A Sufficient Introduction to R

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This set of notes has grown out of teaching applied statistics courses at NAU to graduate students in Biology, Ecology and Forestry. Typically these students do not have a background in programming the scripting aspect of R is very challenging. I attempt to be clear and emphasize the major ideas but leave the documentation of the fine details to references that actually cost money or can be found on coding forums such as Stack Exchange.

While there is a definite statistical flair to the chosen examples, the reader is not assumed to have much statistical knowledge, and thus this tutorial can be read prior to an introductory statistical methods course, or more likely, concurrently with such a course.

Finally, I wish to thank the R community that has created such a wonderful resource and the package developers that have enriched it so greatly.

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To Aubrey, Elise, and Casey because they make coming home the best part of my day.

Contents

Chapter 1

Introducing simple calculations and scripts

R is a open-source program that is commonly used in Statistics. It runs on almost every platform and is completely free and is available at r-project.org. Most of the cutting-edge statistical research is first available on R.

R is a script based language, so there is no point and click interface. (Actually there are packages that attempt to provide a point and click interface, but they are still somewhat primitive.) While the initial learning curve will be steeper, understanding how to write scripts will be valuable because it leaves a clear description of what steps you performed in your data analysis. Typically you will want to write a script in a separate file and then run individual lines. The saves you from having to retype a bunch of commands and speeds up the debugging process.

This document is a very brief introduction to using R in my course. I highly recommend downloading and reading/skimming the manual *"An Introduction to R"* which is located at `http://cran.r-project.org/doc/manuals/R-intro.pdf`.

Finding help about a certain function is very easy. At the prompt, just type `help(function.name)` or `?function.name`. If you don't know the name of the function, your best bet is to go the the web page `www.rseek.org` which will search various R resources for your keyword(s). Another great resource is the coding question and answer site `stackoverflow.com`.

The basic editor that comes with R works fairly well, but you should consider running R through the program RStudio which is located at `www.rstudio.org`.

The prompt `>` is waiting for you to input a command. The prompt `+` tells you that the current command is spanning multiple lines. In a script file you might have typed something like this:

```
for( i in 1:5 ){
print(i)
}
```

But when you copy and paste it into the console in R you'll see something like this:

```
> for (i in 1:5) {
+ print(i)
+ }
```

If you type your commands into a file, you won't type the $>$ or $+$ prompts. For the rest of the tutorial, I will show the code as you would type it into a script and I will show the output being shown with two hashtags (##) before it to designate that it is output.

When doing anything more difficult than simple algebra, you should write your commands in a script instead of directly to the console. The reason why is that unless you are a perfect typist and never make a mistake, creating a script file with the correct commands will save a massive amount

of re-typing. Furthermore, having a script file fully documents how you did your analysis, which can help when writing the methods section of a paper. Finally, having a script makes it easy to re-run an analysis after a change in the data (additional data values, transformed data, or removal of outliers).

It often makes your script more readable if you break a single command up into multiple lines. R will disregard all whitespace (including line breaks) so you can safely spread your command over as multiple lines. Finally, it is useful to leave comments in the script for things such as explaining a tricky step, who wrote the code and when, or why you chose a particular name for a variable. The `#` sign will denote that the rest of the line is a comment and R will ignore it.

1.1 R as a simple calculator

Assuming that you have started R on whatever platform you like, you can use R as a simple calculator. At the prompt, type `2+3` and hit enter. What you should see is the following:

```
# Some simple addition
2+3

## [1] 5
```

In this fashion you can use R as a very capable calculator.

```
6*8

## [1] 48

4^3

## [1] 64

exp(1)

## [1] 2.718282
```

R has most constants and common mathematical functions you could ever want. `sin()`, `cos()`, and other trigonometry functions are available, as are the exponential and log functions `exp()`, `log()`. The absolute value is given by `abs()`, and `round()` will round a value to the nearest integer.

```
pi

## [1] 3.141593

sin(0)

## [1] 0

log(5)  # Unless you specify the base, R will assume base e

## [1] 1.609438

log(5, base=10)

## [1] 0.69897
```

Whenever I call a function, there will be some arguments that are mandatory, and some that are optional and the arguments are separated by a comma. In the above statements the function `log()`

requires at least one argument, and that is the number(s) to take the log of. However, the `base` argument is optional. If you do not specify what base to use, R will use a default value. You can see that R will default to using base e by looking at the help page (by typing `help(log)` or `?log` at the command prompt).

Arguments can be specified via the order in which they are passed or by naming the arguments. So for the `log()` function which has arguments `log(x, base=exp(1))`. If I specify which arguments are which using the named values, then order doesn't matter.

```
# Demonstrating order does not matter if you specify
# which argument is which
log(x=5, base=10)

## [1] 0.69897

log(base=10, x=5)

## [1] 0.69897
```

But if we don't specify which argument is which, R will decide that `x` is the first argument, and `base` is the second.

```
# If not specified, R will assume the second value is the base...
log(5, 10)

## [1] 0.69897

log(10, 5)

## [1] 1.430677
```

When I specify the arguments, I have been using the `name=value` notation and a student might be tempted to use the `<-` notation here[1]. Don't do that as the `name=value` notation is making an association mapping and not a permanent assignment.

1.2 Assignment

We need to be able to assign a value to a variable to be able to use it later. R does this by using an arrow '`<-`' or an equal sign '`=`'. While R supports either, for readability, I suggest people pick one assignment operator and stick with it. I personally prefer to use the arrow. Variable names cannot start with a number, may not include spaces, and are case sensitive.

```
tau <- 2*pi
my.test.var = 5
tau

## [1] 6.283185

my.test.var

## [1] 5

tau * my.test.var

## [1] 31.41593
```

[1] See next section.

As your analysis gets more complicated, you'll want to save the results to a variable so that you can access the results later[2]. *If you don't assign the result to a variable, you have no way of accessing the result.* [3]

1.3 Scripts and RMarkdown

One of the worst things about a pocket calculator is there is no good way to go several steps and easily see what you did or fix a mistake (there is nothing more annoying than re-typing something because of a typo. To avoid these issues I always work with script (or RMarkdown) files instead of typing directly into the console. You will quickly learn that it is impossible to write R code correctly the first time and you'll save yourself a huge amount of work by just embracing scripts (and RMarkdown) from the beginning.

1.3.1 R Scripts (.R files)

The first type of file that we'll discuss is a traditional script file. To create a new `.R` script in RStudio go to `File -> New File -> R Script`. This opens a new window in RStudio where you can type commands and functions as a common text editor. Type whatever you like in the script window and then you can execute the code line by line (using the run button or its keyboard shortcut to run the highlighted region or whatever line the curser is on) or the entire script (using the source button). Other options for what piece of code to run are available under the `Code` dropdown box.

An R script for a homework assignment might look something like this:

```
# Problem 1
# Calculate the log of a couple of values and make a plot
# of the log function from 0 to 3
log(0)
log(1)
log(2)
x <- seq(.1,3, length=1000)
plot(x, log(x))

# Problem 2
# Calculate the exponential function of a couple of values
# and make a plot of the function from -2 to 2
exp(-2)
exp(0)
exp(2)
x <- seq(-2, 2, length=1000)
plot(x, exp(x))
```

This looks perfectly acceptable as a way of documenting what you did, but this script file doesn't contain the actual results of commands I ran, nor does it show you the plots. Also anytime I want to commend on some output, it needs to be offset with the commenting character `#`. It would be nice to have both the commands *and the results* merged into one document. This is what the `R Markdown` file does for us.

1.3.2 R Markdown (.Rmd files)

When I was a graduate student, I had to tediously copy and past tables of output from the R console and figures I had made into my Microsoft Word document. Far too often I would realize I had made

[2] To paraphrase Beyonce, "Cause if you liked it, then you should have put a name on it."

[3] This isn't strictly true, the variable `.Last.value` always has the result of the last expression evaluated, but you can't go any farther back.

a small mistake in part (b) of a problem and would have to go back, correct my mistake, and then redo all the laborious copying. I often wished that I could write both the code for my statistical analysis and the long discussion about the interpretation all in the same document so that I could just re-run the analysis with a click of a button and all the tables and figures would be updated by magic. Fortunately that magic[4] now exists.

To create a new `R Markdown` document, we use the `File -> New File -> R Markdown...` drop-down option and a menu will appear asking you for the document title, author, and preferred output type. In order to create a PDF, you'll need to have LaTeX installed, but the HTML output nearly always works and I've had good luck with the MS Word output as well.

The `R Markdown` is an implementation of the `Markdown` syntax that makes it extremely easy to write webpages and give instructions for how to do typesetting sorts of things. This syntax was extended to allow use to embed R commands directly into the document. Perhaps the easiest way to understand the syntax is to look at an example:

````
---
output: word_document
---

#Problem 1#
Calculate the log of a couple of values and make a plot of
the log function from 0 to 3. First we will calculate some values...
```{r}
log(0)
log(1)
log(2)
```
Notice that log(0) is equal to -infinity and log(1) == 0. Next we'll make a nice plot.
```{r, fig.height=2, fig.width=4}
x <- seq(.1,3, length=1000)
plot(x, log(x))
```

Notice that this function is only defined for positive values of X and
is monotonically increasing from -infinity to +infinity as X goes from 0 to infinity.

#Problem 2#
Calculate the exponential function of a couple of values and make a
plot of the function from -2 to 2.
```{r}
exp(-2)
exp(0)
exp(2)
```
The most important of these is to notice that e^0=1. Next we'll make a nice plot
```{r}
x <- seq(-2, 2, length=1000)
plot(x, exp(x))
```

Notice that this function is also monotonically increasing but now the X
range is -infinity to +infinity while the output lives in [0, infinity).
This is because the log and exponential functions are inverses of each other.
````

[4] Clark's third law states "Any sufficiently advanced technology is indistinguishable from magic."

The R code in my document is nicely separated from my regular text using the three backticks and an instruction that it is R code that needs to be evaluated. The output of this document looks good as a HTML, PDF, or MS Word document.

This template is sufficient to get a student through STA 570 and its lab section, but more information about `Markdown` syntax and all of its different tricks can be found online. In particular, I've found the following links to be quite useful.

- http://daringfireball.net/projects/markdown/syntax
- http://markdown-guide.readthedocs.org/en/latest/basics.html

1.4 Packages

The packages in R are perhaps the best reason for learning R. There are thousands of packages available for free and most new analysis methods will be available as an R package long before they are available on any other computing platform. Statistical researchers who develop new methodology want to make their methods widely available to researchers and the R package system makes that relatively painless (and free!).

Users will typically download their desired packages from the Comprehensive R Archive Network (CRAN) which is a network of servers (typically called "mirrors") that have all the packages that have been submitted. So to download a package, say the package `Lock5Data`, we just need to tell R to download it from a nearby CRAN mirror.

```
install.packages('Lock5Data', repos='https://cran.cnr.berkeley.edu/')

##
## The downloaded binary packages are in
##  /var/folders/0x/_gvfhyqn1kq6187r8b28cpkr0000gp/T//RtmpLIvNxK/downloaded_packages
```

If you are using RStudio, it is often much easier to download the package using the GUI interface by clicking `Tools -> Install packages...`. By using the GUI, you avoid having to remember the addresses of the nearby CRAN mirrors.

Once a package is downloaded to your computer, it is not yet available. Because a computer might have hundreds or thousands of packages installed, you must load the package into working memory to be able to access the functions and data in the package. You must do this *every* time you start up R. As a result most Rmarkdown files and R scripts will begin with the process of loading the packages that we need for that analysis. In my notes, I often will start the chapter by loading the necessary libraries. You can load the library where ever you want in the script, but recognize that when knitting a RMarkdown file, a completely new session of R is started and you must have the commands loading the library placed above where you use the functions or data from the library.

```
library(Lock5Data)
```

Once the package is loaded using the `library()` command, all the functions are accessible. While most packages will also load their datasets automatically, some packages have so many large datasets that the package authors turned that behavior off. Instead they might require you to explicitly load a dataset using the following:

```
data(ACS)   # load the ACS dataset included in the Lock5Data package.
```

1.5 Exercises

Create an RMarkdown file that solves the following exercises.

1. Calculate $\log(6.2)$ first using base e and second using base 10. To figure out how to do different bases, it might be helpful to look at the help page for the `log` function.

2. Calculate the square root of 2 and save the result as the variable named `sqrt2`. Have R display the decimal value of `sqrt2`.

Chapter 2

Data Structures: Vectors

2.1 Vector Creation

R operates on vectors where we think of a vector as a collection of objects, usually numbers. The first thing we need to be able to do is define an arbitrary collection using the `c()` function[1].

```
# Define the vector of numbers 1, ..., 4
c(1,2,3,4)

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

There are many other ways to define vectors. The function `rep(x, times)` just repeats `x` a the number times specified by `times`.

```
rep(2, 5)

## [1] 2 2 2 2 2

rep( c('A','B'), 3 )

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

Finally, we can also define a sequence of numbers using the `seq(to, from, by, length.out)` function which expects the user to supply 3 out of 4 possible arguments. The possible arguments are `from`, `to`, `by`, and `length.out`. `From` is the starting point of the sequence, `to` is the ending point, `by` is the difference between any two successive elements, and `length.out` is the total number of elements in the vector.

[1] The "c" stands for collection.

```
seq(from=1, to=4, by=1)

## [1] 1 2 3 4

seq(1,4)        # 'by' has a default of 1

## [1] 1 2 3 4

1:4             # a shortcut for seq(1,4)

## [1] 1 2 3 4

seq(1,5, by=.5)

## [1] 1.0 1.5 2.0 2.5 3.0 3.5 4.0 4.5 5.0

seq(1,5, length.out=11)

##  [1] 1.0 1.4 1.8 2.2 2.6 3.0 3.4 3.8 4.2 4.6 5.0
```

If we have two vectors and we wish to combine them, we can again use the `c()` function.

```
vec1 <- c(1,2,3)
vec2 <- c(4,5,6)
vec3 <- c(vec1, vec2)
vec3

## [1] 1 2 3 4 5 6
```

2.2 Accessing Vector Elements

Suppose I have defined a vector

```
foo <- c('A', 'B', 'C', 'D', 'F')
```

and I am interested in accessing whatever is in the first spot of the vector. Or perhaps the 3rd or 5th element. To do that we use the `[]` notation, where the square bracket represents a subscript.

```
foo[1]  # First element in vector foo

## [1] "A"

foo[4]  # Fourth element in vector foo

## [1] "D"
```

This subscripting notation can get more complicated. For example I might want the 2nd and 3rd element or the 3rd through 5th elements.

```
foo[c(2,3)]  # elements 2 and 3

## [1] "B" "C"

foo[ 3:5 ]   # elements 3 to 5

## [1] "C" "D" "F"
```

Finally, I might be interested in getting the entire vector *except* for a certain element. To do this, R allows us to use the square bracket notation with a negative index number.

```
foo[-1]  # everything but the first element

## [1] "B" "C" "D" "F"

foo[ -1*c(1,2) ] # everything but the first two elements

## [1] "C" "D" "F"
```

Now is a good time to address what is the `[1]` doing in our output? Because vectors are often very long and might span multiple lines, R is trying to help us by telling us the index number of the left most value. If we have a very long vector, the second line of values will start with the index of the first value on the second line.

```
# The letters vector is a vector of all 26 lower-case letters
letters

##  [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q"
## [18] "r" "s" "t" "u" "v" "w" "x" "y" "z"
```

Here the `[1]` is telling me that `'a'` is the first element of the vector and the `[18]` is telling me that `'r'` is the 18th element of the vector.

2.3 Scalar Functions Applied to Vectors

It is very common to want to perform some operation on all the elements of a vector simultaneously. For example, I might want take the absolute value of every element. Functions that are inherently defined on single values will almost always apply the function to each element of the vector if given a vector.

```
x <- -5:5
x

##  [1] -5 -4 -3 -2 -1  0  1  2  3  4  5

abs(x)

##  [1] 5 4 3 2 1 0 1 2 3 4 5

exp(x)

##  [1] 6.737947e-03 1.831564e-02 4.978707e-02 1.353353e-01 3.678794e-01
##  [6] 1.000000e+00 2.718282e+00 7.389056e+00 2.008554e+01 5.459815e+01
## [11] 1.484132e+02
```

2.4 Vector Algebra

All algebra done with vectors will be done *element-wise* by default.[2] So two vectors added together result in their individual elements being summed.

[2]For matrix and vector multiplication as usually defined by mathematicians, use `%*%` instead of `*`.

```
x <- 1:4
y <- 5:8
x + y

## [1]  6  8 10 12

x * y

## [1]  5 12 21 32
```

R does another trick when doing vector algebra. If the lengths of the two vectors don't match, R will recycle the elements of the shorter vector to come up with vector the same length as the longer. This is potentially confusing, but is most often used when adding a long vector to a vector of length 1.

```
x <- 1:4
x + 1

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

2.5 Commonly Used Vector Functions

Function	Result
`min(x)`	returns the minimum element of the vector `x`
`max(x)`	maximum element of `x`
`length(x)`	number of elements in `x`
`sum(x)`	sum of all the elements in `x`
`mean(x), median(x)`	mean and median of all the elements in `x`
`var(x)`, `sd(x)`	variance and standard deviations of elements of `x`

Putting this all together, we can easily perform tedious calculations with ease. To demonstrate how scalars, vectors, and functions of them work together, we will calculate the variance of 5 numbers. Recall that variance is defined as

$$Var\left(x\right) = \frac{\sum_{i=1}^{n}\left(x_i - \bar{x}\right)^2}{n-1}$$

```
x <- c(2,4,6,8,10)
xbar <- mean(x)          # calculate the mean
xbar

## [1] 6

x - xbar                 # calculate the errors

## [1] -4 -2  0  2  4

(x-xbar)^2

## [1] 16  4  0  4 16

sum((x-xbar)^2)

## [1] 40

n <- length(x)           # how many data points do we have
n

## [1] 5

sum((x-xbar)^2)/(n-1)    # calculating the variance by hand

## [1] 10

var(x)                   # Same thing using the built-in variance function

## [1] 10
```

2.6 Exercises

1. Create a vector of three elements (2,4,6) and name that vector `vec_a`. Create a second vector, `vec_b`, that contains (8,10,12). Add these two vectors together and name the result `vec_c`.
2. Create a vector, named `vec_d`, that contains only two elements (14,20). Add this vector to `vec_a`. What is the result and what do you think R did (look up the recycling rule in your text book)? What is the warning message that R gives you?
3. Next add `5` to the vector `vec_a`. What is the result and what did R do? Why doesn't in give you a warning message similar to what you saw in the previous problem?
4. Generate the vector of integers $\{1, 2, \ldots 5\}$ in two different ways. First use the `seq()` function and second use the `a:b` shortcut.
5. Generate the vector of even numbers $\{2, 4, 6, \ldots, 20\}$ using both the `seq()` function and using the `a:b` shortcut and some subsequent algebra. *Hint: Generate a vector and multiple it by 2.*
6. Generate a vector of 1001 elements that are evenly placed between 0 and 1 using the `seq()` command and name this vector `x`.
7. Generate the vector $\{2, 4, 8, 2, 4, 8, 2, 4, 8\}$ using the `rep()` command to replicate the vector `c(2,4,8)`.
8. Generate the vector $\{2, 2, 2, 2, 4, 4, 4, 4, 8, 8, 8, 8\}$ using the `rep()` command. You might need to check the help file for `rep()` to see all of the options that `rep()` will accept. In particular, look at the optional argument `each=`.

9. The vector `letters` is a built-in vector to R and contains the lower case English alphabet.

   (a) Extract the 9th element of the `letters` vector.

   (b) Extract the sub-vector that contains the 9th, 11th, and 19th elements.

   (c) Extract the sub-vector that contains everything *except* the last two elements.

Chapter 3

Data Types - Numerical, Strings, Factors, and Logicals

There are some basic data types that are commonly used.

1. Integers - These are the integer numbers $(\dots, -2, -1, 0, 1, 2, \dots)$. To convert a numeric value to an integer you may use the function `as.integer()`.
2. Numeric - These could be any number (whole number or decimal). To convert another type to numeric you may use the function `as.numeric()`.
3. Strings - These are a collection of characters (example: Storing a student's last name). To convert another type to a string, use `as.character()`.
4. Factors - These are strings that can only values from a finite set. For example we might wish to store a variable that records home department of a student. Since the department can only come from a finite set of possibilities, I would use a factor. Factors are categorical variables, but R calls them factors instead of categorical variable. A vector of values of another type can always be converted to a factor using the `as.factor()` command.
5. Logicals - This is a special case of a factor that can only take on the values `TRUE` and `FALSE`. (Be careful to always capitalize `TRUE` and `FALSE`. Because R is case-sensitive, `TRUE` is not the same as true. Using the function `as.logical()` you can convert numeric values to `TRUE` and `FALSE` where 0 is `FALSE` and anything else is `TRUE`.

Depending on the command, R will coerce your data if necessary, but it is a good habit to do the coercion yourself. If a variable is a number, R will automatically assume that it is continuous numerical variable. If it is a character string, then R will assume it is a factor when doing any statistical analysis.

To find the type of an object, the `str()` command gives the type, and if the type is complicated, it describes the structure of the object.

3.1 Integers and Numerics

Integers and numerics are exactly what they sound like. Integers can take on whole number values, while numerics can take on any decimal value. The reason that there are two separate data types is that integers require less memory to store than numerics. For most users, the distinction can be ignored.

```
x <- c(1,2,1,2,1)
# show that x is of type 'numeric'
str(x)

##  num [1:5] 1 2 1 2 1
```

3.2 Character Strings

In R, we can think of collections of letters and numbers as a single entity called a string. Other programming languages think of strings as vectors of letters, but R does not so you can't just pull off the first character using vector tricks. In practice, there are no limits as to how long string can be.

```
x <- "Goodnight Moon"

# Notice x is of type character (chr)
str(x)

##  chr "Goodnight Moon"

# R doesn't care if I use single quotes or double quotes, but don't mix them...
y <- 'Hop on Pop!'

# we can make a vector of character strings
Books <- c(x, y, 'Where the Wild Things Are')
Books

## [1] "Goodnight Moon"            "Hop on Pop!"
## [3] "Where the Wild Things Are"
```

Character strings can also contain numbers and if the character string is in the correct format for a number, we can convert it to a number.

```
x <- '5.2'
str(x)     # x really is a character string

##  chr "5.2"

x

## [1] "5.2"

as.numeric(x)

## [1] 5.2
```

If we try an operation that only makes sense on numeric types (like addition) then R complain unless we first convert it[1].

[1]There are places where R will try to coerce an object to another data type but it happens inconsistently and you should just do the conversion yourself.

```
x+1

## Error in x + 1:  non-numeric argument to binary operator

as.numeric(x) + 1

## [1] 6.2
```

3.3 Factors

Factors are how R keeps track of categorical variables. R does this in a two step pattern. First it figures out how many categories there are and remembers which category an observation belongs two and second, it keeps a vector character strings that correspond to the names of each of the categories.

```
# A charater vector
y <- c('B','B','A','A','C')
y

## [1] "B" "B" "A" "A" "C"

# convert the vector of characters into a vector of factors
z <- factor(y)
str(z)

##  Factor w/ 3 levels "A","B","C": 2 2 1 1 3
```

Notice that the vector `z` is actually the combination of group assignment vector `2,2,1,1,3` and the group names vector `''A'',''B'',''C''`. So we could convert `z` to a vector of numerics or to a vector of character strings.

```
as.numeric(z)

## [1] 2 2 1 1 3

as.character(z)

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

Often we need to know what possible groups there are, and this is done using the `levels()` command.

```
levels(z)

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

Notice that the order of the group names was done alphabetically, which we did not chose. This ordering of the levels has implications when we do an analysis or make a plot and R will always display information about the factor levels using this order. It would be nice to be able to change the order. Also it would be really nice to give more descriptive names to the groups rather than just the group code in my raw data. I find it is usually easiest to just convert the vector to a character vector, and then convert it back using the `levels` argument to define the order of the groups, and `labels` to define the modified names.

```
z <- factor(z, levels=c('B','A','C'), labels=c("B Group", "A Group", "C Group"))
z

## [1] B Group B Group A Group A Group C Group
## Levels: B Group A Group C Group
```

Often we wish to take a continuous numerical vector and transform it into a factor. The function `cut()` takes a vector of numerical data and creates a factor based on your give cut-points.

```
# Define a continuous vector to convert to a factor
x <- 1:10

# divide range of x into three groups of equal length
cut(x, breaks=3)

##  [1] (0.991,4] (0.991,4] (0.991,4] (0.991,4] (4,7]     (4,7]     (4,7]
##  [8] (7,10]    (7,10]    (7,10]
## Levels: (0.991,4] (4,7] (7,10]

# divide x into four groups, where I specify all 5 break points
# Notice that the the outside breakpoints must include all the data points.
# That is, the smallest break must be smaller than all the data, and the largest
# must be larger (or equal) to all the data.
cut(x, breaks = c(0, 2.5, 5.0, 7.5, 10))

##  [1] (0,2.5]  (0,2.5]  (2.5,5]  (2.5,5]  (2.5,5]  (5,7.5]  (5,7.5]
##  [8] (7.5,10] (7.5,10] (7.5,10]
## Levels: (0,2.5] (2.5,5] (5,7.5] (7.5,10]

# divide x into 3 groups, but give them a nicer
# set of group names
cut(x, breaks=3, labels=c('Low','Medium','High'))

##  [1] Low    Low    Low    Low    Medium Medium Medium High   High   High
## Levels: Low Medium High
```

3.4 Logicals

Often I wish to know which elements of a vector are equal to some value, or are greater than something. R allows us to make those tests at the vector level.

Very often we need to make a comparison and test if something is equal to something else, or if one thing is bigger than another. To test these, we will use the `<`, `<=`, `==`, `>=`, `>`, and `!=` operators. These can be used similarly to

```
6 < 10    # 6 less than 10?

## [1] TRUE

6 == 10   # 6 equal to 10?

## [1] FALSE

6 != 10   # 6 not equal to 10?

## [1] TRUE
```

where we used 6 and 10 just for clarity. The result of each of these is a logical value (a TRUE or FALSE). In most cases these would be variables you had previously created and were using. Assign values to variable `a` and to variable `b` and test if `a < b`.

Suppose I have a vector of numbers and I want to get all the values greater than 16. Using the `>` comparison, I can create a vector of logical values that tells me if the specified value is greater than 16. The `which()` takes a vector of logicals and returns the indices that are true.

```
x <- 1:20  # a vector of 20 integers
x > 16     # a vector of 20 logicals

##  [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [12] FALSE FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE

indices <- which( x > 16 )
indices

## [1] 17 18 19 20

x[ indices ]

## [1] 17 18 19 20
```

On function I find to be occasionally useful is the `is.element` function which allows me to figure out which elements of a vector are one of a set of possibilities. For example, I might want to know which elements of the `letters` vector are vowels.

```
letters  # recall this is all 26 english lowercase letters

##  [1] "a" "b" "c" "d" "e" "f" "g" "h" "i" "j" "k" "l" "m" "n" "o" "p" "q"
## [18] "r" "s" "t" "u" "v" "w" "x" "y" "z"

vowels <- c('a','e','i','o','u')
which( is.element(letters, vowels) )

## [1]  1  5  9 15 21
```

This shows me the vowels occur at the 1st, 5th, 9th, 15th, and 21st elements of the alphabet.

Often I want to make multiple comparisons, for example maybe I want to find all undergraduate Forestry majors with a GPA greater than 3.0. Then give my set of university students I want ask two questions: Is their major Forestry, and is their GPA greater than 3.0. So I need to combine those two logical results into a single logical that is true if *both* questions are true. The command `&` means "and" and `|` means "or". We can combine two logical values using these two similarly:

```
TRUE  & TRUE     # both are true so combo so result is true
```

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

```
TRUE  & FALSE    # one true and one false so result is false
```

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

```
FALSE & FALSE    # both are false so the result is false
```

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

```
TRUE  | TRUE     # at least one is true -> TRUE
```

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

```
TRUE  | FALSE    # at least one is true -> TRUE
```

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

```
FALSE | FALSE    # neither is true -> FALSE
```

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

3.5 Exercises

1. Create a vector of character strings with six elements

```
test <- c('red','red','blue','yellow','blue','green')
```

   (a) Transform the `test` vector just you created into a factor.
   (b) Use the `levels()` command to determine the levels (and order) of the factor you just created.
   (c) Transform the factor you just created into integers. Comment on the relationship between the integers and the order of the levels you found in part (b).
   (d) Use some sort of comparison to create a vector that identifies which factor elements are the `red` group.

2. Given the vector of ages,

```
ages <- c(17, 18, 16, 20, 22, 23)
```

   create a factor that has levels `Minor` or `Adult` where any observation greater than or equal to 18 qualifies as an adult.

3. Suppose we vectors that give a students name, their GPA, and their major. We want to come up with a list of forestry students with a GPA of greater than 3.0.

```
Name <- c('Adam','Benjamin','Caleb','Daniel','Ephriam', 'Frank','Gideon')
GPA <- c(3.2, 3.8, 2.6, 2.3, 3.4, 3.7, 4.0)
Major <- c('Math','Forestry','Biology','Forestry','Forestry','Math','Forestry')
```

   (a) Create a vector of `TRUE/FALSE` values that indicate whether the students GPA is greater than 3.0.

(b) Create a vector of `TRUE`/`FALSE` values that indicate whether the students' major is forestry.

(c) Create a vector of `TRUE/FALSE` values that indicates if a student has a GPA greater than 3.0 *and* is a forestry major.

(d) Convert the vector of `TRUE/FALSE` values in part (b) to integer values using the `as.numeric()` function. Which numeric value corresponds to `TRUE`?

(e) Sum the vector of numbers you created in part (c) to count the number of values in `x` that are less than or equal to 0.

4. Make two variables, and call them `a` and `b` where `a=2` and `b=10`. I want to think of these as defining an interval.

(a) Define the vector `x <- c(-1, 5, 12)`

(b) Using the `&`, come up with a comparison that will test if the value of x is in the interval $[a, b]$. (We want the test to return TRUE if $a \leq x \leq b$). That is, test if a is less than x and if x is less than b. Confirm that for `x` defined above you get the correct vector of logical values.

(c) Similarly make a comparison that tests if x is outside the interval $[a, b]$ using the `|` operator. That is, test if x $<$ a or x $>$ b. I want the test to return TRUE is x is less than a or if x is greater than b. Confirm that for `x` defined above you get the correct vector of logical values.

Chapter 4

Data Structures: Matrices, Data Frames, and Lists

4.1 Matrices

We often want to store numerical data in a square or rectangular format and mathematicians will call these "matrices". These will have two dimensions, rows and columns. To create a matrix in R we can create it directly using the `matrix()` command which requires the data to fill the matrix with, and optionally, some information about the number of rows and columns:

The alternative to this is we could create two columns as individual vectors and just push them together. Or we could have made three rows and lump them by rows instead. To do this we'll use a group of functions that *bind* vectors together. To join two column vectors together, we'll use `cbind` and to bind rows together we'll use the `rbind` function

```
first <- c(1,2,3)
second <- c(4,5,6)
cbind(first, second)

##      first second
## [1,]     1      4
## [2,]     2      5
## [3,]     3      6

rbind(first, second)

##        [,1] [,2] [,3]
## first     1    2    3
## second    4    5    6
```

Notice that doing this has provided R with some names for the individual rows and columns. I can change these using the commands `colnames()` and `rownames()`.

```
M <- matrix(1:6, nrow=3, ncol=2, byrow=TRUE)
colnames(M) <- c('Column1', 'Column2')
rownames(M) <- c('Row1', 'Row2','Row3')
M

##      Column1 Column2
## Row1       1       2
## Row2       3       4
## Row3       5       6
```

Accessing a particular element of a matrix is done in a similar manner as with vectors, using the `[]` notation, but this time we must specify which row and which column. Notice that this scheme *always* is `[row, col]`.

```
M1 <- matrix(1:6, nrow=3, ncol=2)
M1

##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
## [3,]    3    6

M1[1,2] # Grab row 1, column 2 value

## [1] 4

M1[1, 1:2]  # grab the 1st and 2nd elements in row 1

## [1] 1 4
```

I might want to grab a single row or a single column out of a matrix, which is sometimes referred to as taking a *slice* of the matrix. I could figure out how long that vector is, but often I'm too lazy. Instead I can just specify the specify the particular row or column I want.

```
M1

##      [,1] [,2]
## [1,]    1    4
## [2,]    2    5
## [3,]    3    6

M1[1,]  # grab the 1st row

## [1] 1 4

M1[,2]  # grab second column

## [1] 4 5 6
```

4.2 Data Frames

Matrices are great for mathematical operations, but I also want to be able to store data that is numerical. For example I might want to store a categorical variable such as manufacturer brand. To generalize our concept of a matrix to include these types of data, we will create a structure called a `data.frame`. These are very much like a simple Excel spreadsheet where each column represents a

different trait or measurement type and each row will represent an individual.

Perhaps the easiest way to create a data frame is to just type the columns of data

```
data <- data.frame(
  Name  = c('Bob','Jeff','Mary'),
  Score = c(90, 75, 92)
)

# Show the data.frame
data
```

```
##   Name Score
## 1  Bob    90
## 2 Jeff    75
## 3 Mary    92
```

Because a data frame feels like a matrix, R also allows matrix notation for accessing particular values.

format	result
`[a,b]`	element in row `a` and column `b`
`[a,]`	all elements in row `a`
`[,b]`	all elements in column `b`

```
data[1,1]
```

```
## [1] Bob
## Levels: Bob Jeff Mary
```

```
data[2,]
```

```
##   Name Score
## 2 Jeff    75
```

```
data[,2]
```

```
## [1] 90 75 92
```

Because the columns have meaning and we have given them column names, it is desirable to want to access an element by the name of the column as opposed to the column number.[1]

```
data$Name
```

```
## [1] Bob  Jeff Mary
## Levels: Bob Jeff Mary
```

```
data$Name[2]
```

```
## [1] Jeff
## Levels: Bob Jeff Mary
```

I can mix the `[]` notation with the column names. The following is also acceptable:

[1] In large Excel spreadsheets I often get annoyed trying to remember which column something was in and muttering "Was total biomass in column P or Q?" A system where I could just name the column `Total.Biomass` and be done with it is much nicer to work with and I make fewer dumb mistakes.

```
data[, 'Name']

## [1] Bob  Jeff Mary
## Levels: Bob Jeff Mary
```

The next thing we might wish to do is add a new column to a preexisting data frame. There are two ways to do this. First, we could use the `cbind()` function to bind two data frames together. Second we could reference a new column name and assign values to it.

```
Second.score <- data.frame(Score2=c(41,42,43))
data <-  cbind( data, Second.score )
data

##   Name Score Score2
## 1  Bob    90     41
## 2 Jeff    75     42
## 3 Mary    92     43

data$Score3 <- c(61,62,63) # the Score3 column will created
data

##   Name Score Score2 Score3
## 1  Bob    90     41     61
## 2 Jeff    75     42     62
## 3 Mary    92     43     63
```

Data frames are very commonly used and many commonly used functions will take a `data` argument and all other arguments are assumed to be in the given data frame. Unfortunately this is not universally supported by all functions and you must look at the help file for the function you are interested in.

4.3 Lists

Data frames are quite useful for storing data but sometimes we'll need to store a bunch of different pieces of information and it won't fit neatly as a data frame. The most general form of a data structure is called a *list*. This can be thought of as a vector of objects where there is no requirement for each element to be the same type of object.

Consider that I might need to store information about person. For example, suppose that I want make an object that holds information about my immediate family. This object should have my spouse's name (just one name) as well as my siblings. But since I have many siblings, I want the siblings to be a vector of names. Likewise I might also include my pets, but we don't want any requirement that the number of pets is the same as the number of siblings (or spouses!).

```
wife <- 'Aubrey'
sibs <- c('Tina','Caroline','Brandon','John')
pets <- c('Beau','Tess','Kaylee')
Derek <- list(Spouse=wife, Siblings=sibs, Pets=pets)
str(Derek) # show the structure of object

## List of 3
##  $ Spouse  : chr "Aubrey"
##  $ Siblings: chr [1:4] "Tina" "Caroline" "Brandon" "John"
##  $ Pets    : chr [1:3] "Beau" "Tess" "Kaylee"
```

Notice that the object `Derek` is a list of three elements. The first is the single string containing my wife's name. The next is a vector of my siblings' names and it a vector of length 4. Finally the vector of pets' names is only of length 3.

To access any element of this list we can use an indexing scheme similar to matrices and vectors. The only difference is that we'll use *two* square brackets instead of one.

```
Derek[[ 1 ]]

## [1] "Aubrey"

Derek[[ 3 ]]

## [1] "Beau"   "Tess"   "Kaylee"
```

There is a second way I can access elements. For data frames it was convenient to use the notation `DataFrame$ColumnName` and we will use the same convention for lists.[2] To access my pets names we can use the following notation:

```
Derek$Pets

## [1] "Beau"   "Tess"   "Kaylee"
```

To add something new to the list object, we can just make an assignment in a similar fashion.

```
Derek$Offspring <- c('Elise')
```

We can also add extremely complicated items to my list. Here we'll add a matrix as another list element.

[2] Actually a data frame is just a list with the requirement that each list element is a vector and all vectors are of the same length.

```
# from the previous section, recall we had
# defined the following data.frame
str(data)

## 'data.frame': 3 obs. of  4 variables:
##  $ Name  : Factor w/ 3 levels "Bob","Jeff","Mary": 1 2 3
##  $ Score : num  90 75 92
##  $ Score2: num  41 42 43
##  $ Score3: num  61 62 63

Derek$foo <- data
str(Derek)

## List of 5
##  $ Spouse   : chr "Aubrey"
##  $ Siblings : chr [1:4] "Tina" "Caroline" "Brandon" "John"
##  $ Pets     : chr [1:3] "Beau" "Tess" "Kaylee"
##  $ Offspring: chr "Elise"
##  $ foo      :'data.frame': 3 obs. of  4 variables:
##   ..$ Name  : Factor w/ 3 levels "Bob","Jeff","Mary": 1 2 3
##   ..$ Score : num [1:3] 90 75 92
##   ..$ Score2: num [1:3] 41 42 43
##   ..$ Score3: num [1:3] 61 62 63

Derek$foo

##   Name Score Score2 Score3
## 1  Bob    90     41     61
## 2 Jeff    75     42     62
## 3 Mary    92     43     63
```

The place that most users will run into lists is that the output of many statistical procedures will return the results in a list object. When a user asks R to perform a regression, the output returned is a list object, and we'll need to grab particular information from that object afterwards. For example, the output from a t-test in R is a list:

```
x <- c(5.1, 4.9, 5.6, 4.2, 4.8, 4.5, 5.3, 5.2)
result <- t.test(x, alternative='less', mu=5)
str(result)

## List of 9
##  $ statistic  : Named num -0.314
##   ..- attr(*, "names")= chr "t"
##  $ parameter  : Named num 7
##   ..- attr(*, "names")= chr "df"
##  $ p.value    : num 0.381
##  $ conf.int   : atomic [1:2] -Inf 5.25
##   ..- attr(*, "conf.level")= num 0.95
##  $ estimate   : Named num 4.95
##   ..- attr(*, "names")= chr "mean of x"
##  $ null.value : Named num 5
##   ..- attr(*, "names")= chr "mean"
##  $ alternative: chr "less"
##  $ method     : chr "One Sample t-test"
##  $ data.name  : chr "x"
##  - attr(*, "class")= chr "htest"
```

We see that `result` is actually a list with 9 elements in it. To access the p-value we could use:

```
result$p.value

## [1] 0.3813385
```

If I ask R to print the object `result`, it will hide the structure from you and print it in a "pretty" fashion because there is a print function defined specifically for objects created by the `t.test()` function.

```
result

##
##  One Sample t-test
##
## data:  x
## t = -0.31399, df = 7, p-value = 0.3813
## alternative hypothesis: true mean is less than 5
## 95 percent confidence interval:
##      -Inf 5.251691
## sample estimates:
## mean of x
##      4.95
```

4.4 Exercises

1. In this problem, we will work with the matrix

$$\begin{bmatrix} 2 & 4 & 6 & 8 & 10 \\ 12 & 14 & 16 & 18 & 20 \\ 22 & 24 & 26 & 28 & 30 \end{bmatrix}$$

   (a) Create the matrix in two ways and save the resulting matrix as `M`.

   i. Create the matrix using some combination of the `seq()` and `matrix()` commands.
   ii. Create the same matrix by some combination of multiple `seq()` commands and either the `rbind()` or `cbind()` command.

(b) Extract the second row out of `M`.

(c) Extract the element in the third row and second column of `M`.

2. Create and manipulate a data frame.

(a) Create a data frame named it `trees` that has the following columns:
   - `Girth = c(8.3, 8.6, 8.8, 10.5, 10.7, 10.8, 11.0)`
   - `Height= c(70, 65, 63, 72, 81, 83, 66)`
   - `Volume= c(10.3, 10.3, 10.2, 16.4, 18.8, 19.7, 15.6)`

(b) Extract the third observation.

(c) Extract the `Girth` column referring to it by name (don't use whatever order you placed the columns in).

(d) Create a data frame of all the observations *except* for the fourth observation. (i.e. Remove the fourth observation/row.)

3. Create and manipulate a list.

(a) Create a list named `my.test` with elements
   - `x = c(4,5,6,7,8,9,10)`
   - `y = c(34,35,41,40,45,47,51)`
   - `slope = 2.82`
   - `p.value = 0.000131`

(b) Extract the second element in the list.

(c) Extract the element named `p.value` from the list.

4. The function `lm()` creates a linear model, which is a general class of model that includes both regression and ANOVA. We will call this on a data frame and examine the results. For this problem, there isn't much to figure out, but rather the goal is to recognize the data structures being used by common analysis functions.

(a) There are many data sets that are included with R and its packages. One of which is the `trees` data which is a data set of $n = 31$ cherry trees. Load this dataset into your current workspace using the command

```
data(trees)     # load trees data.frame
```

(b) Examine the data frame using the `str()` command. Look at the help file for the data using the command `help(trees)` or `?trees`.

(c) Perform a regression relating the volume of lumber produced to the girth and height of the tree using the following command

```
m <- lm( Volume ~ Girth + Height, data=trees)
```

(d) Use the `str()` command to inspect `m`. Extract the model coefficients from this list.

(e) The list `m` can be passed to other functions. For example, the function `summary()` will take the list and recognize that it was produced by the `lm()` function and produce a summary table in the manner that we are used to seeing. Produce that summary table using the command

```
summary(m)
```

```
##
## Call:
## lm(formula = Volume ~ Girth + Height, data = trees)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.4065 -2.6493 -0.2876  2.2003  8.4847
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -57.9877     8.6382  -6.713 2.75e-07 ***
## Girth         4.7082     0.2643  17.816  < 2e-16 ***
## Height        0.3393     0.1302   2.607   0.0145 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.882 on 28 degrees of freedom
## Multiple R-squared:  0.948,Adjusted R-squared:  0.9442
## F-statistic:   255 on 2 and 28 DF,  p-value: < 2.2e-16
```

Chapter 5

Importing Data

Reading data from external sources is necessary. It is most common for data to be in a data-frame like storage, such as a MS Excel workbook, so we will concentrate on reading data into a `data.frame`.

In the typical way data is organized, we think of each column of data representing some trait or variable that we might be interested in. In general, we might wish to investigate the relationship between variables. In contrast, the rows of our data represent a single object on which the column traits are measured. For example, in a grade book for recording students scores throughout the semester, their is one row for every student and columns for each assignment. A green-house experiment dataset will have a row for every plant and columns for treatment type and biomass.

5.1 Comma Separated Data

To consider how data might be stored, we first consider the simplest file format... the comma separated values file. In this file time, each of the "cells" of data are separated by a comma. For example, the data file storing scores for three students might be as follows:

```
Able, Dave, 98, 92, 94
Bowles, Jason, 85, 89, 91
Carr, Jasmine, 81, 96, 97
```

Typically when you open up such a file on a computer with Microsoft Excel installed, Excel will open up the file assuming it is a spreadsheet and put each element in its own cell. However, you can also open the file using a more primitive program (say Notepad in Windows, TextEdit on a Mac) you'll see the raw form of the data.

Having just the raw data without any sort of column header is problematic (which of the three exams was the final??). Ideally we would have column headers that store the name of the column.

```
LastName, FirstName, Exam1, Exam2, FinalExam
Able, Dave, 98, 92, 94
Bowles, Jason, 85, 89, 91
Carr, Jasmine, 81, 96, 97
```

To see another example, open the "Body Fat" dataset from the Lock[5] introductory text book at the website http://www.lock5stat.com/datasets/BodyFat.csv. The first few rows of the file are as follows:

```
Bodyfat,Age,Weight,Height,Neck,Chest,Abdomen,Ankle,Biceps,Wrist
32.3,41,247.25,73.5,42.1,117,115.6,26.3,37.3,19.7
22.5,31,177.25,71.5,36.2,101.1,92.4,24.6,30.1,18.2
22,42,156.25,69,35.5,97.8,86,24,31.2,17.4
12.3,23,154.25,67.75,36.2,93.1,85.2,21.9,32,17.1
20.5,46,177,70,37.2,99.7,95.6,22.5,29.1,17.7
.
.
.
```

To make R read in the data arranged in this format, we need to tell R three things:

1. Where does the data live? Often this will be the name of a file on your computer, but the file could just as easily live on the internet (provided your computer has internet access).
2. Is the first row data or is it the column names?
3. What character separates the data? Some programs store data using tabs to distinguish between elements, some others use white space. R's mechanism for reading in data is flexible enough to allow you to specify what the separator is.

The primary function that we'll use to read data from a file and into R is the function `read.table()`. This function has many optional arguments but the most commonly used ones are outlined in the table below.

argument	default	Interpretation
`file`		A character string denoting the file location
`header`	`FALSE`	Is the first line column names?
`sep`	`""`	What character separates each data value. The default `sep=""` represents any whitespace
`skip`	`0`	The number of lines to skip before reading anything. This is useful when there are multiple lines of text describing how the data was collected or what the columns mean.
`na.strings`	`NA`	What values represent missing data. Can have multiple strings such as `na.strings=c('NA',-9999)`
`quote`	`"` and `'`	For character strings, what characters represent quotations.

So to read in the "Body Fat" dataset we could run the R command:

```
BodyFat <- read.table(
  file   = 'http://www.lock5stat.com/datasets/BodyFat.csv',  # where the data lives
  header = TRUE,                                             # first line is column names
  sep    = ',' )                                             # Data is sparated by commas

str(BodyFat)

## 'data.frame': 100 obs. of  10 variables:
##  $ Bodyfat: num  32.3 22.5 22 12.3 20.5 22.6 28.7 21.3 29.9 21.3 ...
##  $ Age    : int  41 31 42 23 46 54 43 42 37 41 ...
##  $ Weight : num  247 177 156 154 177 ...
##  $ Height : num  73.5 71.5 69 67.8 70 ...
##  $ Neck   : num  42.1 36.2 35.5 36.2 37.2 39.9 37.9 35.3 42.1 39.8 ...
##  $ Chest  : num  117 101.1 97.8 93.1 99.7 ...
##  $ Abdomen: num  115.6 92.4 86 85.2 95.6 ...
##  $ Ankle  : num  26.3 24.6 24 21.9 22.5 22 23.7 21.9 24.8 25.2 ...
##  $ Biceps : num  37.3 30.1 31.2 32 29.1 35.9 32.1 30.7 34.4 37.5 ...
##  $ Wrist  : num  19.7 18.2 17.4 17.1 17.7 18.9 18.7 17.4 18.4 18.7 ...
```

Looking at the help file for `read.table()` we see that there are variants such as `read.csv()` that sets the default arguments to `header` and `sep` more intelligently. Also, there are many options to customize how R responds to different input.

5.2 MS Excel

Commonly our data is stored as a MS Excel file. There are two approaches you could use to import the data into R.

1. From within Excel, export the worksheet that contains your data as a comma separated values (.csv) file and proceed using the tools in the previous section.
2. Use functions within R that automatically convert the worksheet into a `.csv` file and read it in. One package that works nicely for this is the `readxl` package..

I generally prefer using option 2 because all of my collaborators can't live without Excel and I've resigned myself to this. However if you have complicated formulas in your Excel file, it is often times safer to export it as a `.csv` file to guarantee the data imported into R is correct. Furthermore, other spreadsheet applications (such as Google docs) requires you to export the data as a `.csv` file so it is good to know both paths.

Because R can only import a complete worksheet, the desired data worksheet must be free of notes to yourself about how the data was collected, preliminary graphics, or other stuff that isn't the data. I find it very helpful to have a worksheet in which I describe the sampling procedure and describe what each column means (and give the units!), then a second worksheet where the actual data is, and finally a third worksheet where my "Excel Only" collaborators have created whatever plots and summary statistics they need.

The simplest package for importing Excel files seems to be the package `readxl`[1]. This library provides a function `read_exel()` that allows us to specify which sheet within the Excel file to read and what character specifies missing data (it assumes a blank cell is missing data if you don't specifying anything).

From Bblearn, download the `files Example_1.xls, Example_2.xls, Example_3.xls` and `Example_4.xls` Place these files in the same directory that you store your STA 599 course work. Make sure that the working directory that RStudio is using is that same directory (Session -> Set Working Directory).

```
# load the library that has the read.xls function. Unfortunately it overwrites some
# functions in the mosaic package, so you should remove it once the data are loaded.
library(readxl)

# read the first worksheet of the Example_1 file
data.1 <- read_excel('Example_1.xls')

# read the second worksheet where the second worksheet is named 'data'
data.2 <- read_excel('Example_2.xls', sheet=2     )   # both ways
data.2 <- read_excel('Example_2.xls', sheet='data')   # will work
```

There is one additional problem that shows up while reading in Excel files. Blank columns often show up in Excel files because at some point there was some text in a cell that got deleted but a space remains and Excel still thinks there is data in the column. To fix this, you could find the cell with the space in it, or you can select a bunch of columns at the edge and delete the entire columns. Alternatively, you could remove the column after it is read into R.

Open up the file `Example_4.xls` in Excel and confirm that the data sheet has name columns out to `carb`. Read in the data frame using the following code:

[1] Another package that does this is the `XLConnect` which does the Excel -> `.csv` conversion using Java. The `RODBC` package allows R to connect to various databases and it is possible to make it consider an Excel file as an extremely crude database.

```
data.4 <- read_excel('Example_4.xls', sheet='data')   # Extra Column Example
str(data.4)

## Classes 'tbl_df', 'tbl' and 'data.frame': 31 obs. of  13 variables:
##  $ model: chr  "Mazda RX4" "Mazda RX4 Wag" "Datsun 710" "Hornet 4 Drive" ...
##  $ mpg  : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
##  $ cyl  : num  6 6 4 6 8 6 8 4 4 6 ...
##  $ disp : num  160 160 108 258 360 ...
##  $ hp   : num  110 110 93 110 175 105 245 62 95 123 ...
##  $ drat : num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92 ...
##  $ wt   : num  2.62 2.88 2.32 3.21 3.44 ...
##  $ qsec : num  16.5 17 18.6 19.4 17 ...
##  $ vs   : num  0 0 1 1 0 1 0 1 1 1 ...
##  $ am   : num  1 1 1 0 0 0 0 0 0 0 ...
##  $ gear : num  4 4 4 3 3 3 3 4 4 4 ...
##  $ carb : num  4 4 1 1 2 1 4 2 2 4 ...
##  $ NA   : chr  NA NA " " NA ...
```

We notice that after reading in the data, there are an additional two columns (labeled `X` and `X.1` because R had to make up some column name so it chose that) that just has missing data (the `NA` stands for *not available* which means that the data is missing). Go back to the Excel file and go to row 4 column N and notice that the cell isn't actually blank... there is a space. Delete the space, save the file, and then reload the data into R. You should notice that the extra columns are now gone.

5.3 Exercises

1. Download from Bblearn the file `Example_5.xls`. Open it in Excel and figure out which sheet of data we should import into R. At the same time figure out how many initial rows need to be skipped. Import the data set into a data frame and show the structure of the imported data using the `str()` command. Make sure that your data has $n = 31$ observations and the three columns are appropriately named.

Chapter 6

Manipulating Data Frames

Most of the time, our data is in the form of a data frame and we are interested in exploring the relationships. This chapter explores how to manipulate data frames and methods.

6.1 Classical functions for summarizing rows and columns

6.1.1 summary()

The first method is to calculate some basic summary statistics (minimum, 25th, 50th, 75th percentiles, maximum and mean) of each column. If a column is categorical, the summary function will return the number of observations in each category.

```
# use the iris data set which has both numerical and categorical variables
data( iris )
str(iris)    # recall what columns we have
```

```
## 'data.frame': 150 obs. of  5 variables:
##  $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
##  $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
##  $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
##  $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
##  $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...
```

```
# display the summary for each column
summary( iris )
```

```
##   Sepal.Length    Sepal.Width     Petal.Length    Petal.Width
##  Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100
##  1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300
##  Median :5.800   Median :3.000   Median :4.350   Median :1.300
##  Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199
##  3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
##  Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500
##        Species
##  setosa    :50
##  versicolor:50
##  virginica :50
##
##
##
```

6.1.2 apply()

The summary function is convenient, but we want the ability to pick another function to apply to each column and possibly to each row. To demonstrate this, suppose we have data frame that contains students grades over the semester.

```
# make up some data
grades <- data.frame(
  l.name = c('Cox', 'Dorian', 'Kelso', 'Turk'),
  Exam1 = c(93, 89, 80, 70),
  Exam2 = c(98, 70, 82, 85),
  Final = c(96, 85, 81, 92) )
```

The `apply()` function will apply an arbitrary function to each row (or column) of a matrix or a data frame and then aggregate the results into a vector.

```
# Because I can't take the mean of the last names column,
# remove the name column
scores <- grades[,-1]
scores

##   Exam1 Exam2 Final
## 1    93    98    96
## 2    89    70    85
## 3    80    82    81
## 4    70    85    92

# Summarize each column by calculating the mean.
apply( scores,       # what object do I want to apply the function to
       MARGIN=2,     # rows = 1, columns = 2, (same order as [rows, cols]
       FUN=mean      # what function do we want to apply
     )

## Exam1 Exam2 Final
## 83.00 83.75 88.50
```

To apply a function to the rows, we just change which margin we want. We might want to calculate the average exam score for person.

```
apply( scores,       # what object do I want to apply the function to
       MARGIN=1,     # rows = 1, columns = 2, (same order as [rows, cols]
       FUN=mean      # what function do we want to apply
     )

## [1] 95.66667 81.33333 81.00000 82.33333
```

This is useful, but it would be more useful to concatenate this as a new column in my `grades` data frame.

```
average <- apply(
  scores,       # what object do I want to apply the function to
  MARGIN=1,     # rows = 1, columns = 2, (same order as [rows, cols]
  FUN=mean      # what function do we want to apply
)
grades <- cbind( grades, average )
grades

##   l.name Exam1 Exam2 Final  average
## 1    Cox    93    98    96 95.66667
## 2 Dorian    89    70    85 81.33333
## 3  Kelso    80    82    81 81.00000
## 4   Turk    70    85    92 82.33333
```

There are several variants of the `apply()` function, and the variant I use most often is the function `sapply()`, which will apply a function to each element of a list or vector and returns a corresponding list or vector of results.

6.2 Package `dplyr`

Many of the tools to manipulate data frames in R were written without a consistent syntax and are difficult use together. To remedy this, Hadley Wickham (the writer of `ggplot2`) introduced a package called `plyr` which was quite useful. As with many projects, his first version was good but not great and he introduced an improved version that works exclusively with `data.frames` called `dplyr` which we will investigate. The package `dplyr` strives to provide a convenient and consistent set of functions to handle the most common data frame manipulations and a mechanism for chaining these operations together to perform complex tasks.

The author of the `dplyr` package has put together a very nice introduction to the package that explains in more detail how the various pieces work and I encourage you to read it at some point. http://cran.rstudio.com/web/packages/dplyr/vignettes/introduction.html.

The pipe command `%>%` allows for very readable code. The idea is that the `%>%` operator works in the context of functions that take a `data.frame` as their first argument. The `%>%` operator translates `df %>% f()` to the expression `f(df)`. The beauty of this comes when you have functions that takes `data.frames` as arguments and returns a modified `data.frame`. This will allow me to chain together commands in a readable fashion.

6.2.1 Verbs

The foundational operations to perform on a data frame are:

- Subsetting - Returns a `data.frame` with only particular columns or rows
  - `select` - Selecting a subset of columns by name or column number.
  - `filter` - Selecting a subset of rows from a data frame based on logical expressions.
  - `slice` - Selecting a subset of rows by row number.
- `arrange` - Re-ordering the rows of a data frame.
- `mutate` - Add a new column that is some function of another column.
- `summarise` - calculate some summary statistic of a column of data. This collapses a set of rows into a single row.

Each of these operations is a function in the package `dplyr`. These functions all have a similar calling syntax, the first argument is a data frame, subsequent arguments describe what to do with the input data frame and you can refer to the columns without using the `df$column` notation. All of these functions will return a data frame.

6.2.1.1 Subsetting with `select`, `filter`, and `slice`

These function allows you select certain columns and rows of a data frame.

select()

Often you only want to work with a small number of columns of a data frame. It is relatively easy to do this using the standard `[,col.name]` notation, but is often pretty tedious. The dataset `mtcars` contains information about 32 models of cars from the 70s.

```
library(dplyr)
str(mtcars)

## 'data.frame': 32 obs. of  11 variables:
##  $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
##  $ cyl : num  6 6 4 6 8 6 8 4 4 6 ...
##  $ disp: num  160 160 108 258 360 ...
##  $ hp  : num  110 110 93 110 175 105 245 62 95 123 ...
##  $ drat: num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92 ...
##  $ wt  : num  2.62 2.88 2.32 3.21 3.44 ...
##  $ qsec: num  16.5 17 18.6 19.4 17 ...
##  $ vs  : num  0 0 1 1 0 1 0 1 1 1 ...
##  $ am  : num  1 1 1 0 0 0 0 0 0 0 ...
##  $ gear: num  4 4 4 3 3 3 3 4 4 4 ...
##  $ carb: num  4 4 1 1 2 1 4 2 2 4 ...
```

I could select the columns `mpg, cyl, disp, hp` by hand, or by using an extension of the `:` operator

```
small <- mtcars %>% select( mpg, cyl, disp, hp )  # these two commands are
small <- mtcars %>% select( mpg:hp )              # equivalent
str(small)

## 'data.frame': 32 obs. of  4 variables:
##  $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
##  $ cyl : num  6 6 4 6 8 6 8 4 4 6 ...
##  $ disp: num  160 160 108 258 360 ...
##  $ hp  : num  110 110 93 110 175 105 245 62 95 123 ...
```

filter()

It is common to want to select particular rows where we have some logically expression to pick the rows.

```
# recall what the grades are
grades
```

```
##   l.name Exam1 Exam2 Final  average
## 1    Cox    93    98    96 95.66667
## 2 Dorian    89    70    85 81.33333
## 3  Kelso    80    82    81 81.00000
## 4   Turk    70    85    92 82.33333
```

```
# select students with Final grades greater than 90
grades %>% filter(Final > 90)
```

```
##   l.name Exam1 Exam2 Final  average
## 1    Cox    93    98    96 95.66667
## 2   Turk    70    85    92 82.33333
```

You can have multiple logical expressions to select rows and they will be logically combined so that only rows that satisfy **all** of the conditions are selected.[1]

```
# select students with Final grades above 90 and
# average score also above 90
grades %>% filter(Final > 90, average > 90)
```

```
##   l.name Exam1 Exam2 Final  average
## 1    Cox    93    98    96 95.66667
```

```
# we could also use an "and" condition
grades %>% filter(Final > 90 & average > 90)
```

```
##   l.name Exam1 Exam2 Final  average
## 1    Cox    93    98    96 95.66667
```

slice()

When you want to filter rows based on row number, this is called slicing.

```
# grab the first 2 rows
grades %>% slice(1:2)
```

```
##   l.name Exam1 Exam2 Final  average
## 1    Cox    93    98    96 95.66667
## 2 Dorian    89    70    85 81.33333
```

6.2.1.2 arrange()

We often need to re-order the rows of a data frame. For example, we might wish to take our grade book and sort the rows by the average score, or perhaps alphabetically. The `arrange()` function does exactly that. The first argument is the data frame to re-order, and the subsequent arguments are the columns to sort on. The order of the sorting column determines the precedent... the first sorting column is first used and the second sorting column is only used to break ties.

[1] The logicals are joined together using `&` (and) operator or the `|` (or) operator and you may explicitly use other logicals. For example a factor column `type` might be used to select rows where type is either one or two via the following: `type==1 | type==2`.

```
grades %>% arrange(l.name)

##   l.name Exam1 Exam2 Final  average
## 1    Cox    93    98    96 95.66667
## 2 Dorian    89    70    85 81.33333
## 3  Kelso    80    82    81 81.00000
## 4   Turk    70    85    92 82.33333
```

The default sorting is in ascending order, so to sort the grades with the highest scoring person in the first row, we must tell `arrange` to do it in descending order using `desc(column.name)`.

```
grades %>% arrange(desc(Final))

##   l.name Exam1 Exam2 Final  average
## 1    Cox    93    98    96 95.66667
## 2   Turk    70    85    92 82.33333
## 3 Dorian    89    70    85 81.33333
## 4  Kelso    80    82    81 81.00000
```

In a more complicated example, consider the following data and we want to order it first by Treatment Level and secondarily by the y-value. I want the Treatment level in the default ascending order (Low, Medium, High), but the y variable in descending order.

```
# make some data
dd <- data.frame(
  Trt = factor(c("High", "Med", "High", "Low"),
               levels = c("Low", "Med", "High")),
  y = c(8, 3, 9, 9),
  z = c(1, 1, 1, 2))
dd

##    Trt y z
## 1 High 8 1
## 2  Med 3 1
## 3 High 9 1
## 4  Low 9 2

# arrange the rows first by treatment, and then by y (y in descending order)
dd %>% arrange(Trt, desc(y))

##    Trt y z
## 1  Low 9 2
## 2  Med 3 1
## 3 High 9 1
## 4 High 8 1
```

6.2.1.3 mutate()

I often need to create a new column that is some function of the old columns. This was often cumbersome. Consider code to calculate the average grade in my grade book example.

```
grades$average <- (grades$Exam1 + grades$Exam2 + grades$Final) / 3
```

Instead, we could use the `mutate()` function and avoid all the `grades$` nonsense.[2]

[2]There is another way to do this. The command `with(df, expression)` will attach the dataframe `df` to the current

```
grades %>% mutate( average = (Exam1 + Exam2 + Final)/3 )

##   l.name Exam1 Exam2 Final  average
## 1    Cox    93    98    96 95.66667
## 2 Dorian    89    70    85 81.33333
## 3  Kelso    80    82    81 81.00000
## 4   Turk    70    85    92 82.33333
```

You can do multiple calculations within the same `mutate()` command, and you can even refer to columns that were created in the same `mutate()` command.

```
grades %>% mutate( average = (Exam1 + Exam2 + Final)/3,
                   grade = cut(average, c(0,60,70,80,90,100), c('F','D','C','B','A')) )

##   l.name Exam1 Exam2 Final  average grade
## 1    Cox    93    98    96 95.66667     A
## 2 Dorian    89    70    85 81.33333     B
## 3  Kelso    80    82    81 81.00000     B
## 4   Turk    70    85    92 82.33333     B
```

6.2.1.4 summarise()

By itself, this function is quite boring, but will become useful later on. Its purpose is to calculate summary statistics using any or all of the data columns. Notice that we get to chose the name of the new column. The way to think about this is that we are collapsing information stored in multiple rows into a single row of values.

```
# calculate the mean of exam 1
summarise( grades, mean.E1=mean(Exam1))

##   mean.E1
## 1      83
```

We could calculate multiple summary statistics if we like.

```
# calculate the mean of each of the exams
grades %>% summarise( mean.E1=mean(Exam1), stddev.E1=sd(Exam2) )

##   mean.E1 stddev.E1
## 1      83      11.5
```

If we want to apply the same statistic to each column, we use the `summarise_each()` command. We have to be a little careful here because the function you use has to work on every column (that isn't part of the grouping structure (see `group_by()`)).

environment, then evaluate the expression, and then detach the dataframe. However, to assign the result back to the data frame, I still end up typing the name of the dataframe twice.

```
# calculate the mean and stddev of each column
grades %>% summarise_each( funs(mean, sd) )

## Warning in mean.default(structure(1:4, .Label = c("Cox", "Dorian", "Kelso", :
argument is not numeric or logical:  returning NA
## Warning in var(if (is.vector(x) || is.factor(x)) x else as.double(x), na.rm =
na.rm):  Calling var(x) on a factor x is deprecated and will become an error.
##  Use something like 'all(duplicated(x)[-1L])' to test for a constant vector.

##   l.name_mean Exam1_mean Exam2_mean Final_mean average_mean l.name_sd
## 1          NA         83      83.75       88.5     85.08333  1.290994
##   Exam1_sd Exam2_sd Final_sd average_sd
## 1 10.23067     11.5 6.757712   7.078266
```

Miscellaneous functions

There are some more function that are useful but aren't as commonly used. For sampling the functions `sample_n()` and `sample_frac()` will take a subsample of either `n` rows or of a fraction of the data set. The function `n()` returns the number of rows in the data set. Finally `rename()` will rename a selected column.

6.2.2 Split, apply, combine

Aside from unifying the syntax behind the common operations, the major strength of the `dplyr` package is the ability to split a data frame into a bunch of sub-dataframes, apply a sequence of one or more of the operations we just described, and then combine results back together. We'll consider data from an experiment from spinning wool into yarn. This experiment considered two different types of wool (A or B) and three different levels of tension on the thread. The response variable is the number of breaks in the resulting yarn. For each of the 6 `wool:tension` combinations, there are 9 replicated observations.

```
data(warpbreaks)
str(warpbreaks)

## 'data.frame': 54 obs. of  3 variables:
##  $ breaks : num  26 30 54 25 70 52 51 26 67 18 ...
##  $ wool   : Factor w/ 2 levels "A","B": 1 1 1 1 1 1 1 1 1 1 ...
##  $ tension: Factor w/ 3 levels "L","M","H": 1 1 1 1 1 1 1 1 1 2 ...
```

The first we must do is to create a data frame with additional information about how to break the data into sub-dataframes. In this case, I want to break the data up into the 6 wool-by-tension combinations. Initially we will just figure out how many rows are in each wool-by-tension combination.

```
# what variable(s) shall we group one
grouped.warpbreaks <- warpbreaks %>% group_by( wool, tension)

# n() is a function that returns how many rows are in the
# currently selected sub-dataframe
summarise(grouped.warpbreaks, n = n() )

## Source: local data frame [6 x 3]
## Groups: wool [?]
##
##     wool tension     n
##   (fctr)  (fctr) (int)
## 1      A       L     9
## 2      A       M     9
## 3      A       H     9
## 4      B       L     9
## 5      B       M     9
## 6      B       H     9
```

Using the same `summarise` function, we could calculate the group mean and standard deviation for each wool-by-tension group.

```
warpbreaks %>% group_by(wool, tension) %>%
  summarise( n           = n(),             # I added some formatting to tell the
             mean.breaks = mean(breaks),    # reader I am calculating several
             sd.breaks   = sd(breaks)       # statistics.
)

## Source: local data frame [6 x 5]
## Groups: wool [?]
##
##     wool tension     n mean.breaks sd.breaks
##   (fctr)  (fctr) (int)       (dbl)     (dbl)
## 1      A       L     9    44.55556 18.097729
## 2      A       M     9    24.00000  8.660254
## 3      A       H     9    24.55556 10.272671
## 4      B       L     9    28.22222  9.858724
## 5      B       M     9    28.77778  9.431036
## 6      B       H     9    18.77778  4.893306
```

If instead of summarizing each split, we might want to just do some calculation and the output should have the same number of rows as the input data frame. In this case I'll tell `dplyr` that we are *mutating* the data frame instead of summarizing it. For example, suppose that I want to calculate the residual value

$$e_{ijk} = y_{ijk} - \bar{y}_{ij\cdot}$$

where $\bar{y}_{ij\cdot}$ is the mean of each `wool:tension` combination.

```
temp <- warpbreaks %>%
   group_by(wool, tension) %>%
   mutate(resid = breaks - mean(breaks))
head( temp )  # show the first couple of rows of the result

## Source: local data frame [6 x 4]
## Groups: wool, tension [1]
##
##   breaks   wool tension      resid
##    (dbl) (fctr)  (fctr)      (dbl)
## 1     26      A       L -18.555556
## 2     30      A       L -14.555556
## 3     54      A       L   9.444444
## 4     25      A       L -19.555556
## 5     70      A       L  25.444444
## 6     52      A       L   7.444444
```

6.2.3 Chaining commands together

Suppose we have the results of a small 5K race. The data given to us is in the order that the runners signed up but we want to calculate the results for each gender, calculate the placings, and the sort the data frame by gender and then place. We can think of this process as having three steps: 1) Splitting 2) Ranking 3) Re-arranging.

```
# input the initial data
race.results <- data.frame(
  name=c('Bob', 'Jeff', 'Rachel', 'Bonnie', 'Derek', 'April','Elise','David'),
  time=c(21.23, 19.51, 19.82, 23.45, 20.23, 24.22, 28.83, 15.73),
  gender=c('M','M','F','F','M','F','F','M')
)

# how should I group?
grouped.results <- race.results %>% group_by( gender)

# calculate the rankings using the rank() function
temp.df1 <- grouped.results %>% mutate( place = rank(time) )

# arrange the rows based on gender and then place
temp.df2 <- temp.df1 %>% arrange( gender, place )
```

```
# output the result
temp.df2

## Source: local data frame [8 x 4]
## Groups: gender [2]
##
##     name  time gender place
##   (fctr) (dbl) (fctr) (dbl)
## 1 Rachel 19.82      F     1
## 2 Bonnie 23.45      F     2
## 3  April 24.22      F     3
## 4  Elise 28.83      F     4
## 5  David 15.73      M     1
## 6   Jeff 19.51      M     2
## 7  Derek 20.23      M     3
## 8    Bob 21.23      M     4
```

It would be nice if I didn't have to save all these intermediate results because keeping track of `temp1` and `temp2` gets pretty annoying if I keep changing the order of how things or calculated or add/subtract steps. The way this is typically handled in R is to to just nest one command inside the next. The same set of commands could be run as follows:

```
arrange(
  mutate(
    group_by(
      race.results,          # using race.results
      gender),               # group by gender
    place = rank( time )),   # mutate to calculate the place column
  gender, place)             # arrange the result by gender and place

## Source: local data frame [8 x 4]
## Groups: gender [2]
##
##     name  time gender place
##   (fctr) (dbl) (fctr) (dbl)
## 1 Rachel 19.82      F     1
## 2 Bonnie 23.45      F     2
## 3  April 24.22      F     3
## 4  Elise 28.83      F     4
## 5  David 15.73      M     1
## 6   Jeff 19.51      M     2
## 7  Derek 20.23      M     3
## 8    Bob 21.23      M     4
```

This is extremely hard to read because the commands are separated from the arguments (e.g. the `arrange` function call was at the top, but the columns to arrange by are on the last line). To get around this, the author of `dplyr` gives us an operator to combine these simple operations smoothly. The composition operation `%>%` takes the following `A %>% f(B)` and converts it to the statement `f(A, B)`. This allows us to write the following code that does exactly what the above two code chunks did.

```
race.results %>%                    # what data frame am I interested in
  group_by(gender) %>%              # break things by gender
  mutate(place=rank(time)) %>%      # calculate the placings within each gender
  arrange(gender, place)            # arrange the result by gender and place

## Source: local data frame [8 x 4]
## Groups: gender [2]
##
##     name  time gender place
##   (fctr) (dbl) (fctr) (dbl)
## 1 Rachel 19.82      F     1
## 2 Bonnie 23.45      F     2
## 3  April 24.22      F     3
## 4  Elise 28.83      F     4
## 5  David 15.73      M     1
## 6   Jeff 19.51      M     2
## 7  Derek 20.23      M     3
## 8    Bob 21.23      M     4
```

If I only wanted the top three finishers in each gender, we could simply add a `filter` command after the `place` column was calculated.

```
race.results %>%                    # what data frame am I interested in
  group_by(gender) %>%              # break things by gender
  mutate(place=rank(time)) %>%      # calculate the placings within each gender
  filter( place <= 3 ) %>%          # only get the top 3 finishers within each gender
  arrange(gender, place)            # arrange the result by gender and place

## Source: local data frame [6 x 4]
## Groups: gender [2]
##
##     name  time gender place
##   (fctr) (dbl) (fctr) (dbl)
## 1 Rachel 19.82      F     1
## 2 Bonnie 23.45      F     2
## 3  April 24.22      F     3
## 4  David 15.73      M     1
## 5   Jeff 19.51      M     2
## 6  Derek 20.23      M     3
```

6.3 Exercises

1. The dataset `ChickWeight` which tracks the weights of 48 baby chickens (chicks) feed four different diets.

   (a) Load the dataset using

   ```
   data(ChickWeight)
   ```

   (b) Look at the help files for the description of the columns.

   (c) Remove all the observations except for the weights on day 10 and day 20.

   (d) Calculate the mean and standard deviation for each diet group on days 10 and 20.

2. The *OpenIntro* textbook on statistics includes a data set on body dimensions.

(a) Load the file using

```
Body <- read.csv('http://www.openintro.org/stat/data/bdims.csv')
```

(b) The column `sex` is coded as a `1` if the individual is male and `0` if female. This is a non-intuitive labeling system. Create a new column `sex.MF` that uses labels `Male` and `Female`.

(c) The columns `wgt` and `hgt` measure weight and height in kilograms and centimeters (respectively). Use these to calculate the Body Mass Index (BMI) for each individual where

$$BMI = \frac{Weight\,(kg)}{[Height\,(m)]^2}$$

Notice you should get values between 18 to 30.

(d) Double check that your calculated BMI column is correct by examining the summary statistics of the column.

(e) The function `cut` takes a vector of continuous numerical data and creates a factor based on your give cut-points.

```
# Define a continuous vector to convert to a factor
x <- 1:10

# divide range of x into three groups of equal length
cut(x, breaks=3)
```

```
##  [1] (0.991,4] (0.991,4] (0.991,4] (0.991,4] (4,7]     (4,7]     (4,7]
##  [8] (7,10]    (7,10]    (7,10]
## Levels: (0.991,4] (4,7] (7,10]
```

```
# divide x into four groups, where I specify all 5 break points
cut(x, breaks = c(0, 2.5, 5.0, 7.5, 10))
```

```
##  [1] (0,2.5]  (0,2.5]  (2.5,5]  (2.5,5]  (2.5,5]  (5,7.5]  (5,7.5]
##  [8] (7.5,10] (7.5,10] (7.5,10]
## Levels: (0,2.5] (2.5,5] (5,7.5] (7.5,10]
```

```
# divide x into 3 groups, but give them a nicer
# set of group names
cut(x, breaks=3, labels=c('Low','Medium','High'))
```

```
##  [1] Low    Low    Low    Low    Medium Medium Medium High   High   High
## Levels: Low Medium High
```

Create a new column of in the data frame that divides the `age` into decades (10-19, 20-29, 30-39, etc). Notice the oldest person in the study is 67.

(f) Find the average BMI for each Sex and Age group.

Chapter 7

Pivot Tables

Most of the time, our data is in the form of a data frame and we are interested in exploring the relationships. This chapter explores how to manipulate data frames and methods.

7.1 Package `tidyr`

There is a common issue with obtaining data with many columns that you wish were organized as rows. For example, I might have data in a grade book that has several homework scores and I'd like to produce a nice graph that has assignment number on the x-axis and score on the y-axis. Unfortunately this is incredibly hard to do when the data is arranged in the following way:

```
grade.book <- rbind(
  data.frame(name='Alison',  HW.1=8, HW.2=5, HW.3=8),
  data.frame(name='Brandon', HW.1=5, HW.2=3, HW.3=6),
  data.frame(name='Charles', HW.1=9, HW.2=7, HW.3=9))
grade.book
```

```
##      name HW.1 HW.2 HW.3
## 1  Alison    8    5    8
## 2 Brandon    5    3    6
## 3 Charles    9    7    9
```

What we want to do is turn this data frame from a *wide* data frame into a *long* data frame. In MS Excel this is called *pivoting*. Essentially I'd like to create a data frame with three columns: `name`, `assignment`, and `score`. That is to say that each homework datum really has three pieces of information: who it came from, which homework it was, and what the score was. It doesn't conceptually matter if I store it as 5 columns or 5 rows so long as there is a way to identify how a student scored on a particular homework. So we want to reshape the HW1 to HW5 columns into two columns (assignment and score).

This package was built by the sample people that created `dplyr` and `ggplot2` and there is a nice introduction at:
http://blog.rstudio.org/2014/07/22/introducing-tidyr/

`gather()` and `spread()`

As with the `dplyr` package, there are two main verbs to remember:

1. Gather - Gather multiple columns that are related into two columns that contain the original column name and the value. For example for columns `HW1`, ..., `HW5` we would gather them into two column `HomeworkNumber` and `Score`. In this case, we refer to `HomeworkNumber` as the key

column and `Score` as the value column. So for any key:value pair you know everything you need.

2. Spread - This is the opposite of gather. Takes a key column (or columns) and a results column and forms a new column for each level of the key column(s).

```
library(tidyr)
# first we gather the score columns into columns we'll name Assesment and Score
tidy.scores <- grade.book %>% gather( Assessement, Score, HW.1:HW.3 )
tidy.scores

##      name Assessement Score
## 1  Alison        HW.1     8
## 2 Brandon        HW.1     5
## 3 Charles        HW.1     9
## 4  Alison        HW.2     5
## 5 Brandon        HW.2     3
## 6 Charles        HW.2     7
## 7  Alison        HW.3     8
## 8 Brandon        HW.3     6
## 9 Charles        HW.3     9
```

To spread the key:value pairs out into a matrix, we use the `spread()` command.

```
# first we gather the score columns into columns we'll name Assesment and Score
tidy.scores %>% spread( Assessement, Score )

##      name HW.1 HW.2 HW.3
## 1  Alison    8    5    8
## 2 Brandon    5    3    6
## 3 Charles    9    7    9
```

7.2 Exercises

Chapter 8

Using R for Statistical Tables

Statistics makes use of a wide variety of distributions and before the days of personal computers, every statistician had books with hundreds and hundreds of pages of tables allowing them to look up particular values. Fortunately in the modern age, we don't need those books and tables, but we do still need to access those values. To make life easier and consistent for R users, every distribution is accessed in the same manner.

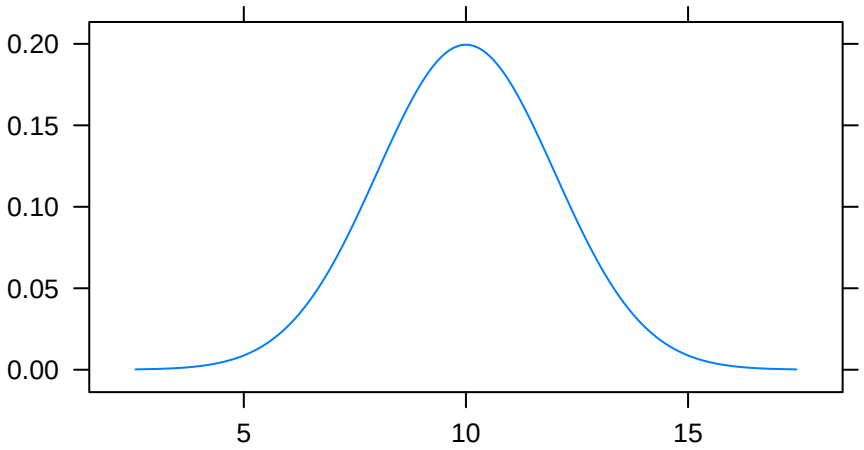
8.1 `mosaic::plotDist()` function

The `mosaic` package provides a very useful routine for understanding a distribution. The `plotDist()` function takes the R name of the distribution along with whatever parameters are necessary for that function and show the distribution. For reference below is a list of common distributions and their R name and a list of necessary parameters.

Distribution	R stem	parameters (and defaults)	parameter interpretation
Binomial	`binom`	`size` `prob`	number of trials probability of success
Poisson	`pois`	`lambda`	mean of the distribution
Exponential	`exp`	`rate`	mean is 1/rate
Normal	`norm`	`mean=0` `sd=1`	mean standard deviation
Uniform	`unif`	`min=0` `max=1`	lower bound upper bound

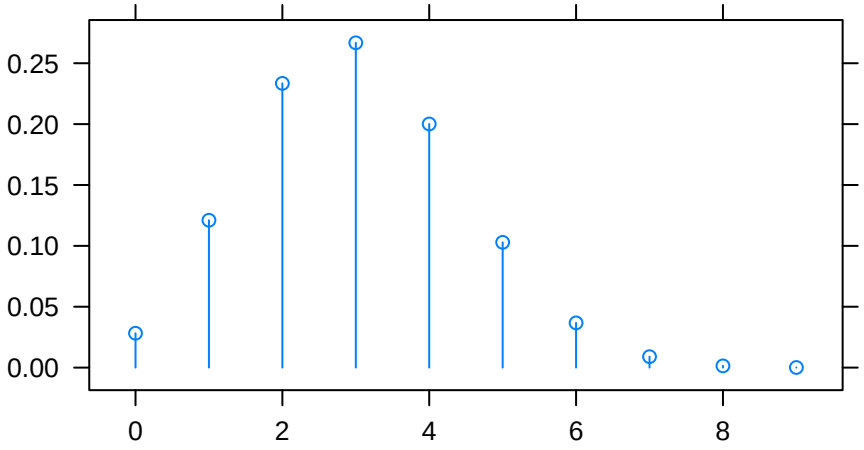
For example, to see the normal distribution with mean $\mu = 10$ and standard deviation $\sigma = 2$, we use

```
library(mosaic)
plotDist('norm', mean=10, sd=2)
```



This function works for discrete distributions as well

```
plotDist('binom', size=10, prob=.3)
```



8.2 Base R functions

All the probability distributions available in R are accessed in exactly the same way, using a `d-function`, `p-function`, `q-function`, and `r-function`. For the rest of this section suppose that X is a random variable from the distribution of interest and x is some possible value that X could take on.

Function	Result
`d-function(x)`	the height of the probability distribution at x
`p-function(x)`	$P(X \leq x)$
`q-function(q)`	x such that $P(X \leq x) = q$
`r-function(n)`	n random observations from the distribution

Notice that the `p-function` is the inverse of the `q-function`.

For each distribution in R, there will be be this set of functions but we replace the "-function" with the distribution name or a shortened version. `norm, exp, binom, t, f` are the names for the normal, exponential, binomial, T and F distributions. Furthermore, most distributions have additional parameters that define the distribution and will also be passed as arguments to these functions, although, if a reasonable default value for the parameter exists, there will be a default.

8.2.1 d-function

The purpose of the d-function is to calculate the height of a probability mass function or a density function.

We start with an example of the Binomial distribution. For $X \sim Binomial\,(n = 10, \pi = .2)$ suppose we wanted to know $P(X = 0)$? We know the probability mass function is

$$P(X = x) = \binom{n}{x} \pi^x (1 - \pi)^{n-x}$$

thus

$$\begin{aligned} P(X = 0) &= \binom{10}{0} 0.2^0 (0.8)^{10} \\ &= 1 \cdot 1 \cdot 0.8^{10} \\ &\approx 0.107 \end{aligned}$$

but that calculation is fairly tedious. To get R to do the same calculation, we just need the height of the probability mass function at 0. To do this calculation, we need to know the x value we are interested in along with the distribution parameters n and π.

The first thing we should do is check the help file for the binomial distribution functions to see what parameters are needed and what they are named.

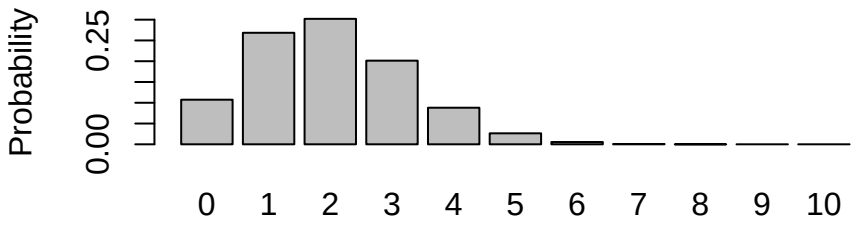
```
?dbinom
```

The help file shows us the parameters n and π are called `size` and `prob` respectively. So to calculate the probability that $X = 0$ we would use the following command:

```
dbinom(0, size=10, prob=.2)

## [1] 0.1073742
```

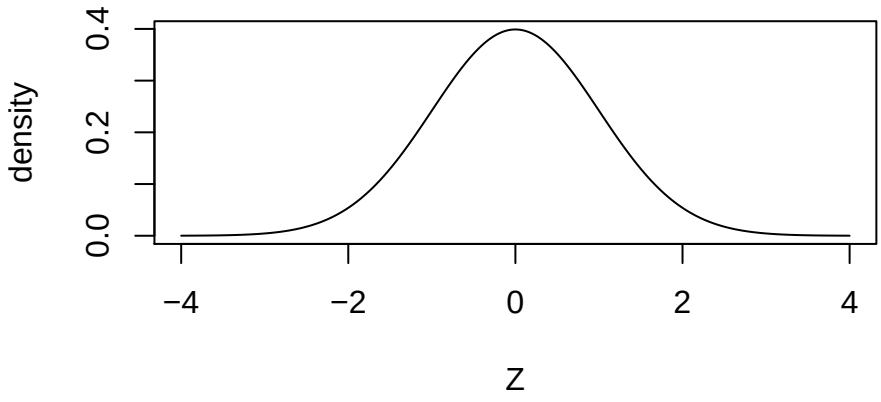
To graph all the probabilities (from 0 to 10 successes) we can do the following:

```r
# Plotting Binomial(n=10, p=.2) distribution
x <- 0:10
heights <- dbinom(x, size=10, prob=.2)
barplot(heights, names.arg=x, ylab='Probability')
```



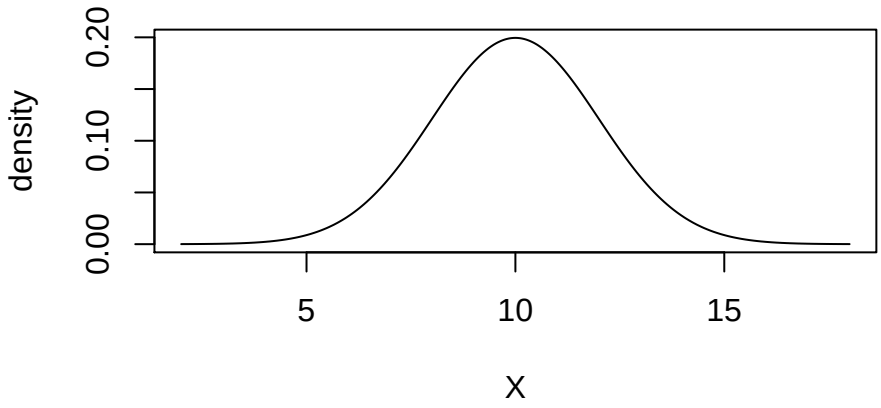
Next we plot the Standard Normal distribution using `dnorm()` to give use the height of the density function. Notice I haven't given the mean and standard deviation to the `dnorm()` function. If I don't specify anything, R will default to using `mean=0` and `sd=1`.

```r
# Plotting a standard normal distribution
z <- seq(-4,4,by=.01) # grid of 801 z values
heights <- dnorm(z)   # get density value for each
plot(z, heights, type='l', ylab='density', xlab='Z') # make a plot
```



In the previous plot, we essentially drew the line by asking R to "connect the dots" and we had *a lot* of dots, so the graph looks very smooth. We will cover more about graphing in later chapters. We could make a similar plot of a non-standard normal as well.

```
# Plotting a non-standard normal distribution
x <- seq(2,18,length=801)             # grid of 801 x values
heights <- dnorm(x, mean=10, sd=2)    # get density value for each
plot(x, heights, type='l', ylab='density', xlab='X') # make a plot
```



8.2.2 p-function

Often we are interested in the probability of observing some value or anything less. P-values will be calculated this way, so we want a nice easy way to do this.

To start our example with the binomial distribution, again let $X \sim Binomial\,(n = 10, \pi = 0.2)$. Suppose I want to know what the probability of observing a 0, 1, or 2? That is, what is $P\,(X \leq 2)$? I could just find the probability of each and add them up.

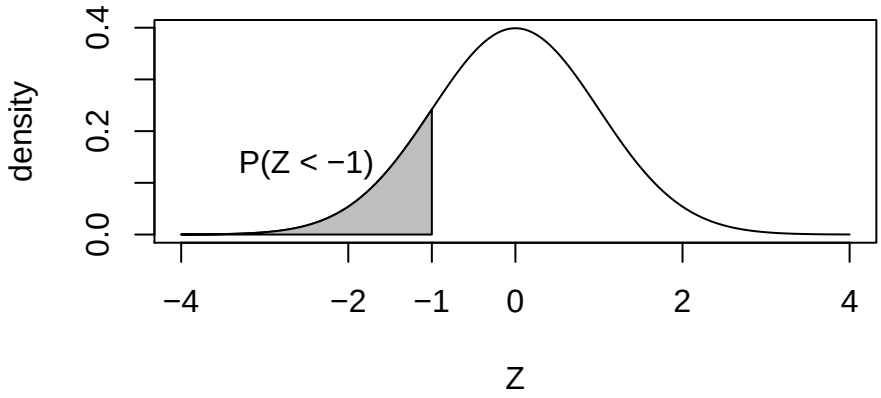
```
dbinom(0, size=10, prob=.2)   +
  dbinom(1, size=10, prob=.2) +
  dbinom(2, size=10, prob=.2)

## [1] 0.6777995
```

but this would get tedious for binomial distributions with a large number of trials. The shortcut is to use the `pbinom()` function.

```
pbinom(2, size=10, prob=.2)

## [1] 0.6777995
```

For discrete distributions, you must be careful because R will give you the probability of *less than or equal to 2*. If you wanted less than two, you should use `dbinom(1,10,.2)`.

The normal distribution works similarly. Suppose for $Z \sim N\,(0, 1)$ and we wanted to know $P\,(Z \leq -1)$?



The answer is easily found via `pnorm()`

```
pnorm(-1)

## [1] 0.1586553
```

Notice for continuous random variables, the probability $P(Z = -1) = 0$ so we can ignore the issue of "less than" vs "less than or equal to".

Often times we will want to know the probability of *greater than* some value. That is, we might want to find $P(Z \geq 1)$. For the normal distribution, there are a number of tricks we could use. Notably

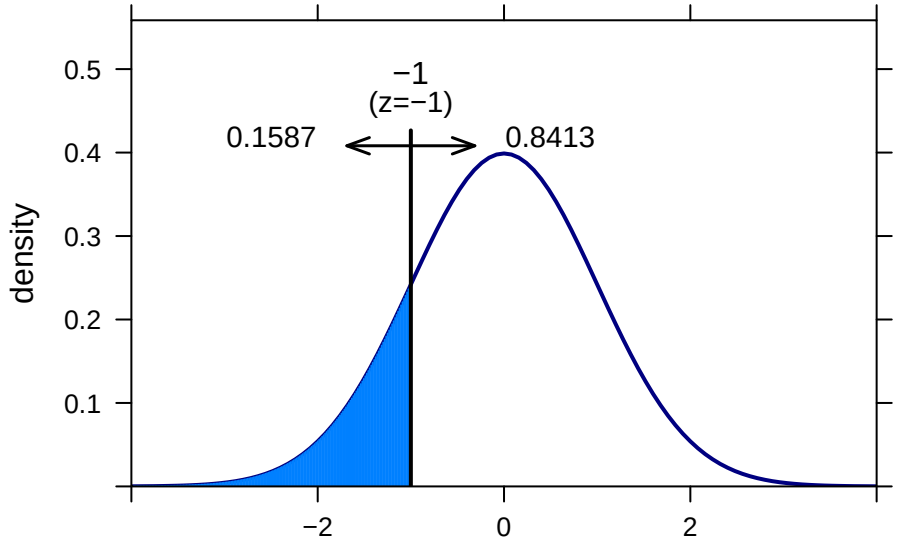
$$P(Z \geq -1) \quad = \quad P(Z \leq 1) = 1 - P(Z < -1)$$

but sometimes I'm lazy and would like to tell R to give me the area to the right instead of area to the left (which is the default). This can be done by setting the argument `lower.tail=FALSE`.

The `mosaic` package includes an augmented version of the `pnorm()` function called `xpnorm()` that calculates the same number but includes some extra information and produces a pretty graph to help us understand what we just calculated and do the tedious "1 minus" calculation to find the upper area.[1]

[1] Unfortunately this `x`-variant only exists for the normal distribution.

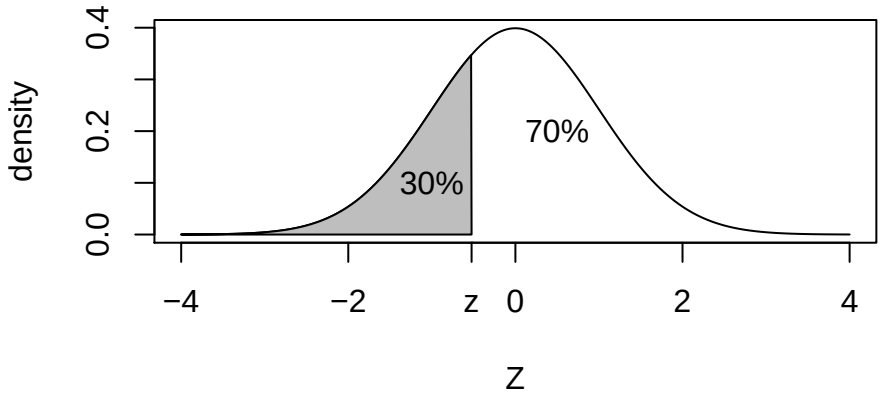
```
library(mosaic)
xpnorm(-1)

##
## If X ~ N(0,1), then
##
##  P(X <= -1) = P(Z <= -1) = 0.1587
##  P(X >  -1) = P(Z >  -1) = 0.8413
```




```
## [1] 0.1586553
```

8.2.3 q-function

In class, we will also find ourselves asking for the quantiles of a distribution. For example, I might want to find the 0.30 quantile, which is the value such that 30% of the distribution is less than it, and 70% is greater. Mathematically, I wish to find the value z such that $P(Z < z) = 0.30$.

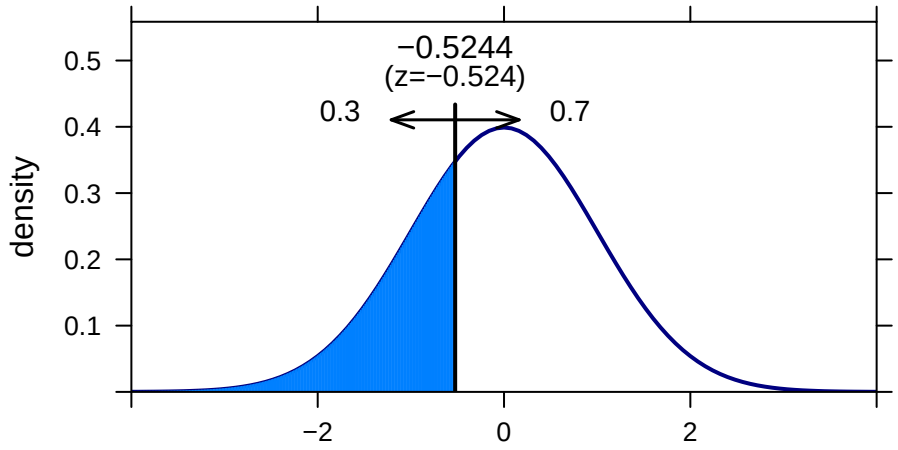


To find this value in the tables in the book, we use the table in reverse. R gives us a handy way to do this with the `qnorm()` function.

```
qnorm(0.30)

## [1] -0.5244005

# if we take that and stuff it back into the
# pnorm() function, we should get 0.30 back out again
pnorm(-0.5244005)

## [1] 0.3
```

The `mosaic` package also provides an augmented version of the `qnorm()` function named `xqnorm()` that calculates the same value but also includes a nice graph to help us understand what we just calculated.

```
xqnorm(0.30)

##  P(X <= -0.524400512708041) = 0.3
##  P(X >  -0.524400512708041) = 0.7
```




```
## [1] -0.5244005
```

8.2.4 r-function

Finally, I often want to be able to generate random data from a particular distribution. R does this with the r-function. The first argument to this function the number of random variables to draw and any remaining arguments are the parameters of the distribution.

```
rnorm(5, mean=20, sd=2)

## [1] 22.76926 18.64821 15.94490 19.99659 20.69094

rbinom(4, size=10, prob=.8)

## [1] 10 10  9  9
```

8.3 Exercises

1. We will examine how to use the probability mass functions (a.k.a. d-functions) and cumulative probability function (a.k.a. p-function) for the Poisson distribution.

   (a) Create a graph of the distribution of a Poisson random variable with rate parameter $\lambda = 2$ using the `mosaic` function `plotDist()`.

   (b) Calculate the probability that a Poisson random variable (with rate parameter $\lambda = 2$) is exactly equal to 3 using the `dpois()` function. Be sure that this value matches the graphed distribution in part (a).

   (c) For a Poisson random variable with rate parameter $\lambda = 2$, calculate the probability it is less than or equal to 3, by summing the four values returned by the Poisson d-function.

(d) Perform the same calculation as the previous question but using the cumulative probability function `ppois()`.

2. We will examine how to use the cumulative probability functions (a.k.a. p-functions) for the normal distributions.

   (a) Use the `mosaic` function `plotDist()` to produce a graph of the standard normal distribution.

   (b) For a standard normal, use the `pnorm()` function or its `mosaic` augmented version `xpnorm()` to calculate

      i. $P(Z < -1)$
      ii. $P(Z \geq 1.5)$

   (c) Use the `mosaic` function `plotDist()` to produce a graph of an exponential distribution with `rate` parameter 2.

   (d) Suppose that $Y \sim Exp(2)$, as above, use the `pexp()` function to calculate $P(Y \leq 1)$.

3. We next examine how to use the quantile functions for the normal and exponential distributions using R's q-functions.

   (a) Find the value of a standard normal distribution ($\mu = 0$, $\sigma = 1$) such that 5% of the distribution is to the left of the value using the `qnorm()` function or the `mosaic` augmented version `xqnorm()`.

   (b) Find the value of an exponential distribution with rate 2 such that 60% of the distribution is less than it using the `qexp()` function.

4. Finally we will look at generating random deviates from a distribution.

   (a) Generate a value of 1 from a uniform distribution with minimum 0, and maximum 1 using the `runif()` function. Repeat this step several times and confirm you are getting different values each time.

   (b) Generate a sample of size 20 from the same uniform distribution and save it as a column in a data frame. Then produce a histogram of the sample using the `mosaic` function `histogram()`.

   (c) Generate a sample of 2000 from a normal distribution with `mean=10` and standard deviation `sd=2` using the `rnorm()` function. Create a histogram the the resulting sample.

Chapter 9

Graphing using `ggplot2`

There are three major "systems" of making graphs in R. The basic plotting commands in R are quite effective but the commands do not have a way of being combined in easy ways. Lattice graphics (which the `mosaic` package uses) makes it possible to create some quite complicated graphs but it is very difficult to do make non-standard graphs. The last package, `ggplot2` tries to not anticipate what the user wants to do, but rather provide the mechanisms for pulling together different graphical concepts and the user gets to decide elements to combine.

To make the most of `ggplot2` it is important to wrap your mind around "The Grammar of Graphics". The act of building a graph can be broken down into three steps.

1. Define what data we are using.
2. What is the major relationship we wish to exam.
3. Third, in what way should we present that relationship. These relationships can be presented in multiple ways, and the process of creating a good graph relies on building layers upon layers of information. For example, we might start with printing the raw data and then overlay a regression line over the top.

Next, it should be noted that `ggplot2` is designed to act on data frames. It is actually hard to just draw three data points and for simple graphs (like I might make for a lecture) I prefer to use the base graphing system in R. However for any real data analysis project, the data will already be in a data frame and this is not an annoyance.

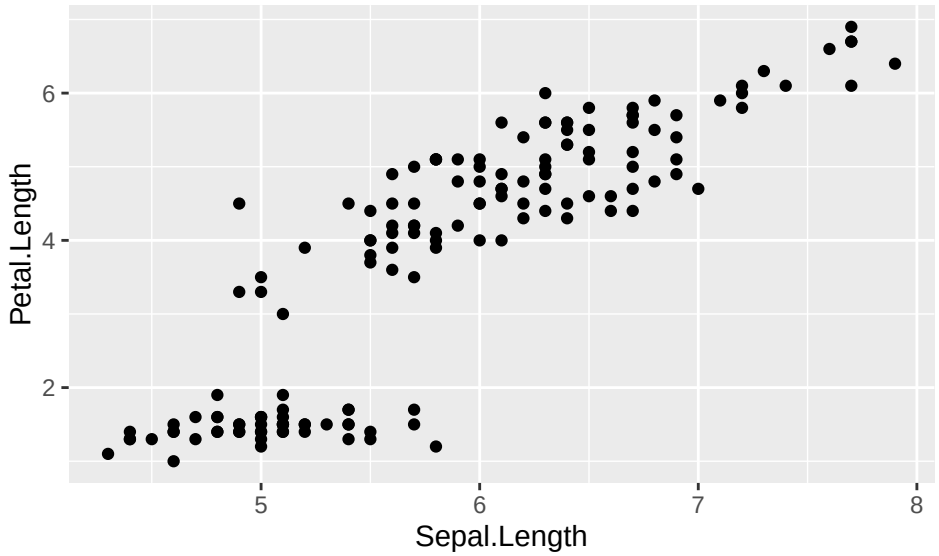
These notes are in no sufficient for graphing, particularly with `ggplot2`. There are many places online to get help with `ggplot2`. One very nice resource is the website http://www.cookbook-r.com/Graphs/ which gives much of the information available in the book *R Graphics Cookbook* which I highly recommend. Second is just googling your problems and see what you can find on websites such as StackExchange.

In this chapter we will use three different data sets. The first is the `iris` data that shows the dimensions of petals and sepals for three varieties of iris. The `mtcars` dataset shows some cars from a *Motor Trend* magazine and gives information about gas efficiency, number of cylinders, volume of cylinders, etc. Finally the `diamond` data set looks at the price versus a number of other covariates such as carats, cut, and clarity of the diamond.

9.1 A simple scatterplot

To start with, we'll make a very simple scatterplot using the `iris` dataset that will make a scatterplot of `Sepal.Length` versus `Petal.Length`.

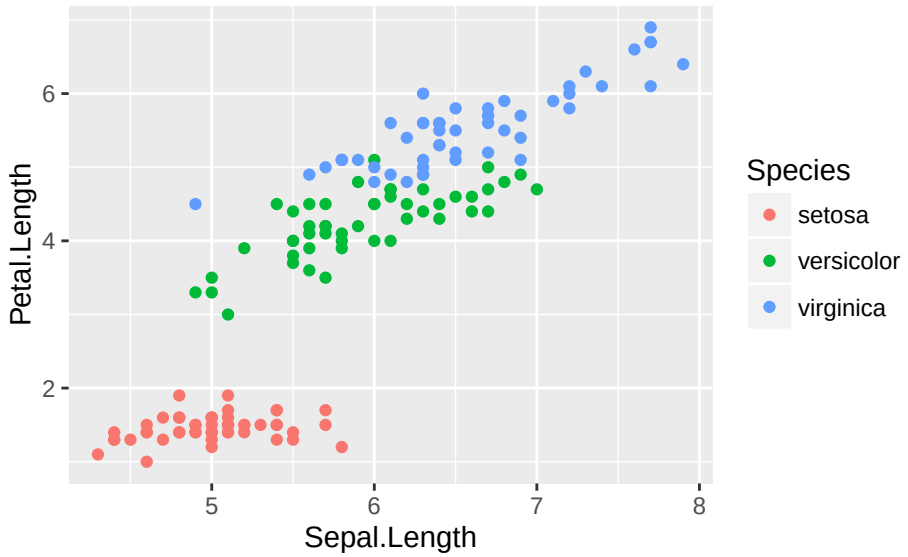
```
library(ggplot2)
ggplot( data=iris, aes(x=Sepal.Length, y=Petal.Length) ) +
        geom_point(  )
```



1. The data set we wish to use is specified using `data=iris`.
2. The relationship we want to explore is `x=Sepal.Length` and `y=Petal.Length`. This means the x-axis will be the Sepal Length and the y-axis will be the Petal Length.
3. The way we want to display this relationship is through graphing 1 point for every observation.

We can define other attributes that might reflect other aspects of the data. For example, we might want for the of the data point to change dynamically based on the species of iris.

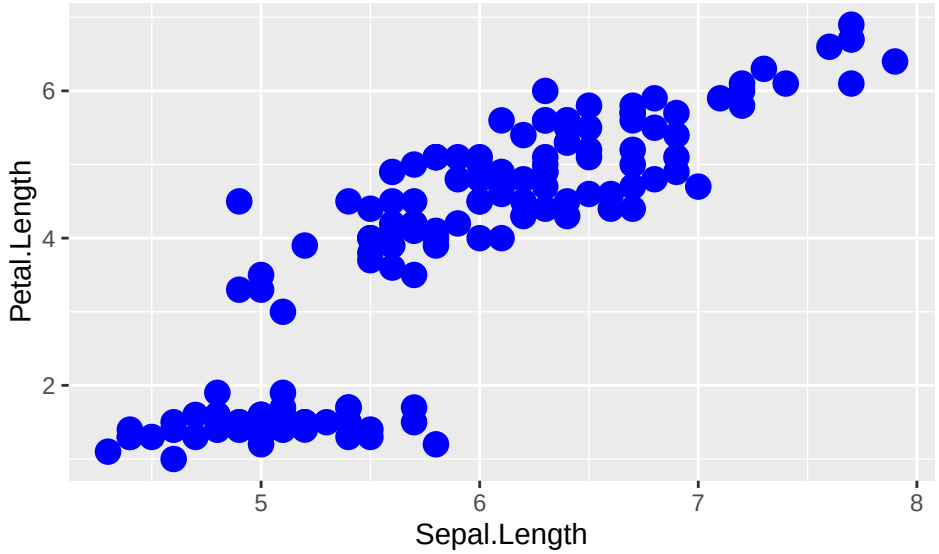
```
ggplot( data=iris, aes(x=Sepal.Length, y=Petal.Length, color=Species) ) +
        geom_point(  )
```



The `aes()` command inside the previous section of code is quite mysterious. The way to think about the `aes()` is that it gives you a way to define relationships that are data dependent. In the

previous graph, the x-value and y-value for each point was defined dynamically by the data, as was the color. If we just wanted all the data points to be colored blue and larger, then the following code would do that

```
ggplot( data=iris, aes(x=Sepal.Length, y=Petal.Length) ) +
        geom_point( color='blue', size=4 )
```



The important part isn't that `color` and `size` were defined in the `geom_point()` but that they were defined *outside of an `aes()` function!*

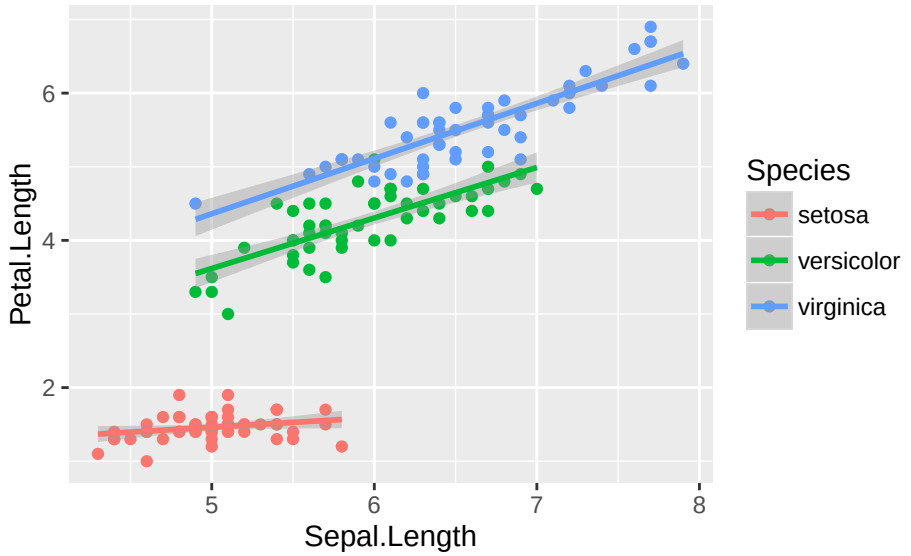
1. Anything set inside an `aes()` command will be of the form `attribute=Column_Name` and will change based on the data.
2. Anything set outside an `aes()` command will be in the form `attribute=value` and will be fixed.

Next, I suppose I want to add a regression line[1] to each of these groups. We can do this by adding another layer to the graph, in this case, a `smoother` layer. The `geom_smoother` is intended to take a scatterplot of points and draw the best-fitting curve to the data. There are several options for how it choses to do this, but I'll tell it to fit a regression line to each set of data. Below, we have a graph of data points, a regression line, *and* a confidence region for the line[2].

[1] The line that best summarizes the relationship between `Sepal.Length` and `Petal.Length`.

[2] I typically don't use this method because it has too many limitations as to how I fit the smoother. I prefer to fit a model to the data and calculate the predicted values along with whatever confidence intervals I want and plot those directly using `geom_ribbon()`.

```
ggplot( data=iris, aes(x=Sepal.Length, y=Petal.Length, color=Species) ) +
  geom_point( ) +
  geom_smooth( method='lm' ) # fit a regression to each species
```



9.2 Geometries

One way that ggplot2 makes it easy to form very complicated graphs is that it provides a large number of basic building blocks that, when stacked upon each other, can produce extremely complicated graphs. A full list is available at http://docs.ggplot2.org/current/ but the following list gives some idea of different building blocks.

Geom	Description
geom_bar	A barplot
geom_boxplot	Boxplots
geom_density	A smoothed histogram
geom_errorbar	Error bars
geom_histogram	A histogram
geom_line	Draw a line (after sorting x-values)
geom_path	Draw a line (without sorting x-values)
geom_point	Draw points (for a scatterplot)
geom_ribbon	Enclose a region, and color the interior
geom_smooth	Add a ribbon that summarizes a scatterplot
geom_text	Add text to a graph

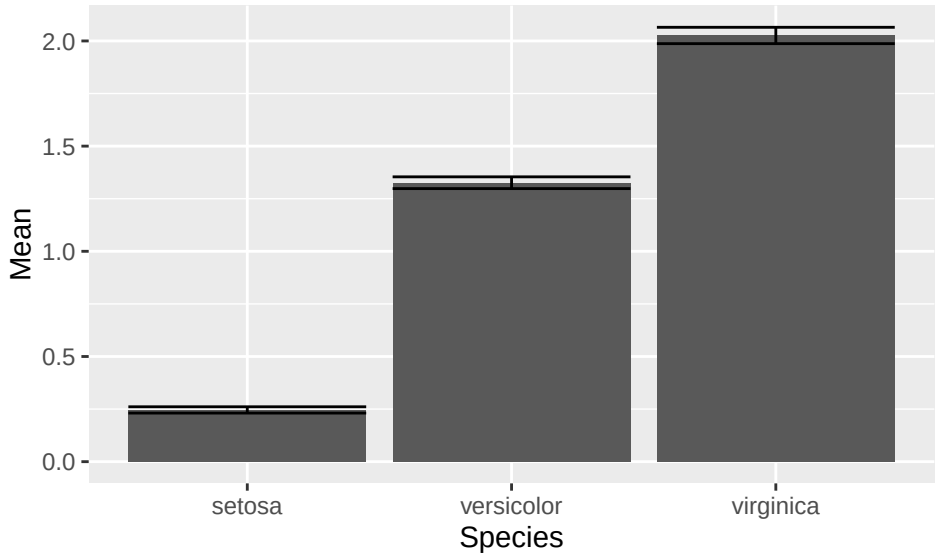
9.2.1 Bar plots

These different geometries are different ways to display the relationship between variables and can be combined in many interesting ways. Suppose that you just want make some barplots and add ± S.E. bars. This should be really easy to do, but in the base graphics in R, it is a pain. Fortunately in ggplot2 this is easy. First, define a data frame with the bar heights you want to graph and the ± values you wish to use.

```
# Calculate the mean and sd of the Petal Widths for each species
library(dplyr)
stats <- iris %>%
  group_by(Species) %>%
  summarize( Mean = mean(Petal.Width),                    # Mean   = ybar
             StdErr = sd(Petal.Width)/sqrt(n()) ) %>%  # StdErr = s / sqrt(n)
  mutate( lwr = Mean - StdErr,
          upr = Mean + StdErr )
stats

## Source: local data frame [3 x 5]
##
##      Species  Mean     StdErr       lwr       upr
##       (fctr) (dbl)      (dbl)     (dbl)     (dbl)
## 1     setosa 0.246 0.01490377 0.2310962 0.2609038
## 2 versicolor 1.326 0.02796645 1.2980335 1.3539665
## 3  virginica 2.026 0.03884138 1.9871586 2.0648414
```

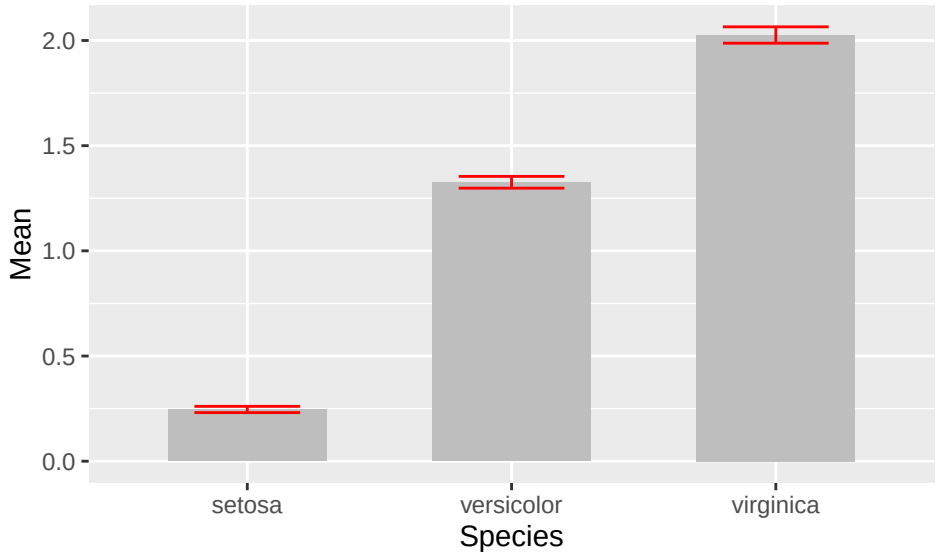
Next we take these summary statistics and define the following graph which makes a bar graph of the means and error bars that are ± 1 estimated standard deviation of the mean (usually referred to as the *standard errors* of the means). By default, `geom_bar()` tries to draw a bar plot based on how many observations each group has. What I want, though, is to draw bars of the height I specified, so to do that I have to add `stat='identity'` to specify that it should just use the heights I tell it.

```
ggplot(stats, aes(x=Species)) +
  geom_bar( aes(y=Mean), stat='identity') +
  geom_errorbar( aes(ymin=lwr, ymax=upr) )
```



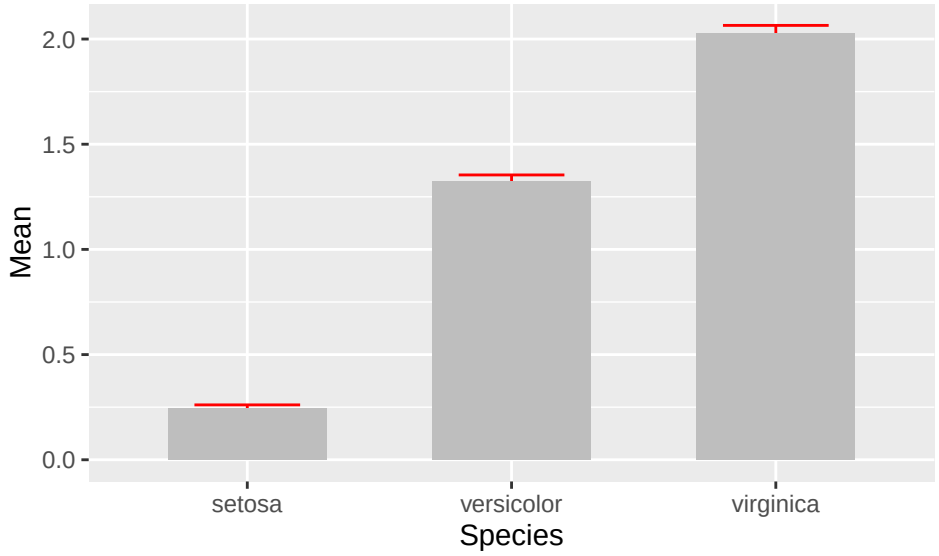
While this isn't too bad, we would like to make this a bit more pleasing to look at. Each bars is a little too wide and the error bars should be a tad narrower than then bar. Also, the fill color for the bars is too dark. So I'll change all of these, by setting those attributes *outside of an* `aes()` *command.*

```
ggplot(stats, aes(x=Species)) +
  geom_bar( aes(y=Mean), stat='identity', fill='grey', width=.6) +
  geom_errorbar( aes(ymin=lwr, ymax=upr), color='red', width=.4 )
```



The last thing to notice is that the *order* in which the different layers matter. This is similar to photoshop or GIS software where the layers added last can obscure prior layers. In the graph below, the lower part of the error bar is obscured by the grey bar.

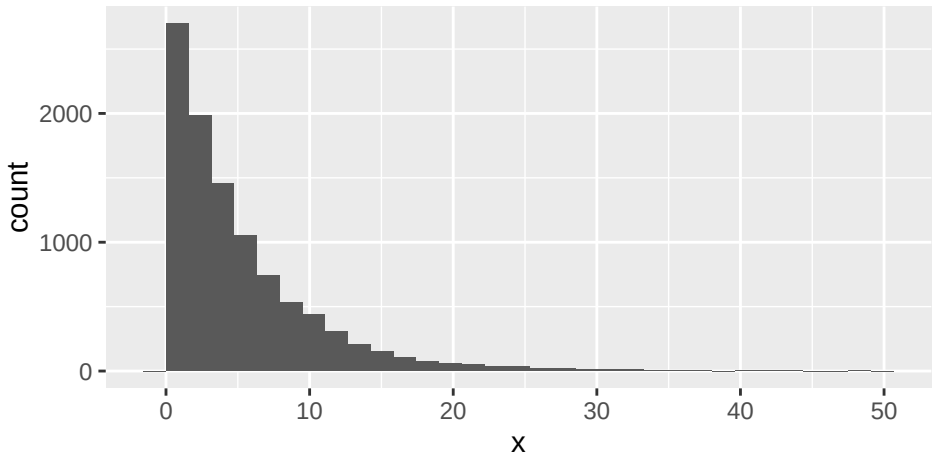
```
ggplot(stats, aes(x=Species)) +
  geom_errorbar( aes(ymin=lwr, ymax=upr), color='red', width=.4 ) +
  geom_bar( aes(y=Mean), stat='identity', fill='grey', width=.6)
```



9.2.2 Histograms

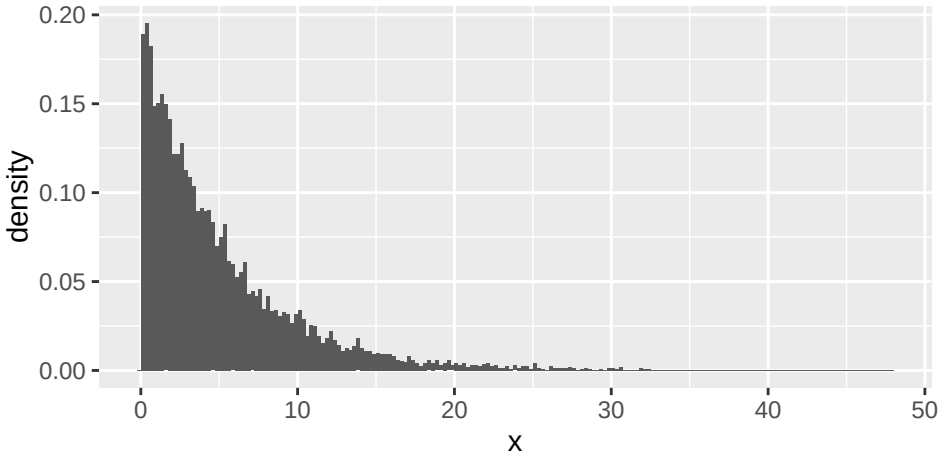
Creating histograms of continuous data is a very common thing to do. The simplest way to do this in `ggplot()` is using the `geom_histogram` function. The simplest form is the the following:

```
data <- data.frame(x=rexp(10000, rate=1/5))
ggplot(data, aes(x=x)) +
  geom_histogram()

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



Somewhat annoyingly, `ggplot2` does not include an easy way for use intelligent choices for how many bins to use.[3] Instead we are stuck investigating different bin widths by hand. To do this, we can set the number of bins via the `binwidth` argument. Notice that the y-axis is the number of observations in each bin. If we want the y-axis to be *density*[4] we just need to tell `geom_histogram` to have `y=..density..` instead of the default.

```
ggplot(data, aes(x=x, y=..density..)) +
  geom_histogram(binwidth=.25)
```

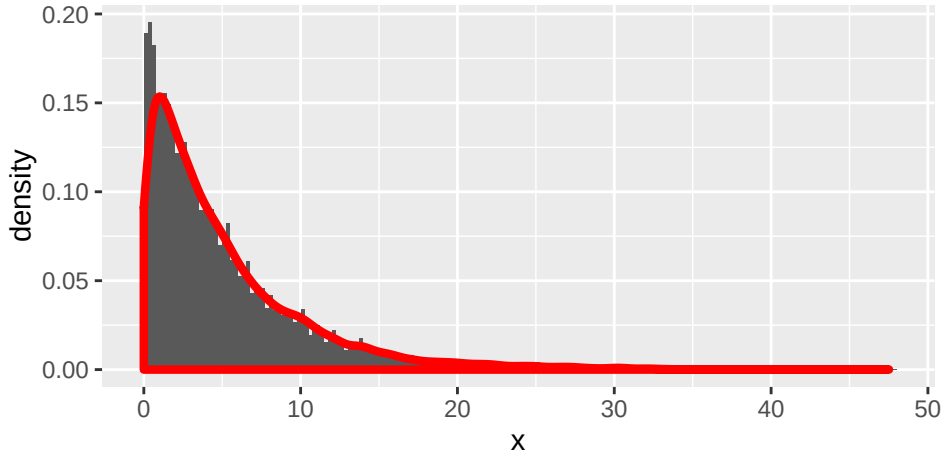


Often I want to also add some sort of smoothed density plot to my histogram. The geom to do that is `geom_density()` which takes your x-values and creates a smoothed density function using kernel density algorithm with a normal kernel. To do this, we need both layers of my plot to have a y-axis of density.

[3] To use Scott's rule or Freedman-Draconis rule and we have to calculate those by hand. Letting the binwidth by $\hat{h}$ these are $\hat{h}_S = 3.49\hat{\sigma}n^{-1/3}$ and $\hat{h}_{FD} = 2 * IQR * n^{-1/3}$ where $\hat{\sigma}$ is the standard deviation of the observations plotted and IQR is the inter-quartile range.

[4] So that the area shaded has area 1, so that when I compare a distribution to the data, the y-axes are on the same scale.

```
ggplot(data, aes(x=x, y=..density..)) +
  geom_histogram(binwidth=.25) +
  geom_density(color='red', size=1.5)
```

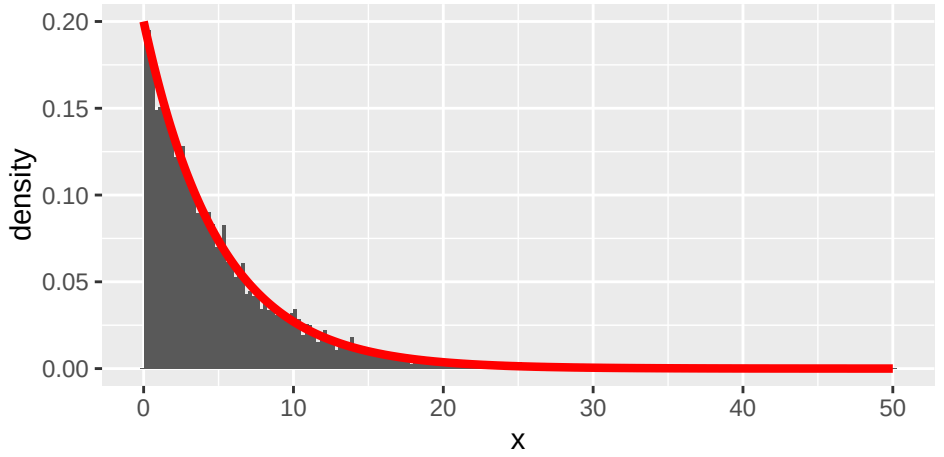


In this case, we know the distribution the data came from, so we add the exponential distribution that the data was drawn from over the top of the histogram, mostly to demonstrate building a plot layer by layer. We first need to create another data frame that has the distribution we wish to plot.

```
x <- seq(0, 50, by=0.1)
y <- dexp(x, rate=1/5)
density.data <- data.frame(x=x, y=y)
```

Now to build our plot, we first by creating the histogram, and then add the layer with the exponential distribution on top. Notice that we must pass the data frame in which we stored the density information to the `geom_line()` function because the data we are using for this graph are in two different data frames.

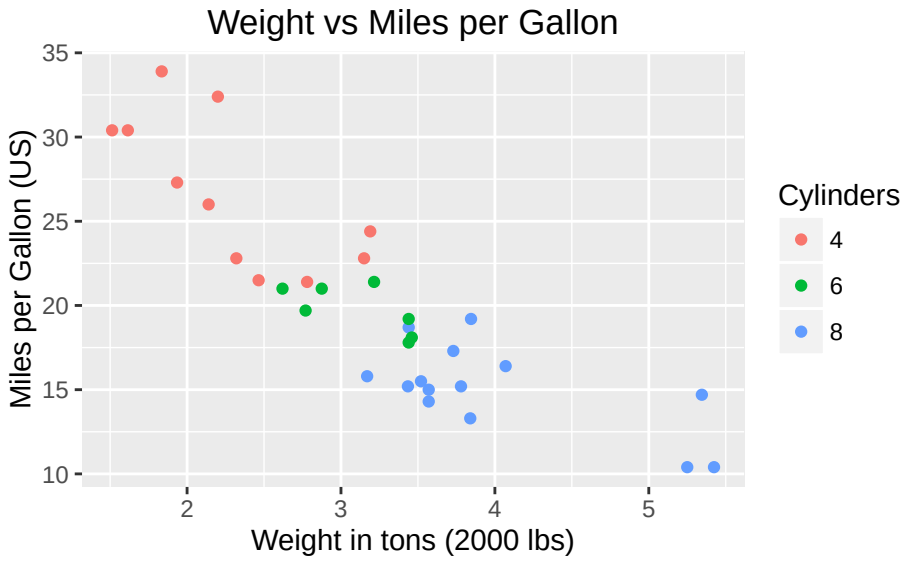
```
ggplot(data, aes(x=x)) +
  geom_histogram(aes(y=..density..), binwidth=.25) +
  geom_line( data=density.data, aes(x=x, y=y),
             color='red', size=1.5 )
```



9.3 Adjusting labels

To make a graph more understandable, it is necessary to tweak labels for the axes and add a main title and such. Here we'll adjust labels in a graph, including the legend labels.

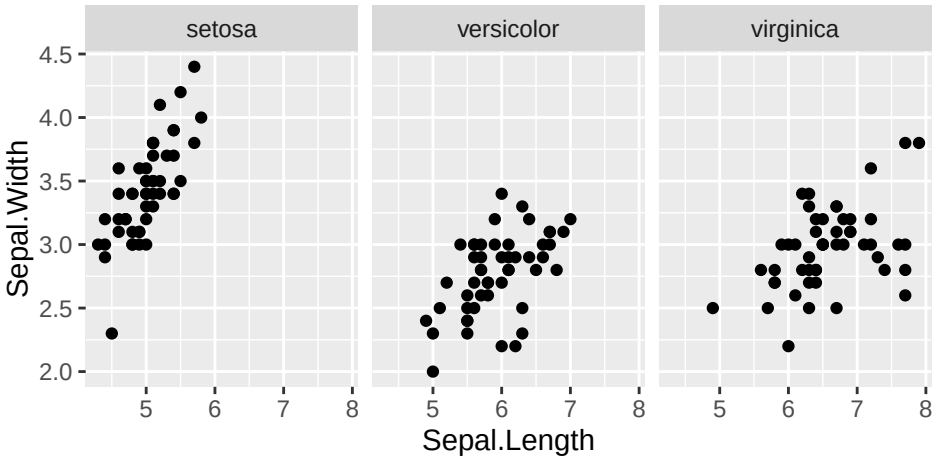
```
# Treat the number of cylinders in a car as a
# categorical variable (4,6 or 8)
mtcars$cyl <- factor(mtcars$cyl)
ggplot(mtcars, aes(x=wt, y=mpg, col=cyl)) +
   geom_point() +
  labs( title='Weight vs Miles per Gallon') +
  labs( x="Weight in tons (2000 lbs)" ) +
  labs( y="Miles per Gallon (US)") +
  labs( color="Cylinders")
```



9.4 Faceting

The goal with faceting is to make many panels of graphics where each panel represents the same relationship between variables, but something changes between each panel. For example using the `iris` dataset we could look at the relationship between `Sepal.Length` and `Petal.Length` either with all the data in one graph, or one panel per species.

```
library(ggplot2)
ggplot(iris, aes(x=Sepal.Length, y=Sepal.Width)) +
  geom_point() +
  facet_grid( . ~ Species )
```



The line `facet_grid( formula )` tells `ggplot2` to make panels, and the formula tells how to orient the panels. Recall that a formula is always in the order `y ~ x` and because I want the species to change as we go across the page, but don't have anything I want to change vertically we use `. ~ Species` to represent that. If we had wanted three graphs stacked then we could use `Species ~ .`.

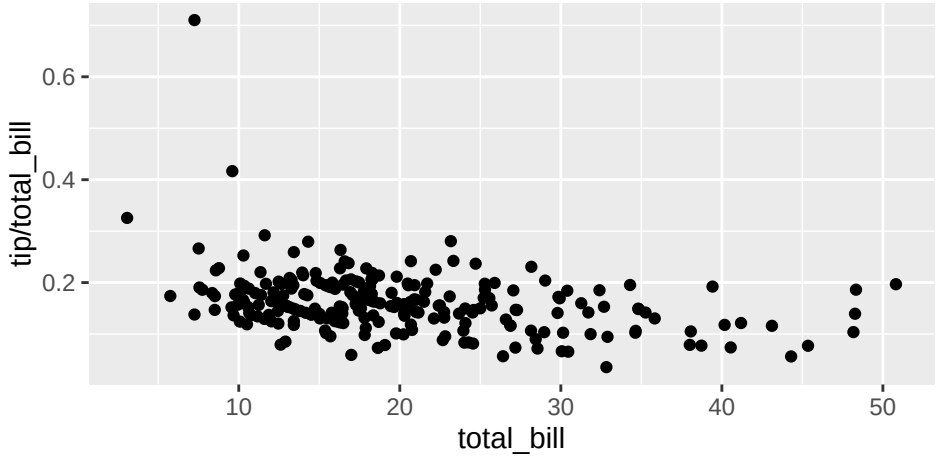
For a second example, we look at a dataset that examines the amount a waiter was tipped by 244 parties. Covariates that were measured include the day of the week, size of the party, total amount of the bill, amount tipped, whether there were smokers in the group[5] and the gender of the person paying the bill[6]

```
library(reshape2)
data(tips)
head(tips)

##   total_bill  tip    sex smoker day   time size
## 1      16.99 1.01 Female     No Sun Dinner    2
## 2      10.34 1.66   Male     No Sun Dinner    3
## 3      21.01 3.50   Male     No Sun Dinner    3
## 4      23.68 3.31   Male     No Sun Dinner    2
## 5      24.59 3.61 Female     No Sun Dinner    4
## 6      25.29 4.71   Male     No Sun Dinner    4
```

It is easy to look at the relationship between the size of the bill and the percent tipped.

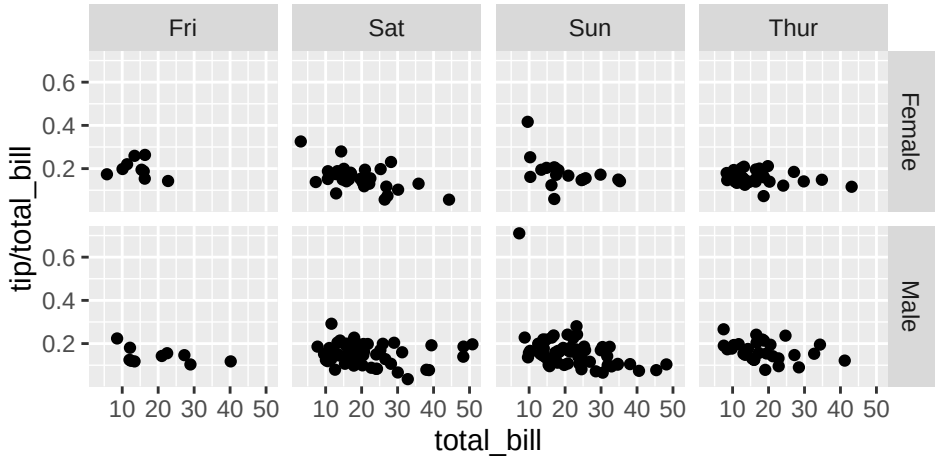
[5] Old data set when smoking in restaurants was allowed.
[6] Mis-labeled as `sex`.

```
# make a graph and save it as an object
p2 <- ggplot(tips, aes(x = total_bill, y = tip / total_bill )) +
  geom_point()
# Now print the graph
p2
```



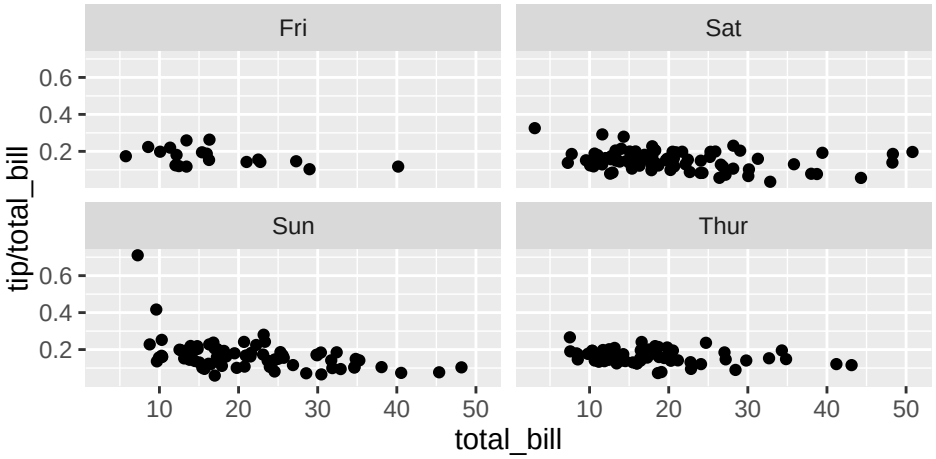
Next we ask if there is a difference in tipping percent based on gender or day of the week by plotting this relationship for each combination of gender and day.

```
p2 + facet_grid( sex ~ day )
```



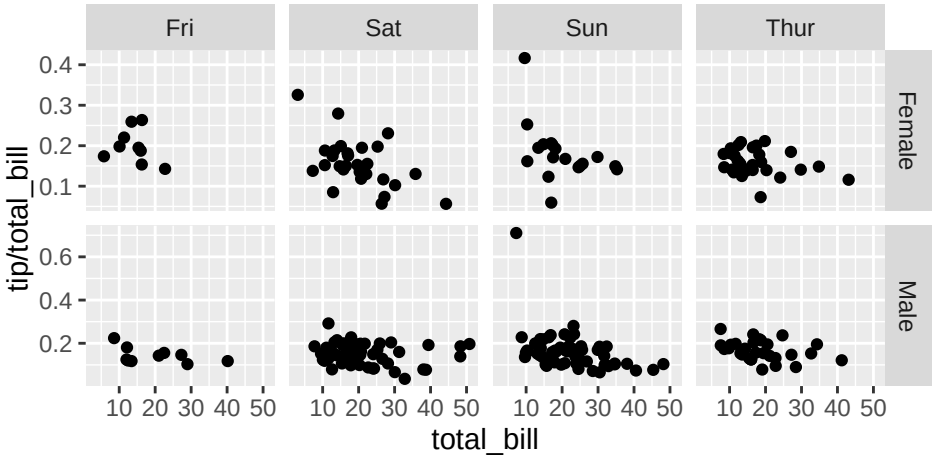
Sometimes we want multiple rows and columns of facets, but there is only one categorical variable with many levels. In that case we use `facet_wrap` which takes a one-sided formula.

```
p2 + facet_wrap( ~ day )
```



Finally we can allow the x and y `scales` to vary between the panels by setting "`free`", "`free_x`", or "`free_y`". In the following code, the y-axis scale changes between the gender groups.

```
p2 + facet_grid( sex ~ day, scales="free_y" )
```



9.5 Exercises

1. The `mosaic` package includes a function that allows for a point and click interface to building a graph in `ggplot2`. The point of the `mplot()` command is to allow you to do some point and click selection to build a graph and then click the button that produces the R commands that produced the graph. You then copy and past the R commands into your markdown file. Once you know the ggplot2 system better, you won't ever bother with `mplot()`, you'll just type it in directly. Until then it is nice to have some help in formatting the plotting commands.

   (a) Load the `mosaic` library.

   ```
   library(mosaic)
   ```

   (b) For the dataset `trees`, which should already be pre-loaded[7], we wish to build a scatterplot that compares the height and girth of these cherry trees to the volume of lumber that was

[7] Look at the help file `?trees` for more information about this data set.

produced. The `mosaic` function `mplot()` will allow you to explore many different ways of visualizing the data. Run the command

```
library(mosaic)
mplot(trees)
```

and create a graph using `ggplot2` with `Height` on the x-axis, `Volume` on the y-axis, and `Girth` as the either the size of the data point or the color of the data point.

(c) Have `mplot()` produce the code to produce this graph and copy that code into your RMarkdown file for this lab. Because `mplot()` *requires* user input via the mouse, it is a pointless command for a document that will be printed and will cause an error when you try to knit your results. Instead you'll use `mplot()` to help produce the code for a graphic, and then do any final tweaking on the graph that is necessary. In your write up, I would recommend that you include the `mplot()` command so that you can go back and remember how it was called but then comment it out using the '#' character.

(d) Add appropriate labels for the x and y axes along with a title.

2. Consider the following small dataset that represents the number of times per day my wife plays "Ring around the Rosy" with my daughter relative to the number of days since she has learned this game. The column `yhat` represents the best fitting line through the data, and `lwr` and `upr` represent a 95% confidence interval for the predicted value on that day.[8]

```
Rosy <- data.frame(
  times = c(15, 11, 9, 12, 5, 2, 3),
  day   = 1:7,
  yhat  = c(14.36, 12.29, 10.21, 8.14,
              6.07,  4.00,  1.93),
  lwr   = c(9.54,  8.5, 7.22, 5.47, 3.08,
            0.22, -2.89),
  upr   = c(19.18, 16.07, 13.2, 10.82,
              9.06,  7.78,  6.75))
```

(a) Using `ggplot()` and `geom_point()`, create a scatterplot with `day` along the x-axis and `times` along the y-axis.

(b) Add a line to the graph where the x-values are the `day` values but now the y-values are the predicted values which we've called `yhat`. Notice that you have to set the aesthetic `y=times` for the points and `y=yhat` for the line. Because each `geom_` will accept and `aes()` command, you can specify the y attribute to be different for different layers of the graph.

(c) Add a ribbon that represents the confidence region of the regression line. The `geom_ribbon()` function requires and `x, ymin, ymax` columns to be defined inside an `aes()` command. For the `x=day`, `ymin=lwr`, and `ymax=upr`.

(d) What happened when you added the ribbon? Did some points get hidden? If so, why?

(e) Reorder the statements that created the graph so that the ribbon is on the bottom and the data points are on top and the regression line is visible.

(f) The color of the ribbon `fill` is ugly. Use google to find a list of named colors available to `ggplot2`. For example, I googled "ggplot2 named colors" and found the following link: http://sape.inf.usi.ch/quick-reference/ggplot2/colour. Choose a color for the fill that is pleasing to you.

[8] This is actually a repeated measures study because we are taking repeated observations on the same child so this analysis is *way* too simplistic, but our purpose here is just to make a pretty graph.

(g) Add labels for the x-axis and y-axis that are appropriate along with a main title.

3. We'll next make some density plots that relate several factors towards the birthweight of a child.

   (a) Load the `MASS` library, which includes the dataset `birthwt` which contains information about 189 babies and their mothers.

   (b) Add better labels to the `race` and `smoke` variables using the following:

```
library(MASS)

##
## Attaching package:  'MASS'
## The following object is masked from 'package:dplyr':
##
##    select

birthwt$race  <- factor(birthwt$race,  labels=c('White','Black','Other'))
birthwt$smoke <- factor(birthwt$smoke, labels=c('No Smoke', 'Smoke'))
```

   (c) Graph a histogram of the birthweights `bwt` using `ggplot(birthwt, aes(x=bwt)) + geom_histogram()`.

   (d) Make separate graphs that denote whether a mother smoked during pregnancy using the `facet_grid()` command.

   (e) Perhaps race matters in relation to smoking. Make our grid of graphs vary with smoking status changing vertically, and race changing horizontally (that is the formula in `facet_grid()` should have smoking be the y variable and race as the x).

   (f) Remove race from the facet grid, (so go back to the graph you had in part d). I'd like to next add an estimated density line to the graphs, but to do that, I need to first change the y-axis to be density (instead of counts), which we do by using `aes(y=..density..)` in the `ggplot()` aesthetics command.

   (g) Next we can add the estimated smooth density using the `geom_density()`

   (h) To really make this look nice, lets change the fill color of the histograms to be something less dark, lets use `fill='cornsilk'` and `color='grey60'`.

   (i) Change the order in which the histogram and the density line are added to the plot. Does it matter and which do you prefer?

4. Load the dataset `ChickWeight` and remind yourself what the data was using `?ChickWeight`. Using `facet_wrap()`, produce a scatter plot of weight vs age for each chick. Use color to distinguish the four different `Diet` treatments.

```
# load the data
data(ChickWeight)
```

Chapter 10

Graphing using `ggplot2`: Lab 2

10.1 Multiple Plots in one Figure

Give a link to the multi-plot command

10.2 Saving plots consistently

Use `ggsave()`

10.3 Themes

Show a few of my favorite themes. In part using the package `ggthemes`

1. theme_bw()
2. theme_economist
3. theme_wsj
4. theme_excel - If you really must...

10.4 Googling to get help

Chapter 11

Flow Control Structures

Often it is necessary to write scripts that perform different action depending on the data or to automate a task that must be repeated many times. To address these issues we will introduce the `if` statement and its closely related cousin `if else`. To address repeated tasks we will define two types of loops, a `while` loop and a `for` loop.

11.1 Decision statements

An `if` statement takes on the following two formats

```
# Simplest version
if( logical ){
  expression
}

# Including the optional else
if( logical ){
  expression
}else{
  expression
}
```

where the `else` part is optional.

Suppose that I have a piece of code that generates a random variable from the Binomial distribution with one sample (essentially just flipping a coin) but I'd like to label it head or tails instead of one or zero.

```
# Flip the coin, and we get a 0 or 1
result <- rbinom(n=1, size=1, prob=0.5)
result

## [1] 1

# convert the 0/1 to Tail/Head
if( result == 0 ){
  result <- 'Tail'
}else{
  result <- 'Head'
}

result

## [1] "Head"
```

What is happening is that the test expression inside the `if()` is evaluated and if it is true, then the subsequent statement is executed. If the test expression is false, the next statement is skipped. The way the R language is defined, only the first statement after the `if` statement is executed (or skipped) depending on the test expression. If we want multiple statements to be executed (or skipped), we will wrap those expressions in curly brackets `{}`. I find it easier to follow the `if else` logic when I see the curly brackets so I use them even when there is only one expression to be executed. Also notice that the RStudio editor indents the code that might be skipped to try help give you a hint that it will be conditionally evaluated.

```
# Flip the coin, and we get a 0 or 1
result <- rbinom(n=1, size=1, prob=0.5)
result

## [1] 1

# convert the 0/1 to Tail/Head
if( result == 0 ){
  result <- 'Tail'
  print(" in the if statement, got a Tail! ")
}else{
  result <- 'Head'
  print("In the else part!")
}

## [1] "In the else part!"

result

## [1] "Head"
```

There are cases where you have two alternative routes of computation. Instead of writing two `if` statements you could use the `if else` construct. This will evaluate the test expression and, if true, execute the statement following the `if`. If the test expression is false, it will execute the statement in the `else` section.

Finally we can nest `if else` statements together to allow you to write code that has many different execution routes.

```
# randomly grab a number between 0,5 and round it up to 1,2, ..., 5
birth.order <- ceiling( runif(1, 0,5) )
if( birth.order == 1 ){
  print('The first child had more rules to follow')
}else if( birth.order == 2 ){
  print('The second child was ignored')
}else if( birth.order == 3 ){
  print('The third child was spoiled')
}else{
  # if birth.order is anything other than 1, 2 or 3
  print('No more unfounded generalizations!')
}

## [1] "No more unfounded generalizations!"
```

To provide a more statistically interesting example of when we might use an `if else` statement, consider the calculation of a p-value in a 1-sample t-test with a two-sided alternative. Recall the calculate was:

- If the test statistic t is negative, then $p - value = 2 * P\left(T_{df} < t\right)$
- If the test statistic t is positive, then $p - vlaue = 2 * P\left(T_{df} > t\right)$

```
# create some fake data
n  <- 20   # suppose this had a sample size of 20
x  <- rnorm(n, mean=2, sd=1)

# testing H0: mu = 0  vs Ha: mu =/= 0
t  <- ( mean(x) - 0 ) / ( sd(x)/sqrt(n) )
df <- n-1
if( t < 0 ){
  p.value <- 2 * pt(t, df)
}else{
  p.value <- 2 * (1-pt(t, df))
}

# print the resulting p-value
p.value

## [1] 9.246968e-07
```

This sort of logic is necessary for the calculation of p-values and so something similar is found somewhere inside the `t.test()` function.

When my code expressions in the if/else sections are short, I can use the command `ifelse()` that is a little more space efficient and responds correctly to vectors. The syntax is `ifelse( logical.expression, TrueValue, FalseValue )`.

```
x <- 1:10
ifelse( x <= 5, 'Small Value', 'Large Value')

##  [1] "Small Value" "Small Value" "Small Value" "Small Value" "Small Value"
##  [6] "Large Value" "Large Value" "Large Value" "Large Value" "Large Value"
```

11.2 Loops

It is often desirable to write code that does the same thing over and over, relieving you of the burden of repetitive tasks. To do this we'll need a way to tell the computer to repeat some section of code over and over. However we'll usually want something small to change each time through the loop and some way to tell the computer how many times to run the loop or when to stop repeating.

11.2.1 While Loops

The basic form of a `while` loop is as follows:

```
# while loop with 1 line
while( logical )
  expression

# while loop with multiple lines to be repeated
while( logical ){
  expression1
  expression2
}
```

The computer will first evaluate the test expression. If it is true, it will execute the code once. It will then evaluate the test expression again to see if it is still true, and if so it will execute the code section a third time. The computer will continue with this process until the test expression finally evaluates as false.

```
x <- 2
while( x < 100 ){
  x <- 2*x
  print(x)
}

## [1] 4
## [1] 8
## [1] 16
## [1] 32
## [1] 64
## [1] 128
```

It is very common to forget to update the variable used in the test expression. In that case the test expression will never be false and the computer will never stop. This unfortunate situation is called an *infinite loop*.

```
x <- 1
while( x < 10 ){
  print(x)
}
```

11.2.2 For Loops

Often we know ahead of time exactly how many times we should go through the loop. We could use a `while` loop, but there is also a second construct called a `for` loop that is quite useful.

The format of a for loop is as follows: `for( index in vector ) statement` where the `index` will take on each value in `vector` in succession and then `statement` will be evaluated. As always,

`statement` can be multiple statements wrapped in curly brackets {}.

```
for( i in 1:5 ){
  print(i)
}
```

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

What is happening is that `i` starts out as the first element of the vector `c(1,2,3,4,5)`, in this case, `i` starts out as 1. After `i` is assigned, the statements in the curly brackets are then evaluated. Once we get to the end of those statements, `i` is reassigned to the next element of the vector `c(1,2,3,4,5)`. This process is repeated until `i` has been assigned to each element of the given vector. It is somewhat traditional to use `i` and `j` and the index variables, but they could be anything.

We can use this loop to calculate the first 10 elements of the Fibonacci sequence. Recall that the Fibonacci sequence is defined by $F_n = F_{n-1} + F_{n-2}$ where $F_1 = 0$ and $F_2 = 1$.

```
F <- rep(0, 10)
F[1] <- 0
F[2] <- 1
cat('F = ', F, '\n')            # concatenate for pretty output
```

```
## F =  0 1 0 0 0 0 0 0 0 0
```

```
for( n in 3:10 ){
  F[n] <- F[n-1] + F[n-2]
  cat('F = ', F, '\n')
}
```

```
## F =  0 1 1 0 0 0 0 0 0 0
## F =  0 1 1 2 0 0 0 0 0 0
## F =  0 1 1 2 3 0 0 0 0 0
## F =  0 1 1 2 3 5 0 0 0 0
## F =  0 1 1 2 3 5 8 0 0 0
## F =  0 1 1 2 3 5 8 13 0 0
## F =  0 1 1 2 3 5 8 13 21 0
## F =  0 1 1 2 3 5 8 13 21 34
```

For a more statistical case where we might want to perform a loop, we can consider the creation of the bootstrap estimate of a sampling distribution. We will show how to create the bootstrap sampling distribution using `mosaic` syntax and using the base R `for` loop.

```
# mosaic way
library(mosaic)
library(dplyr)
mosaic.SampDist <- do(1000) * {
  resample(trees) %>% summarise(xbar=mean(Height))
}


baseR.SampDist <- data.frame() # Make a vector to store the means
for( i in 1:1000 ){
  temp <- resample(trees) %>% summarise(xbar=mean(Height)) # 1x1 data frame
  baseR.SampDist[i,'xbar'] <- temp[1,1]
}
```

11.3 Exercises

1. The $Uniform\,(a,b)$ distribution is defined on $x \in [a,b]$ and represents a random variable that takes on any value of between a and b with equal probability.[1] It has the density function

$$f\,(x) = \begin{cases} \frac{1}{b-a} & a \leq x \leq b \\ 0 & \text{otherwise} \end{cases}$$

   The R function `dunif()`

```
a <- 4
b <- 10

x <- runif(n=1, 0,10)  # one random value between 0 and 10
x

## [1] 2.2758

# what is value of f(x) at the randomly selected x value?
dunif(x, a, b)

## [1] 0
```

   evaluates this density function for the above defined values of `x`, `a`, and `b`. Somewhere in that function, there is a chunk of code that evaluates the density for arbitrary values of x. Write a sequence of statements that utilizes an `if` statements to appropriately calculate the density of `x` assuming that `a`, `b` , and `x` are given to you, but your code won't know if `x` is between `a` and `b`. That is, your code needs to figure out if it is and give either `1/(b-a)` or `0`.

   (a) We could write a set of `if/else` statements

[1] Technically since there are an infinite number of values between a and b, each value has a probability of 0 of being selected and I should say each interval of width d has equal probability.

```
a <- 4
b <- 10
x <- runif(n=1, 0,10)  # one random value between 0 and 10
x


if( x < a ){
  result <- ???
}else if( x <= b ){
  result <- ???
}else{
  result <- ???
}
```

Replace the `???` with the appropriate value, either 0 or $1/(b-a)$.

(b) We could perform the logical comparison all in one comparison. Recall that we can use `&` to mean "and" and `|` to mean "or". In the following two code chunks, replace the `???` with either `&` or `|` to make the appropriate result.

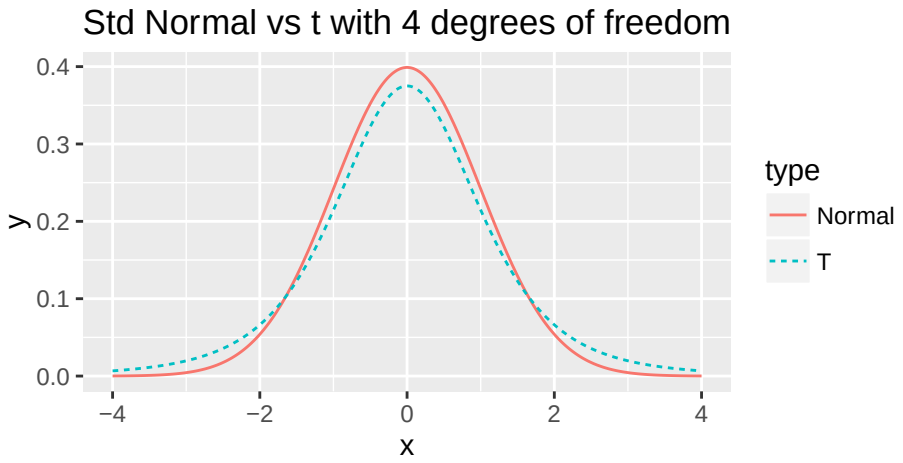
i.
```
x <- runif(n=1, 0,10)  # one random value between 0 and 10
if( (a<=x) ??? (x<=b) ){
  result <- 1/(b-a)
}else{
  result <- 0
}
```

ii.
```
x <- runif(n=1, 0,10)  # one random value between 0 and 10
if( (x<a) ??? (b<x) ){
  result <- 0
}else{
  result <- 1/(b-a)
}
```

iii.
```
x <- runif(n=1, 0,10)  # one random value between 0 and 10
ifelse( a<x & x<b, ???, ??? )
```

2. I often want to repeat some section of code some number of times. For example, I might want to create a bunch plots that compare the density of a t-distribution with specified degrees of freedom to a standard normal distribution.

```
library(ggplot2)
df <- 4
N <- 1000
x <- seq(-4, 4, length=N)
data <- data.frame(
  x = c(x,x),
  y = c(dnorm(x), dt(x, df)),
  type = c( rep('Normal',N), rep('T',N) ) )

# make a nice graph
myplot <- ggplot(data, aes(x=x, y=y, color=type, linetype=type)) +
  geom_line() +
  labs(title = paste('Std Normal vs t with', df, 'degrees of freedom'))

# actually print the nice graph we made
print(myplot)
```



(a) Use a `for` loop to create similar graphs for degrees of freedom $2, 3, 4, \ldots, 29, 30$.

(b) In retrospect, perhaps we didn't need to produce all of those. Rewrite your loop so that we only produce graphs for $\{2, 3, 4, 5, 10, 15, 20, 25, 30\}$ degrees of freedom. *Hint: you can just modify the vector in the for statement to include the desired degrees of freedom.*

3. The `for` loop usually is the most natural one to use, but occasionally we have occasions where it is too cumbersome and a different sort of loop is appropriate. One example is taking a random sample from a truncated distribution. For example, I might want to take a sample from a normal distribution with mean μ and standard deviation σ but for some reason need the answer to be larger than zero. One solution is to just sample from the given normal distribution until I get a value that is bigger than zero.

```
mu    <- 0
sigma <- 1
x <- rnorm(1, mean=mu, sd=sigma)
# start the while loop checking if x < 0
#    generate a new x value
# end the while loop
```

Replace the comments in the above code so that x is a random observation from the truncated normal distribution.

Chapter 12

User Defined Functions

It is very important to be able to define a piece of programing logic that is repeated often. For example, I don't want to have to always program the mathematical code for calculating the sample variance of a vector of data. Instead I just want to call a function that does everything for me and I don't have to worry about the details.

While hiding the computational details is nice, fundamentally writing functions allows us to think about our problems at a higher layer of abstraction. For example, most scientists just want to run a t-test on their data and get the appropriate p-value out; they want to focus on their problem and not how to calculate what the appropriate degrees of freedom are. Functions let us do that.

12.1 Basic function definition

In the course of your analysis, it can be useful to define your own functions. The format for defining your own function is

```
function.name <- function(arg1, arg2, arg3)
  statement
```

where `arg1` is the first argument passed to the function and `arg2` is the second. As usual `statement` is a single statement or multiple statements wrapped in the familiar curly brackets `{}`.

To illustrate how to define your own function, we will define a variance calculating function.

```
# define my function
my.var <- function(x){
  n <- length(x)                # calculate sample size
  xbar <- mean(x)               # calculate sample mean
  SSE <- sum( (x-xbar)^2 )      # calculate sum of squared error
  v <- SSE / ( n - 1 )          # "average" squared error
  return(v)                     # result of function is v
}
```

```
# create a vector that I wish to calculate the variance of
test.vector <- c(1,2,2,4,5)
```

```
# calculate the variance using my function
calculated.var <- my.var( test.vector )
calculated.var

## [1] 2.7
```

Notice that even though I defined my function using `x` as my vector of data, and passed my

function something named `test.vector`, R does the appropriate renaming.[1] Think of the variable `x` as a placeholder, with it being replaced by whatever gets passed into the function.

When I call a function, the function might cause something to happen (e.g. draw a plot) or it might do some calculates the result is returned by the function and we might want to save that. Inside a function, if I want the result of some calculation saved, I return the result as the output of the function. The way I specify to do this is via the `return` statement.[2]

By writing a function, I can use the same chunk of code repeatedly. This means that I can do all my tedious calculations inside the function and just call the function whenever I want and happily ignore the details. Consider the function `t.test()` which we have used to do all the calculations in a t-test. We could write a similar function using the following code:

```
# define my function
one.sample.t.test <- function(input.data, mu0){
  n    <- length(input.data)
  xbar <- mean(input.data)
  s    <- sd(input.data)
  t    <- (xbar - mu0)/(s / sqrt(n))
  if( t < 0 ){
    p.value <- 2 * pt(t, df=n-1)
  }else{
    p.value <- 2 * (1-pt(t, df=n-1))
  }
  # we haven't addressed how to print things in a organized
  # fashion, the following is ugly, but works...
  # Notice that this function returns a character string
  # with the necessary information in the strong.
  return( paste('t =', t, ' and p.value =', p.value) )
}
```

```
# create a vector that I wish apply a one-sample t-test on.
test.data <- c(1,2,2,4,5,4,3,2,3,2,4,5,6)
```

```
# calculate the variance using my function
one.sample.t.test( test.data, 2 )

## [1] "t = 3.15682074900988  and p.value = 0.00826952416706961"
```

Nearly every function we use to do data analysis is written in a similar fashion. Somebody decided it would be convenient to have a function that did an ANOVA analysis and they wrote something similar to the above function, but is a bit grander in scope. Even if you don't end up writing any of your own functions, knowing how to will help you understand why certain functions you use are designed the way they are.

12.2 Parameter Defaults

When I define a function and can let it take as many arguments as I want and I can also give default values to the arguments. For example we can define the normal density function using the following code which gives a default mean of 0 and default standard deviation of 1.

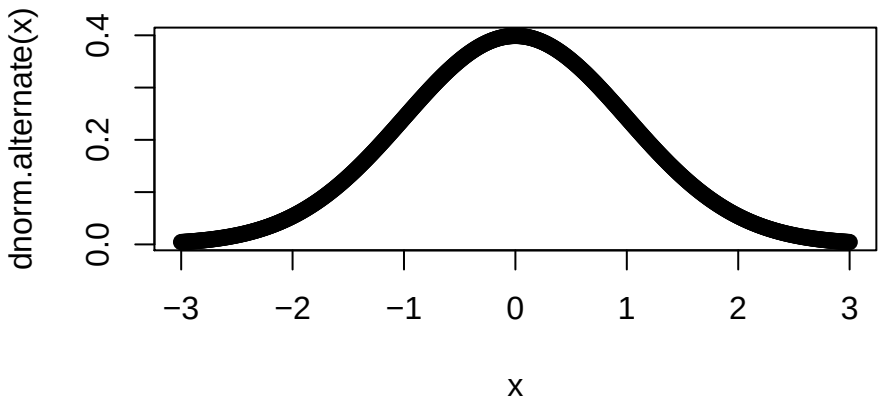
[1] If my function doesn't modify its input arguments, then R just passes a pointer to the inputs to avoid copying large amounts of data when you call a function. If your function modifies its input, then R will take the input data, copy it, and then pass that new copy to the function. This means that a function cannot modify its arguments. In Computer Science parlance, R does not allow for procedural side effects.

[2] Actually R doesn't completely require this. But the alternative method is less intuitive and I strongly recommend using the `return()` statement for readability.

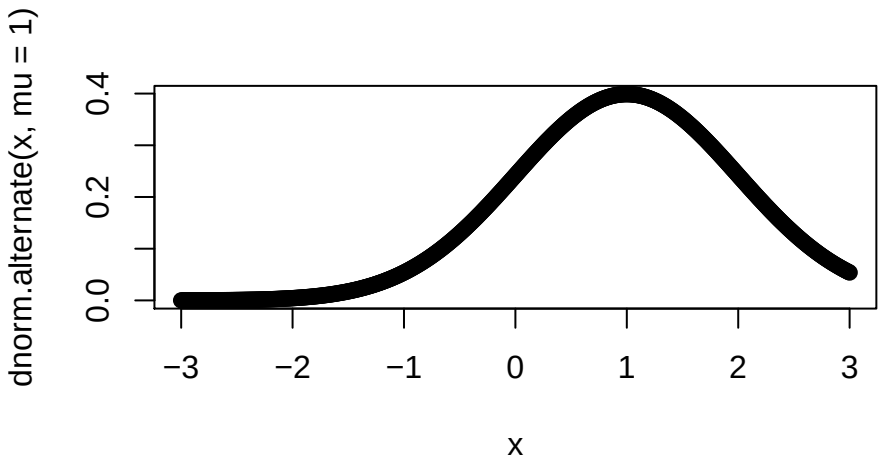
```r
# a function that defines the shape of a normal distribution.
# by including mu=0, we give a default value that the function
# user can override
dnorm.alternate <- function(x, mu=0, sd=1){
  out <- 1 / (sd * sqrt(2*pi)) * exp( -(x-mu)^2 / (2 * sd^2) )
  return(out)
}
```

```r
# test the function to see if it works
dnorm.alternate(1)

## [1] 0.2419707

dnorm.alternate(1, mu=1)

## [1] 0.3989423
```

```r
# Lets test the function a bit more by drawing the height
# of the normal distribution a lots of different points
# ... First the standard normal!
x <- seq(-3, 3, length=601)
plot( x, dnorm.alternate(x) )  # use default mu=0, sd=1
```



```
# next a normal with mean 1, and standard deviation 1
plot( x, dnorm.alternate(x, mu=1) ) # override mu, but use sd=1
```



Many functions that we use have defaults that we don't normally mess with. For example, the function `mean()` has an option the specifies what it should do if your vector of data has missing data. The common solution is to remove those observations, but we might have wanted to say that the mean is unknown one component of it was unknown.

```
x <- c(1,2,3,NA)    # fourth element is missing
mean(x)             # default is to return NA if any element is missing

## [1] NA

mean(x, na.rm=TRUE) # Only average the non-missing data

## [1] 2
```

As you look at the help pages for different functions, you'll see in the function definitions what the default values are. For example, the function `mean` has another option, `trim`, which specifies what percent of the data to trim at the extremes. Because we would expect `mean` to not do any trimming by default, the authors have appropriately defined the default amount of trimming to be zero via the definition `trim=0`.

12.3 Ellipses

When writing functions, I occasionally have a situation where I call function `a()` and function `a()` needs to call another function, say `b()`, and I want to pass an unusual parameter to that function. To do this, I'll use a set of three periods called an *ellipses.* What these do is represent a set of parameter values that will be passed along to a subsequent function.

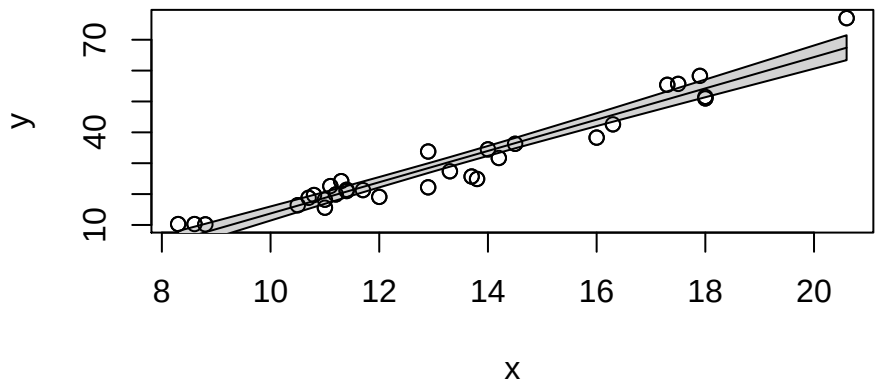
For example the following code takes the result of a simple linear regression and plots the data and the regression line and confidence region (*basically I'm recreating a function that does the same thing as `ggplot2`'s geom_smooth() layer).* I might not want to specify (and give good defaults) to every single graphical parameter that the `plot()` function supports. Instead I'll just use the `'...'` argument and pass any additional parameters to the plot function.

```
# a function that draws the regression line and confidence interval
# notice it doesn't return anything... all it does is draw a plot
show.lm <- function(m, interval.type='confidence', fill.col='light grey', ...){
  x <- m$model[,2]        # extract the predictor variable
  y <- m$model[,1]        # extract the response
  pred <- predict(m, interval=interval.type)
  plot(x, y, ...)
  polygon( c(x,rev(x)),                          # draw the ribbon defined
           c(pred[,'lwr'], rev(pred[,'upr'])),   # by lwr and upr - polygon
           col='light grey')                     # fills in the region defined by
  lines(x, pred[, 'fit'])                        # a set of vertices, need to reverse
  points(x, y)                                  # the uppers to make a nice figure
}
```

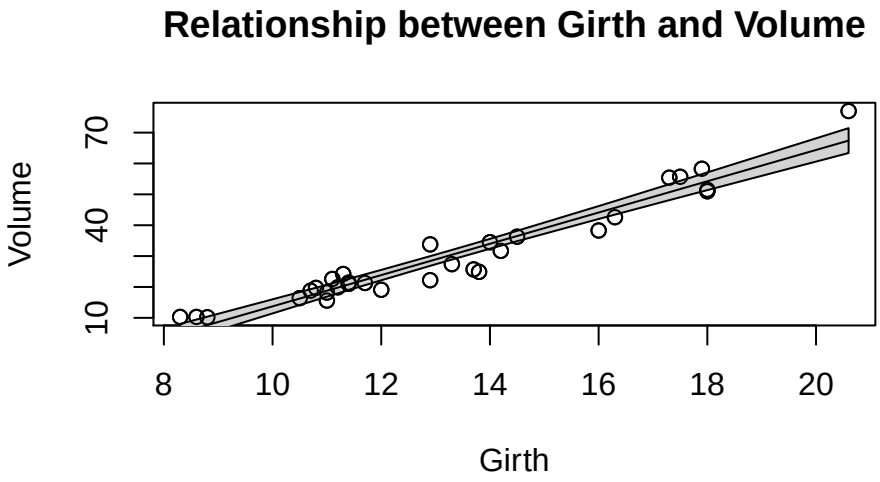
This function looks daunting, but we experiment to see what it does.

```
# first define a simple linear model from our cherry tree data
m <- lm( Volume ~ Girth, data=trees )
```

```
# call the function with no extraneous parameters
show.lm( m )
```



```
# Pass arguments that will just be passed along to the plot function
show.lm( m, xlab='Girth', ylab='Volume',
         main='Relationship between Girth and Volume')
```



This type of trick is done commonly. Look at the help files for `hist()` and `qqnorm()` and you'll see the ellipses used to pass graphical parameters along to sub-functions. Functions like `lm()` use the ellipses to pass arguments to the low level regression fitting functions that do the actual calculations. By only including these parameters via the ellipses, must users won't be tempted to mess with the parameters, but experts who know the nitty-gritty details can still modify those parameters.

12.4 Function Overloading

Frequently the user wants to inspect the results of some calculation and display a variable or object to the screen. The `print()` function does exactly that, but it acts differently for matrices than it does for vectors. It especially acts different for lists that I obtained from a call like `lm()` or `aov()`.

The reason that the print function can act differently depending on the object type that I pass it is because the function `print()` is *overloaded*. What this means is that there is a `print.lm()` function that is called whenever I call `print(obj)` when `obj` is the output of an `lm()` command.

Recall that we initially introduced a few different classes of data, Numerical, Factors, and Logicals. It turns out that I can create more types of classes.

```
x <- seq(1:10)
y <- 3+2*x+rnorm(10)

h <- hist(y)  # h should be of class "Histogram"
class(h)

## [1] "histogram"

model <- lm( y ~ x ) # model is something of class "lm"
class(model)

## [1] "lm"
```

Many common functions such as `plot()` are overloaded so that when I call the plot function with an object, it will in turn call `plot.lm()` or `plot.histogram()` as appropriate. When building

statistical models I am often interested in different quantities and would like to get those regardless of the model I am using. Below are a list of functions that work whether I fit a model via `aov()`, `lm()`, `glm()`, or `gam()`.

Quantity	Function name
Residuals	`resid( obj )`
Model Coefficients	`coef( obj )`
Summary Table	`summary( obj )`
ANOVA table	`anova( obj )`
AIC value	`AIC( obj )`

For the residual function, there actually exists a `resid.aov()` function, and `resid.lm()`, `resid.glm()`, and `resid.gam()` and it is these functions are called when we run the command `resid( obj )`.

12.5 Scope

Consider the case where we make a function that calculates the trimmed mean. A good implementation of the function is given here.

```
trimmed.mean <- function(x, k){
  x <- sort(x)
  n <- length(x)
  if( k > 0){
    x <- x[c(-1*(1:k), -1*((n-k+1):n))]
  }
  tm <- sum(x)/ length(x)
  return( tm )
}
x <- c(10:1,50)                          # 10, 9, 8, ..., 1
output <- trimmed.mean(x, k=2)
output

## [1] 6

x                                  # x is unchanged

##  [1] 10  9  8  7  6  5  4  3  2  1 50
```

Notice that even though I passed `x` into the function and then sorted it, `x` remained unsorted outside the function.[3] But what if I didn't bother with passing `x` and `k`. If I don't pass in the values of `x` and `k`, then R will try to find them in my current workspace.

[3] When I modified `x`, R made a copy of `x` and sorted the copy that belonged to the function so that I didn't modify a variable that was defined outside of the scope of my function. The only way you can do that is to use the assignment operator ' `<<-` '. This can lead to all sorts of weird behavior and I recommend against it.

```
trimmed.mean <- function(){
  x <- sort(x)
  n <- length(x)
  if( k > 0){
    x <- x[c(-1*(1:k), -1*((n-k+1):n))]
  }
  tm <- sum(x)/length(x)
  return( tm )
}
x <- c( 1:10, 50 )
k <- 2
output <- trimmed.mean()  # amazingly this still works
output                    # this is actually the correct output!

## [1] 6

x                         # still the same x vector

##  [1]  1  2  3  4  5  6  7  8  9 10 50
```

So if I forget to pass some variable into a function, but it happens to be defined outside the function, R will find it. It is not good practice to rely on that because how do I take the trimmed mean of a vector named `z`? Worse yet, what if the variable `x` changes between runs of your function? What should be consistently giving the same result keeps changing. This is especially insidious when you have defined most of the arguments the function uses, but missed one. Your function happily goes to the next higher scope and sometimes finds it.

When executing a function, R will have access to all the variables defined in the function, all the variables defined in the function that called your function and so on until the base workspace. However, you should never let your function refer to something that is not either created in your function or passed in via a parameter.

12.6 Exercises

1. The following function augments the `t.test()` so that it calculates the usual t test information along with the bootstrap confidence interval.

```
x.t.test <- function( formula, data, conf.level=0.95, M=10000, ... ){
  alpha <- 1-conf.level
  SampDist <- rep(NA, M)
  for( i in 1:M ){
    SampDist[i] <- t.test(formula, data)$statistic
  }
  bootCI <- quantile(SampDist, probs=c(alpha/2, 1-alpha/2))  # vector of 2 numbers
  bootCI <- paste( bootCI, collapse=TRUE )                   # Character string
  t.test(formula, data, mu, conf.level, ... )
  print(paste('Bootstrap Confidence Interval:', bootCI))
}
```

2. Write a function that calculates the density function of a *Uniform* continuous variable on the interval (a, b). The function is defined as

$$f(x) = \begin{cases} \frac{1}{b-a} & \text{if } a \leq x \leq b \\ 0 & \text{otherwise} \end{cases}$$

which looks like this

We want to write a function `duniform(x, a, b)` that takes an arbitrary value of x and parameters `a` and `b` and return the appropriate height of the density function. For various values of `x`, `a`, and `b`, demonstrate that your function returns the correct density value. Ideally, your function should be able to take a vector of values for `x` and return a vector of densities.

3. I very often want to provide default values to a parameter that I pass to a function. For example, it is so common for me to use the `pnorm()` and `qnorm()` functions on the standard normal, that R will automatically use `mean=0` and `sd=1` parameters unless you tell R otherwise. To get that behavior, we just set the default parameter values in the definition. When the function is called, the user specified value is used, but if none is specified, the defaults are used. Look at the help page for the functions `dunif()`, and notice that there are a number of default parameters.

   For your `duniform()` function provide default values of 0 and 1 for `a` and `b`. Demonstrate that your function is appropriately using the given default values.

Chapter 13

Manipulating Strings

Strings make up a very important class of data. Data being read into R often come in the form of character strings where different parts might mean different things. For example a sample ID of "R1_P2_C1_2012_05_28" might represent data from Region 1, Park 2, Camera 1, taken on May 28, 2012. It is important that we have a set of utilities that allow us to split and combine character strings in a easy and consistent fashion.

Unfortunately, the utilities included in the base version of R are somewhat inconsistent and were not designed to work nicely together. Hadley Wickham, the developer of `ggplot2` and `dplyr` has this to say:

> R provides a solid set of string operations, but because they have grown organically over time, they can be inconsistent and a little hard to learn. Additionally, they lag behind the string operations in other programming languages, so that some things that are easy to do in languages like Ruby or Python are rather hard to do in R. – Hadley Wickham

For this chapter we will introduce the most commonly used functions from the base version of R that you might use or see in other people's code. Second, we introduce Dr Wickham's `stringr` package that provides many useful functions that operate in a consistent manner.

13.1 Base function

13.1.1 `paste()`

The most basic thing we will want to do is to combine two strings or to combine a string with a numerical value. The `paste()` command will take one or more R objects and converts them to character strings and then pastes them together to form one or more character strings. It has the form:

```
paste( ..., sep = ' ', collapse = NULL )
```

The `...` piece means that we can pass any number of objects to be pasted together. The `sep` argument gives the string that separates the strings to be joined and the `collapse` argument that specifies if a simplification should be performed before pasting together.

Suppose we want to combine the strings "`Peanut butter`" and "`Jelly`" then we could execute:

```
paste( "PeanutButter", "Jelly" )

## [1] "PeanutButter Jelly"
```

Notice that without specifying the separator character, R chose to put a space between the two strings. We could specify whatever we wanted:

```
paste( "Hello", "World", sep='_' )

## [1] "Hello_World"
```

Also we can combine strings with numerical values

```
paste( "Pi is equal to", pi )

## [1] "Pi is equal to 3.14159265358979"
```

We can combine vectors of similar or different lengths as well. By default R assumes that you want to produce a vector of character strings as output.

```
paste( "n =", c(5,25,100) )

## [1] "n = 5"   "n = 25"  "n = 100"

first.names <- c('Robb','Stannis','Daenerys')
last.names <- c('Stark','Baratheon','Targaryen')
paste( first.names, last.names)

## [1] "Robb Stark"         "Stannis Baratheon"  "Daenerys Targaryen"
```

If we want `paste()` produce just a single string of output, use the `collapse=` argument to first paste together each input vector (separated by the `collapse` character).

```
paste( paste( "n =", c(5,25,100) ) )

## [1] "n = 5"   "n = 25"  "n = 100"

paste( "n =", c(5,25,100), collapse=':' )

## [1] "n = 5:n = 25:n = 100"

paste(first.names, last.names, sep='.', collapse=' : ')

## [1] "Robb.Stark : Stannis.Baratheon : Daenerys.Targaryen"
```

Notice we could use the `paste()` command with the `collapse` option to combine a vector of character strings together.

```
paste(first.names, collapse=':')

## [1] "Robb:Stannis:Daenerys"
```

13.2 Package `stringr`: basic operations

The goal of `stringr` is to make a consistent user interface to a suite of functions to manipulate strings.

> "(`stringr`) is a set of simple wrappers that make R's string functions more consistent, simpler and easier to use. It does this by ensuring that: function and argument names (and positions) are consistent, all functions deal with NA's and zero length character appropriately, and the output data structures from each function matches the input data structures of other functions." - Hadley Wickham

We'll investigate the most commonly used function but there are many we will ignore.

Function	Description
str_c()	string concatenation, similar to `paste()`
str_length()	number of characters in the string
str_sub()	extract a substring
str_trim()	remove leading and trailing whitespace
str_pad	pad a string with empty space to be a designated length

Concatenating with `str_c()` or `str_join()`

The first thing we do is to concatenate two strings or two vectors of strings similarly to the `paste()` command. The `str_c()` and `str_join()` functions are a synonym for the exact same function, but `str_join()` might be a more natural verb to use and remember. The syntax is:

```
str_join( ..., sep='', collapse=NULL)
```

You can think of the inputs building a matrix of strings, with each input creating a column of the matrix. For each row, `str_join()` first joins all the columns (using the separator character given in `sep`) into a single column of strings. If the `collapse` argument is non-`NULL`, the function takes the vector and joins each element together using `collapse` as the separator character.

```
# load the stringr library
library(stringr)

# envisioning the matrix of strings
cbind(first.names, last.names)

##      first.names last.names
## [1,] "Robb"      "Stark"
## [2,] "Stannis"   "Baratheon"
## [3,] "Daenerys"  "Targaryen"

# join the columns together
full.names <- str_c( first.names, last.names, sep='.')
cbind( first.names, last.names, full.names)

##      first.names last.names  full.names
## [1,] "Robb"      "Stark"     "Robb.Stark"
## [2,] "Stannis"   "Baratheon" "Stannis.Baratheon"
## [3,] "Daenerys"  "Targaryen" "Daenerys.Targaryen"

# Join each of the rows together separated by collapse
str_join( first.names, last.names, sep='.', collapse=' : ')

## Warning:  'str_join' is deprecated.
## Use 'str_c' instead.
## See help("Deprecated")

## [1] "Robb.Stark : Stannis.Baratheon : Daenerys.Targaryen"
```

Calculating string length with `str_length()`

The `str_length()` function calculates the length of each string in the vector of strings passed to it.

```
text <- c('WordTesting', 'With a space', NA, 'Night')
str_length( text )

## [1] 11 12 NA  5
```

Notice that `str_length()` correctly interprets the missing data as missing and that the length ought to also be missing.

Extracting substrings with `str_sub()`

If we know we want to extract the 3^{rd} through 6^{th} letters in a string, this function will grab them.

```
str_sub(text, start=3, end=6)

## [1] "rdTe" "th a" NA     "ght"
```

If a given string isn't long enough to contain all the necessary indices, `str_sub()` returns only the letters that where there (as in the above case for `"Night"`

Pad a string with `str_pad()`

Sometimes we to make every string in a vector the same length to facilitate display or in the creation of a uniform system of assigning ID numbers. The `str_pad()` function will add spaces at either the beginning or end of the of every string appropriately.

```
str_pad(first.names, width=8)

## [1] "    Robb" " Stannis" "Daenerys"

str_pad(first.names, width=8, side='right', pad='*')

## [1] "Robb****" "Stannis*" "Daenerys"
```

Trim a string with str_trim()

This removes any leading or trailing whitespace where whitespace is defined as spaces `' '`, tabs `'\t'`, or returns `'\n'`.

```
text <- ' Some text. \n  '
print(text)

## [1] " Some text. \n  "

str_trim(text)

## [1] "Some text."
```

13.3 Package `stringr`: Pattern Matching

The previous commands are all quite useful but the most powerful string operation is take a string and match some pattern within it. The following commands are available within `stringr`.

Function	Description
`str_detect()`	Detect if a pattern occurs in the input string
`str_locate()` `str_locate_all()`	Locates the first (or all) position(s) of a pattern
`str_extract()` `str_extract_all()`	Extracts the first (or all) substrings corresponding to a pattern
`str_replace()` `str_replace_all()`	Replaces the matched substrings with a new pattern
`str_split()` `str_split_fixed()`	Splits the input string based on the input pattern

We will first examine these functions using a very simple pattern matching algorithm where we are matching a specific pattern. For most people, this is as complex as we need. The next section will introduce using regular expressions[1] in these functions. Suppose that we have a vector of strings that contain a date in the form "2012-May-27" and we want to manipulate them to extract certain information.

```
test.vector <- c('2008-Feb-10', '2010-Sept-18', '2013-Jan-11', '2016-Jan-2')
```

Detecting a pattern using `str_detect()`

Suppose we want to know which dates are in September. We want to detect if the pattern "Sept" occurs in the strings. It is important that I used `fixed("Sept")` in this code to "turn off" the complicated regular expression matching rules and just look for exactly what I specified.

```
str_detect( test.vector, pattern=fixed('Sept') )

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

Here we see that the second string in the test vector included the substring "Sept" but none of the others did.

Locating a pattern using `str_locate()`

To figure out where the "-" characters are, we can use the `str_locate()` function.

```
str_locate(test.vector, pattern=fixed('-') )

##      start end
## [1,]     5   5
## [2,]     5   5
## [3,]     5   5
## [4,]     5   5
```

which shows that the first dash occurs as the 5^{th} character in each string. If we wanted all the dashes in the string the following works.

[1] Regular expressions are a way to specify very complicated patterns. Go look at https://xkcd.com/208/ to gain insight into just how geeky regular expressions are.

```
str_locate_all(test.vector, pattern=fixed('-') )

## [[1]]
##      start end
## [1,]     5   5
## [2,]     9   9
##
## [[2]]
##      start end
## [1,]     5   5
## [2,]    10  10
##
## [[3]]
##      start end
## [1,]     5   5
## [2,]     9   9
##
## [[4]]
##      start end
## [1,]     5   5
## [2,]     9   9
```

The output of `str_locate_all()` is a list of matrices that gives the start and end of each matrix. Using this information, we could grab the Year/Month/Day information out of each of the dates. We won't do that here because it will be easier to do this using `str_split()`.

Replacing substrings using `str_replace()`

Suppose we didn't like using "-" to separate the Year/Month/Day but preferred a space, or an underscore, or something else. This can be done by replacing all of the "-" with the desired character. The `str_replace()` function only replaces the first match, but `str_replace_all()` replaces all matches.

```
str_replace(test.vector, pattern=fixed('-'), replacement=fixed(':') )

## [1] "2008:Feb-10"  "2010:Sept-18" "2013:Jan-11"  "2016:Jan-2"

str_replace_all(test.vector, pattern=fixed('-'), replacement=fixed(':') )

## [1] "2008:Feb:10"  "2010:Sept:18" "2013:Jan:11"  "2016:Jan:2"
```

Splitting into substrings using `str_split()`

We can split each of the dates into three smaller substrings using the `str_split()` command, which returns a list where each element of the list is a vector containing pieces of the original string (excluding the pattern we matched on).

```
str_split(test.vector, pattern=fixed('-'))

## [[1]]
## [1] "2008" "Feb"  "10"
##
## [[2]]
## [1] "2010" "Sept" "18"
##
## [[3]]
## [1] "2013" "Jan"  "11"
##
## [[4]]
## [1] "2016" "Jan"  "2"
```

If we know that all the strings will be split into a known number of substrings (we have to specify how many substrings to match), we can use `str_split_fixed()` to get a matrix of substrings instead of list of substrings. It is somewhat unfortunate that the `_fixed` modifier to the function name is the same as what we use to specify to use simple pattern matching.

```
str_split_fixed(test.vector, pattern=fixed('-'), n=3)

##      [,1]   [,2]   [,3]
## [1,] "2008" "Feb"  "10"
## [2,] "2010" "Sept" "18"
## [3,] "2013" "Jan"  "11"
## [4,] "2016" "Jan"  "2"
```

13.4 Regular Expressions

Regular expressions are a way of precisely writing out patterns that are very complicated. The `stringr` package `pattern` arguments can be given using standard regular expressions (not perl-style!) instead of using fixed strings.

Regular expressions are extremely powerful for sifting through large amounts of text. For example, we might want to extract all of the 4 digit substrings (the years) out of our dates vector, or I might want to find all cases in a paragraph of text of words that begin with a capital letter and are at least 5 letters long. In another, somewhat nefarious example, spammers might have downloaded a bunch of text from webpages and want to be able to look for email addresses. So as a first pass, they want to match a pattern:

$$\underbrace{\texttt{Username}}_{\text{1 or more letters}}\ \texttt{@}\ \underbrace{\texttt{OrganizationName}}_{\text{1 or more letter}}\ \texttt{.}\ \begin{cases}\texttt{com}\\ \texttt{org}\\ \texttt{edu}\end{cases}$$

where the `Username` and `OrganizationName` can be pretty much anything, but a valid email address looks like this. We might get even more creative and recognize that my list of possible endings could include country codes as well.

For most people, I don't recommend opening the regular expression can-of-worms, but it is good to know that these pattern matching utilities are available within R and you don't need to export your pattern matching problems to Perl or Python.

13.5 Exercises

1. Using the `test.vector` of dates given in the text, create a vector of the years using `stringr` functions.

2. The following file names were used in a camera trap study. The `S` number represents the site, `P` is the plot within a site, `C` is the camera number within the plot, the first string of numbers is the YearMonthDay and the second string of numbers is the HourMinuteSecond.

```
file.names <- c( 'S123.P2.C10_20120621_213422.jpg',
                 'S10.P1.C1_20120622_050148.jpg',
                 'S187.P2.C2_20120702_023501.jpg')
```

   Use a combination of `str_sub()` and `str_split`() to produce a data frame with columns corresponding to the site, plot, camera, year, month, day, hour, minute, and second for these three file names. So we want to produce code that will create the data frame:

```
##   Site Plot Camera Year Month Day Hour Minute Second
## 1 S123   P2    C10 2012    06  21   21     34     22
## 2  S10   P1     C1 2012    06  22   05     01     48
## 3 S187   P2     C2 2012    07  02   02     35     01
```

   Hint: Split the file names first by the underscore, and save the resulting three pieces as SiteInfo, DateInfo and TimeInfo and then further break each of those apart in whatever way is appropriate.

Chapter 14

Dates and Times using the `lubridate` package

Dates within a computer require some special organization because there are several competing conventions for how to write a date (some of them more confusing than others) and because the sort order should be in the order that the dates occur in time.

One useful tidbit of knowledge is that computer systems store a time point as the number of seconds from set point in time, called the epoch. So long as your system uses the same epoch, the use doesn't have to worry about when the epoch is, but if you are switching between software systems, you might run into problems if they use different epochs.[1] In R, we use midnight on Jan 1, 1970. In Microsoft Excel, they use Jan 0, 1900.

For many years, R users hated dealing with dates because it was difficult to remember how to get R to take a string that represents a date (e.g. `"June 26, 1997"`) because users were required to specify how the format was arranged using a relatively complex set of rules. For example `%y` represents the two digit year, `%Y` represents the four digit year, `%m` represents the month, but `%b` represents the month written as Jan or Mar. Into this mess came Hadley Wickham (of `ggplot2` and `dplyr` fame) and his student Garrett Grolemund. The internal structure of R dates and times is quite robust, but the functions we use to manipulate them are horrible. To fix this, Dr Wickham and his then PhD student Dr Grolemund introduced the `lubridate` package.

14.1 Creating Date and Time objects

To create a `Date` object, we need to take a string or number that represents a date and tell the computer how to figure out which bits are the year, which are the month, and which are the day. The `lubridate` package uses the following functions:

Common Orders	
`ymd()`	Year Month Day
`mdy()`	Month Day Year
`dmy()`	Day Month Year

Uncommon Orders	
`dym()`	Day Year Month
`myd()`	Month Year Day
`ydm()`	Year Day Month

The uncommon orders aren't likely to be used, but the `lubridate` package includes them for completeness. Once the order has been specified, the `lubridate` package will try as many different ways to parse the date that make sense. As a result, so long as the order is consistent, all of the following will work:

[1] http://en.wikipedia.org/wiki/Epoch_(reference_date)#Computing

```
library( lubridate )

mdy( 'June 6, 1997', 'Jun 6 97', '6-26-97', '6-6-1997', '6/6/97', '6-6/97' )

## [1] "1997-06-06 UTC" "1997-06-06 UTC" "0097-06-26 UTC" "1997-06-06 UTC"
## [5] "1997-06-06 UTC" "1997-06-06 UTC"
```

Unfortunately `lubridate()` is inconsistency recognizing the two digit year as either 97, 1997, or 2097. This illustrates that you should ALWAYS fully specify the year.

The `lubridate` functions will also accommodate if an integer representation of the date, but it has to have enough digits to uniquely identify the month and day.

```
ymd(20090110)

## [1] "2009-01-10 UTC"

ymd(2009722) # only one digit for month --- error!

## Warning:  All formats failed to parse.  No formats found.

## [1] NA

ymd(2009116) # this is ambiguous! 1-16 or 11-6?

## Warning:  All formats failed to parse.  No formats found.

## [1] NA
```

If we want to add a time to a date, we will use a function with the suffix `_hm` or `_hms`. Suppose that we want to encode a date and time, for example, the date and time of my wedding ceremony[2].

```
mdy_hm('Sept 18, 2010 5:30 PM', '9-18-2010 17:30')

## Warning:  1 failed to parse.

## [1] NA                        "2010-09-18 17:30:00 UTC"
```

In the above case, `lubridate` is having trouble understanding `AM/PM` differences and it is better to always specify times using 24 hour notation and skip the AM/PM designations.

By default, R codes the time of day using as if the event occurred in the UMT time zone (also know as Greenwich Mean Time GMT). To specify a different time zone, use the `tz=` option. For example:

```
mdy_hm('9-18-2010 17:30', tz='MST') # Mountain Standard Time

## [1] "2010-09-18 17:30:00 MST"
```

This isn't bad, but Loveland, Colorado is on MST in the winter and MDT in the summer because of daylight savings time. So to specify the time zone that could switch between standard time and daylight savings time, I should specify `tz='US/Mountain'`

```
mdy_hm('9-18-2010 17:30', tz='US/Mountain') # US mountain time

## [1] "2010-09-18 17:30:00 MDT"
```

As Arizonans, we recognize that Arizona is weird and doesn't use daylight savings time. Fortunately R has a built-in time zone just for us.

[2] It is convenient to have this written down in many places in case I really need to figure it out.

```
mdy_hm('9-18-2010 17:30', tz='US/Arizona') # US Arizona time

## [1] "2010-09-18 17:30:00 MST"
```

R recognizes 582 different time zone locals and you can find these using the function `OlsonNames()`. To find out more about what these mean you can check out the Wikipedia page on timezones[3].

14.2 Extracting information

The `lubridate` package provides many functions for extracting information from the date. Suppose we have defined

```
x <- mdy_hm('9-18-2010 17:30', tz='US/Mountain') # US Mountain time
```

Command	Output
`year(x)`	2010
`month(x)`	9
`day(x)`	18

Command	Output
`hour(x)`	17
`minute(x)`	30
`second(x)`	0

Command	Output
`wday(x)`	7
`mday(x)`	18
`yday(x)`	261

Here we get the output as digits, where September is represented as a 9 and the day of the week is a number between 1-7. To get nicer labels, we can use `label=TRUE` for some commands.

Command	Output
`wday(x, label=TRUE)`	Sat
`month(x, label=TRUE)`	Sep
`tz(x)`	US/Mountain

All of these functions can also be used to update the value. For example, we could move the day of the wedding from September 18^{th} to October 18^{th} by changing the month.

```
month(x) <- 10
x

## [1] "2010-10-18 17:30:00 MDT"
```

Often I want to consider some point in time, but need to convert the timezone the date was specified into another timezone. The function `with_tz()` will take a given moment in time and figure out when that same moment is in another timezone. For example, *Game of Thrones* is made available on HBO's streaming service at 9pm on Sunday evenings Eastern time. I need to know when I can start watching it here in Arizona.

```
GoT <- ymd_hm('2015-4-26 21:00', tz='US/Eastern')
with_tz(GoT, tz='US/Arizona')

## [1] "2015-04-26 18:00:00 MST"
```

This means that *Game of Thrones* is available for streaming at 6 pm Arizona time.

14.3 Arithmetic on Dates

Once we have two or more Date objects defined, we can perform appropriate mathematical operations. For example, we might want to the know the number of days there are between two dates.

[3] http://en.wikipedia.org/wiki/List_of_tz_database_time_zones

```
Wedding <- ymd('2010-Sep-18')
Elise <- ymd('2013-Jan-11')
Childless <- Elise - Wedding
Childless

## Time difference of 846 days
```

Because both dates were recorded without the hours or seconds, R defaults to just reporting the difference in number of days.

Often I want to add two weeks, or 3 months, or one year to a date. However it is not completely obvious what I mean by "add 1 year". Do we mean to increment the year number (eg Feb 2, 2011 -> Feb 2, 2012) or do we mean to add 31,536,000 seconds? To get around this, `lubridate` includes functions of the form `dunits()` and `units()` where the "unit" portion could be `year`, `month`, `week`, etc. The "d" prefix will stand for duration when appropriate.

```
x <- ymd("2011-Feb-21")
x + years(2)

## [1] "2013-02-21 UTC"

# 2012 was a leap year, so Feb 21, 2011 + 2*365 days results in Feb 20, 2013
x + dyears(2)

## [1] "2013-02-20 UTC"
```

14.4 Exercises

1. For the following formats for a date, transform them into a date/time object. Which formats can be handled nicely and which are not?

September 13, 1978
Sept 13, 1978
Sep 13, 1978
9-13-78
9/13/78

2. Suppose that we have a vector of character strings but obnoxiously they are all in the form "9/13/76" and we want to turn them into dates where the year is 1976.

   ```
   my.dates <- c('10/5/72', '8/23/74', '9/13/76')
   ```

   To convert these to dates that have the proper year, I could use the `stringr` package to tear them apart, append a "19" in front of the year, and then put it back together with the following code:

   ```
   library(stringr)
   d2 <- str_split_fixed(my.dates, pattern=fixed('/'), n=3)
   d3 <- str_c( d2[,1], d2[,2], str_c('19',d2[,3]), sep = '-' )
   mdy(d3)
   ```

   Or we could use the `mdy()` function to convert these to dates and subtract 100 years. Write code to do the second solution.

3. Suppose you have arranged for a phone call to be at 3 pm on May 8, 2015 at Arizona time. However, the recipient will be in Auckland, NZ. What time will it be there?

4. Number of births per day.

   (a) Using the `mosaicData` package, load the data set `Births78` which records the number of children born on each day in the United States in 1978.

```
library(mosaicData)
data(Births78)
```

   (b) There is already a date column in the data set that is called, appropriately, `date`. Notice that `ggplot2` knows how to represent dates in a pretty fashion and the following chart looks nice.

```
library(ggplot2)
ggplot(Births78, aes(x=date, y=births)) +
  geom_point()
```

   What stands out to you? Why do you think we have this trend?

   (c) To test your assumption, we need to figure out the what day of the week each observation is. Use `dplyr::mutate` to add a new column named `dow` that is the day of the week (Monday, Tuesday, etc). This calculation will involve some function in the `lubridate` package.

   (d) Plot the data with the point `color` being determined by the `dow` variable.