little room for adding extra elements, while the plots on the right of those figures have much more room for additions.

One quick way to increase data density in `ggplot2` is to change the *theme* for the plot. The theme specifies a number of the "background" elements to a plot, including elements like the plot grid, background color, and the font used for labeling. Some themes come with `ggplot2`, including:

- `theme_bw`
- `theme_minimal`
- `theme_void`

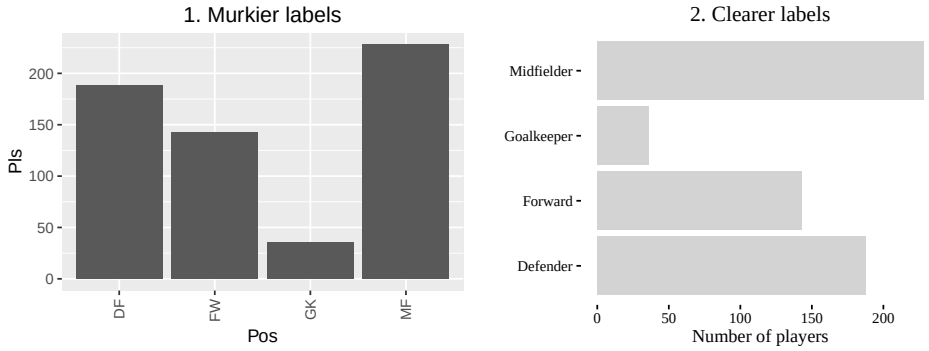
You can find more themes in packages that extend `ggplot2`. The `ggthemes` package, in particular, has some excellent additional themes.

Figures 23 shows some examples of the effects of using different themes. All show the same information– a plot of daily deaths in Chicago in July 1995. The top left graph shows the graph with the default theme. The other plots show the effects of adding different themes, including the black-and-white theme that comes with `ggplot2` (top right) and various themes from the `ggthemes` package. You can even use themes to add some questionable choices for different elements, like the Excel theme (bottom left).

0.28.1 Meaningful labels

Guideline 2: **Use clear, meaningful labels.**

Graph defaults often use abbreviations for axis labels and other labeling. Furthermore, text labels can sometimes be aligned in a way that makes them hard to read. The plots below give an example of the same information shown without (left) and with (right) clear, meaningful labels.



There are a few strategies you can use to make labels clearer:

- Add `xlab` and `ylab` elements to the plot, rather than relying on the column names in the original data. This can also be done with `scale` elements (e.g., `scale_x_continuous`), which give you more power to also make other changes to the x- and y-axes.
- Include units of measurement in axis titles when relevant. If units are dollars or percent, check out the `scales` package, which allows you to add labels directly to axis elements by including arguments like `labels = percent` in `scale` elements.
- If the x-variable requires longer labels (player positions in the example above), consider flipping the coordinates, rather than abbreviating or rotating the labels. You can use `coord_flip` to do this.

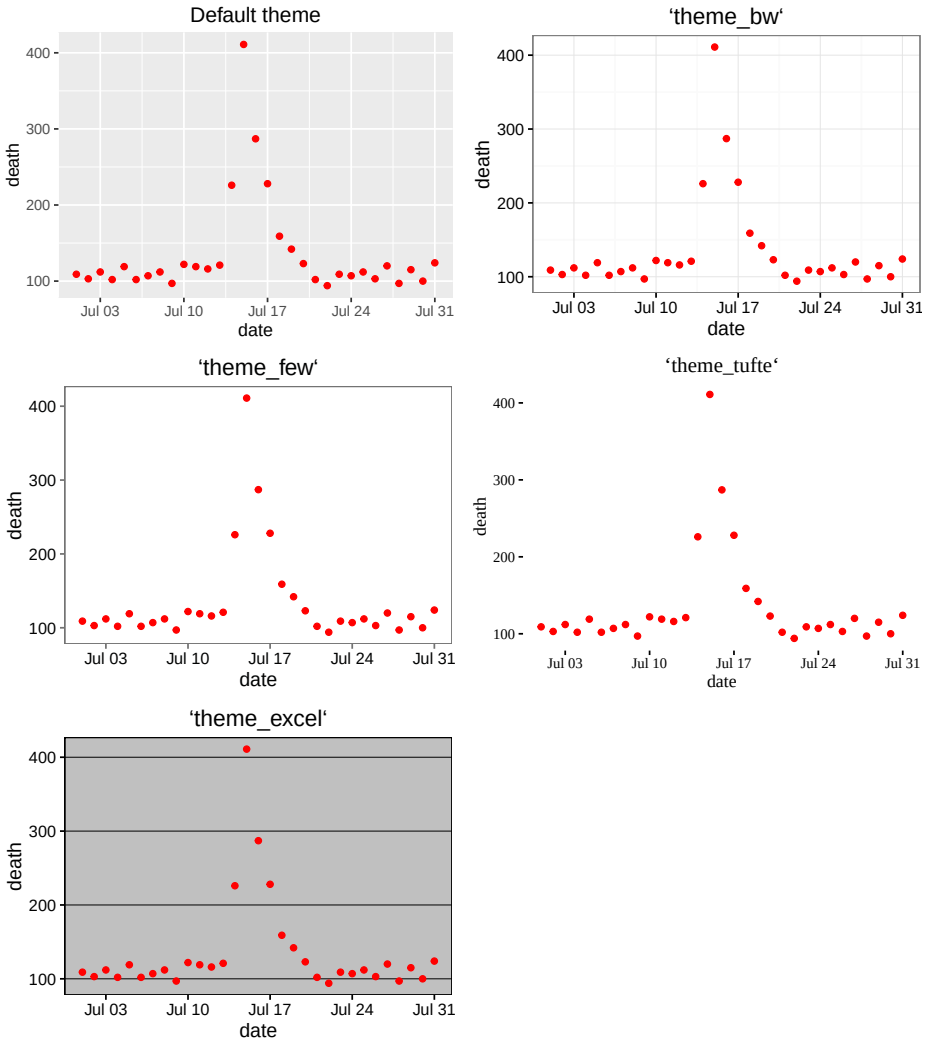
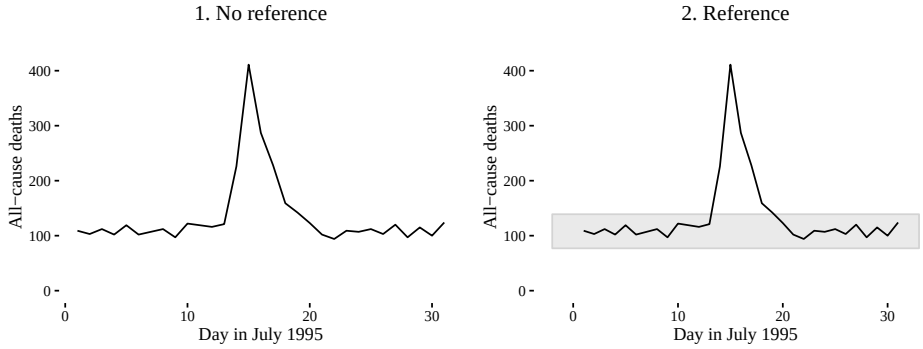


Figure 23: Daily mortality in Chicago, IL, in July 1995. This figure gives an example of the plot using different themes.

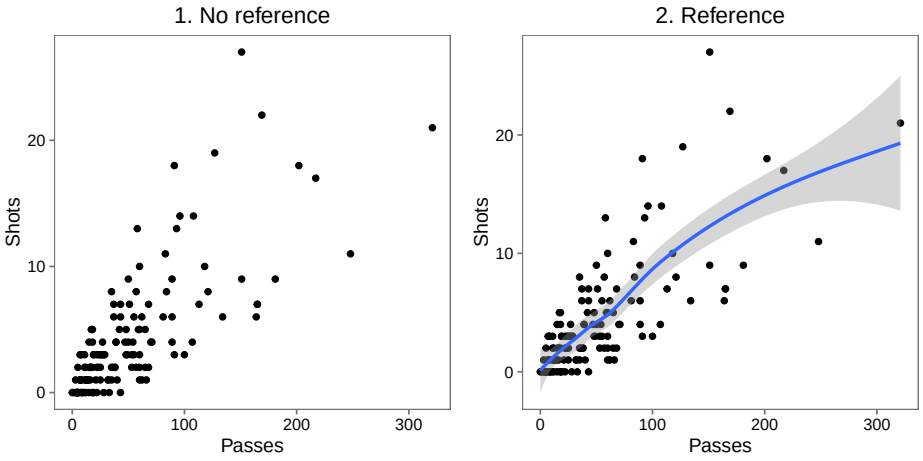
0.29 References

Guideline 3: **Provide useful references.**

Data is easier to interpret when you add references. For example, if you show what it typical, it helps viewers interpret how unusual outliers are. The graph below on the right has added shading showing the range of daily deaths in July in Chicage for 1990–1994 and 1996–2000, to clarify how unusual July 1995 was.

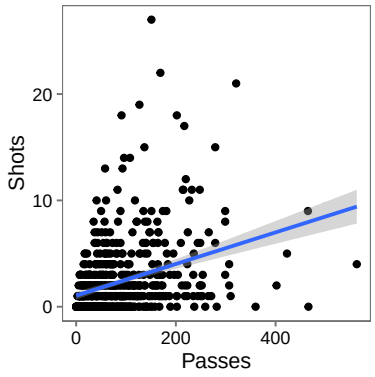


Another useful way to add references is to add a linear or smooth fit to the data, to help clarify trends in the data.



You can use the function `geom_smooth` to add a smooth or linear reference line:

```
ggplot(worldcup, aes(x = Passes, y = Shots)) +
  geom_point() + theme_few() +
  geom_smooth(method = "lm")
```



The most useful `geom_smooth` parameters to know are:

- `method`: The default is to add a loess curve if the data includes less than 1000 points and a generalized additive model for 1000 points or more. However, you can change to show the fitted line from a linear model using `method = "lm"` or from a generalized linear model using `method = "glm"`.
- `span`: How wiggly or smooth the smooth line should be (smaller value: more wiggly; larger value: more smooth)
- `se`: TRUE or FALSE, indicating whether to include shading for 95% confidence intervals.
- `level`: Confidence level for confidence interval (e.g., `0.90` for 90% confidence intervals)

Lines and polygons can also be useful for adding references. Useful geoms include:

- `geom_hline`, `geom_vline`: Add a horizontal or vertical line
- `geom_abline`: Add a line with an intercept and slope
- `geom_polygon`: Add a filled polygon
- `geom_path`: Add an unfilled polygon

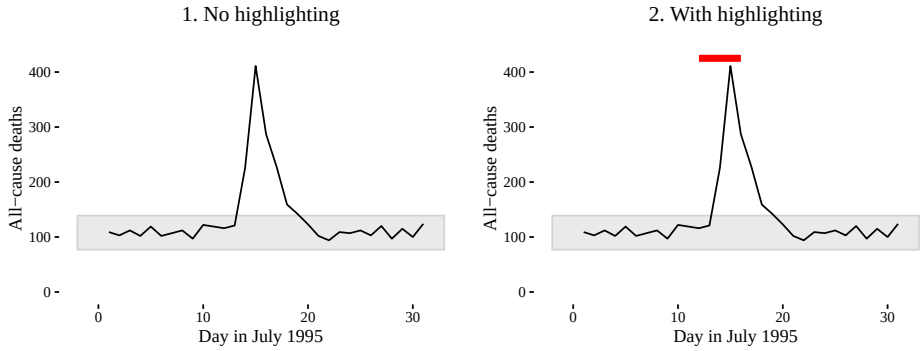
When adding these references:

- Add reference elements first, so they will be plotted under the data, instead of on top of it.
- Use `alpha` to add transparency to these elements.
- Use colors that are unobtrusive (e.g., grays)
- For lines, consider using non-solid line types (e.g., `linetype = 3`)

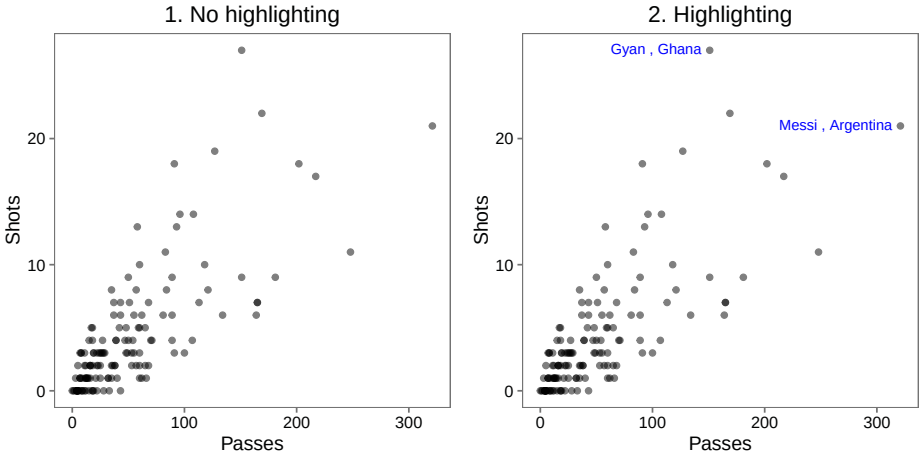
0.30 Highlighting

Guideline 3: **Highlight interesting aspects.**

Consider adding elements to highlight noteworthy elements of the data. For example, in the graph on the right, the days of a major heat wave have been highlighted with a red line.



In the below graphs, the names of the players with the most shots and passes have been added to highlight these unusual points.

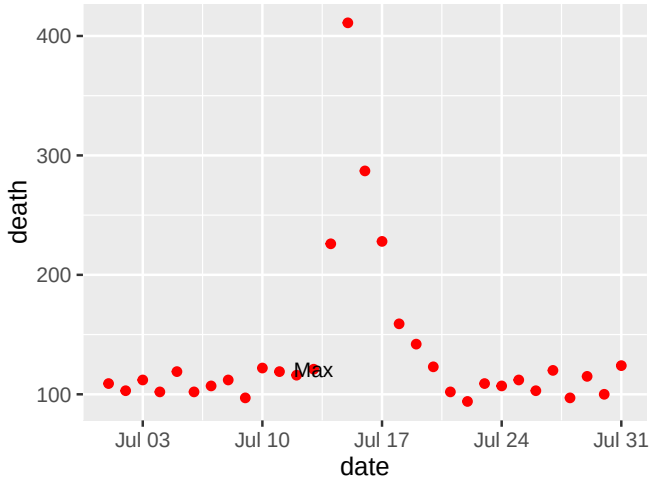


One helpful way to annotate is with text, using `geom_text()`. For this, you'll first need to create a dataframe with the hottest day in the data:

```
hottest_day <- chic_july %>%
  filter(temp == max(temp))
hottest_day[ , 1:6]
```

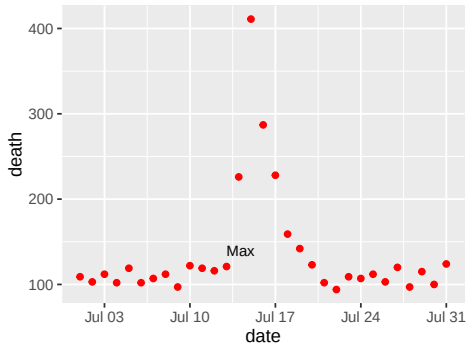
```
##         date time year month doy      dow
## 1 1995-07-13 3116 1995     7 194 Thursday
```

```
chic_plot + geom_text(data = hottest_day,
                      label = "Max",
                      size = 3)
```



With `geom_text`, you'll often want to use position adjustment (the `position` parameter) to move the text so it won't be right on top of the data points:

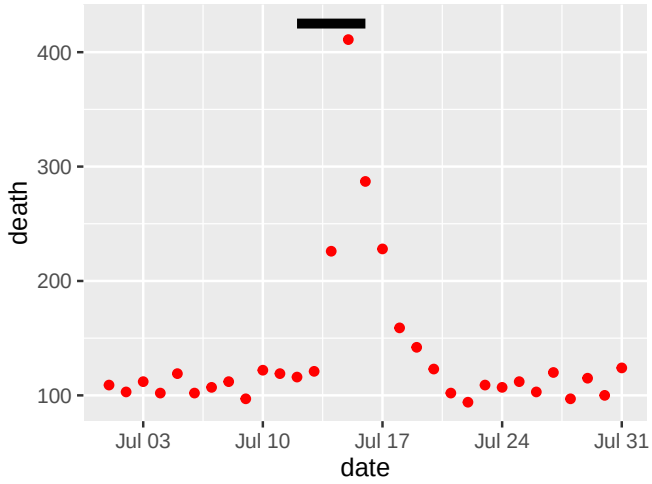
```
chic_plot + geom_text(data = hottest_day,
                      label = "Max",
                      size = 3, hjust = 0, vjust = -1)
```



You can also use lines to highlight. For this, it is often useful to create a new dataframe with data for the reference. To add a line for the Chicago heat wave, I've added a dataframe called `hw` with the relevant date range. I'm setting the y-value to be high enough (425) to ensure the line will be placed above the mortality data.

```
hw <- data.frame(date = c(as.Date("1995-07-12"),
                          as.Date("1995-07-16")),
                 death = c(425, 425))

b <- chic_plot +
        geom_line(data = hw,
                  aes(x = date, y = death),
                  size = 2)
```

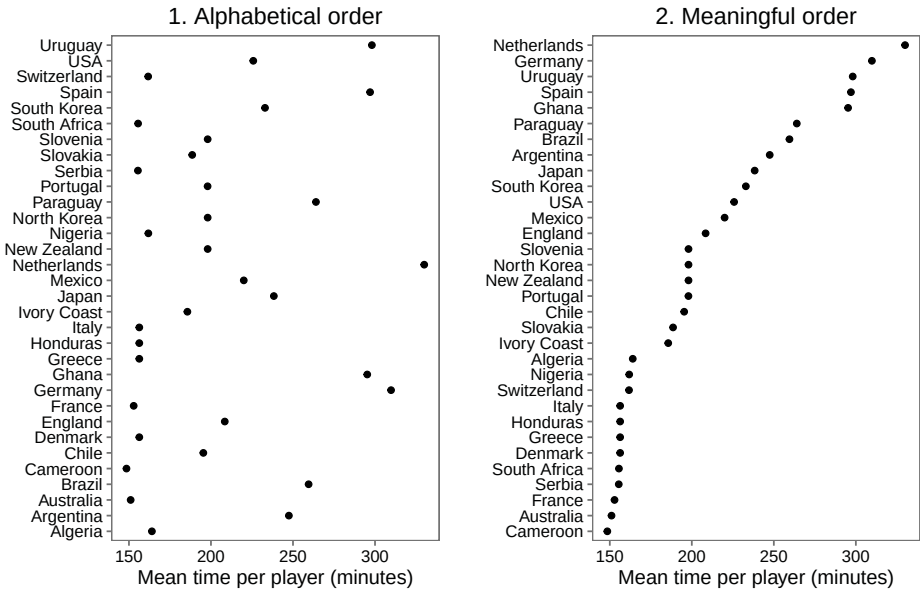
```
b
```



0.31 Order

Guideline 4: **Make order meaningful.**

You can make the ranking of data clearer from a graph by using order to show rank. Often, factor or categorical variables are ordered by something that is not interesting, like alphabetical order.



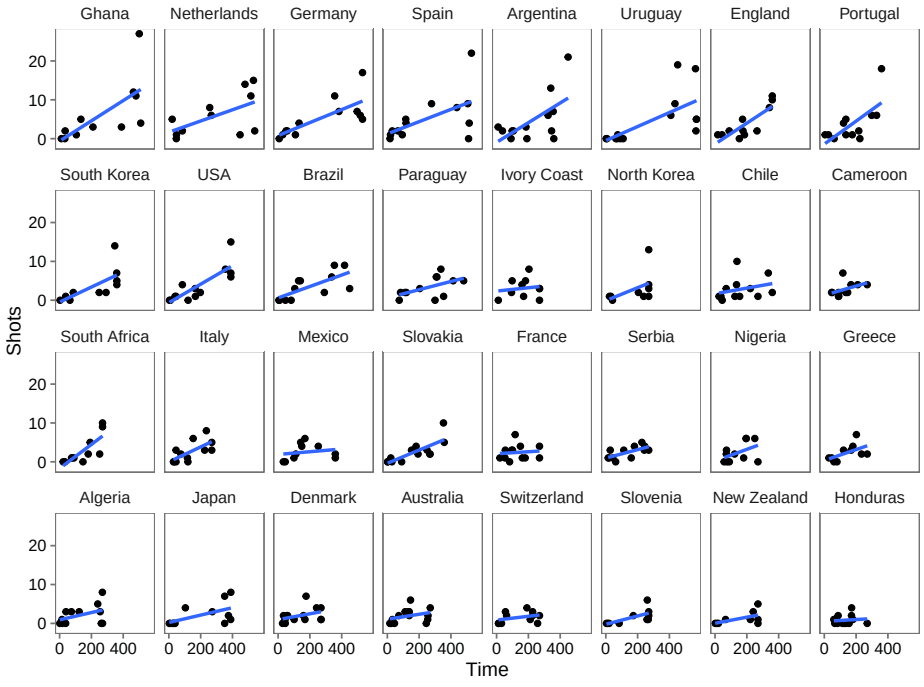
You can re-order factor variables in a graph by resetting the factor using the `factor` function and changing the order that levels are included in the `levels` parameter.

0.32 Small multiples

Guideline 5: **When possible, use small multiples.**

Small multiples are graphs that use many small plots showing the same thing for different facets of the data. For example, instead of using color in a single plot to show data for males and females, you could use two small plots, one each for males and females.

Typically, in small multiples, all plots use the same x- and y-axes. This makes it easier to compare across plots, and it also allows you to save room by limiting axis annotation.



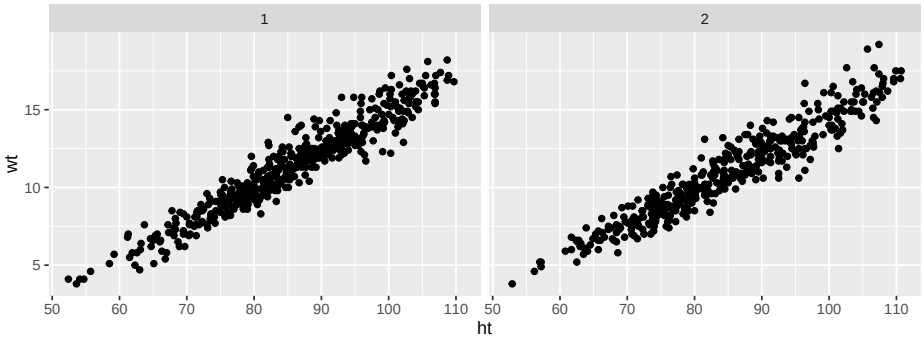
You can use the `facet` functions to create small multiples. This separates the graph into several small graphs, one for each level of a factor.

The `facet` functions are:

- `facet_grid()`
- `facet_wrap()`

For example, to create small multiples by sex for the Nepali dataset, when plotting height versus weight, you can call:

```
ggplot(nepali, aes(ht, wt)) +
       geom_point() +
       facet_grid(. ~ sex)
```



The `facet_grid` function can facet by one or two variables. One will be shown by rows, and one by columns:

```
## Generic code
facet_grid([factor for rows] ~ [factor for columns])
```

The `facet_wrap()` function can only facet by one variable, but it can "wrap" the small graphs for that variable, so the don't all have to be in one row or column:

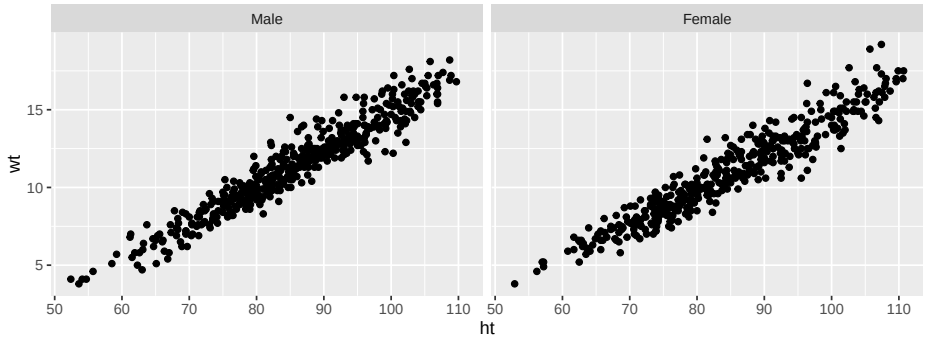
```
## Generic code
facet_wrap(~ [factor for faceting], ncol = [number of columns])
```

Often, when you do faceting, you'll want to re-name your factors levels or re-order them. For this, you'll need to use the `factor()` function on the original vector. For example, to rename the `sex` factor levels from "1" and "2" to "Male" and "Female", you can run:

```
nepali <- nepali %>%
  mutate(sex = factor(sex, levels = c(1, 2),
                      labels = c("Male", "Female")))
```

Notice that the labels for the two graphs have now changed:

```
ggplot(nepali, aes(ht, wt)) +
        geom_point() +
        facet_grid(. ~ sex)
```

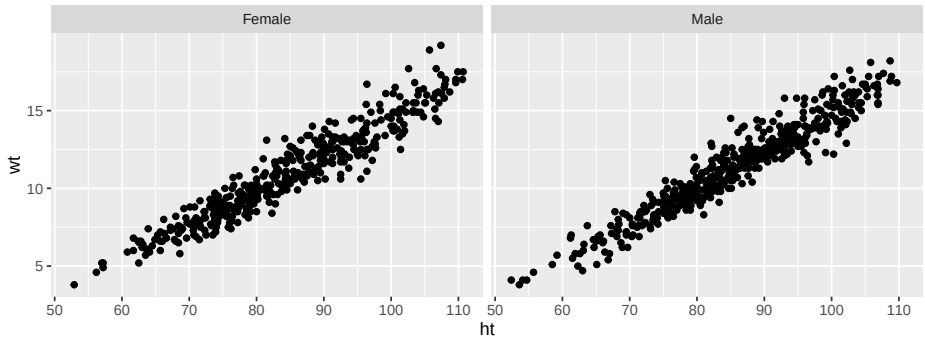


To re-order the factor, and show the plot for "Female" first, you can use `factor` to change the order of the levels:

```
nepali <- nepali %>%
  mutate(sex = factor(sex, levels = c("Female", "Male")))
```

Now notice that the order of the plots has changed:

```
ggplot(nepali, aes(ht, wt)) +
        geom_point() +
        facet_grid(. ~ sex)
```



0.33 Advanced customization

0.33.1 Scales

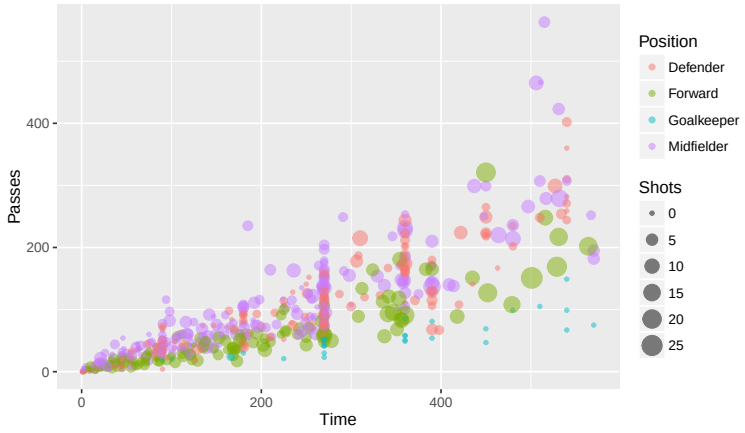
There are a number of different functions for adjusting scales. These follow the following convention:

```
## Generic code
scale_[aesthetic]_[vector type]
```

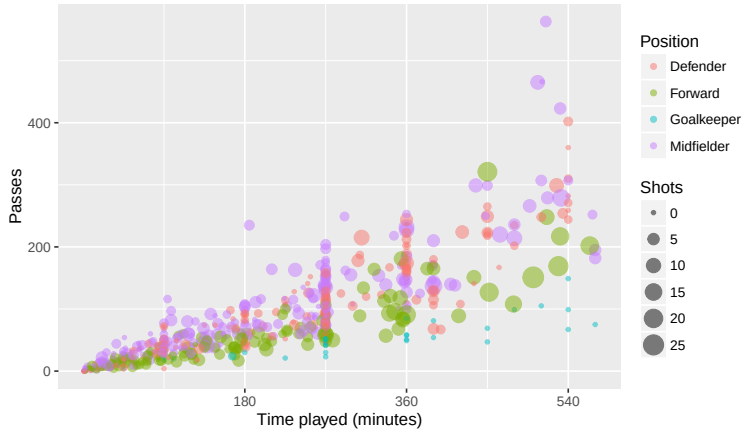
For example, to adjust the x-axis scale for a continuous variable, you'd use `scale_x_continuous`. You can use a `scale` function for an axis to change things like the axis label (which you could also change with `xlab` or `ylab`) as well as position and labeling of breaks.

For example, here is the default for plotting time versus passes for the `worldcup` dataset, with the number of shots taken shown by size and position shown by color:

```
ggplot(worldcup, aes(x = Time, y = Passes,
                     color = Position, size = Shots)) +
  geom_point(alpha = 0.5)
```




```
ggplot(worldcup, aes(x = Time, y = Passes,
                     color = Position, size = Shots)) +
  geom_point(alpha = 0.5) +
  scale_x_continuous(name = "Time played (minutes)",
                     breaks = 90 * c(2, 4, 6),
                     minor_breaks = 90 * c(1, 3, 5))
```

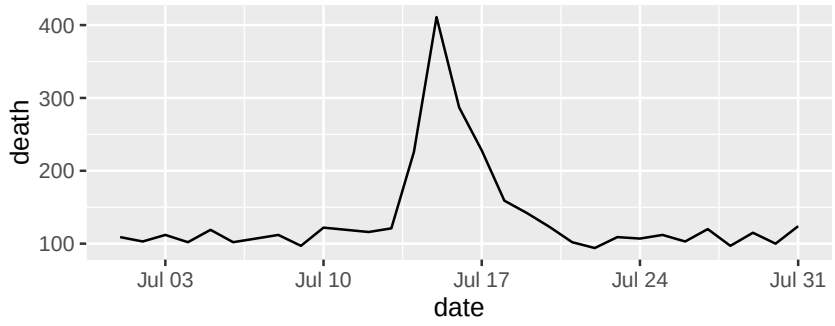


Parameters you might find useful in `scale` functions include:

Parameter	Description
name	Label or legend name
breaks	Vector of break points
minor_breaks	Vector of minor break points
labels	Labels to use for each break
limits	Limits to the range of the axis

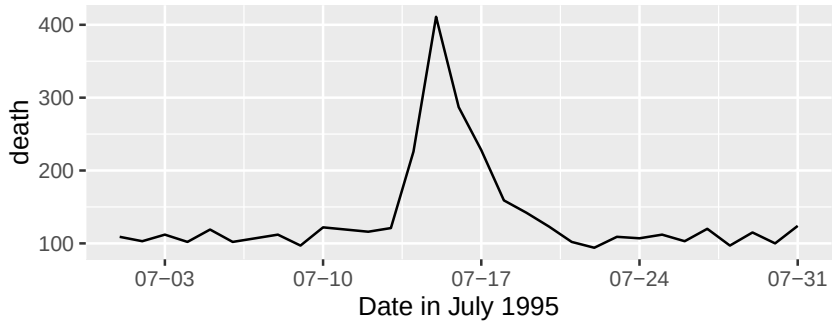
For dates, you can use `scale` functions like `scale_x_date` and `scale_x_datetime`. For example, here's a plot of deaths in Chicago in July 1995 using default values for the x-axis:

```
ggplot(chic_july, aes(x = date, y = death)) +
  geom_line()
```



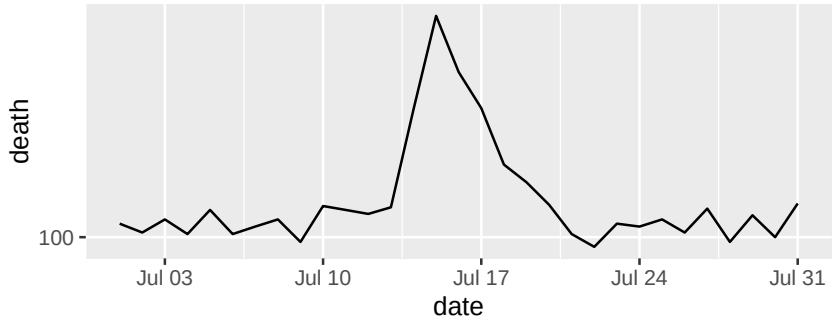
And here's an example of changing the formating and name of the x-axis:

```
ggplot(chic_july, aes(x = date, y = death)) +
  geom_line() +
  scale_x_date(name = "Date in July 1995",
               date_labels = "%m-%d")
```



You can also use the `scale` functions to transform an axis. For example, to show the Chicago plot with "deaths" on a log scale, you can run:

```
ggplot(chic_july, aes(x = date, y = death)) +
  geom_line() +
  scale_y_log10()
```



For colors and fills, the conventions for the names of the `scale` functions can vary. For example, to adjust the color scale when you're mapping a discrete variable (i.e., categorical, like gender or animal breed) to color, you'd use `scale_color_hue`. To adjust the color scale for a continuous variable, like age, you'll use `scale_color_gradient`.

For any color scales, consider starting with `brewer` first (e.g., `scale_color_brewer`, `scale_color_distiller`). Scale functions from `brewer` allow you to

set colors using different palettes. You can explore these palettes at `http://colorbrewer2.org/`.

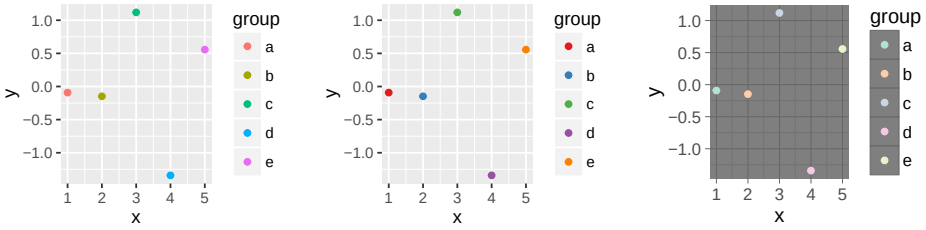
The Brewer palettes fall into three categories: sequential, divergent, and qualitative. You should use sequential or divergent for continuous data and qualitative for categorical data. Use `display.brewer.pal` to show the palette for a given number of colors.

```
library(RColorBrewer)
display.brewer.pal(name = "Set1", n = 8)
display.brewer.pal(name = "PRGn", n = 8)
display.brewer.pal(name = "PuBuGn", n = 8)
```

Set1 (qualitative) PRGn (divergent) PuBuGn (sequential)

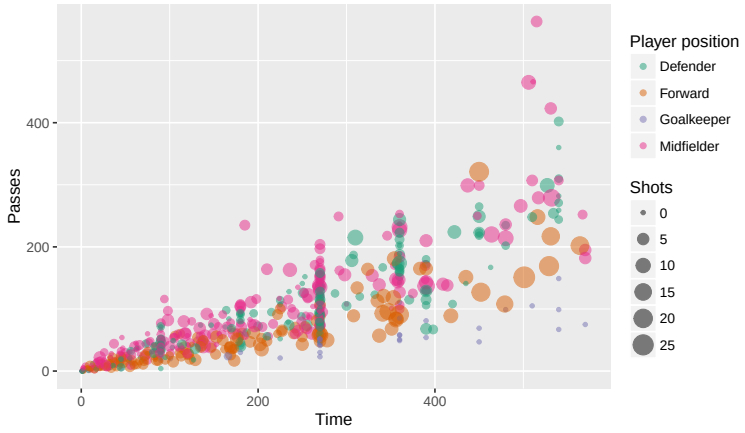
Use the `palette` argument within a `scales` function to customize the palette:

```
a <- ggplot(data.frame(x = 1:5, y = rnorm(5),
                       group = letters[1:5]),
            aes(x = x, y = y, color = group)) +
  geom_point()
b <- a + scale_color_brewer(palette = "Set1")
c <- a + scale_color_brewer(palette = "Pastel2") +
  theme_dark()
grid.arrange(a, b, c, ncol = 3)
```



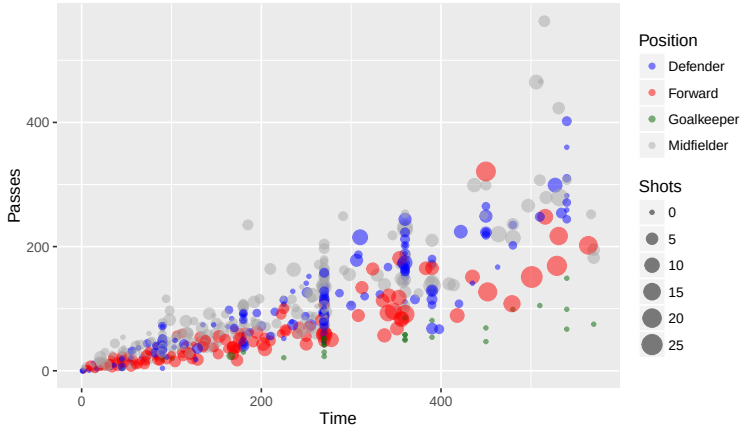

```
ggplot(worldcup, aes(x = Time, y = Passes,
                     color = Position, size = Shots)) +
```

```
  geom_point(alpha = 0.5) +
  scale_color_brewer(palette = "Dark2",
                     name = "Player position")
```



You can also set colors manually:

```
ggplot(worldcup, aes(x = Time, y = Passes,
                     color = Position, size = Shots)) +
  geom_point(alpha = 0.5) +
  scale_color_manual(values = c("blue", "red",
                                "darkgreen", "darkgray"))
```



0.34 To find out more

Some excellent further references for plotting are:

- R Graphics Cookbook (book and website)
- Google images

For more technical details about plotting in R:

- ggplot2: Elegant Graphics for Data Analysis, Hadley Wickham
- R Graphics, Paul Murrell

0.35 In-course exercise

0.35.1 Designing a plot

For today's exercise, you'll be building a plot using the `worldcup` data from the `faraway` package. First, load in that data.

Next, say you want to look at the relationship between the number of minutes that a player played in the 2010 World Cup (`Time`) and the number of shots the player took on goal (`Shots`). On a sheet of paper, and talking with your partner, decide how the two of you would design a plot to explore and present this relationship. How would you incorporate some of the principles of creating good graphs?

0.35.1.1 Example R code

```
library(faraway)
data(worldcup)
head(worldcup, 2)
```

```
##           Team   Position Time Shots Passes Tackles Saves
## Abdoun Algeria Midfielder   16     0      6       0     0
## Abe      Japan Midfielder  351     0    101      14     0
```

This dataset has the players' names as rownames, rather than in a column. Once we start using `dplyr` functions, we'll lose these rownames. Therefore, start by converting the rownames to a column called `Player`:

```
library(dplyr)
worldcup <- worldcup %>%
  mutate(Player = rownames(worldcup))
head(worldcup, 2)
```

```
##      Team   Position Time Shots Passes Tackles Saves Player
## 1 Algeria Midfielder   16     0      6       0     0 Abdoun
## 2   Japan Midfielder  351     0    101      14     0    Abe
```

0.35.2 Basic scatterplots with R base graphics and ggplot

Perform the following tasks:

- Install and load the `ggplot2` and `ggthemes` packages.
- For the `worldcup` data, plot a scatterplot of Time (on the x-axis) versus Shots.
- Add some ggplot elements to make this plot a bit more attractive. (For example, change the x- and y-axis labels and add a title.)

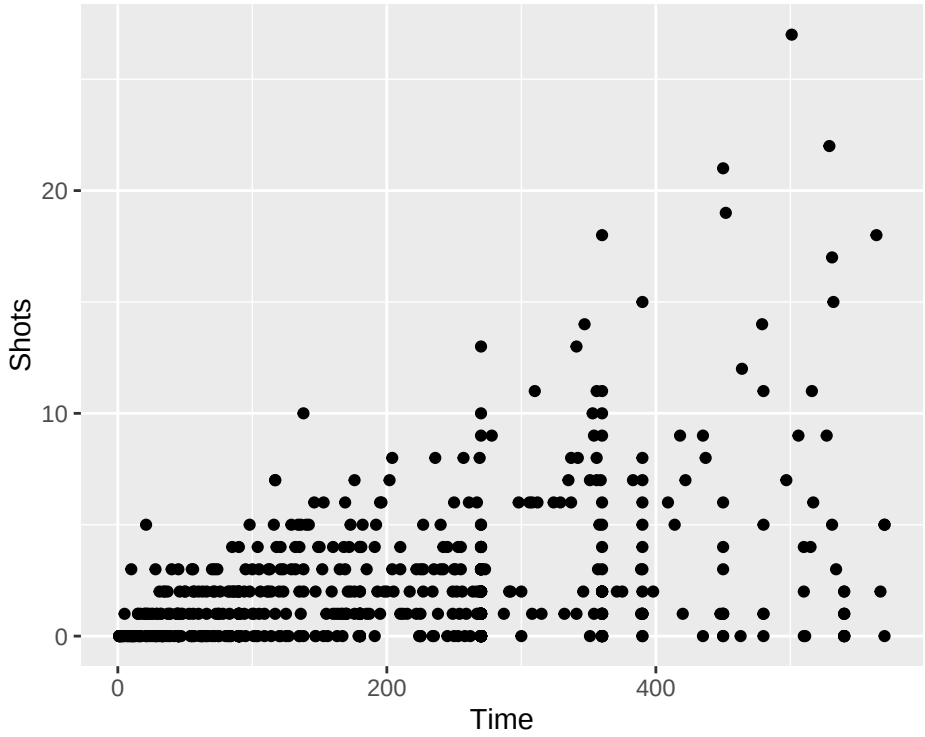
0.35.2.1 Example R code

Install and load the `ggplot2` package:

```
# install.packages("ggplot2")
library(ggplot2)
# install.packages("ggthemes")
library(ggthemes)
```

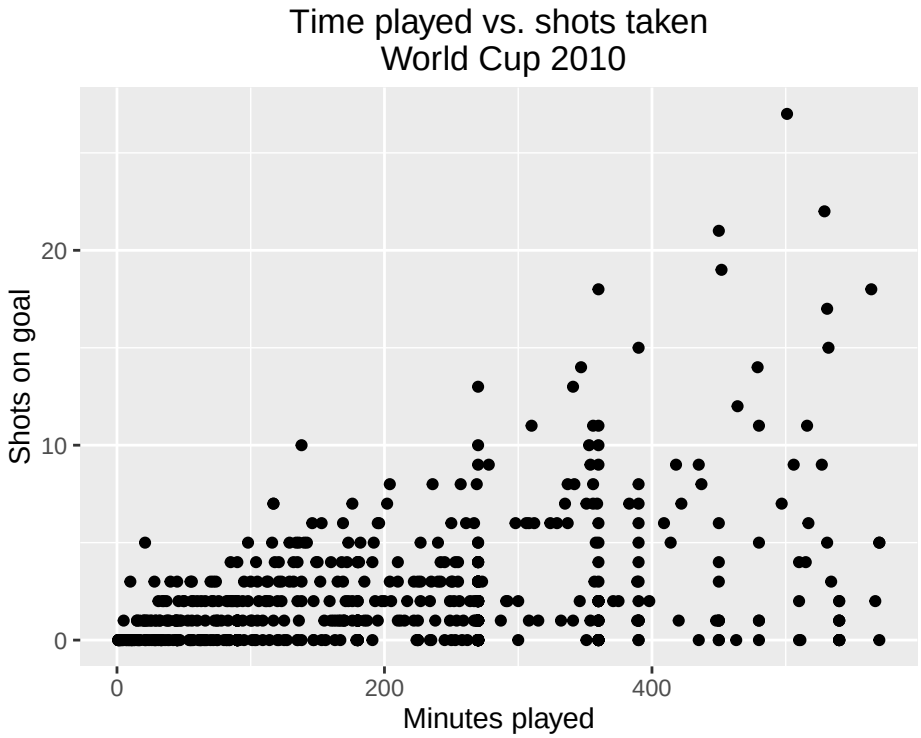
Use the R base graphics to create a scatterplot of Time versus Shots:

```
ggplot(worldcup, aes(x = Time, y = Shots)) +
        geom_point()
```



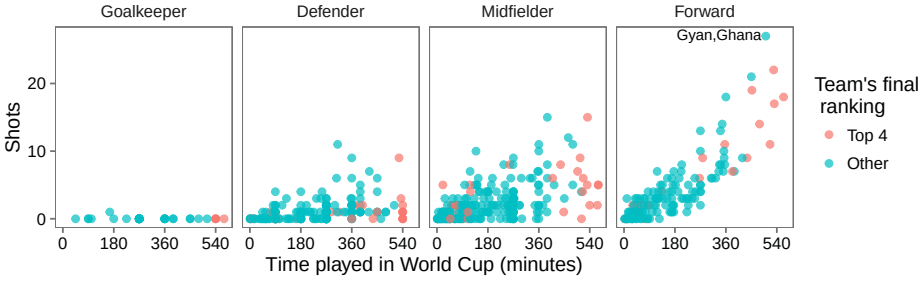
Use some of the plotting options to improve the graph's appearance:

```
ggplot(worldcup, aes(x = Time, y = Shots)) +
  geom_point() +
  xlab("Minutes played") +
  ylab("Shots on goal") +
  ggtitle("Time played vs. shots taken\n World Cup 2010")
```



0.35.3 Fancier graphs

In this section, we'll work on creating a plot like this:



Try the following tasks:

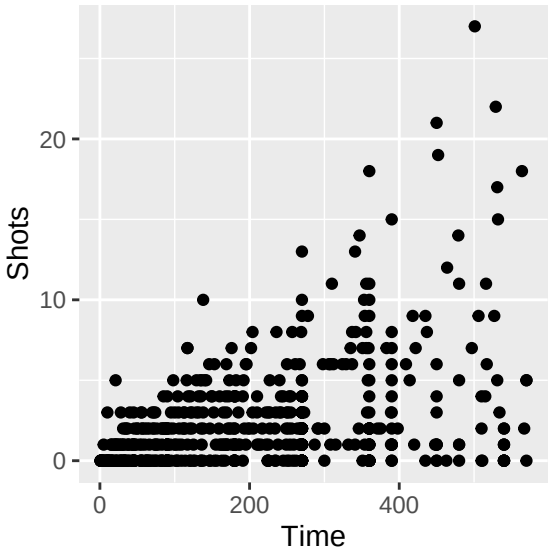
- First, before you start coding, talk with your group members about how this graph is different from the simple one you created with `ggplot` in the last section. Also discuss what you can figure out from this new graph that was less clear from the simpler one you created before.
- Use the `xlab()` function to make a clearer title for the x-axis. (You may have already written this code in the last section of this exercise.)

- Often, in graphs with a lot of points, it's hard to see some of the points, because they overlap other points. Three strategies to address this are: (a) make the points smaller; (b) make the points somewhat transparent; and (c) jitter the points. Try doing the first two with the simple ggplot scatterplot you created in the previous section of Shots by Time.
- Create a new column in the `worldcup` data called `top_four` that specifies whether or not the `Team` for that observation was one of the top four teams in the tournament (Netherlands, Uruguay, Spain, and Germany). Make the colors of the points correspond to whether the team was a top-four team.
- Create small multiples. The relationship between time played and shots taken is probably different by the players' positions. Use faceting to create different graphs for each position.
- Make order count: What order are the faceted graphs currently in? Offensive players have more chances to take shots than defensive players, so that might be a useful ordering for the facets. Re-order the `Position` factor column to go from nearest your own goal to nearest the opponents goal, and then re-plot the graph from the previous step.
- Highlighting interesting data: Who had the most shots in the 2010 World Cup? Was he on a top-four team? Use `geom_text()` to label his point on the graph with his name.
- Increase data density: Try changing the theme, to come up with a graph with a bit less non-data ink. From the `ggthemes` package (you'll need to install it if you don't already have it), try some of the following themes: `theme_few()`, `theme_tufte()`, `theme_stata()`, `theme_fivethirtyeight()`, `theme_economist_white()`, and `theme_wsj()`.

0.35.3.1 Example R code

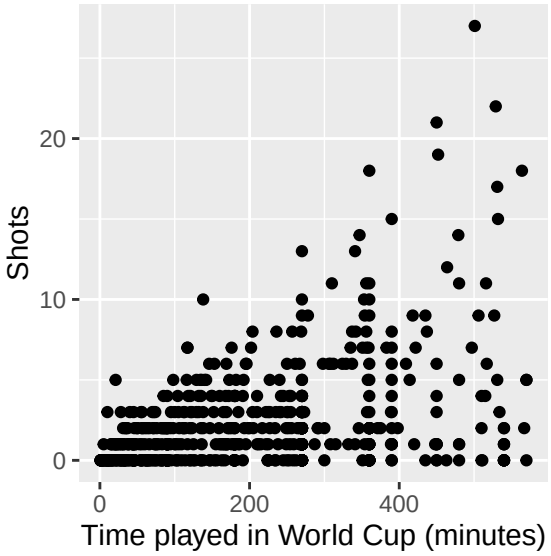
As a reminder, here's the code to do a simple scatterplot ot Shots by Time for the `worldcup` data:

```
ggplot(worldcup, aes(x = Time, y = Shots)) +
        geom_point()
```



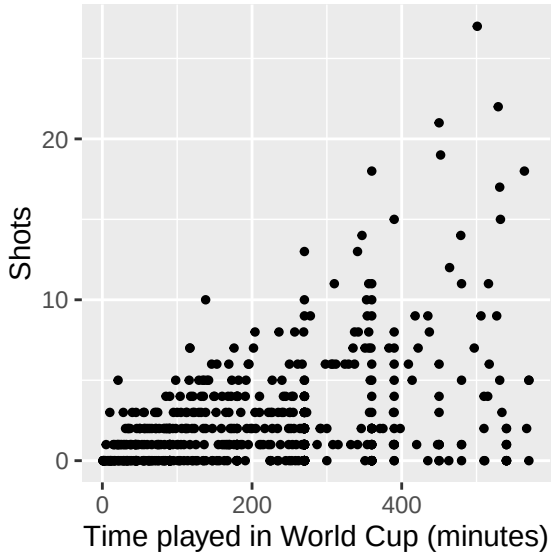
To add a clearer x-axis label that the current one, use `xlab()`:

```
ggplot(worldcup, aes(x = Time, y = Shots)) +
        geom_point() +
        xlab("Time played in World Cup (minutes)")
```



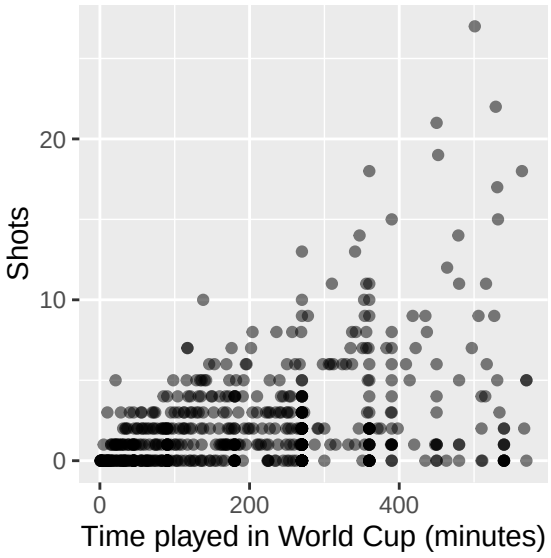
To make the points smaller, use the `size` option in `geom_point()` (smaller than about 2 = smaller than default, larger than about 2 = larger than default):

```
ggplot(worldcup, aes(x = Time, y = Shots)) +
        geom_point(size = 1)  +
        xlab("Time played in World Cup (minutes)")
```



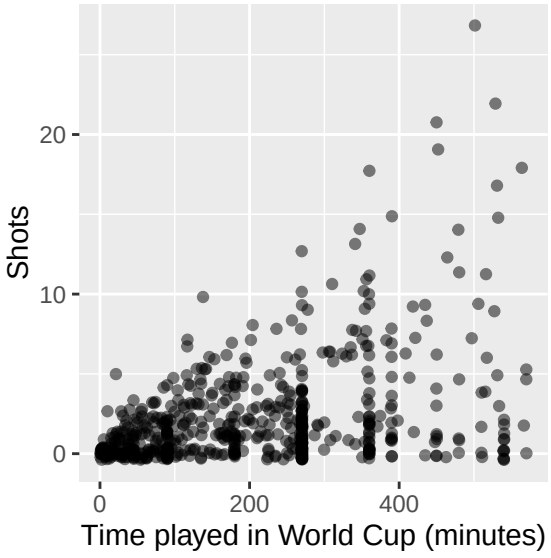
To make the points semi-transparent, use the `alpha` option in `geom_point()` (closer to 0 = more tranparent, closer to 1 = more opaque):

```
ggplot(worldcup, aes(x = Time, y = Shots)) +
        geom_point(alpha = 0.5)  +
        xlab("Time played in World Cup (minutes)")
```



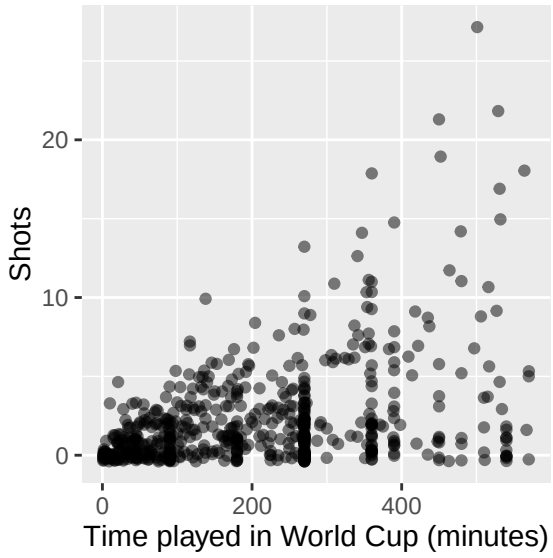
To jitter the points some, use the `position = "jitter"` option in `geom_point()`:

```
ggplot(worldcup, aes(x = Time, y = Shots)) +
        geom_point(size = 1.5, position = "jitter",
                   alpha = 0.5)  +
        xlab("Time played in World Cup (minutes)")
```



As an alternative, you could also jitter the points by using `geom_jitter` rather than `geom_point`:

```
ggplot(worldcup, aes(x = Time, y = Shots)) +
        geom_jitter(size = 1.5, alpha = 0.5, width = 0.25)  +
        xlab("Time played in World Cup (minutes)")
```



"Jittering" the points means adding some extra random noise in either the x- or y-direction, or in both directions. This technique can be particularly useful when you are trying to plot points for which one dimension is categorical, rather than continuous. You can specify which direction (x and / or y) is jittered, as well as the amount of noise to add. To find out more, check out the helpfile for the `geom_jitter` function.

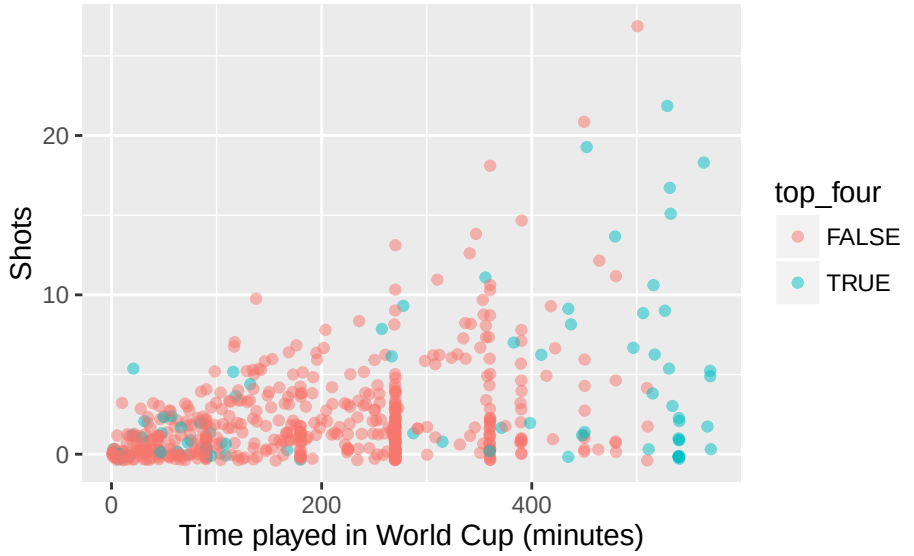
To create a new column called `top_four`, first create vector that lists those top four teams, then create a logical vector in the dataframe for whether the team for that observation is in one of the top four teams:

```
worldcup <- worldcup %>%
  mutate(top_four = Team %in% c("Spain", "Germany",
                                "Uruguay", "Netherlands"))
summary(worldcup$top_four)
```

```
##    Mode   FALSE    TRUE    NA's
## logical     517      78       0
```

To color points by this variable, use `color =` in the `aes()` part of the `ggplot()` call:

```
ggplot(worldcup, aes(x = Time, y = Shots,
                     color = top_four)) +
        geom_point(size = 1.5, position = "jitter",
                   alpha = 0.5)  +
        xlab("Time played in World Cup (minutes)")
```

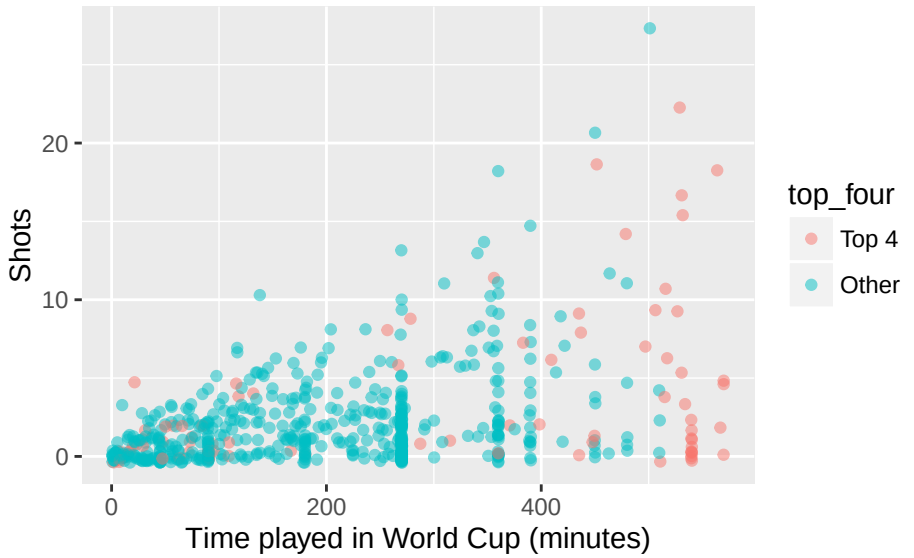


To create nicer labels for the legend for color, convert the `top_four` column into the factor class, with the labels you want to use in the figure legend:

```
worldcup <- worldcup %>%
  mutate(top_four = factor(top_four, levels = c(TRUE, FALSE),
                           labels = c("Top 4", "Other")))
summary(worldcup$top_four)
```

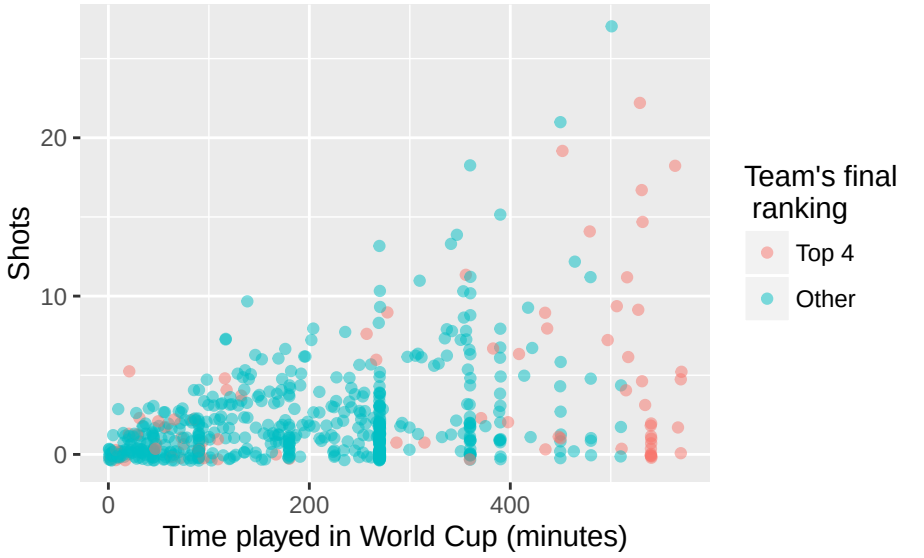
```
## Top 4 Other
##    78   517
```

```
ggplot(worldcup, aes(x = Time, y = Shots,
                     color = top_four)) +
        geom_point(size = 1.5, position = "jitter",
                   alpha = 0.5)  +
        xlab("Time played in World Cup (minutes)")
```



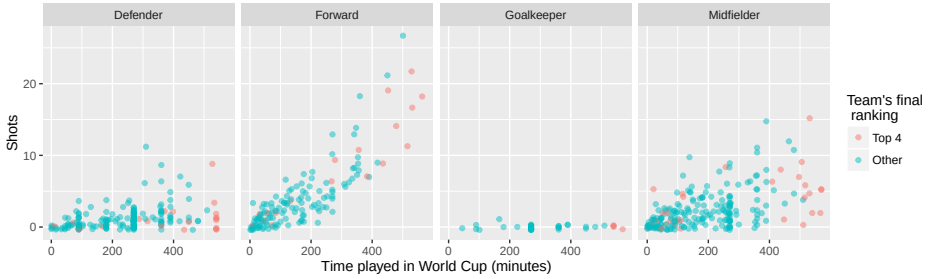
As a note, you can use the `scale_color_discrete()` function to put in a nicer legend title:

```
ggplot(worldcup, aes(x = Time, y = Shots,
                     color = top_four)) +
        geom_point(size = 1.5, position = "jitter",
                   alpha = 0.5)  +
        xlab("Time played in World Cup (minutes)") +
        scale_color_discrete(name = "Team's final\n ranking")
```



To create small multiples, use the `facet_grid()` command:

```
ggplot(worldcup, aes(x = Time, y = Shots,
                     color = top_four)) +
        geom_point(size = 1.5, position = "jitter",
                   alpha = 0.5)  +
        xlab("Time played in World Cup (minutes)") +
        scale_color_discrete(name = "Team's final\n ranking") +
        facet_grid(. ~ Position)
```



To re-order the `Position` column of the dataframe, use the `levels` option of the `factor()` function. This re-sets how R saves the order of the levels of this factor.

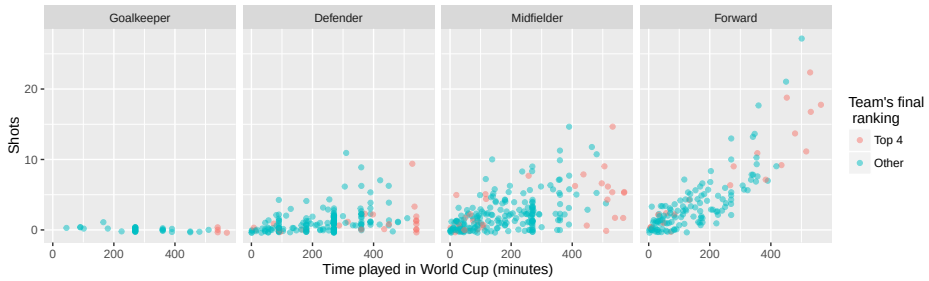
```
worldcup <- worldcup %>%
  mutate(Position = factor(Position,
                           levels = c("Goalkeeper", "Defender",
                                      "Midfielder", "Forward")))
levels(worldcup$Position)
```

```
## [1] "Goalkeeper" "Defender"   "Midfielder" "Forward"
```

Note from this code example that you can use the `levels` function to find out the levels and their order for a factor-class vector.

Then use the same code from before for your plot:

```
ggplot(worldcup, aes(x = Time, y = Shots,
                     color = top_four)) +
        geom_point(size = 1.5, position = "jitter",
                   alpha = 0.5)  +
        xlab("Time played in World Cup (minutes)") +
        scale_color_discrete(name = "Team's final\n ranking") +
        facet_grid(. ~ Position)
```



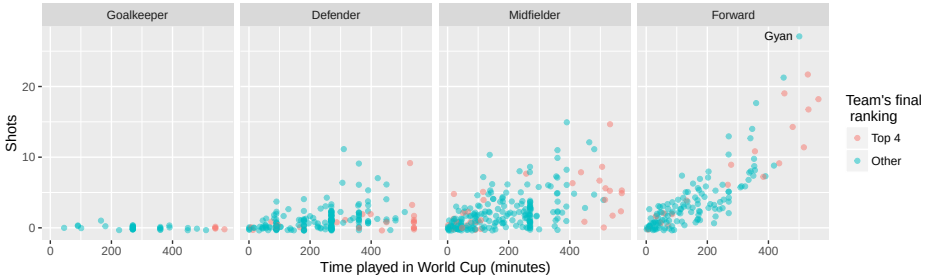
You can use the `filter` function with a logical statement comparing `Shots` to the maximum value of `Shots` (`max(Shots)`) to filter down to the row or rows of the player or players with the most shots:

```
most_shots <- worldcup %>%
  filter(Shots == max(Shots))
most_shots
```

```
##    Team Position Time Shots Passes Tackles Saves Player top_four
## 1 Ghana  Forward  501    27    151       1     0   Gyan    Other
```

Use `geom_text()` to label his point on the graph with his name. You may need to mess around with some of the options in `geom_text()`, like `size`, `hjust`, and `vjust` (`hjust` and `vjust` say where, in relation to the point location, to put the label), to get something you're happy with. Also, I pasted on an extra space at the end of the player's name, to add some padding so the label wouldn't be right on top of the point.

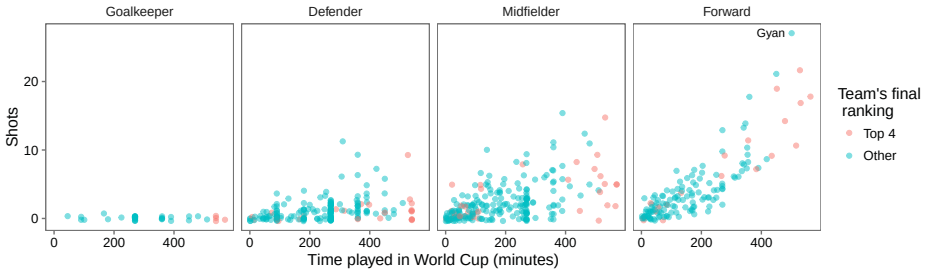
```
ggplot(worldcup, aes(x = Time, y = Shots,
                     color = top_four)) +
        geom_point(size = 1.5, position = "jitter",
                   alpha = 0.5)  +
        xlab("Time played in World Cup (minutes)") +
        scale_color_discrete(name = "Team's final\n ranking") +
        facet_grid(. ~ Position) +
        geom_text(data = most_shots,
                  aes(label = paste(Player, " ")),
                  colour = "black", size = 3,
                  hjust = 1, vjust = 0.4)
```



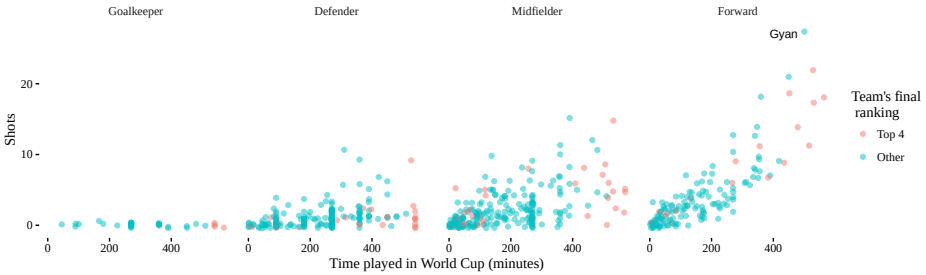
Try out different themes for the plot. First, I'll save everything we've done so far as the object `shot_plot`, then I'll try adding different themes:

```
shot_plot <- ggplot(worldcup, aes(x = Time, y = Shots,
                     color = top_four)) +
        geom_point(size = 1.5, position = "jitter",
                   alpha = 0.5)  +
        xlab("Time played in World Cup (minutes)") +
        scale_color_discrete(name = "Team's final\n ranking") +
        facet_grid(. ~ Position) +
        geom_text(data = most_shots,
```

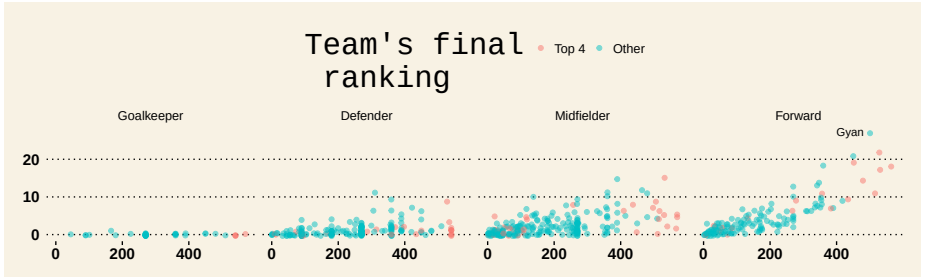
```
                aes(label = paste(Player, " ")),
                colour = "black", size = 3,
                hjust = 1, vjust = 0.4)

shot_plot + theme_few()
```



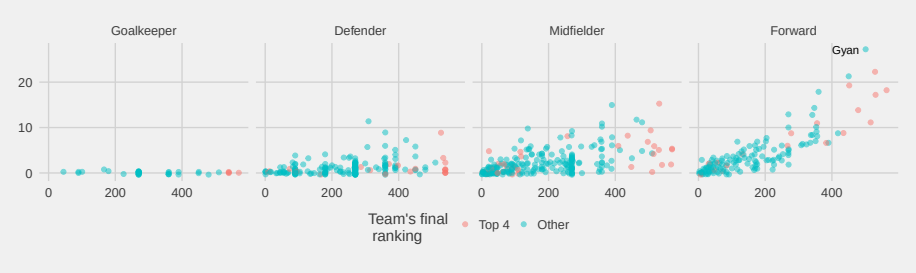

```
shot_plot + theme_tufte()
```



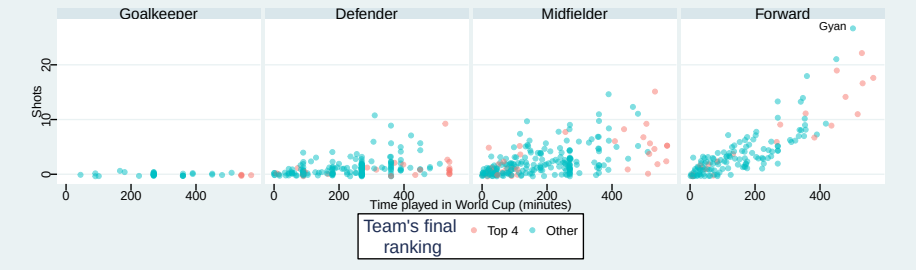

```
shot_plot + theme_wsj()
```



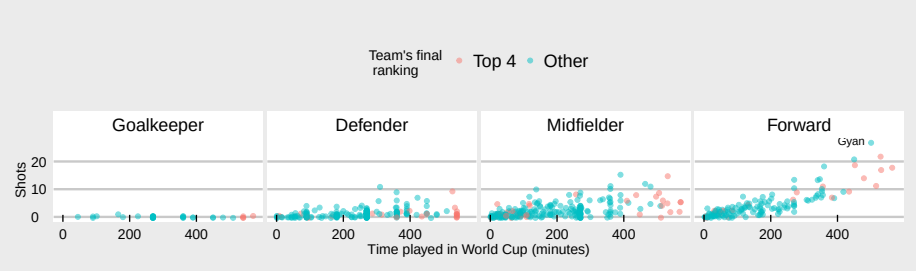
```
shot_plot + theme_fivethirtyeight()
```




```
shot_plot + theme_stata()
```




```
shot_plot + theme_economist_white()
```



0.35.4 Data visualization cheatsheet

RStudio comes with some excellent cheatsheets, which provide quick references to functions and code you might find useful for different tasks. For this part of

the group exercise, you'll explore their cheatsheet for data visualization, both to learn some new `ggplot2` code and to become familiar with how to use this cheatsheet as you do your own analysis.

- Open the data visualization cheatsheet. You can do this from RStudio by going to "Help" -> "Cheatsheets" -> "Data Visualization with ggplot2".
- Notice that different sections give examples with some datasets that come with either base R or ggplot2. For example, under the "Graphical Primitives" section, there is code defining the object `a` as a ggplot object using the "seals" dataset: `a <- ggplot(seals, aes(x = long, y = lat))`.
- Go through the cheatsheet and list all of the example datasets that are used in this cheatsheet. Open their helpfiles to learn more about the data.
- Create the example datasets `a` through `l` and `s` through `t` using the code given on the cheatsheet.
- Pick at least one example to try out from each of the following sections: "Graphical Primitives", "One Variable", at least three subsections of "Two Variables", "Three Variables", "Scales", "Faceting", and "Position Adjustments". As you try these, try to figure out any aesthetics that you aren't familiar with (e.g., `ymin`, `ymax`). Also, use helpfiles for the geoms to look up parameters you aren't familiar with (e.g., `stat` for `geom_area`). If you can't figure out how to interpret a plot, check the helpfile for the associated geom. **Note**: For the `n` geom used in "scales", it should be defined as `n <- d + geom_bar(aes(fill = fl))`.

0.35.4.1 Example R code

The code for opening the helpfiles for the example datasets is:

```
?seals
?economics
?mpg
?diamonds
?USArrests
```

Note that, for `USArrests`, only some of the columns are pulled out (e.g., `murder = USArrests$murder`) to use in the `data` example dataframe. Further, the "Visualizing error" examples use a dataframe created specifically for these examples, called `df`.

Some of the base R and ggplot2 example datasets have become fairly well-known. Some that you'll see very often in examples are the `iris`, `mpg`, and `diamonds` datasets.

All of the code to create the datasets `a` through `l` and `s` through `t` is given somewhere on the cheatsheet. Here it is in full:

```
a <- ggplot(seals, aes(x = long, y = lat))
b <- ggplot(economics, aes(date, unemploy))
c <- ggplot(mpg, aes(hwy))
d <- ggplot(mpg, aes(fl))
e <- ggplot(mpg, aes(cty, hwy))
f <- ggplot(mpg, aes(class, hwy))
g <- ggplot(diamonds, aes(cut, color))
h <- ggplot(diamonds, aes(carat, price))
i <- ggplot(economics, aes(date, unemploy))
df <- data.frame(grp = c("A", "B"), fit = 4.5, se = 1:2)
j <- ggplot(df, aes(grp, fit, ymin = fit - se, ymax = fit + se))
data <- data.frame(murder = USArrests$Murder,
                   state = tolower(rownames(USArrests)))
map <- map_data("state")
k <- ggplot(data, aes(fill = murder))
seals$z <- with(seals, sqrt(delta_long^2 + delta_lat^2))
l <- ggplot(seals, aes(long, lat))
s <- ggplot(mpg, aes(fl, fill = drv))
t <- ggplot(mpg, aes(cty, hwy)) + geom_point()
```

Notice that, in some places, the aesthetics are defined using the full aesthetic name-value pair (e.g., `aes(x = long, y = lat)`), while in other places the code relies on position for defining which column of a dataframe maps to which aesthetic (e.g., `aes(cty, hwy)` or `aes(fl)`). Either is fine, although relying on position can result in errors if you are not very familiar with the order in which parameters are defined for a function.

This code will vary based on the examples you try, but here is some code for one set of examples:

```
b + geom_ribbon(aes(ymin = unemploy - 900, ymax = unemploy + 900))
c + geom_dotplot()
f + geom_violin(scale = "area")
h + geom_hex()
j + geom_pointrange()
k + geom_map(aes(map_id = state), map = map) +
  expand_limits(x = map$long, y = map$lat)
l + geom_contour(aes(z = z))
n <- d + geom_bar(aes(fill = fl))
n + scale_fill_brewer(palette = "Blues")
```

```
o <- c + geom_dotplot(aes(fill = ..x..))
o + scale_fill_gradient(low = "red", high = "yellow")
t + facet_grid(year ~ fl)
s + geom_bar(position = "fill")
```

Reproducible research #1

Download a pdf of the lecture slides covering this topic.

0.36 What is reproducible research?

A data analysis is **reproducible** if all the information (data, files, etc.) required is available for someone else to re-do your entire analysis.

This includes:

- Data available
- All code for cleaning raw data
- All code and software (specific versions, packages) for analysis

Some advantages of making your research reproducible are:

- You can (easily) figure out what you did six months from now.
- You can (easily) make adjustments to code or data, even early in the process, and re-run all analysis.
- When you're ready to publish, you can (easily) do a last double-check of your full analysis, from cleaning the raw data through generating figures and tables for the paper.
- You can pass along or share a project with others.
- You can give useful code examples to people who want to extend your research.

Here is a famous research example of the dangers of writing code that is hard to double-check or confirm:

- The Economist
- The New York Times
- Simply Statistics

Some of the steps required to making research reproducible are:

- All your raw data should be saved in the project directory. You should have clear documentation on the source of all this data.
- Scripts should be included with all the code used to clean this data into the data set(s) used for final analyses and to create any figures and tables.
- You should include details on the versions of any software used in analysis (for R, this includes the version of R as well as versions of all packages used).
- If possible, there should be no "by hand" steps used in the analysis; instead, all steps should be done using code saved in scripts. For example, you should use a script to clean data, rather than cleaning it by hand in Excel. If any "non-scriptable" steps are unavoidable, you should very clearly document those steps.

There are several software tools that can help you improve the reproducibility of your research:

- `knitr`: Create files that include both your code and text. These can be rendered to create final reports and papers. They keep code within the final file for the report.
- **`knitr` complements**: Create fancier tables and figures within RMarkdown documents. Packages include `tikzDevice`, `animate`, `xtables`, and `pander`.
- `packrat`: Save versions of each package used for the analysis, then load those package versions when code is run again in the future.

In this section, I will focus on using `knitr` and RMarkdown files.

0.37 Markdown

R Markdown files are mostly written using Markdown. To write R Markdown files, you need to understand what markup languages like Markdown are and how they work.

In Word and other word processing programs you have used, you can add formatting using buttons and keyboard shortcuts (e.g., "Ctrl-B" for bold). The file saves the words you type. It also saves the formatting, but you see the final output, rather than the formatting markup, when you edit the file (WYSIWYG – what you see is what you get).

In markup languages, on the other hand, you markup the document directly to show what formatting the final version should have (e.g., you type `**bold**` in the file to end up with a document with **bold**).

Examples of markup languages include:

view-source:www.colostate.edu

```
168
169                         <li>
170                             <a href="http://source.colostate.edu/beloved-mascot-cam-the-ram-
dies-at-age-6/"><img src="http://wwwmanager.colostate.edu/uploaded/1677.4.1.jpg" alt="Beloved
Mascot CAM the Ram Dies at Age 6" /></a>
171                             <div class="sDescription"><div class="dWrap">
172                                 <h3>Beloved Mascot CAM the Ram Dies at Age 6</h3>
173                                 <p>CAM the Ram, Colorado State University's beloved four-
legged mascot, died Saturday of natural causes. Many expressed their sadness after learning
of CAM 24's death. CAM had met thousands of people and had his picture taken thousands of
times while making numerous public appearances over the past four years.</p>
174                                 <p><a href="http://source.colostate.edu/beloved-mascot-cam-
the-ram-dies-at-age-6/">Read his Obituary</a></p>
175                             </div></div>
176                         </li>
177
```

Figure 24: Example of the source of an HTML file.

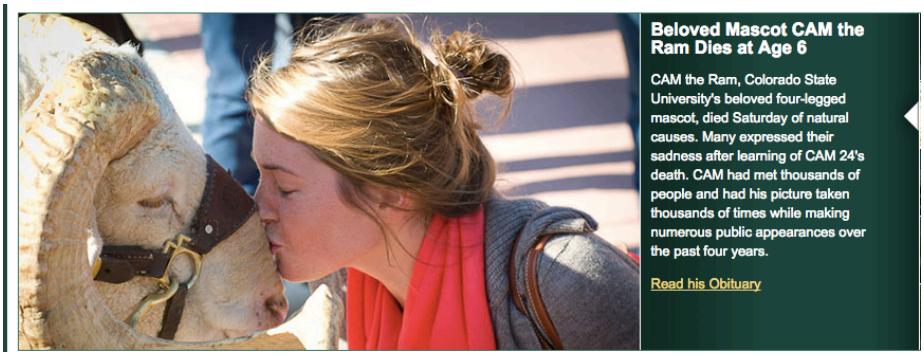


Figure 25: Example of a rendered HTML file.

- HTML (HyperText Markup Language)
- LaTex
- Markdown (a "lightweight" markup language)

For example, Figure 24 some marked-up HTML code from CSU's website, while Figure 25 shows how that file looks when it's rendered by a web browser.

To write a file in Markdown, you'll need to learn the conventions for creating formatting. This table shows what you would need to write in a flat file for some common formatting choices:

Code	Rendering	Explanation
‘**text**‘	**text**	boldface
‘*text*‘	*text*	italicized
‘[text](www.google.com)‘	[text](www.google.com)	hyperlink
‘# text‘		first-level header
‘## text‘		second-level header

Some other simple things you can do in Markdown include:

- Lists (ordered or bulleted)
- Equations
- Tables
- Figures from file
- Block quotes
- Superscripts

For more Markdown conventions, see RStudio's R Markdown Reference Guide (link also available through "Help" in RStudio).

0.38 Literate programming in R

Literate programming, an idea developed by Donald Knuth, mixes code that can be executed with regular text. The files you create can then be rendered, to run any embedded code. The final output will have results from your code and the regular text.

The `knitr` package can be used for literate programming in R. In essence, `knitr` allows you to write an R Markdown file that can be rendered into a pdf, Word, or HTML document.

Here are the basics of opening and rendering an R Markdown file in RStudio:

- To open a new R Markdown file, go to "File" -> "New File" -> "RMarkdown…" -> for now, chose a "Document" in "HTML" format.
- This will open a new R Markdown file in RStudio. The file extension for R Markdown files is ".Rmd".
- The new file comes with some example code and text. You can run the file as-is to try out the example. You will ultimately delete this example code and text and replace it with your own.
- Once you "knit" the R Markdown file, R will render an HTML file with the output. This is automatically saved in the same directory where you saved your .Rmd file.
- Write everything besides R code using Markdown syntax.

To include R code in an RMarkdown document, you need to separate off the code chunk using the following syntax:

````
```{r}
my_vec <- 1:10
```
````

This syntax tells R how to find the start and end of pieces of R code when the file is rendered. R will walk through, find each piece of R code, run it and create

output (printed output or figures, for example), and then pass the file along to another program to complete rendering (e.g., Tex for pdf files).

You can specify a name for each chunk, if you'd like, by including it after "r" when you begin your chunk. For example, to give the name `load_nepali` to a code chunk that loads the `nepali` dataset, specify that name in the start of the code chunk:

````
```{r load_nepali}
library(faraway)
data(nepali)
```
````

Here are a couple of tips for naming code chunks:

- Chunk names must be unique across a document.
- Any chunks you don't name are given numbers by `knitr`.

You do not have to name each chunk. However, there are some advantages:

- It will be easier to find any errors.
- You can use the chunk labels in referencing for figure labels.
- You can reference chunks later by name.

You can add options when you start a chunk. Many of these options can be set as TRUE / FALSE and include:

Option	Action
'echo'	Print out the R code?
'eval'	Run the R code?
'messages'	Print out messages?
'warnings'	Print out warnings?
'include'	If FALSE, run code, but don't print code or results

Other chunk options take values other than TRUE / FALSE. Some you might want to include are:

Option	Action
`results`	How to print results (e.g., `hide` runs the code, but doesn't print the results)
`fig.width`	Width to print your figure, in inches (e.g., `fig.width = 4`)
`fig.height`	Height to print your figure

Add these options in the opening brackets and separate multiple ones with commas:

````
```{r  messages = FALSE, echo = FALSE}
nepali[1, 1:3]
```
````

I will cover other chunk options later, once you've gotten the chance to try writting R Markdown files.

You can set "global" options at the beginning of the document. This will create new defaults for all of the chunks in the document. For example, if you want `echo`, `warning`, and `message` to be `FALSE` by default in all code chunks, you can run:

````
```{r  global_options}
knitr::opts_chunk$set(echo = FALSE, message = FALSE,
  warning = FALSE)
```
````

If you set both global and local chunk options that you set specifically for a chunk will take precedence over global options. For example, running a document with:

````
```{r  global_options}
knitr::opts_chunk$set(echo = FALSE, message = FALSE,
  warning = FALSE)
```


```{r  check_nepali, echo = TRUE}
head(nepali, 1)
```
````

would print the code for the `check_nepali` chunk, because the option specified for that specific chunk (`echo = TRUE`) would override the global option (`echo = FALSE`).

You can also include R output directly in your text ("inline") using backticks:

"There are `` `r nrow(nepali)` `` observations in the `nepali` data set. The average age is `` `r mean(nepali$age, na.rm = TRUE)` `` months."

Once the file is rendered, this gives:

"There are 1000 observations in the `nepali` data set. The average age is 37.662 months."

Here are two tips that will help you diagnose some problems rendering R Markdown files:

- Be sure to save your R Markdown file before you run it.
- All the code in the file will run "from scratch"– as if you just opened a new R session.
- The code will run using, as a working directory, the directory where you saved the R Markdown file.

You'll want to try out pieces of your code as you write an R Markdown document. There are a few ways you can do that:

- You can run code in chunks just like you can run code from a script (Ctrl-Return or the "Run" button).
- You can run all the code in a chunk (or all the code in all chunks) using the different options under the "Run" button in RStudio.
- All the "Run" options have keyboard shortcuts, so you can use those.

You can render R Markdown documents to other formats:

- Word
- Pdf (requires that you've installed "Tex" on your computer.)
- Slides (ioslides)

Click the button to the right of "Knit" to see different options for rendering on your computer.

You can freely post your RMarkdown documents at RPubs. If you want to post to RPubs, you need to create an account. Once you do, you can click the "Publish" button on the window that pops up with your rendered file. RPubs can also be a great place to look for interesting example code, although it sometimes can be pretty overwhelmed with MOOC homework.

If you'd like to find out more, here are two good how-to books on reproducible research in R (the CSU library has both in hard copy):

- *Reproducible Research with R and RStudio*, Christopher Gandrud
- *Dynamic Documents with R and knitr*, Yihui Xie

0.39 Style guidelines

R style guidelines provide rules for how to format code in an R script. Some people develop their own style as they learn to code. However, it is easy to get in the habit of following style guidelines, and they offer some important advantages:

- Clean code is easier to read and interpret later.
- It's easier to catch and fix mistakes when code is clear.
- Others can more easily follow and adapt your code if it's clean.
- Some style guidelines will help prevent possible problems (e.g., avoiding `.` in function names).

For this course, we will use R style guidelines from two sources:

- Google's R style guidelines
- Hadley Wickham's R style guidelines

These two sets of style guidelines are very similar.

Hear are a few guidelines we've already covered in class:

- Use `<-`, not `=`, for assignment.
- Guidelines for naming objects:
  - All lowercase letters or numbers
  - Use underscore (`_`) to separate words, not camelCase or a dot (`.`) (this differs for Google and Wickham style guides)
  - Have some consistent names to use for "throw-away" objects (e.g., `df`, `ex`, `a`, `b`)
- Make names meaningful
  - Descriptive names for R scripts ("random_group_assignment.R")
  - Nouns for objects (`todays_groups` for an object with group assignments)
  - Verbs for functions (`make_groups` for the function to assign groups)

0.39.1 Line length

Google: **Keep lines to 80 characters or less**

To set your script pane to be limited to 80 characters, go to "RStudio" -> "Preferences" -> "Code" -> "Display", and set "Margin Column" to 80.

```
# Do
my_df <- data.frame(n = 1:3,
                    letter = c("a", "b", "c"),
                    cap_letter = c("A", "B", "C"))

# Don't
my_df <- data.frame(n = 1:3, letter = c("a", "b", "c"), cap_letter = c("A", "B", "C"))
```

This guideline helps ensure that your code is formatted in a way that you can see all of the code without scrolling horizontally (left and right).

0.39.2 Spacing

- Binary operators (e.g., `<-`, `+`, `-`) should have a space on either side
- A comma should have a space after it, but not before.
- Colons should not have a space on either side.
- Put spaces before and after `=` when assigning parameter arguments

```
# Do
shots_per_min <- worldcup$Shots / worldcup$Time
#Don't
shots_per_min<-worldcup$Shots/worldcup$Time

#Do
ave_time <- mean(worldcup[1:10 , "Time"])
#Don't
ave_time<-mean(worldcup[1 : 10 ,"Time"])
```

0.39.3 Semicolons

Although you can use a semicolon to put two lines of code on the same line, you should avoid it.

```
# Do
a <- 1:10
b <- 3

# Don't
a <- 1:10; b <- 3
```

0.39.4 Commenting

- For a comment on its own line, use `#`. Follow with a space, then the comment.
- You can put a short comment at the end of a line of R code. In this case, put two spaces after the end of the code, one `#`, and one more space before the comment.
- If it helps make it easier to read your code, separate sections using a comment character followed by many hyphens (e.g., `#----------`). Anything after the comment character is "muted".

```
# Read in health data ---------------------------

# Clean exposure data ---------------------------
```

0.39.5 Indentation

Google:

- Within function calls, line up new lines with first letter after opening parenthesis for parameters to function calls:

Example:

```
# Relabel sex variable
nepali$sex <- factor(nepali$sex,
                     levels = c(1, 2),
                     labels = c("Male", "Female"))
```

0.39.6 Code grouping

- Group related pieces of code together.
- Separate blocks of code by empty spaces.

```r
# Load data
library(faraway)
data(nepali)

# Relabel sex variable
nepali$sex <- factor(nepali$sex,
                     levels = c(1, 2),
                     labels = c("Male", "Female"))
```

Note that this grouping often happens naturally when using tidyverse functions, since they encourage piping (`%>%` and `+`).

0.39.7 Broader guidelines

- Omit needless code.
- Don't repeat yourself.

We'll learn more about satisfying these guidelines when we talk about writing your own functions in the next part of the class.

0.40 More with knitr

0.40.1 Equations in `knitr`

You can write equations in RMarkdown documents by setting them apart with dollar signs (`$`). For an equation on a line by itself (**display equation**), you two `$`s before and after the equation, on separate lines, then use LaTex syntax for writing the equations.

To help with this, you may want to use this LaTex math cheat sheet.. You may also find an online LaTex equation editor like Codecogs.com helpful.

Note: Equations denoted this way will always compile for pdf documents, but won't always come through on Markdown files (for example, GitHub won't compile math equations).

For example, writing this in your R Markdown file:

```
$$
E(Y_{t}) \sim \beta_{0} + \beta_{1}X_{1}
$$
```

will result in this rendered equation:

$$E(Y_t) \sim \beta_0 + \beta_1 X_1$$

To put math within a sentence (**inline equation**), just use one `$` on either side of the math. For example, writing this in a R Markdown file:

```
"We are trying to model $E(Y_{t})$."
```

The rendered document will show up as:

"We are trying to model $E(Y_t)$."

0.40.2 Figures from file

You can include not only figures that you create with R, but also figures that you have saved on your computer.

The best way to do that is with the `include_graphics` function in `knitr`:

```
library(knitr)
include_graphics("figures/CSU_ram.png")
```

This example would include a figure with the filename "MyFigure.png" that is saved in the "figures" sub-directory of the parent directory of the directory where your .Rmd is saved. Don't forget that you will need to give an absolute pathway or the relative pathway **from the directory where the .Rmd file is saved**.

0.40.3 Saving graphics files

You can save figures that you create in R. Typically, you won't need to save figures for an R Markdown file, since you can include figure code directly. However, you will sometimes want to save a figure from a script. You have two options:

- Use the "Export" choice in RStudio
- Write code to export the figure in your R script

To make your research more reproducible, use the second choice.

To use code export a figure you created in R, take three steps:

1. Open a graphics device (e.g., `pdf("MyFile.pdf")`).
2. Write the code to print your plot.
3. Close the graphics device using `dev.off()`.

For example, the following code would save a scatterplot of time versus passes as a pdf named "MyFigure" in the "figures" subdirectory of the current working directory:

```
pdf("figures/MyFigure.pdf", width = 8, height = 6)
ggplot(worldcup, aes(x = Time, y = Passes)) +
        geom_point(aes(color = Position)) +
        theme_bw()
dev.off()
```

If you create multiple plots before you close the device, they'll all save to different pages of the same pdf file.

You can open a number of different graphics devices. Here are some of the functions you can use to open graphics devices:

- `pdf`
- `png`
- `bmp`
- `jpeg`
- `tiff`
- `svg`

0.41 Saving graphics files

You will use a device-specific function to open a graphics device (e.g., `pdf`). However, you will always close these devices with `dev.off`.

Most of the functions to open graphics devices include parameters like `height` and `width`. These can be used to specify the size of the output figure. The units for these depend on the device (e.g., inches for `pdf`, pixels by default for `png`). Use the helpfile for the function to determine these details.

0.41.1 Tables in R Markdown

If you want to create a nice, formatted table from an R dataframe, you can do that using `kable` from the `knitr` package.

```
my_df <- data.frame(letters = c("a", "b", "c"),
                    numbers = 1:3)
kable(my_df)
```

letters	numbers
a	1
b	2
c	3

There are a few options for the `kable` function:

arg	expl
`colnames`	Column names (default: column name in the dataframe)
`align`	A vector giving the alignment for each column ('l', 'c', 'r')
`caption`	Table caption
`digits`	Number of digits to round to. If you want to round columns different amounts, use a vector with one element for each column.

```
my.df <- data.frame(letters = c("a", "b", "c"),
                    numbers = rnorm(3))
kable(my.df, digits = 2, align = c("r", "c"),
      caption = "My new table",
```

Table 10: My new table

First 3 letters	First 3 numbers
a	0.27
b	0.64
c	1.48

```
      col.names = c("First 3 letters",
                    "First 3 numbers"))
```

From Yihui:

> "**Want more features?** No, that is all I have. You should turn to other packages for help. I'm not going to reinvent their wheels."

If you want to do fancier tables, you may want to explore the `xtable` and `pander` packages. As a note, these might both be more effective when compiling to pdf, rather than html.

0.42 In-course exercise

For all of today's tasks, you'll use the code from last week's in-course exercise to do the exercises. This week we are not focusing on writing new code, but rather on how to take R code and put it in an R Markdown file, so we can create reports from files that include the original code.

0.42.1 Creating a Markdown document

First, you'll create a Markdown document, without any R code in it yet.

In RStudio, go to "File" -> "New File" -> "R Markdown". From the window that brings up, choose "Document" on the left-hand column and "HTML" as the output format. A new file will open in the script pane of your RStudio session. Save this file (you may pick the name and directory). The file extension should be ".Rmd".

First, before you try to write your own Markdown, try rendering the example that the script includes by default. (This code is always included, as a template, when you first open a new RMarkdown file using the RStudio "New file" interface we used in this example.) Try rendering this default R Markdown example by clicking the "Knit" button at the top of the script file.

For some of you, you may not yet have everything you need on your computer to be able to get this to work. If so, let me know. RStudio usually includes all the necessary tools when you install it, but there may be some exceptions.

If you could get the document to knit, do the following tasks:

- Look through the HTML document that was created. Compare it to the R Markdown script that created it, and see if you can understand, at least broadly, what's going on.
- Look in the directory where you saved the R Markdown file. You should now also see a new, .html file in that folder. Try opening it with a web browser like Safari.
- Go back to the R Markdown file. Delete everything after the initial header information (everything after the 6th line). In the header information, make sure the title, author, and date are things you're happy with. If not, change them.
- Using Markdown syntax, write up a description of the data (`worldcup`) we used last week to create the fancier figure. Try to include the following elements:
  - Bold and italic text
  - Hyperlinks
  - A list, either ordered or bulleted
  - Headers

0.42.2 Adding in R code

Now incorporate the R code from last week's exercise into your document. Once you get the document to render with some basic pieces of code in it, try the following:

- Try some different chunk options. For example, try setting `echo = FALSE` in some of your code chunks. Similarly, try using the options `results = "hide"` and `include = FALSE`.
- You should have at least one code chunk that generates figures. Try experimenting with the `fig.width` and `fig.height` options for the chunk to change the size of the figure.
- Try using the global commands. See if you can switch the `echo` default value for this document from TRUE (the usual default) to FALSE.

0.42.3 Working with R Markdown documents

Finally, try the following tasks to get some experience working with R Markdown files in RStudio:

- Go to one of your code chunks. Locate the small gray arrow just to the left of the line where you initiate the code chunk. Click on it and see what happens. Then click on it again.
- Put your cursor inside one of your code chunks. Try using the "Run" button (or Ctrl-Return) to run code in that chunk at your R console. Did it work?
- Pick a code chunk in your document. Put your cursor somewhere in the code in that chunk. Click on the "Run" button and choose "Run All Chunks Above". What did that do? If it did not work, what do you think might be going on? (Hint: Check `getwd()` and think about which directory you've used to save your R Markdown file.)
- Pick another chunk of code. Put the cursor somewhere in the code for that chunk. Click on the "Run" button and choose "Run Current Chunk". Then try "Run Next Chunk". Try to figure out all the options the "Run" button gives you and when each might be useful.
- Click on the small gray arrow to the right of the "Knit HTML" button. If the option is offered, select "Knit Word" and try it. What does this do?

0.42.4 R style guidelines

Go through all the R code in your R Markdown file. Are there are places where your code is not following style conventions for R? Clean up your code to correct any of these issues.

0.42.5 Trying out `knitr` with your own data

Pick a dataset either from your own research or something interesting available online (if you're struggling to find something, check out Five Thirty Eight's GitHub data repository).

- Create an R Markdown document. Add some text to describe the data you're using.
- Write some code to read in the data (you can save it to your computer and read it from a file or, if the data's online, read it in directly).
- Use `dplyr` functions (especially `summarize`) to create a dataframe with some summary statistics for the data. Print this out (just as R output, not as a formatted table, for now).
- Try using `kable` to create a formatted version of the summary table you created.
- Create at least one plot using the data. Try using `fig.width` and `fig.height` chunk options to change the size of the figure in the output.
- Find an image online related to your data. Save it to your computer and use `include_graphics` from the `knitr` package to include it in your R Markdown document.

Appendix A: Vocabulary

You will be responsible for knowing the following functions and vocabulary for the weekly quizzes.

.1 Week 1 (Quiz 1)

- `c()`
- `data.frame()`
- `dim()`
- `ncol()`
- `nrow()`
- `head()`, option `n =`
- `read.csv`, options `head =`, `skip =`, `nrow =`
- `[...]`, `[..., ...]`
- `getwd()`
- `setwd()`, including `setwd("~")`
- `list.files()`
- `install.packages()`
- `library()`
- `<-`
- `=`
- `subset()`
- `length()`
- open source software
- "free as in beer"
- "free as in speech"
- CRAN
- GitHub
- R packages
- R working directory
- How to download a csv file from GitHub
- Nate Silver
- FiveThirtyEight

- Grading policies for the course
- Course requirements / policies for in-class quizzes and weekly journal entries
- Style rules for naming R objects
- Difference between R and RStudio
- Vectors
- Dataframes
- Note: Pay attention in the course notes and exercise to where the code uses quotation marks and where it does not– this will help you in the quiz

.2 Week 2 (Quiz 2)

- `source()`
- `setwd()`, including `setwd("~")`, `setwd("..")`, `setwd("..\..")`
- `list.files()`, option `path =`
- functions in the `read.table()` family, including `read.csv()` and `read.delim()`. What are defaults of the `sep =` and `dec =` options for each? For all, the options `header =`, `sep =`, `as.is =`, `na.strings =`, `nrows =`, `skip =`, and `col.names =`.
- The tidyverse
- functions in the `read_*` family (e.g., `read_csv`)
- Advantages of the `read_*` family of functions compared to their base R analogues (the `read.table` functions)
- `paste()`, option `sep =`
- `paste0()`
- `readxl` package and its `read_excel()` function
- `haven` package and its `read_sas()` function
- `$`
- `class()`
- `str()`
- `as.Date()`, option `format =`
- `lubridate` functions, include `ymd`, `ymd_hm`, and `mdy`
- `range()`
- `dplyr` package
- `rename()`
- `mutate()`
- `arrange()`
- `%>%`, advantages of piping
- `filter()`
- Reading in data from either a local or online flat file
- `save()`, option `file =`
- `load()`
- `rm()`
- `ls()`

- Main types of vector classes in R: character, numeric, factor, date, logical
- Which classes of vectors don't always look like numbers, but R assigns an underlying numeric value to? (Hint: This include the logical class, which R saves with an underlying number, with TRUE = 1 and FALSE = 0.)
- Common abbreviations for telling R date formats (e.g., "%m", "%y")
- Common logical expressions to use in `filter()`
- relative pathnames
- absolute pathnames
- delimited files
- fixed width files
- R script file (How would you make a new one? What file extension would it have? Why is it important to use? How do you run code from a script file in RStudio?)
- What kinds of data can be read into R?
- How to read flat files of data that are online directly into R if they are on:
  - A "http:" site
  - A "https:" site
- When you might want to save an R object as a `.RData` file and when (and why) you might not want to

.3 Week 3 (Quiz 3)

- `data()` (with and without the name of a dataset as an option)
- `library()` (with and without an argument in the parentheses)
- common addition for all these plotting functions: `ggtitle`, `xlab`, `ylab`, `xlim`, `ylim`
- `aes` function and common aesthetics, including `color`, `shape`, `x`, `y`, and `fill`
- Some common geoms: `geom_histogram`, `geom_points`, `geom_lines`, `geom_boxplot()` (both for a single numeric variable and for a numeric vector stratified by a factor)
- `ggpairs()` from the `GGally` package
- `range()`
- `min()`
- `max()`
- `mean()`
- `median()`
- `table()`
- `cor()`, both for two variables in a dataframe, and to get the correlation matrix for several variables in a dataframe
- `summary()`, as applied to: different classes of vectors (numeric, factor, logical), dataframes, `lm` objects, and `glm` objects
- `lm()`, `data=` option

- `glm()`, options `data=`, `family=`
- Functions to apply to a `lm` or `glm` object: `summary()`, `coef()`, `residuals()`, `fitted()`, `plot()`, `abline()`
- The following elements that you can pull from the `summary` of a `lm` call: `summary(mod_1)$call`, `summary(mod_1)$coef`, `summary(mod_1)$r.squared`, `summary(mod_1)$cov.unscaled`
- How to create a logical vector and how to use one to (1) index a data frame and (2) count the number of times a certain condition is true in a vector
- What the bang operator (`!`) does to a logical operator
- What to do if you want to apply a summary statistic function to a vector with missing values (you do not need to know every option name for all the functions, just know that you would need to include an option like `na.rm=` or `use=`, and that you can use the help file for a function to figure out the option call for that function).
- The following about object-oriented programming: In R, it means that some functions, like `summary()`, will do different things depending on what type of object you call it on.
- The basic structure of regression formulae in R (for example, `y ~ x1 + x2`)
- Difference between using `lm()` and `glm()` to fit a linear regression model
- Difference between the code you would use to fit a linear, Poisson, or logistic model using `glm()`

.4 Week 4 (Quiz 4)

- Guidelines for good graphics
- Data density / data-to-ink ratio
- Small multiples
- Edward Tufte
- Hadley Wickham
- Where to put the `+` in ggplot statements to avoid problems (ends of lines instead of starts of new lines)
- Can you save a ggplot object as an R object that you can reference later? If so, how would you add elements on to that object? How would you print it when you were ready to print the graph to your RStudio graphics window?
- `geom_hline()`, `geom_vline()`
- `geom_text()`
- `facet_grid()`, `facet_wrap()`
- `grid.arrange()` from the `gridExtra` package
- `ggthemes` package, including `theme_few()` and `theme_tufte()`
- Setting point color for `geom_point()` both as a constant (all points red) and as a way to show the level of a factor for each observation

- `size`, `alpha`, `color`
- Re-naming and re-ordering factors
- **Note:** If you read this and find and bring in an example of a "small multiples" graph (from a newspaper, a website, an academic paper), you can get one extra point on this quiz

.5 Week 5 (Quiz 5)

- `as.Date`, including `format=` option
- `format` applied to Date objects (including what class the output of this function will be)
- Reproducible research, including what it is and advantages to aiming to make your research reproducible
- R style guidelines on variable names, `attach()`, `<-` vs. `=`, line length, spacing, semicolons, commenting, indentation, and code grouping
- Markup languages (concept and examples)
- Basic conventions for Markdown (bold, italics, links, headers, lists)
- Literate programming
- What working directory R uses for code in an .Rmd document
- Basic syntax for RMarkdown chunks, including how to name them
- Options for RMarkdown chunks: `echo`, `eval`, `messages`, `warnings`, `include`, `fig.width`, `fig.height`, `results`
- Difference between global options and chunk options, and which takes precendence
- What inline code is and how to write it in RMarkdown
- How to set global options
- Why style is important in coding
- RPubs

.6 Week 6 (Quiz 6)

- `with()`
- Three characteristics of tidy data
- Five common problems with tidy data and how to resolve them (make sure you understand the examples shown, which you can find out more about in the Hadley Wickham paper I reference)
- `select()`
- `filter()`
- `mutate()`
- `summarize()`
- `group_by()`
- `arrange()`
- `gather()`

- `spread()`
- `%>%`
- Go through the examples where I've chained together several functions to clean up a dataset and make sure you can follow through these chained examples

.7 Week 7 (Quiz 7)

- `for` loops
- basics of writing a function
- figuring out the output of a loop based on its code
- figuring the the output of a function based on its code
- parentheses around a full assignment statement (e.g., `(ex <- 1)`)
- in-class exercise and example analysis from Oct. 12 course
- `kable()` from the `knitr` package

.8 Week 8 (Quiz 8)

- `apply` family of functions
- `*_join` family of functions
- `matrix` objects, including how to subset
- `list` objects, including how to subset
- `Titanic` example analysis from Oct. 19 course
- Using `color =`, `size =`, or `shape =` in the `aes()` statement of a `ggplot()` call
- `geom_bar()`
- `geom_smooth()`, including the `se =` and `method =` options
- jittering, the `position = position_jitter()` option in ggplot geoms

Appendix B: Homework

The following are six homework assignments for the course.

.9 Homework #1

Due date: Sept. 14

For your first homework assignment, you'll be working through a few swirl lessons that are relevant to the material we've covered so far. Swirl is a platform that helps you learn R **in** R - you can complete the lessons right in your R console.

.9.1 Getting started

First, you'll need to install the swirl package:

```
install.packages("swirl")
```

Next, load the swirl package. We're going to download a course from swirl's course repository called R Programming E using the function `install_course_github`. Then call the `swirl()` function to enter the interactive platform:

```
library(swirl)
uninstall_course("R_Programming_E") # Only run if you have an old version of
                                    # R_Programming_E installed
install_course_github("swirldev", "R_Programming_E")
swirl()
```

After calling `swirl()`, you may be prompted to clear your workspace variables by running `rm=(list=ls())`. Running this code will clear any variables you already have saved in your global environment. While swirl recommends that you do this, it's not necessary.

.9.2 Swirl lessons

Sign in with your name, and choose *R Programming E* when swirl asks you to choose a course. For this homework, you will need to work through the following lessons in that course (the lesson number is in parentheses):

- Basic Building Blocks (1)
- Vectors (4)
- Missing Values (5)
- Subsetting Vectors (6)
- Logic (8)
- Looking at Data (12)
- Dates and Times (14)

Each lesson should take about 10-15 minutes, but some are much shorter. You can complete the lessons in any order you want, but you may find it easiest to start with the lowest-numbered lessons and work your way up, in the order we've listed the lessons here.

You'll be able to get started on some of these lessons after your first day in class (Basic Building Blocks, for example), but others cover topics that we'll get to in weeks 2 and 3. Whether or not we've covered a swirl topic in class, you should be able to successfully work through the lesson. At the end of each lesson, you'll be prompted to "`inform someone about your successful completion of this lesson via email`." after answering `2` for 'Yes,' enter your full name, and enter `rachel.severson@colostate.edu` as the email address of the person you'd like to notify. You should be sending 7 emails in total.

After telling swirl that you would like to send a notification email, an already-populated email should pop up with the lesson you just completed in the subject line - you just need to push send. This might not happen if you access your email through a web browser instead of an app. In this case, just send an email manually with a screenshot of the end of the lesson, and the name of the lesson you just completed.

.9.3 Special swirl commands

In the swirl environment, knowing about the following commands will be helpful:

- Within each lesson, the prompt `...` indicates that you should hit Enter to move on to the next section.
- `play()`: temporarily exit swirl. It can be useful during a swirl lesson to play around in the R console to try things out.
- `nxt()`: regain swirl's attention after `play()`ing around in the console.
- `main()`: return to swirl's main menu.
- `bye()`: exit swirl. Swirl will save your progress if you exit in the middle of a lesson. You can also hit the Esc. key to exit. (To re-enter swirl, run `swirl()`. In a new R session you will have to first load the swirl library: `library(swirl)`.)

.9.3.1 For fun

While they aren't required for class, you should consider trying out some other swirl lessons later in the course. The `Functions` lesson, as well as `lapply and sapply` and `vapply and tapply` could be particularly useful. You can also look through the course directory to see what other courses and lessons are available.

If you are doing extra swirl courses on your own, you probably want to do them through the "R Programming", rather than the "R Programming E", course, since you won't need to let us know by email. To get this, you can run:

```
library(swirl)
install_course("R_Programming")
swirl()
```

.10 Homework #2

Due date: Sept. 28

For Homework 2, recreate the R Markdown document that you can download from here.

Here are some initial tips:

- Your goal is to create an R Markdown document that you can compile to create a Word document that looks just like the example document we've linked above.

- You will turn in (by email) both the compiled Word document and the .Rmd original file.
- Add your name as "Author" and the due date of the assignment as "Date". You should add these within the R Markdown document, rather than changing them in the final, compiled Word document.
- If you want to get started before you know how to use R Markdown, you can go ahead and write all of the necessary code to replicate the output and figures in the document in an R script.
- The code chunks here have been hidden with the option `echo = FALSE`, but you should include your code in your final document.
- Set the chunk options `warning = FALSE` and `message = FALSE` to prevent warnings and messages from being printed out. You will get some messages and warnings in the code from things like missing values and from loading packages, but you want to hide all of those messages in your final document.
- For things like templates, colors, level of transparency, and point size, you will receive full credit if you create figures that are visually similar to the ones shown in the example document. In other words, if the example document shows some transparency in points, you will get full credit if you also include some transparency in the points in your plot, but you do not have to include the exact same value of `alpha`.
- In R, there are often many different ways to achieve something. As long as your code *works*, it's fine if you haven't coded it exactly like we have in our version. However, your output should look identical to ours (or, in the case of color, transparency, point size, and themes, visually similar).
- You will not lose points if you cannot recreate the table in the document (although you should try to!).
- The last section, under the heading "Extra challenge– not graded", is not graded. However, if you'd like an extra challenge, you're welcome to try it out and include it in your final submission!

If you need them, here are some further tips:

- Functions from the tidyverse (especially from `dplyr`, `readr`, and `ggplot` packages) will make your life much easier for this exercise. You can now install and load the `tidyverse` package to load them all at once.
- To rename column names with "special" characters in them, wrap the whole old column name in backticks. For example, to change a column name that has a dollar sign in it, you would use something like "rename(new_col_name = `old_col_name$`)".
- To change the size of a figure in a report, use the "fig.width" and "fig.height" chunk options.
- You will want to use `scale_fill_brewer` in several of the figures.
- Don't forget that, within functions like `scale_x_continuous`, you can use the argument `breaks` to set where the axis has breaks, and then `labels` to set what will actually be shown at each break.

- The string "\n" can be included in legends and labels to include a carriage return.
- Coordinates can be flipped in a graph with the `coord_flip` geom. So, if you can figure out a way to make a graph with the coordinates flipped, use that code and just add `coord_flip` at the end.

.11 Homework #3

Due date: Oct. 12

[`dplyr`, tidy data homework assignment]

.12 Homework #4

Due date: Oct. 26

[Advanced R Markdown homework assignment]

.13 Homework #5

Due date: Nov. 9

[Homework on functions, regular expressions, and web data assignment]

.14 Homework #6

Due date: Nov. 30

[Mapping homework assignment]

Bibliography