A Sufficient Introduction to R

Derek L. Sonderegger

2017-10-17

Contents

Preface

This book is intended to guide people that are completely new to programming along a path towards a useful skill level using R. I belive that while people can get by with just copying code chunks, that doesn't give them the background information to modify the code in non-trivial ways. Therefore we will spend more time on foundational details than a "crash-course" would.

There is a manuel that shows how to use R that avoids many of the additional packages that I will use. cran.r-project.org/doc/manuals/R-intro.pdf.

Garrett Grolemund and Hadley Wickham have a book, R for Data Science that is very good and lays out the foundational ideas behind Hadley's *tidyverse*.

Chapter 1

Introduction

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 www.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.

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.

The basic editor that comes with R works fairly well, but you should consider running R through the program RStudio which is located at rstudio.com. This is a completely free Integrated Developement Environment that works on Macs, Windows and a couple of flavors of Linux. It simplifies a bunch of more annoying aspects of the standard R GUI and supports things like tab completion.

When you first open up R (or RStudio) the console window gives you some information about the version of R you are running and then it gives the prompt `>`. This 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.

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)   # exp() is the exponential function
```

```
## [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     # the constant 3.14159265...
```

```
## [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)  # 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. 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       # create two variables
my.test.var = 5   # notice they show up in 'Environment' tab in RStudio!
tau
```

```
## [1] 6.283185
```

```
my.test.var
```

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

```
tau * my.test.var
```

```
## [1] 31.41593
```

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

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. 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.

1.3.1 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 comment 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 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 now exists.

To create a new R Markdown document, we use the `File -> New File -> R Markdown...` dropdown 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 at the RMarkdown website.

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. I have actually created this entire book using RMarkdown.

1.4 Packages

One of the greatest strengths about R is that so many people have devloped add-on packages to do some additional function. For example, plant community ecologists have a large number of multivariate methods that are useful but were not part of R. So Jari Oksanen got together with some other folks and put together a package of functions that they found useful. The result is the package `vegan`.

To download and install the package from the Comprehensive R Archive Network (CRAN), you just need to ask RStudio it to install it via the menu `Tools -> Install Packages...`

Many major analysis types are available via downloaded packages as well as problem sets from various books (e.g. `Sleuth3` or `faraway`) and can be easily downloaded and installed via the menu.

Once a package is downloaded and installed on your computer, it is available, but it is not loaded into your current R session by default. The reason it isn't loaded is that there are thousands of packages, some of which are quite large and only used occasionally. So to improve overall performance only a few packages are loaded by default and the you must explicitly load packages whenever you want to use them. You only need to load them once per session/script.

For a similar performance reason, many packages do not automatically load their datasets unless explicitly asked. Therefore when loading datasets from a package, you might need to do a *two-step* process of loading the package and then loading the dataset.

```
library(faraway)      # load the package into memory
data("babyfood")      # load the dataset into memory
```

If you don't need to load any functions from a package and you just want the datasets, you can do it in one step.

```
data('babyfood', package='faraway')   # just load the dataset, not anything else
```

To get information about a package, you can use either of the following afer the library has been loaded:

```
library(help='faraway')
```

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. *Hint: use Google to find the square root function. Perhaps search on the keywords "R square root function".*
3. This exercise walks you through installing a package with all the datasets used in the textbook *The Statistical Sleuth*.
    a) Install the package `Sleuth3` on your computer using RStudio.
    b) Load the package using the `library()` command.
    c) Print out the dataset `case0101`

Chapter 2

Vectors

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)              # repeat 2 five times... 2 2 2 2 2
```

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

```
rep( c('A','B'), 3 )   # repeat A B three times  A B A B A B
```

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

Finally, we can also define a sequence of numbers using the `seq(from, to, 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.

```
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
```

[1] The "c" stands for collection.

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
```

2.1 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.

2.2 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
```

2.3 Vector Algebra

All algebra done with vectors will be done element-wise by default.For matrix and vector multiplication as usually defined by mathematicians, use `%*%` instead of `*`. So two vectors added together result in their individual elements being summed.

```
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
```

2.4 Commonly Used Vector Functions

Function	Result
`min(x)`	Minimum value in vector x
`max(x)`	Maximum value in vector x
`length(x)`	Number of elements in vector x
`sum(x)`	Sum of all the elements in vector x
`mean(x)`	Mean of the elements in vector x
`median(x)`	Median of the elements in vector x

Function	Result
`var(x)`	Variance of the elements in vector x
`sd(x)`	Standard deviation of the elements in 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
```

2.5 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 using Google)? 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.
   a) First using the `seq()` function
   b) Using the `a:b` shortcut.
5. Generate the vector of even numbers $\{2, 4, 6, \ldots, 20\}$

a) Using the seq() function and
b) Using the a:b shortcut and some subsequent algebra. *Hint: Generate the vector 1-10 and then multiple it by 2.*

6. Generate a vector of 21 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

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.

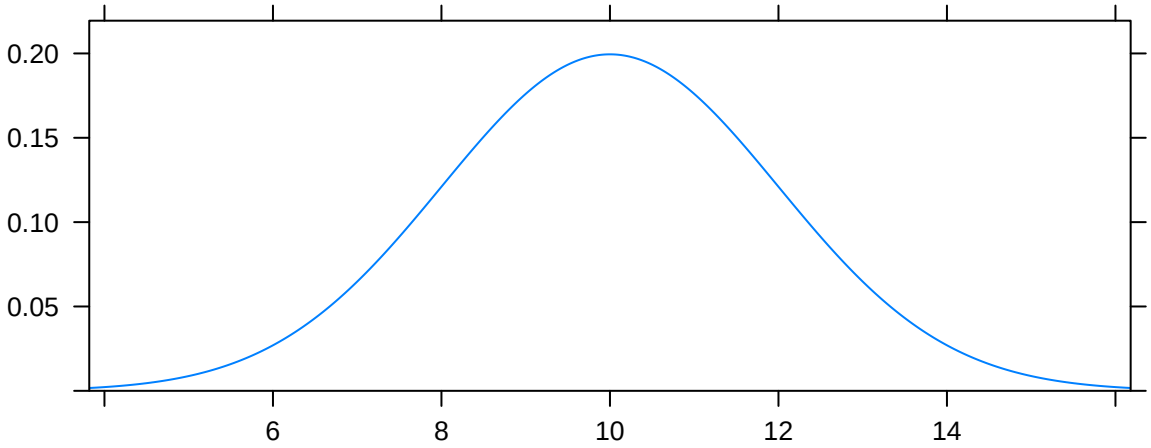
3.1 `mosaic::plotDist()` function

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	Stem	Parameters	Parameter Interpretation
Binomial	`binom`	`size prob`	Number of Trials Probability of Success (per Trial)
Exponential	`exp`	`rate`	Mean of the distribution
Normal	`norm`	`mean=0 sd=1`	Center of the distribution Standard deviation
Uniform	`unif`	`min=0 max=1`	Minimum of the distribution Maximum of the distribution

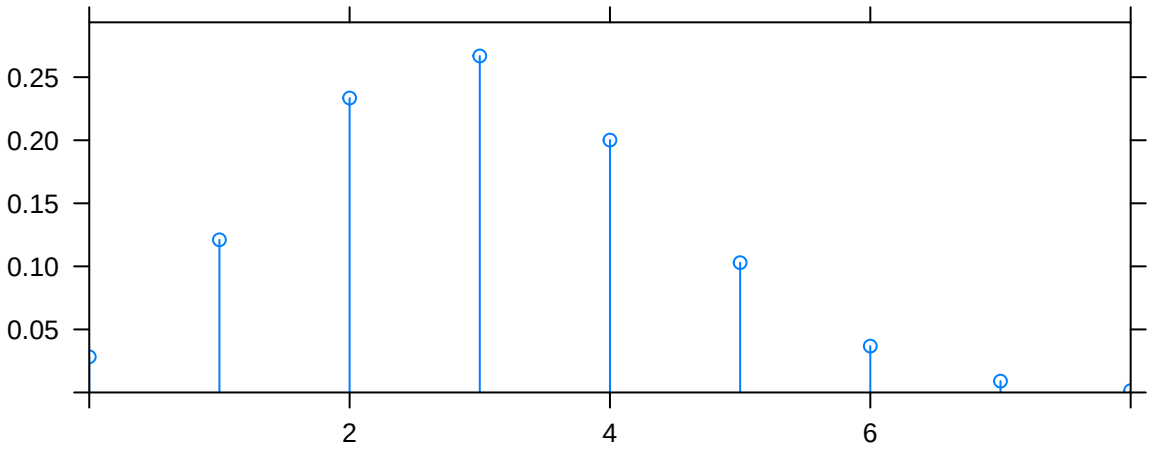
For example, to see the normal distribution with mean $mu = 10$ and standard deviation $\sigma = 2$, we use

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



This function works for discrete distributions as well.

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



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

Function	Result
`d`-function(x)	The height of the probability distribution/density at given x
`p`-function(x)	Find q such that $P(X \leq x) = q$ where x is given
`q`-function(q)	Find x such that $P(X \leq x) = q$ where q is given
`r`-function(n)	Generate n random observations from the distribution

For each distribution in R, there will 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.

3.2.1 d-function

The purpose of the d-function is to calculate the height of a probability mass function or a density function (The "d" actually stands for density). Notice that for discrete distributions, this is the probability of observing that particular value, while for continuous distributions, the height doesn't have a nice physical interpretation.

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

$$P\,(X = 0) = \binom{10}{0} 0.2^0\,(0.8)^{10} = 1 \cdot 1 \cdot 0.8^{10} \approx 0.107$$

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
```

3.2.2 p-function

Often we are interested in the probability of observing some value or anything less (In probability theory, we call this the cumulative density function or CDF). 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)   +       #   P(X==0) +
  dbinom(1, size=10, prob=.2) +       #     P(X==1) +
  dbinom(2, size=10, prob=.2)         #     P(X==2)
```

```
## [1] 0.6777995
```

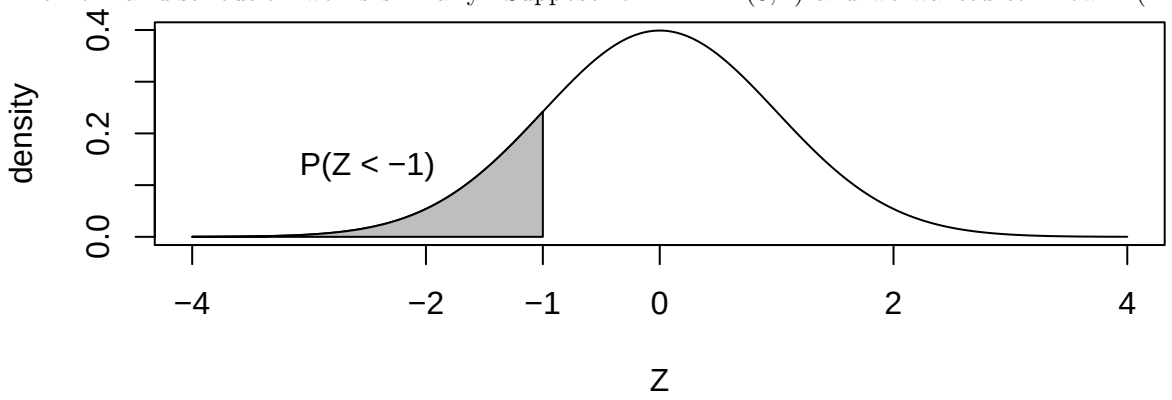
but this would get tedious for binomial distributions with a large number of trials. The shortcut is to use the `pbinom()` function.

```
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

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

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. Fortunately this x-variant exists for the Normal, Chi-squared, F, Gamma continuous distributions and the discrete Poisson, Geometric, and Binomial distributions.

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

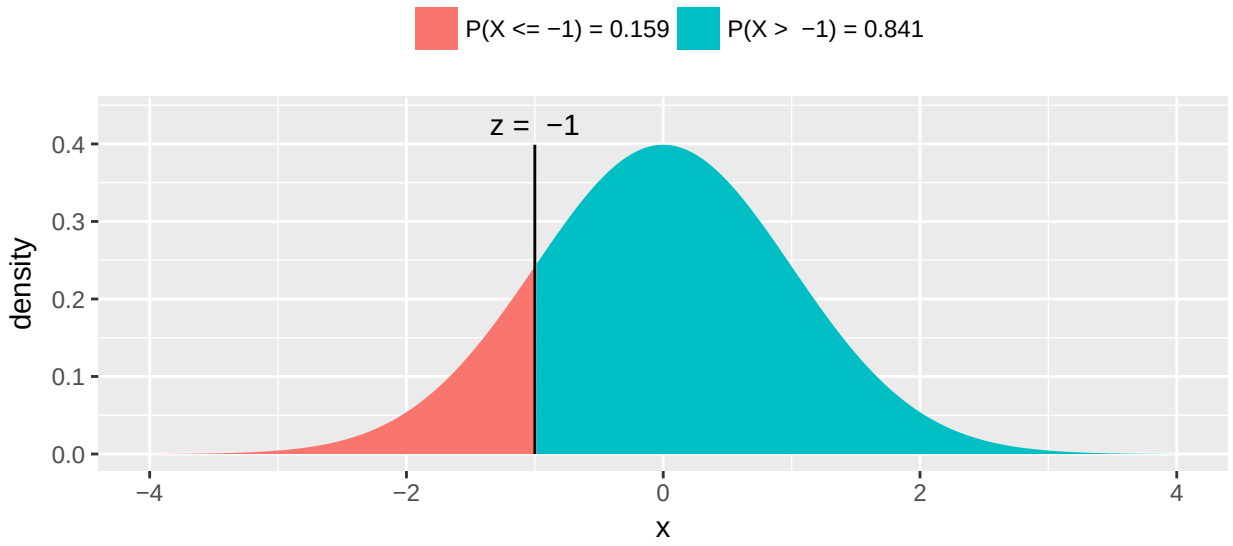
```
##
```

```
## 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
```

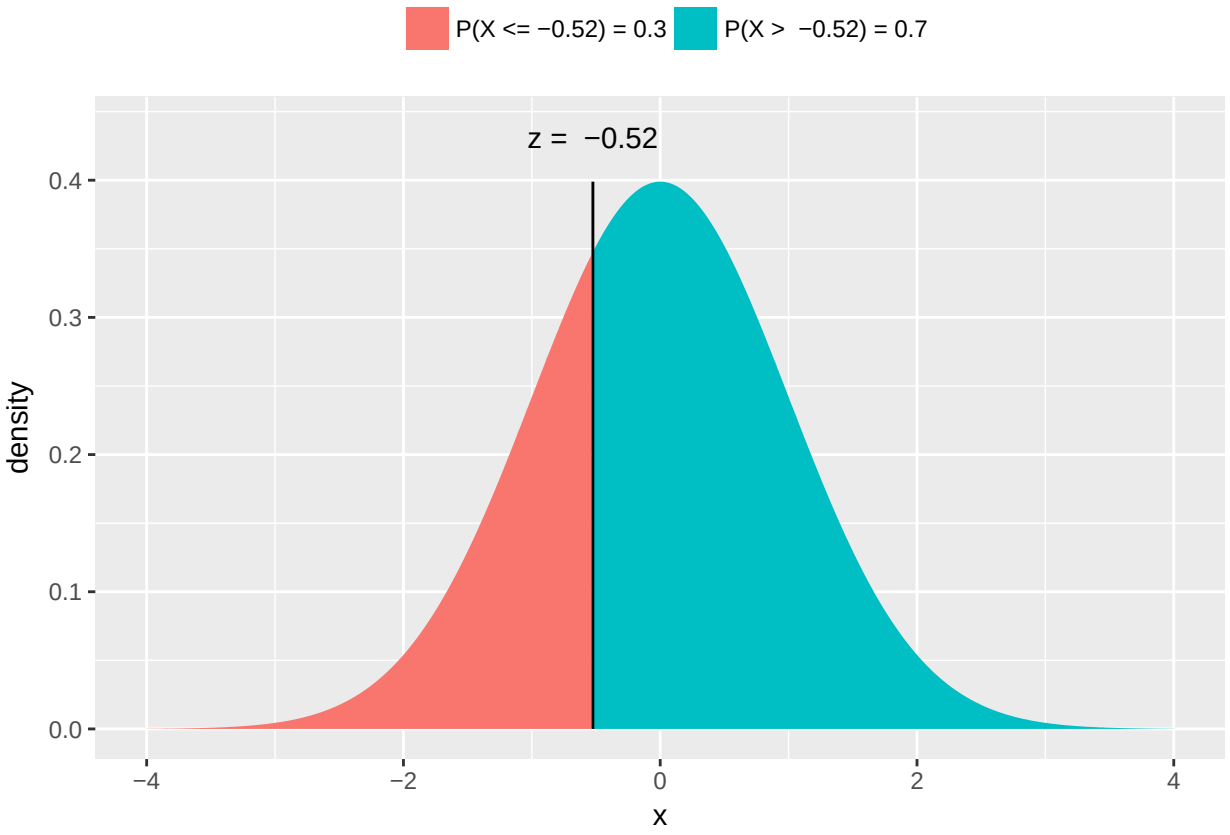
3.2.3 q-function

In class, we will also find ourselves asking for the quantiles of a distribution. Percentiles are by definition 1/100, 2/100, etc but if I am interested in something that isn't and even division of 100, we get fancy can call them quantiles. This is a small semantic quibble, but we ought to be precise. That being said, I won't correct somebody if they call these percentiles. 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 a book, we use the table in reverse. R gives us a handy way to do this with the `qnorm()` function and the mosaic package provides a nice visualization using the augmented `xqnorm()`. Below, I specify that I'm using a function in the `mosaic` package by specifying it via `PackageName::FunctionName()` but that isn't strictly necessary but can improve readability of your code.

```
mosaic::xqnorm(0.30)   # Give me the value along with a pretty picture
```

```
##
## If X ~ N(0, 1), then
##  P(X <= -0.5244005) = 0.3
##  P(X >  -0.5244005) = 0.7
##
```




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

```
qnorm(.30)              # No pretty picture, just the value
```

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

3.2.4 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] 23.96150 18.94976 17.12487 21.37702 18.74837
```

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

```
## [1] 9 7 9 7
```

3.3 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 and exponential distributions.

a) Use the mosaic function `plotDist()` to produce a graph of the standard normal distribution (that is a normal distribution with mean $\mu = 0$ and standard deviation $\sigma = 1$.

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 $P(Y \leq 1)$. (Unfortunately there isn't a mosaic augmented `xpexp()` function.)

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.

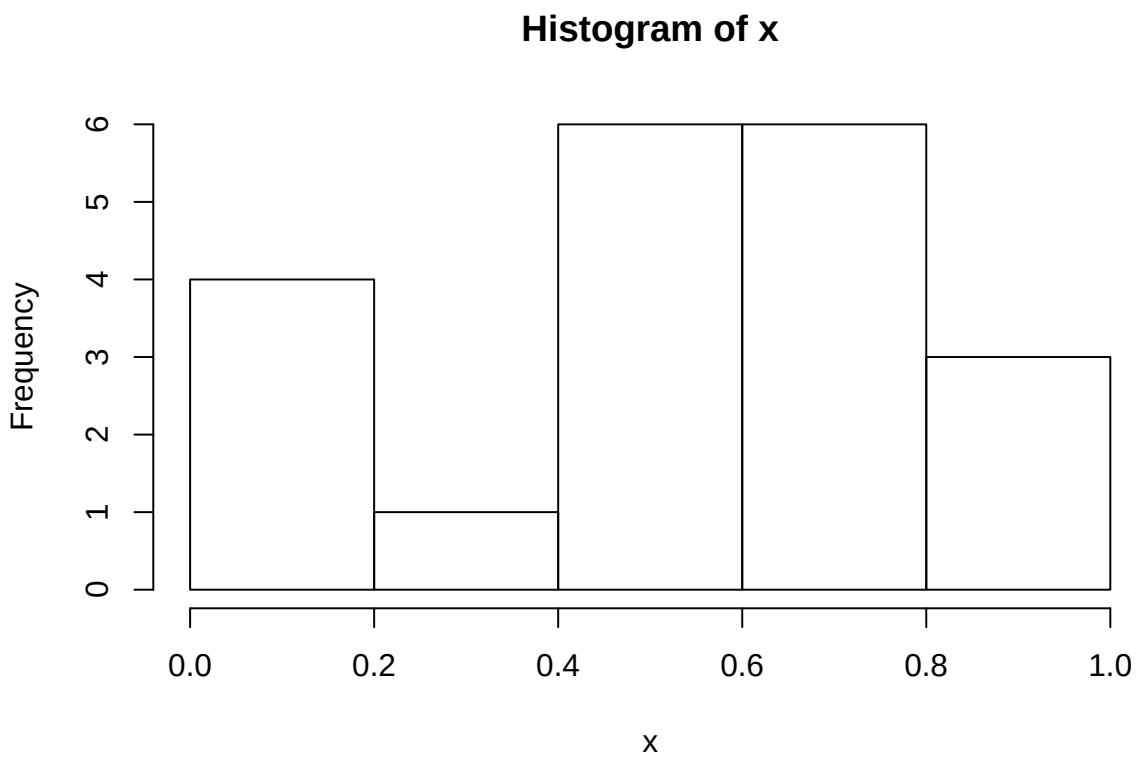
a) Generate a single value from a uniform distribution with minimum 0, and maximum 1 using the `runif()` function. Repeat this step several times and confirm you are getting different values each time.

b) Generate a sample of size 20 from the same uniform distribution and save it as the vector `x` using the following:

```
x <- runif(20, min=0, max=1)
```

Then produce a histogram of the sample using the function `hist()`

```
hist(x)
```



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 4

Data Types

There are some basic data types that are commonly used.

1. Integers - These are the integer numbers $(\ldots, -2, -1, 0, 1, 2, \ldots)$. 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. For converting numeric values to factors, I will often use the function `cut()`.
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.

4.1 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)   # the str() command show the STRucture of the object
```

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

4.2 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. 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
```

4.3 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"
```

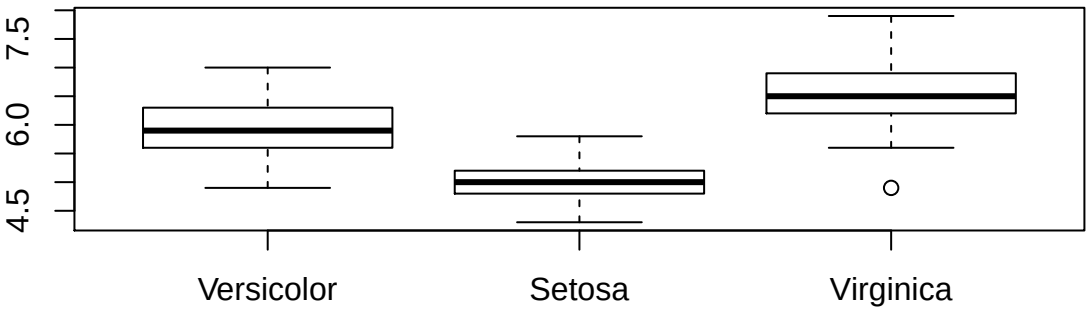
Notice that the order of the group names was done alphabetically, which we did not chose. This ordering of the levels has implications when we do an analysis or make a plot and R will always display information about the factor levels using this order. It would be nice to be able to change the order. 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,                        # vector of data levels to convert
            levels=c('B','A','C'),    # Order of the levels
            labels=c("B Group", "A Group", "C Group")) # Pretty labels to use
z
```

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

For the Iris data, the species are ordered alphabetically. We might want to re-order how they appear in a graphs to place Versicolor first. The `Species` names are not capitalized, and perhaps I would like them to begin with a capital letter.

```
iris$Species <- factor( iris$Species,
                        levels = c('versicolor','setosa','virginica'),
                        labels = c('Versicolor','Setosa','Virginica'))
boxplot( Sepal.Length ~ Species, data=iris)
```



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
```

4.4 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.

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 <- -10:10     # a vector of 20 values, (11th element is the 0)
x
```

```
##  [1] -10  -9  -8  -7  -6  -5  -4  -3  -2  -1   0   1   2   3   4   5   6
## [18]   7   8   9  10
```

```
x > 0           # a vector of 20 logicals
```

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

```
which( x > 0 )  # which vector elements are > 0
```

```
##  [1] 12 13 14 15 16 17 18 19 20 21
```

```
x[ which(x>0) ] # Grab the elements > 0
```

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

On function I find to be occasionally useful is the `is.element(el, set)' 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  # 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 given a bunch of students and a vector of their GPAs and another vector of their major, maybe I want to find all undergraduate Forestry majors with a GPA greater than 3.0. Then, given 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
```

4.5 Exercises

1. Create a vector of character strings with six elements

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

   and then

   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. Also, make sure that the order of the levels is `Minor` first and `Adult` second.

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 (c) to integer values using the `as.numeric()` function. Which numeric value corresponds to TRUE?
   e) Sum (using the `sum()` function) the vector you created to count the number of students with GPA > 3.0 and are a forestry major.

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 5

Matrices, Data Frames, and Lists

5.1 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:

```
W <- matrix( c(1,2,3,4,5,6), nrow=2, ncol=3 )
W
```

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

Notice that because we only gave it six values, the information the number of columns is redundant and could be left off and R would figure out how many columns are needed. Next notice that the order that R chose to fill in the matrix was to fill in the first column then the second, and then the third. If we wanted to fill the matrix in order of the rows first, then we'd use the optional `byrow=TRUE` argument.

```
W <- matrix( c(1,2,3,4,5,6), nrow=2, byrow=TRUE )
W
```

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

The alternative to the `matrix()` command 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

```
a <- c(1,2,3)
b <- c(4,5,6)
cbind(a,b)  # Column Bind:  a,b are columns in resultant matrix
```

```
##      a b
## [1,] 1 4
## [2,] 2 5
## [3,] 3 6
```

```
rbind(a,b)  # Row Bind:     a,b are   rows  in resultant matrix
```

```
##   [,1] [,2] [,3]
## a    1    2    3
## b    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')       # set column labels
rownames(M) <- c('Row1', 'Row2','Row3')      # set row labels
M
```

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

This is actually a pretty peculiar way of setting the *attributes* of the object `M` because it looks like we are evaluating a function and assigning some value to the function output. Yes it is weird, but R was developed in the 70s and it seemed like a good idea at the time.

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 row 1, and columns 1 and 2.
```

```
## [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 (the spaces are optional...)
```

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

5.2 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 of row `a`
`[,b]`	All of column `b`

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.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       # The $-sign means to reference a column by its label
```

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

```
data$Name[2]    # Notice that data$Name results in a vector, which I can manipulate
```

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

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

```
data[, 'Name']   # Grab the column labeled '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))  # another data.frame
data <-  cbind( data, Second.score )            # squish them together
```

```
data
```

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

```
# if you assign a value to a column that doesn't exist, R will create it
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.

Data frames are also very restricive in that the shape of the data must be rectangular. If I try to create a new column that doesn't have enough rows, R will complain.

```
data$Score4 <- c(1,2)
```

```
## Error in `$<-.data.frame`(`*tmp*`, "Score4", value = c(1, 2)): replacement has 2 rows, data has 3
```

5.3 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 because 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) # Create the list
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 is a vector of length four. Finally the vector of pets' names is only of length three.

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 ]]    # First element of the list is Spouse!
```

```
## [1] "Aubrey"
```

```
Derek[[ 3 ]]    # Third element of the list is the vector of pets
```

```
## [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. 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. To access my pets names we can use the following notation:

```
Derek$Pets         # Using the '$' notation
```

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

```
Derek[[ 'Pets' ]]  # Using the '[[ ]]' notation
```

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

To add something new to the list object, we can just make an assignment in a similar fashion as we did for `data.frame` and just assign a value to a slot that doesn't (yet!) exist.

```
Derek$Spawn <- c('Elise', 'Casey')
```

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

```
# Recall that we previous had defined a data.frame called "data"
Derek$RandomDataFrame <- data  # Assign it to be a list element
str(Derek)
```

```
## List of 5
##  $ Spouse         : chr "Aubrey"
##  $ Siblings       : chr [1:4] "Tina" "Caroline" "Brandon" "John"
##  $ Pets           : chr [1:3] "Beau" "Tess" "Kaylee"
##  $ Spawn          : chr [1:2] "Elise" "Casey"
##  $ RandomDataFrame:'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
```

Now we see that the list `Derek` has five elements and some of those elements are pretty complicated. In fact, I could happily have lists of lists and have a very complicated nesting structure.

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)   # some toy data
results <- t.test(x, alternative='less', mu=5)   # do a t-test
str(results)                                     # examine the resulting object
```

```
## 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:

```
results$p.value
```

```
## [1] 0.3813385
```

If I ask R to print the object `results`, 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.

```
results
```

```
##
##  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
```

5.4 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 `my.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 (i.e. the third row)
c) Extract the Girth column referring to it by name (don't use whatever order you placed the columns in).
d) Print out a data frame of all the observations *except* for the fourth observation. (i.e. Remove the fourth observation/row.)
e) Use the `which()` command to create a vector of row indices that have a `girth` greater than 10. Call that vector `index`.
f) Use the `index` vector to create a small data set with just the small girth trees.
g) Use the `index` vector to create a small data set with just the large girth trees.

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 in 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 6

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 greenhouse experiment dataset will have a row for every plant and columns for treatment type and biomass.

6.1 Working directory

One concept that will be important is to recognize that every time you start up RStudio, it picks an appropriate working directory. This is the directory where it will first look for script files or data files. By default when you double click on an R script or Rmarkdown file to launch RStudio, it will set the working directory to be the directory that the file was in. Similarly, when you knit an Rmarkdown file, the working directory will be set to the directory where the Rmarkdown file is. For both of these reasons, I always program my scripts assuming that paths to any data files will be relative to where where my Rmarkdown file is. To set the working directory explicitly, you can use the GUI tools `Session -> Set Working Directory....`

The functions that we will use in this lab all accept a character string that denotes the location of the file. This location could be a web address, it could be an absolute path on your computer, or it could be a path relative to the location of your Rmarkdown file.

`'MyFile.csv'`	Look in the working directory for `MyFile.csv`.
`'MyFolder/Myfile.csv'`	In the working directory, there is a subdirectory called `MyFolder` and inside that folder there is a filed called `MyFile.csv`.

6.2 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	What it does
`file`		A character string denoting the file location
`header`	FALSE	Is the first line column headers?
`sep`	" "	What character separates columns. " " == any whitespace
`skip`	`0`	The number of lines to skip before reading data. This is useful when there are lines of text that describe the data or aren't actual data
`na.strings`	'NA'	What values represent missing data. Can have multiple. E.g. `c('NA', -9999)`
`quote`	" and '	For character strings, what characters represent quotes.

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.

6.3 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 sheets) 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`. Another package that does this is the XLConnect which does the Excel -> .csv conversion using Java. Another package the works well is the `xlsx` package, but it also requires Java to be installed. The nice thing about these two packages is that they also allow you to write Excel files as well. 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.

The `readxl` package 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). One annoying change between `read.table()` and `read_excel()` is that the argument for specifying where the file is is different (`path=` instead of `file=`). Another difference between the two is that `read_excel()` does not yet have the capability of handling a path that is a web address.

From GitHub, download the files `Example_1.xls`, `Example_2.xls`, `Example_3.xls` and `Example_4.xls` from the directory [https://github.com/dereksonderegger/570L/tree/master/data-raw]. Place these files in the same directory that you store your course work or make a subdirectory data to store the files in. 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.
library(readxl)

# Where does the data live relative to my current working location?
#
# In my directory where this Rmarkdown file lives, I have made a subdirectory
#    named 'data-raw' to store all the data files. So the path to my data
#    file will be 'data-raw/Example_1.xls'.
# If you stored the files in the same directory as your RMarkdown script, you
#    don't have to add any additional information and you can just tell it the
#    file name 'Example_1.xls'
# Alternatively I could give the full path to this file starting at the root
#    directory which, for me, is '~/GitHub/STA570L_Book/data-raw/Example_1.xls'
#    but for Windows users it might be 'Z:/570L/Lab7/Example_1.xls'. This looks
#    odd because Windows usually uses a backslash to represent the directory
#    structure, but a backslash has special meaning in R and so it wants
#    to separate directories via forwardslashes.

# read the first worksheet of the Example_1 file
data.1 <- read_excel( 'data-raw/Example_1.xls'  )   # relative to this Rmarkdown file
data.1 <- read_excel('~/GitHub/570L/data-raw/Example_1.xls')  # absolute path

# read the second worksheet where the second worksheet is named 'data'
data.2 <- read_excel('data-raw/Example_2.xls', sheet=2     )
data.2 <- read_excel('data-raw/Example_2.xls', sheet='data')
```

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 using tools we'll learn when we get to the *Manipulating Data* chapter.

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:

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

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    34 obs. of  14 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 ...
##  $ X__1 : logi  NA NA NA NA NA NA ...
##  $ X__2 : logi  NA NA NA NA NA NA ...
```

We notice that after reading in the data, there is an additional column that just has missing data (the NA stands for not available which means that the data is missing) and a row with just a single blank. 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.

6.4 Exercises

1. Download from GitHub the data 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 7

Data Manipulation

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 Classical functions for summarizing rows and columns

7.1.1 `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
##
##
```

##

7.1.2 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 ) # squish together
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.

7.2 Package `dplyr`

```
library(dplyr)   # load the dplyr package!
```

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 Dr Wickham 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].

One of the aspects about the `data.frame` object is that R does some simplification for you, but it does not do it in a consistent manner. Somewhat obnoxiously character strings are always converted to factors and subsetting might return a `data.frame` or a `vector` or a `scalar`. This is fine at the command line, but can be problematic when programming. Furthermore, many operations are pretty slow using `data.frame`. To get around this, Dr Wickham introduced a modified version of the `data.frame` called a `tibble`. A `tibble` is a `data.frame` but with a few extra bits. For now we can ignore the differences.

The pipe command `%>%` allows for very readable code. The idea is that the `%>%` operator works by translating the command `a %>% f(b)` to the expression `f(a,b)`. This operator works on any function and was introduced in the `magrittr` package. The beauty of this comes when you have a suite of functions that takes input arguments of the same type as their output.

For example if we wanted to start with `x`, and first apply function `f()`, then `g()`, and then `h()`, the usual R command would be `h(g(f(x)))` which is hard to read because you have to start reading at the innermost set of parentheses. Using the pipe command `%>%`, this sequence of operations becomes `x %>% f() %>% g() %>% h()`.

Dr Wickham gave the following example of readability:

```
bopping(
  scooping_up(
    hopping_through(foo_foo),
    field_mice),
  head)
```

is more readably written:

```
foo_foo %>%
  hopping_through(forest) %>%
  scooping_up( field_mice) %>%
  bopping( head )
```

In `dplyr`, all the functions below take a data set as its first argument and outputs an appropriately modified data set. This will allow me to chain together commands in a readable fashion.

7.2.1 Verbs

The foundational operations to perform on a data set are:

- Subsetting - Returns a 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 other columns.
- `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 set, 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 set.

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

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

7.2.1.1.1 `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.

```
# 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
```

I could select the columns Exam columns by hand, or by using an extension of the `:` operator

```
grades %>% select( Exam1, Exam2 )   # Exam1 and Exam2
```

```
##   Exam1 Exam2
## 1    93    98
## 2    89    70
## 3    80    82
## 4    70    85
```

```
grades %>% select( Exam1:Final )    # Columns Exam1 through Final
```

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

```
grades %>% select( -Exam1 )          # Negative indexing by name works
```

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

```
grades %>% select( 1:2 )             # Can select column by column position
```

```
##   l.name Exam1
## 1    Cox    93
## 2 Dorian    89
## 3  Kelso    80
## 4   Turk    70
```

The `select()` command has a few other tricks. There are functional calls that describe the columns you wish to select that take advantage of pattern matching. I generally can get by with `starts_with()`, `ends_with()`, and `contains()`, but there is a final operator `matches()` that takes a regular expression.

```
grades %>% select( starts_with('Exam') )    # Exam1 and Exam2
```

```
##   Exam1 Exam2
## 1    93    98
## 2    89    70
## 3    80    82
## 4    70    85
```

7.2.1.1.2 `filter()`

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

```
# 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. 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`.

```
# 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
```

7.2.1.1.3 slice()

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

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

```
## # A tibble: 2 x 5
##   l.name Exam1 Exam2 Final  average
##   <fctr> <dbl> <dbl> <dbl>    <dbl>
## 1    Cox    93    98    96 95.66667
## 2 Dorian    89    70    85 81.33333
```

7.2.1.2 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.

```
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
```

7.2.1.3 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.

```
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),  # cut takes numeric variable
                       c( 'F','D','C','B','A')) )  # and makes a factor
```

```
##   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
```

We might look at this data frame and want to do some rounding. For example, I might want to take each numeric column and round it. In this case, the functions `mutate_at()` and `mutate_if()` allow us to apply a function to a particular column and save the output.

```
# for each column, if it is numeric, apply the round() function to the column
# while using any additional arguments.  So round two digits.
grades %>%
  mutate_if( is.numeric, round, digits=2 )
```

```
##   l.name Exam1 Exam2 Final average
## 1    Cox    93    98    96   95.67
## 2 Dorian    89    70    85   81.33
## 3  Kelso    80    82    81   81.00
## 4   Turk    70    85    92   82.33
```

The `mutate_at()` function works similarly, but we just have to specify with columns.

```
# round columns 2 through 5
grades %>%
  mutate_at( 2:5, round, digits=2 )
```

```
##   l.name Exam1 Exam2 Final average
## 1    Cox    93    98    96   95.67
## 2 Dorian    89    70    85   81.33
## 3  Kelso    80    82    81   81.00
## 4   Turk    70    85    92   82.33
```

```
# round columns that start with "ave"
grades %>%
  mutate_at( vars(starts_with("ave")), round )
```

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

```
# These do not work because they doesn't evaluate to column indices.
# I can only hope that at some point, this syntax works
#
# grades %>%
#   mutate_at( starts_with("ave"), round )
#
# grades %>%
#   mutate_at( Exam1:average, round, digits=2 )
```

7.2.1.4 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
grades %>% summarise( mean.E1=mean(Exam1))
```

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

We could calculate multiple summary statistics if we like.

```
# calculate the mean and standard deviation
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_all()` 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()`)). There are two variants `summarize_at()` and `summarize_if()` that give you a bit more flexibility.

```
# calculate the mean and stddev of each column - Cannot do this to Names!
grades %>%
  select( Exam1:Final ) %>%
  summarise_all( funs(mean, sd) )
```

```
##   Exam1_mean Exam2_mean Final_mean Exam1_sd Exam2_sd Final_sd
## 1         83      83.75       88.5 10.23067     11.5 6.757712
```

```
grades  %>%
  summarise_if(is.numeric, funs(Xbar=mean, SD=sd) )
```

```
##   Exam1_Xbar Exam2_Xbar Final_Xbar average_Xbar Exam1_SD Exam2_SD Final_SD
## 1         83      83.75       88.5     85.08333 10.23067     11.5 6.757712
##   average_SD
## 1   7.078266
```

7.2.1.5 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.

7.2.2 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 per `wool:tension` level.

```
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.

```
# group_by:  what variable(s) shall we group one
# n() is a function that returns how many rows are in the
#   currently selected sub-dataframe
warpbreaks %>%
  group_by( wool, tension) %>%    # grouping
  summarise(n = n() )             # how many in each group
```

```
## # A tibble: 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
```

The `group_by` function takes a data.frame and returns the same data.frame, but with some extra information so that any subsequent function acts on each unique combination defined in the `group_by`. If you wish to remove this behavior, use `group_by()` to reset the grouping to have no grouping variable.

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 show the
             mean.breaks = mean(breaks),    # reader I am calculating several
             sd.breaks   = sd(breaks))      # statistics.
```

```
## # A tibble: 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.

```
warpbreaks %>%
   group_by(wool, tension) %>%                  # group by wool:tension
   mutate(resid = breaks - mean(breaks)) %>%    # mean(breaks) of the group!
   head(  )                                     # show the first couple of rows
```

```
## # A tibble: 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
```

7.2.3 Chaining commands together

In the previous examples we have used the %>% operator to make the code more readable but to really appreciate this, we should examine the alternative.

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'))
```

We could run all the commands together using the following code:

```
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
```

```
## # A tibble: 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 very difficult to read because you have to read the code *from the inside out.*

Another (and slightly more readable) way to complete our task is to save each intermediate step of our process and then use that in the next step:

```
temp.df0 <- race.results %>% group_by( gender)
temp.df1 <- temp.df0 %>% mutate( place = rank(time) )
temp.df2 <- temp.df1 %>% arrange( gender, place )
```

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. This is exactly what %>% does for me.

```
race.results %>%
  group_by( gender ) %>%
  mutate( place = rank(time)) %>%
  arrange( gender, place )
```

```
## # A tibble: 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
```

7.3 Exercises

1. The dataset `ChickWeight` 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 ones on day 10 or day 20.
   d) Calculate the mean and standard deviation of the chick weights 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

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

   d) Double check that your calculated BMI column is correct by examining the summary statistics of the column. BMI values should be between 18 to 40 or so. Did you make an error in your calculation?
   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]
```

```
# (0,2.5] (2.5,5] means 2.5 is included in first group
# right=FALSE changes this to make 2.5 included in the second

# 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.

```
Body <- Body %>%
  mutate( Age.Grp = cut(age,
                        breaks=c(10,20,30,40,50,60,70),
                        right=FALSE))
```

f) Find the average BMI for each Sex-by-Age combination.

Chapter 8

Data Reshaping

```
library(tidyr)   # for the gather/spread commands
library(dplyr)   # for the join stuff
```

Most of the time, our data is in the form of a data frame and we are interested in exploring the relationships. However most procedures in R expect the data to show up in a 'long' format where each row is an observation and each column is a covariate. In practice, the data is often not stored like that and the data comes to us with repeated observations included on a single row. This is often done as a memory saving technique or because there is some structure in the data that makes the 'wide' format attractive. As a result, we need a way to convert data from 'wide' to 'long' and vice-versa.

8.1 `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, HW.4=4),
  data.frame(name='Brandon', HW.1=5, HW.2=3, HW.3=6, HW.4=9),
  data.frame(name='Charles', HW.1=9, HW.2=7, HW.3=9, HW.4=10))
grade.book
```

```
##      name HW.1 HW.2 HW.3 HW.4
## 1  Alison    8    5    8    4
## 2 Brandon    5    3    6    9
## 3 Charles    9    7    9   10
```

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 3 rows of 4 columns or 12 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 HW4 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/]

8.1.1 Verbs

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, HW2, HW3 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. This takes a key column (or columns) and a results column and forms a new column for each level of the key column(s).

```
# first we gather the score columns into columns we'll name Assesment and Score
tidy.scores <- grade.book %>%
  gather( key=Assessement,  # What should I call the key column
          value=Score,      # What should I call the values column
          HW.1:HW.4         # which columns to apply this to
          )
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
## 10  Alison        HW.4     4
## 11 Brandon        HW.4     9
## 12 Charles        HW.4    10
```

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

```
# Turn the Assessment/Score pair of columns into one column per factor level of Assessment
tidy.scores %>% spread( key=Assessement, value=Score )
```

```
##      name HW.1 HW.2 HW.3 HW.4
## 1  Alison    8    5    8    4
## 2 Brandon    5    3    6    9
## 3 Charles    9    7    9   10
```

One way to keep straight which is the `key` column is that the key is the category, while `value` is the numerical value or response.

8.2 Storing Data in Multiple Tables

In many datasets it is common to store data across multiple tables, usually with the goal of minimizing memory used as well as providing minimal duplication of information so any change that must be made is only made in a single place.

To see the rational why we might do this, consider building a data set of blood donations by a variety of donors across several years. For each blood donation, we will perform some assay and measure certain qualities about the blood and the patients health at the donation.

```
##   Donor Hemoglobin Systolic Diastolic
## 1 Derek       17.4      121        80
## 2  Jeff       16.9      145       101
```

But now we have to ask, what happens when we have a donor that has given blood multiple times? In this case we should just have multiple rows per person along with a date column to uniquely identify a particular donation.

```
donations
```

```
##   Donor       Date Hemoglobin Systolic Diastolic
## 1 Derek 2017-04-14       17.4      120        79
## 2 Derek 2017-06-20       16.5      121        80
## 3  Jeff 2017-08-14       16.9      145       101
```

I would like to include additional information about the donor where that infomation doesn't change overtime. For example we might want to have information about the donar's birthdate, sex, blood type. However, I don't want that information in *every single donation line*. Otherwise if I mistype a birthday and have to correct it, I would have to correct it *everywhere*. For information about the donor, should live in a `donors` table, while information about a particular donation should live in the `donations` table.

Furthermore, there are many Jeffs and Dereks in the world and to maintain a unique identifier (without using Social Security numbers) I will just create a `Donor_ID` code that will uniquely identify a person. Similarly I will create a `Donation_ID` that will uniquely identify a dontation.

```
donors
```

```
##   Donor_ID F_Name L_Name B_Type      Birth       Street      City State
## 1  Donor_1  Derek    Lee     O+ 1976-09-17 7392 Willard Flagstaff    AZ
## 2  Donor_2   Jeff  Smith      A 1974-06-23     873 Vine   Bozeman    MT
```

```
donations
```

```
##   Donation_ID Donor_ID       Date Hemoglobin Systolic Diastolic
## 1  Donation_1  Donor_1 2017-04-14       17.4      120        79
## 2  Donation_2  Donor_1 2017-06-20       16.5      121        80
## 3  Donation_3  Donor_2 2017-08-14       16.9      145       101
```

If we have a new donor walk in and give blood, then we'll have to create a new entry in the `donors` table as well as a new entry in the `donations` table. If an experienced donor gives again, we just have to create a new entry in the donations table.

```
donors
```

```
##   Donor_ID F_Name L_Name B_Type      Birth       Street      City State
## 1  Donor_1  Derek    Lee     O+ 1976-09-17 7392 Willard Flagstaff    AZ
## 2  Donor_2   Jeff  Smith      A 1974-06-23     873 Vine   Bozeman    MT
## 3  Donor_3 Aubrey    Lee     O+ 1980-12-15 7392 Willard Flagstaff    AZ
```

```
donations
```

```
##   Donation_ID Donor_ID       Date Hemoglobin Systolic Diastolic
## 1  Donation_1  Donor_1 2017-04-14       17.4      120        79
## 2  Donation_2  Donor_1 2017-06-20       16.5      121        80
## 3  Donation_3  Donor_2 2017-08-14       16.9      145       101
## 4  Donation_4  Donor_1 2017-08-26       17.6      120        79
## 5  Donation_5  Donor_4 2017-08-26       16.1      137        90
```

This data storage set-up might be flexible enough for us. However what happens if somebody moves? If we don't want to keep the historical information, then we could just change the person's `Street_Address`, `City`,

and `State` values. If we do want to keep that, then we could create `donor_addresses` table that contains a `Start_Date` and `End_Date` that denotes the period of time that the address was valid.

```
donor_addresses
```

```
##   Donor_ID       Street      City State Start_Date   End_Date
## 1  Donor_1 346 Treeline   Pullman    WA 2015-01-26 2016-06-27
## 2  Donor_1     645 Main Flagstsff    AZ 2016-06-28 2017-07-02
## 3  Donor_1 7392 Willard Flagstaff    AZ 2017-07-03       <NA>
## 4  Donor_2     873 Vine   Bozeman    MT 2015-03-17       <NA>
## 5  Donor_3 7392 Willard Flagstaff    AZ 2017-06-01       <NA>
```

Given this data structure, we can now easily create new donations as well as store donor information. In the event that we need to change something about a donor, there is only *one* place to make that change.

However, having data spread across multiple tables is challenging because I often want that information squished back together. For example, the blood donations services might want to find all 'O' or 'O+' donors in Flagstaff and their current mailing address and send them some notification about blood supplies being low. So we need someway to join the `donors` and `donor_addresses` tables together in a sensible manner.

8.3 Table Joins

Often we need to squish together two data frames but they do not have the same number of rows. Consider the case where we have a data frame of observations of fish and a separate data frame that contains information about lake (perhaps surface area, max depth, pH, etc). I want to store them as two separate tables so that when I have to record a lake level observation, I only input it *one* place. This decreases the chance that I make a copy/paste error.

To illustrate the different types of table joins, we'll consider two different tables.

```
# tibbles are just data.frames that print a bit nicer and don't automatically
# convert character columns into factors.  They behave a bit more consistently
# in a wide variety of situations compared to data.frames.
Fish.Data <- tibble(
  Lake_ID = c('A','A','B','B','C','C'),
  Fish.Weight=rnorm(6, mean=260, sd=25) ) # make up some data
Lake.Data <- tibble(
  Lake_ID = c(    'B','C','D'),
  Lake_Name = c('Lake Elaine', 'Mormon Lake', 'Lake Mary'),
  pH=c(6.5, 6.3, 6.1),
  area = c(40, 210, 240),
  avg_depth = c(8, 10, 38))
```

```
Fish.Data
```

```
## # A tibble: 6 x 2
##   Lake_ID Fish.Weight
##     <chr>       <dbl>
## 1       A    256.7093
## 2       A    258.2189
## 3       B    270.7256
## 4       B    292.8283
## 5       C    218.2320
## 6       C    264.9899
```

```
Lake.Data
```

```
## # A tibble: 3 x 5
##   Lake_ID   Lake_Name    pH  area avg_depth
##     <chr>       <chr> <dbl> <dbl>     <dbl>
## 1       B Lake Elaine   6.5    40         8
## 2       C Mormon Lake   6.3   210        10
## 3       D   Lake Mary   6.1   240        38
```

Notice that each of these tables has a column labled `Lake_ID`. When we join these two tables, the row that describes lake `A` should be duplicated for each row in the `Fish.Data` that corresponds with fish caught from lake `A`.

```
full_join(Fish.Data, Lake.Data)
```

```
## Joining, by = "Lake_ID"
```

```
## # A tibble: 7 x 6
##   Lake_ID Fish.Weight   Lake_Name    pH  area avg_depth
##     <chr>       <dbl>       <chr> <dbl> <dbl>     <dbl>
## 1       A    256.7093        <NA>    NA    NA        NA
## 2       A    258.2189        <NA>    NA    NA        NA
## 3       B    270.7256 Lake Elaine   6.5    40         8
## 4       B    292.8283 Lake Elaine   6.5    40         8
## 5       C    218.2320 Mormon Lake   6.3   210        10
## 6       C    264.9899 Mormon Lake   6.3   210        10
## 7       D          NA   Lake Mary   6.1   240        38
```

Notice that because we didn't have any fish caught in lake `D` and we don't have any Lake information about lake `A`, when we join these two tables, we end up introducing missing observations into the resulting data frame.

The other types of joins govern the behavor or these missing data.

`left_join(A, B)` For each row in A, match with a row in B, but don't create any more rows than what was already in A.

`inner_join(A,B)` Only match row values where both data frames have a value.

```
left_join(Fish.Data, Lake.Data)
```

```
## Joining, by = "Lake_ID"
```

```
## # A tibble: 6 x 6
##   Lake_ID Fish.Weight   Lake_Name    pH  area avg_depth
##     <chr>       <dbl>       <chr> <dbl> <dbl>     <dbl>
## 1       A    256.7093        <NA>    NA    NA        NA
## 2       A    258.2189        <NA>    NA    NA        NA
## 3       B    270.7256 Lake Elaine   6.5    40         8
## 4       B    292.8283 Lake Elaine   6.5    40         8
## 5       C    218.2320 Mormon Lake   6.3   210        10
## 6       C    264.9899 Mormon Lake   6.3   210        10
```

```
inner_join(Fish.Data, Lake.Data)
```

```
## Joining, by = "Lake_ID"
```

```
## # A tibble: 4 x 6
##   Lake_ID Fish.Weight   Lake_Name    pH  area avg_depth
##     <chr>       <dbl>       <chr> <dbl> <dbl>     <dbl>
```

```
## 1       B    270.7256 Lake Elaine   6.5    40         8
## 2       B    292.8283 Lake Elaine   6.5    40         8
## 3       C    218.2320 Mormon Lake   6.3   210        10
## 4       C    264.9899 Mormon Lake   6.3   210        10
```

The above examples assumed that the column used to join the two tables was named the same in both tables. This is good practice to try to do, but sometimes you have to work with data where that isn't the case. In that situation you can use the `by=c("ColName.A"="ColName.B")` syntax where `ColName.A` represents the name of the column in the first data frame and `ColName.B` is the equivalent column in the second data frame.

8.4 Exercises

1. Suppose we are given information about the maximum daily temperature from a weather station in Flagstaff, AZ. The file is available at the GitHub site that this book is hosted on.

   ```
   FlagTemp <-  read.csv(
     'https://github.com/dereksonderegger/570L/raw/master/data-raw/FlagMaxTemp.csv',
      header=TRUE, sep=',')
   ```

   This file is in a wide format, where each row represents a month and the columns X1, X2, ..., X31 represent the day of the month the observation was made.

   a. Convert data set to the long format where the data has only four columns: `Year`, `Month`, `Day`, `Tmax`.

   b. Calculate the average monthly maximum temperature for each Month in the dataset (So there will be 365 mean maximum temperatures). *You'll probably have some issues taking the mean because there are a number of values that are missing and by default R refuses to take means and sums when there is missing data. The argument* `na.rm=TRUE` *to* `mean()` *allows you to force R to remove the missing observations before calculating the mean.*

   c. Convert the average month maximums back to a wide data format where each line represents a year and there are 12 columns of temperature data (one for each month) along with a column for the year. *There will be a couple of months that still have missing data because the weather station was out of commision for those months and there was NO data for the entire month.*

2. A common task is to take a set of data that has multiple categorical variables and create a table of the number of cases for each combination. An introductory statistics textbook contains a dataset summarizing student surveys from several sections of an intro class. The two variables of interest for us are `Gender` and `Year` which are the students gender and year in college.

   a. Download the dataset and correctly order the `Year` variable using the following:

   ```
   Survey <- read.csv('http://www.lock5stat.com/datasets/StudentSurvey.csv', na.strings=c('',' '))
      mutate(Year = factor(Year, levels=c('FirstYear','Sophomore','Junior','Senior')))
   ```

   b. Using some combination of `dplyr` functions, produce a data set with eight rows that contains the number of responses for each gender:year combination. *Notice there are two females that neglected to give their Year and you should remove them first. The function* `is.na(Year)` *will return logical values indicating if the Year value was missing and you can flip those values using the negation operator* `!`*. So you might consider using* `!is.na(Year)` *as the argument to a* `filter()` *command. Alternatively you could sort on* `Year` *and remove the first two rows using* `slice(-2:-1)`*. Next you'll want to summarize each Year/Gender group using the* `n()` *function which gives the number of rows in a data set.*

   c. Using `tidyr` commands, produce a table of the number of responses in the following form:

Gender	First Year	Sophmore	Junior	Senior
Female				
Male				

3. The package `nycflights13` contains information about all the flights that arrived in or left from New York City in 2013. This package contains five data tables, but there are three data tables we will work with. The data table `flights` gives information about a particular flight, `airports` gives information about a particular airport, and `airlines` gives information about each airline. Create a table of all the flights on February 14th by Virgin America that has columns for the carrier, destination, departure time, and flight duration. Join this table with the airports information for the destination. Notice that because the column for the destination airport code doesn't match up between `flights` and `airports`, you'll have to use the `by=c("TableA.Col"="TableB.Col")` argument where you insert the correct names for `TableA.Col` and `TableB.Col`.

Chapter 9

Graphing using ggplot2

```
library(ggplot2)  # my favorite graphing system
library(dplyr)    # data frame manipulations
```

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 examine.
3. 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 it might be easier 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 sufficient for creating simple graphs using `ggplot2`, but are not intended to be exhaustive. 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.

9.1 Basic Graphs

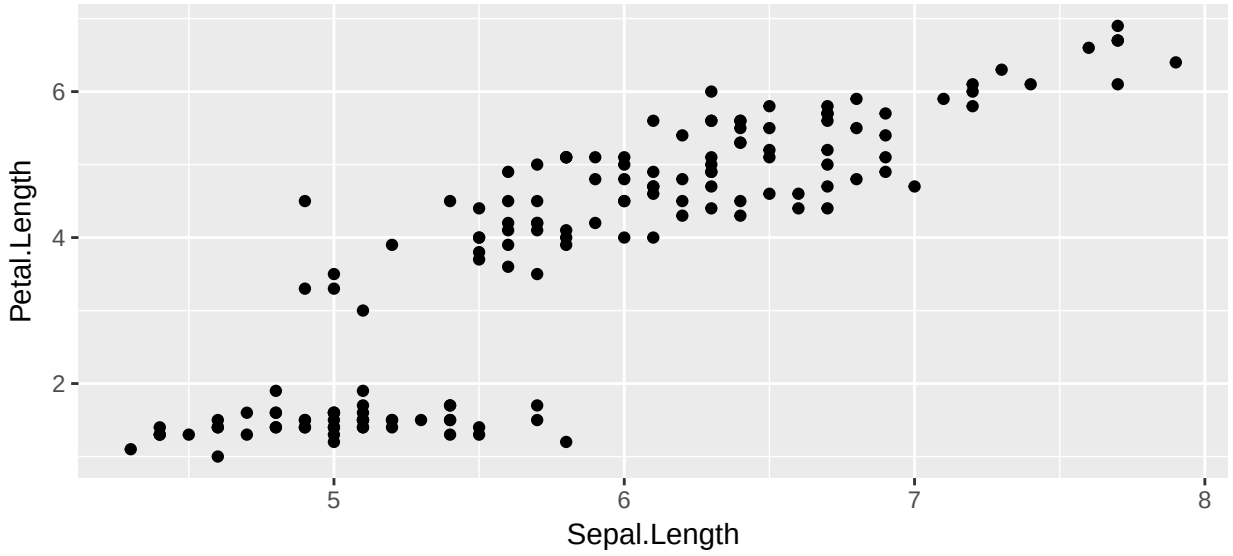
9.1.1 Scatterplots

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`, which are two columns in my dataset.

```
data(iris)  # load the iris dataset that comes with R
str(iris)   # what columns do we have to play with...
```

```
## '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 ...
```

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



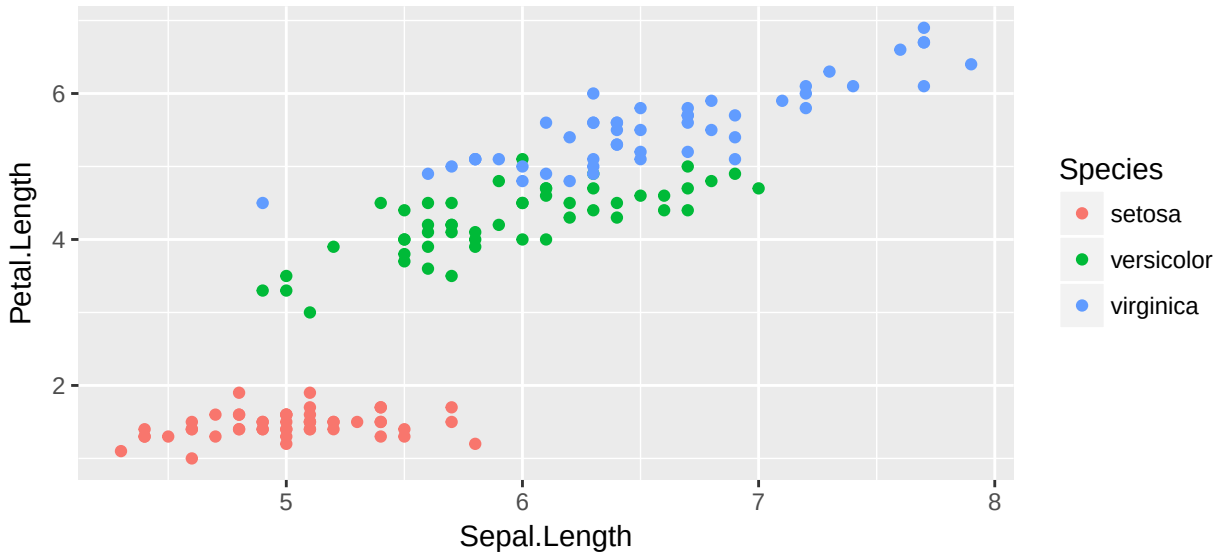
1. The data set we wish to use is specified using `data=iris`.

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.

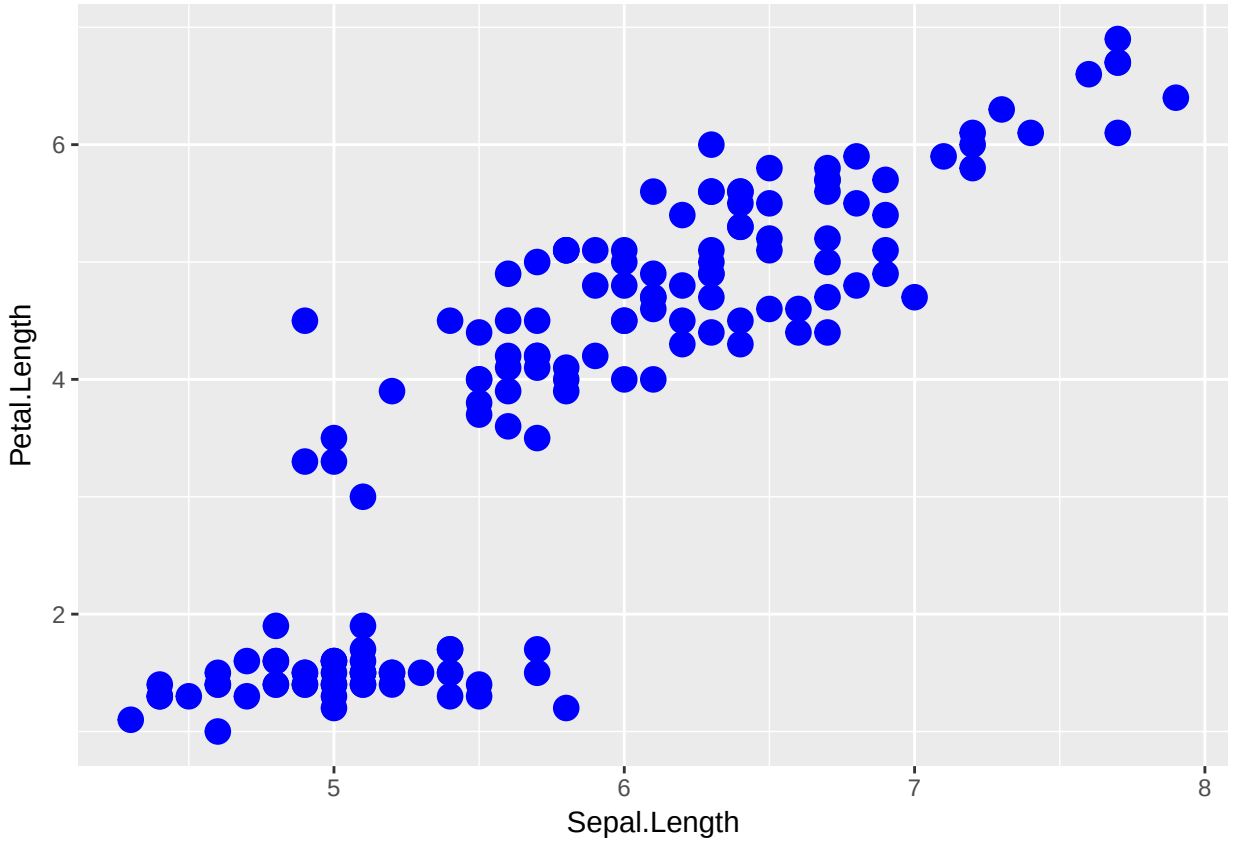
We can define other attributes that might reflect other aspects of the data. For example, we might want for the of the data point to change dynamically based on the species of iris.

```
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 )
```



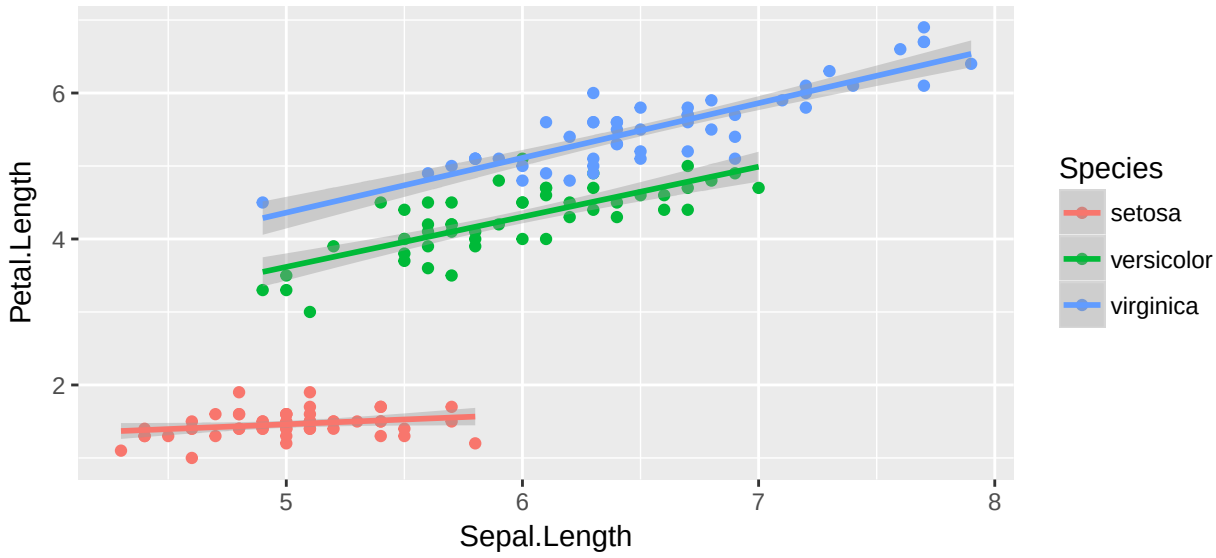
The important part isn't that color and size were defined in the `geom_point()` but that they were defined outside of an `aes()` function!

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.

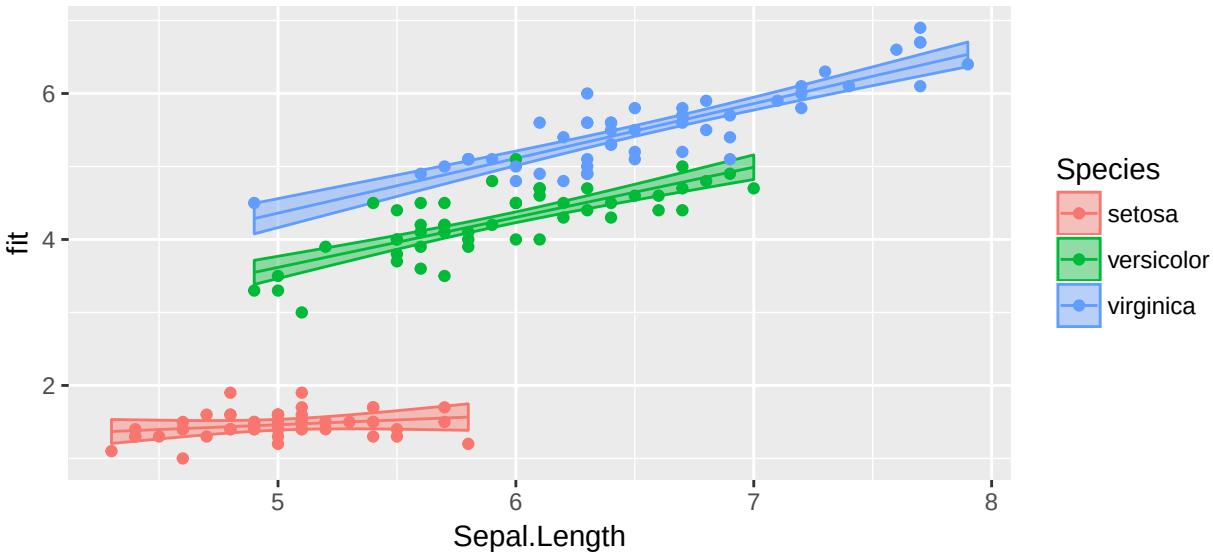
Next, I suppose I want to add a regression line (the line that best summarizes the relationship between Sepal.Length and Petal.Length) to each of these groups. We can do this by adding another layer to the graph, in this case, a `smoother` layer. The `geom_smoother` is intended to take a scatterplot 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.

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



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, calculate the predicted values along with whatever confidence intervals I want, and plot those directly using `geom_line()` and `geom_ribbon()`).

```
model <- lm( Petal.Length ~ Sepal.Length * Species, data=iris) # fit the model
iris <- cbind( iris, predict(model, interval='conf') )         # calc yhat, CI
ggplot(iris, aes(x=Sepal.Length, color=Species, fill=Species)) +
  geom_ribbon( aes(ymin=lwr, ymax=upr), alpha=.4) +  # alpha is the opacity of the ribbon
  geom_line( aes(y=fit)) +
  geom_point( aes(y=Petal.Length))
```



9.1.2 Bar Charts

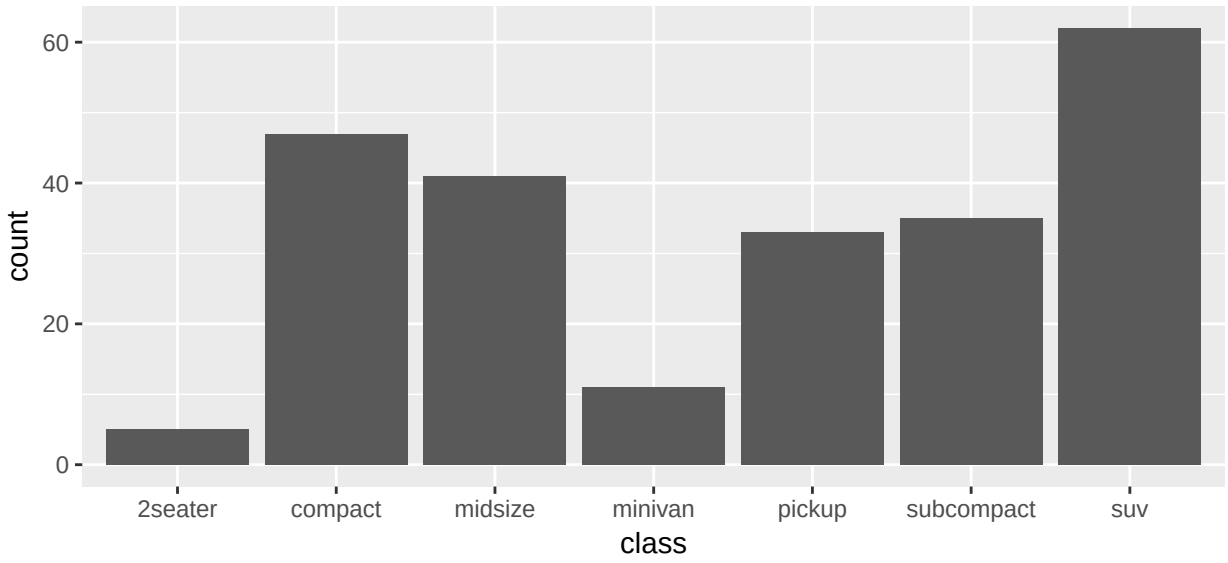
For displaying a categorical variable on the x-axis and a continuous variable on the y-axis, a bar chart is a good option. Here we consider a data set that gives the fuel efficiency of different classes of vehicles in two different years. This is a subset of data that the EPA makes available on [http://fueleconomy.gov]. It contains only model which had a new release every year between 1999 and 2008 and therefore represents the most popular cars sold in the US. It includes information for each model for years 1999 and 2008. The dataset is included in the `ggplot2` package as `mpg`.

```
data(mpg, package='ggplot2')  # load the dataset
str(mpg)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    234 obs. of  11 variables:
##  $ manufacturer: chr  "audi" "audi" "audi" "audi" ...
##  $ model       : chr  "a4" "a4" "a4" "a4" ...
##  $ displ       : num  1.8 1.8 2 2 2.8 2.8 3.1 1.8 1.8 2 ...
##  $ year        : int  1999 1999 2008 2008 1999 1999 2008 1999 1999 2008 ...
##  $ cyl         : int  4 4 4 4 6 6 6 4 4 4 ...
##  $ trans       : chr  "auto(l5)" "manual(m5)" "manual(m6)" "auto(av)" ...
##  $ drv         : chr  "f" "f" "f" "f" ...
##  $ cty         : int  18 21 20 21 16 18 18 18 16 20 ...
##  $ hwy         : int  29 29 31 30 26 26 27 26 25 28 ...
##  $ fl          : chr  "p" "p" "p" "p" ...
##  $ class       : chr  "compact" "compact" "compact" "compact" ...
```

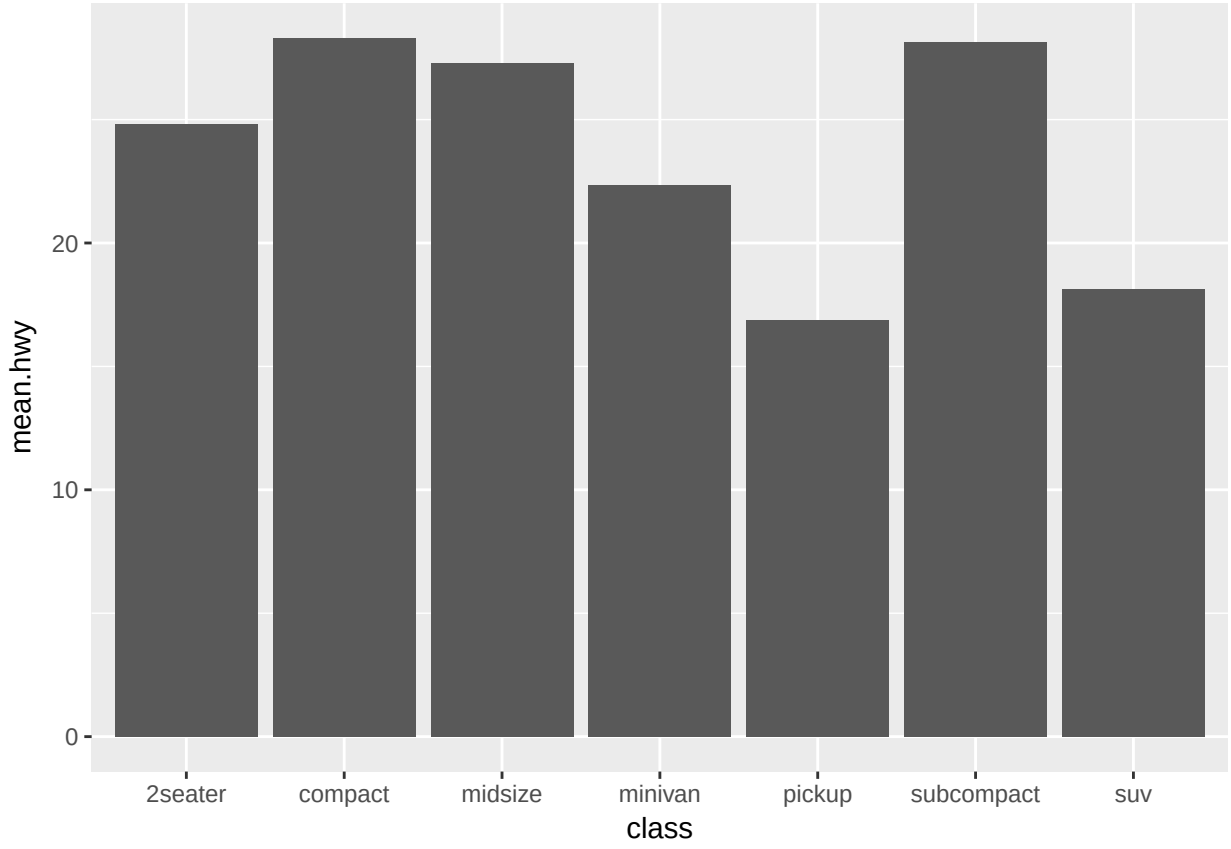
First we could summarize the data by how many of each model there are in the different classes.

```
ggplot(mpg, aes(x=class)) +
  geom_bar()
```



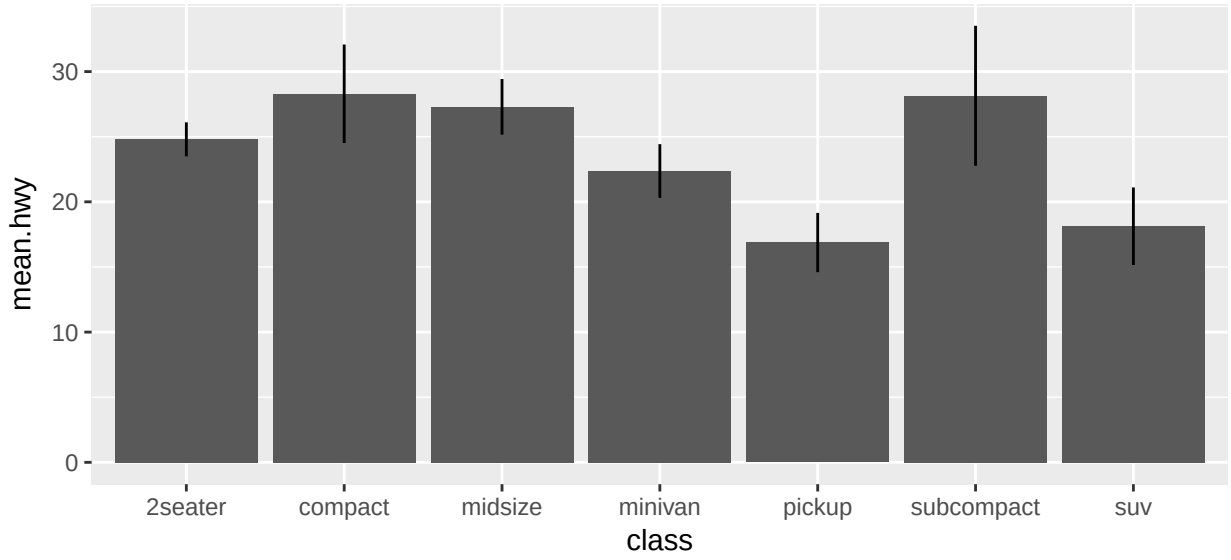
By default, the `geom_box()` just counts the number of cases and displays how many observations were in each class. If we were interested in knowing the mean highway fuel efficiency, we would have to summarize the data and calculate the mean for each class. Fortunately that is pretty easy to do.

```
mpg.small <- mpg %>%
  group_by(class) %>%
  summarise(mean.hwy = mean(hwy),
            sd.hwy   = sd(hwy),
            num.obs  = n() )

ggplot(mpg.small, aes(x=class, y=mean.hwy)) +
  geom_bar( stat = 'identity' )              # no further summarization!
```



The stat='identity' part is necessary to keep `geom_bar()` from doing any default summarization. We can add some error bars to show the standard deviation as well.

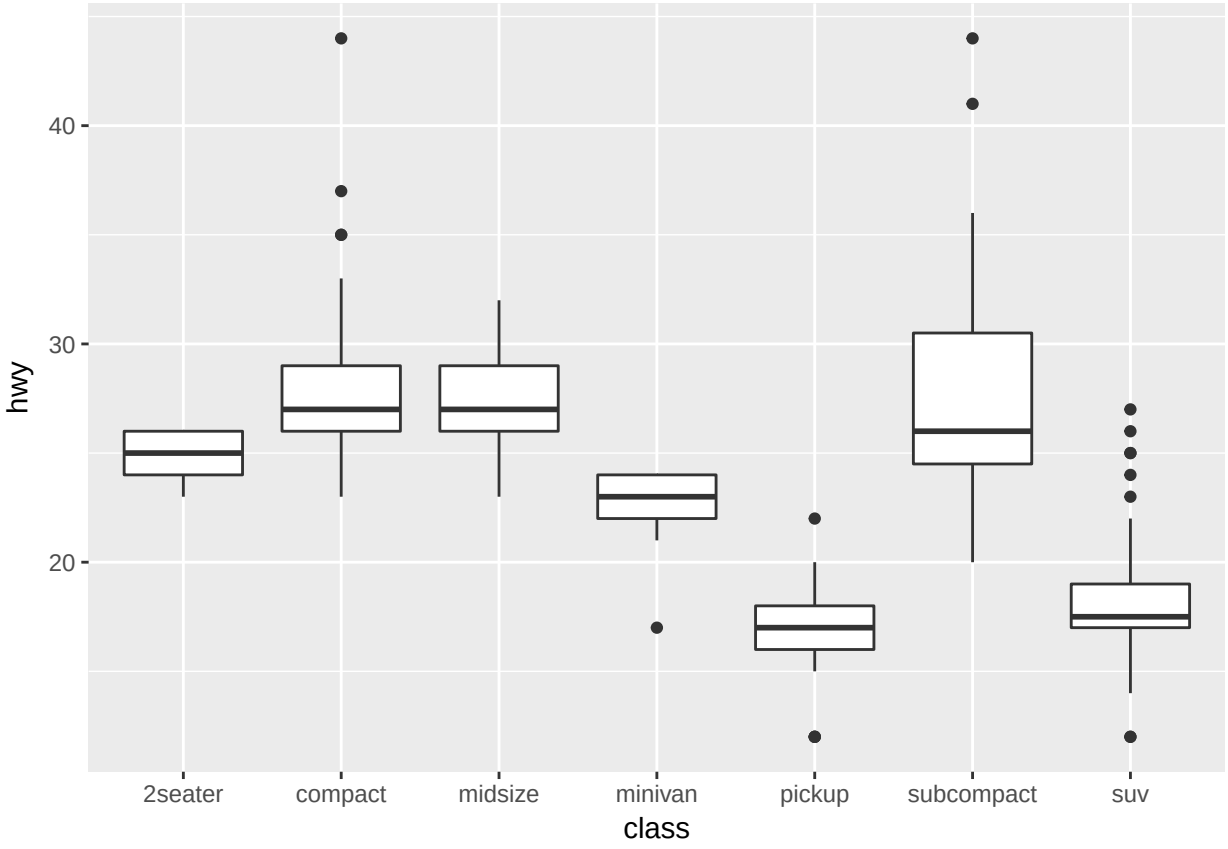
```
ggplot(mpg.small, aes(x=class, y=mean.hwy,
                      ymin = mean.hwy-sd.hwy,
                      ymax = mean.hwy+sd.hwy)) +
  geom_bar( stat = 'identity' ) +
  geom_linerange()
```



9.1.3 Box Plots

Boxplots are a common way to show a categorical variable on the x-axis and continuous on the y-axis. I actually prefer these over the barchart we did prior.

```
ggplot(mpg, aes(x=class, y=hwy)) +
  geom_boxplot()
```



9.1.4 Geometries and Layers

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.

These different geometries are different ways to display the relationship between variables and can be combined in many interesting ways.

Geom	Description	Required Aesthetics
`geom_bar`	A barplot	`x`
`geom_boxplot`	Boxplots	`x`
`geom_density`	A smoothed histogram	`x`
`geom_errorbar`	Error bars	`ymin, ymax`
`geom_histogram`	A histogram	`x`
`geom_line`	Draw a line (after sorting x-values)	`x, y`
`geom_path`	Draw a line (without sorting x-values)	`x, y`

Geom	Description	Required Aesthetics
`geom_point`	Draw points (for a scatterplot)	`x, y`
`geom_ribbon`	Enclose a region, and color the interior	`ymin, ymax`
`geom_smooth`	Add a ribbon that summarizes a scatterplot	`x, y`
`geom_text`	Add text to a graph	`x, y, label`

A graph can be built up layer by layer, where:

- Each layer corresponds to a `geom`, each of which requires a dataset and a mapping between an aesthetic and a column of the data set.

  – If you don't specify either, then the layer inherits everything defined in the ggplot() command. – You can have different datasets for each layer!

- Can add layers with a +, or you can define two plots and add them together (second one over-writes anything that conflicts).

9.2 Getting Fancy

9.2.1 Bar Plot

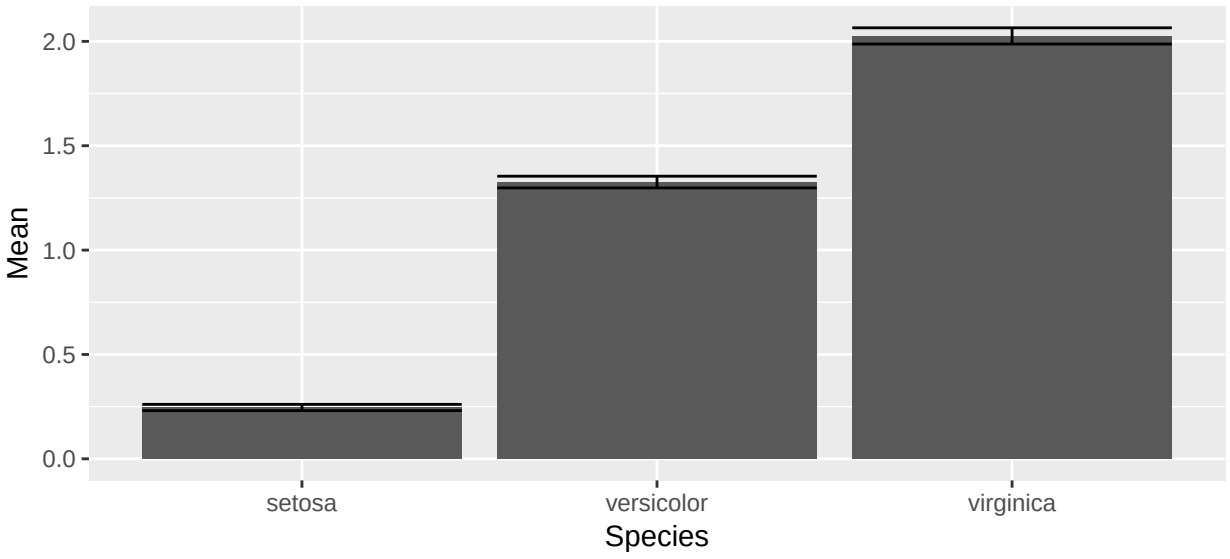
Suppose that you just want make some barplots and add ± S.E. bars. This should be really easy to do, but in the base graphics in R, it is a pain. Fortunately in `ggplot2` this is easy. First, define a data frame with the bar heights you want to graph and the ± values you wish to use.

```
# Calculate the mean and sd of the Petal Widths for each species
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
```

```
## # A tibble: 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
```

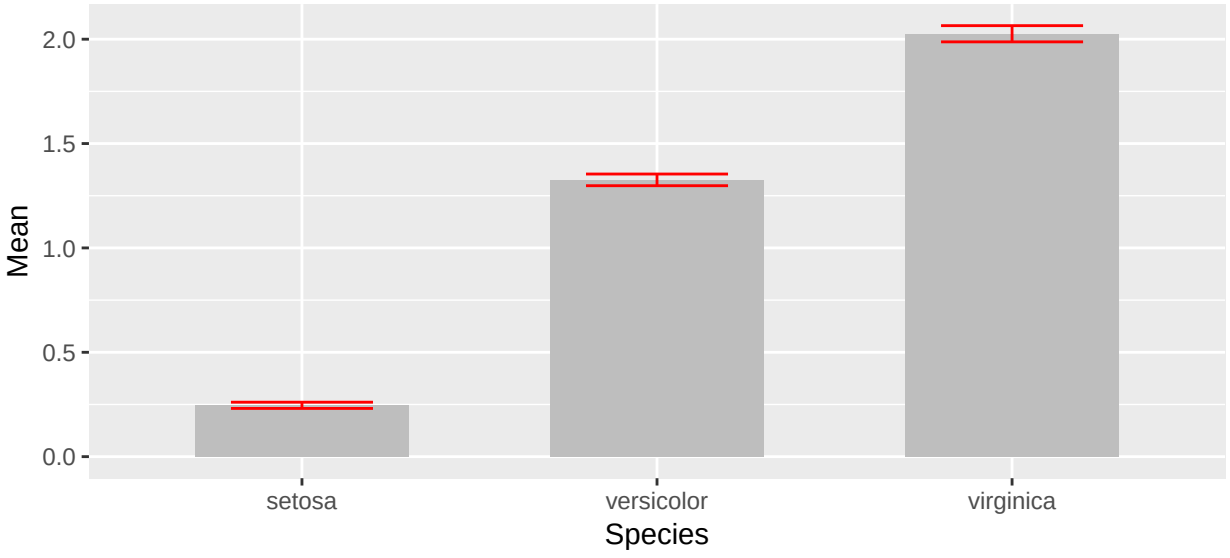
Next we take these summary statistics and define the following graph which makes a bar graph of the means and error bars that are ± 1 estimated standard deviation of the mean (usually referred to as the standard errors of the means). By default, `geom_bar()` tries to draw a bar plot based on how many 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) )
```



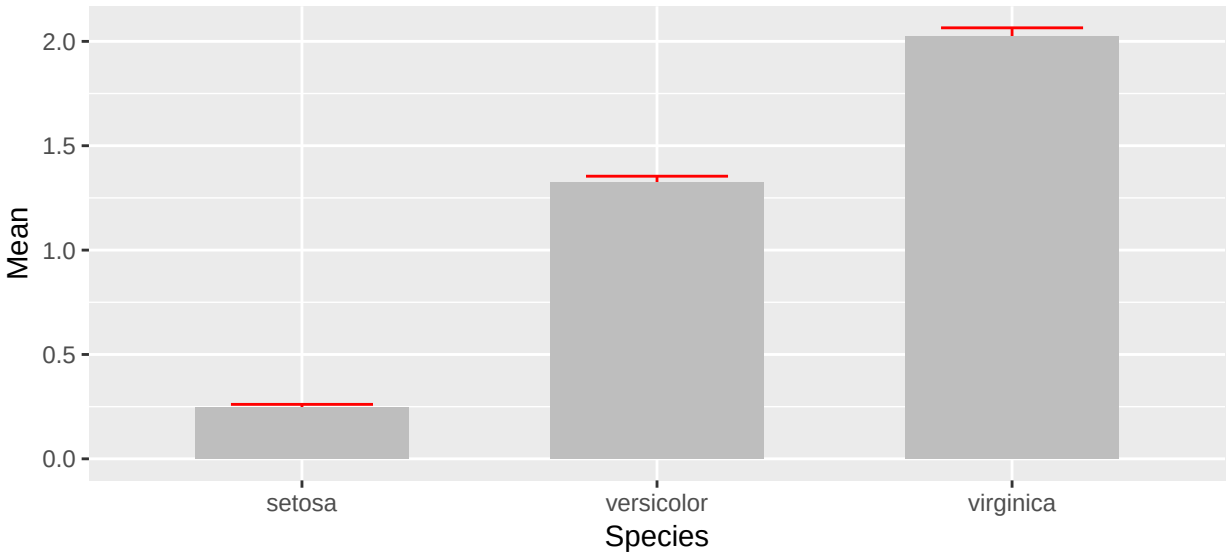
While this isn't too bad, we would like to make this a bit more pleasing to look at. Each of the bars is a little too wide and the error bars should be a tad narrower than then bar. Also, the fill color for the bars is too dark. So I'll change all of these, by setting those attributes *outside of an*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

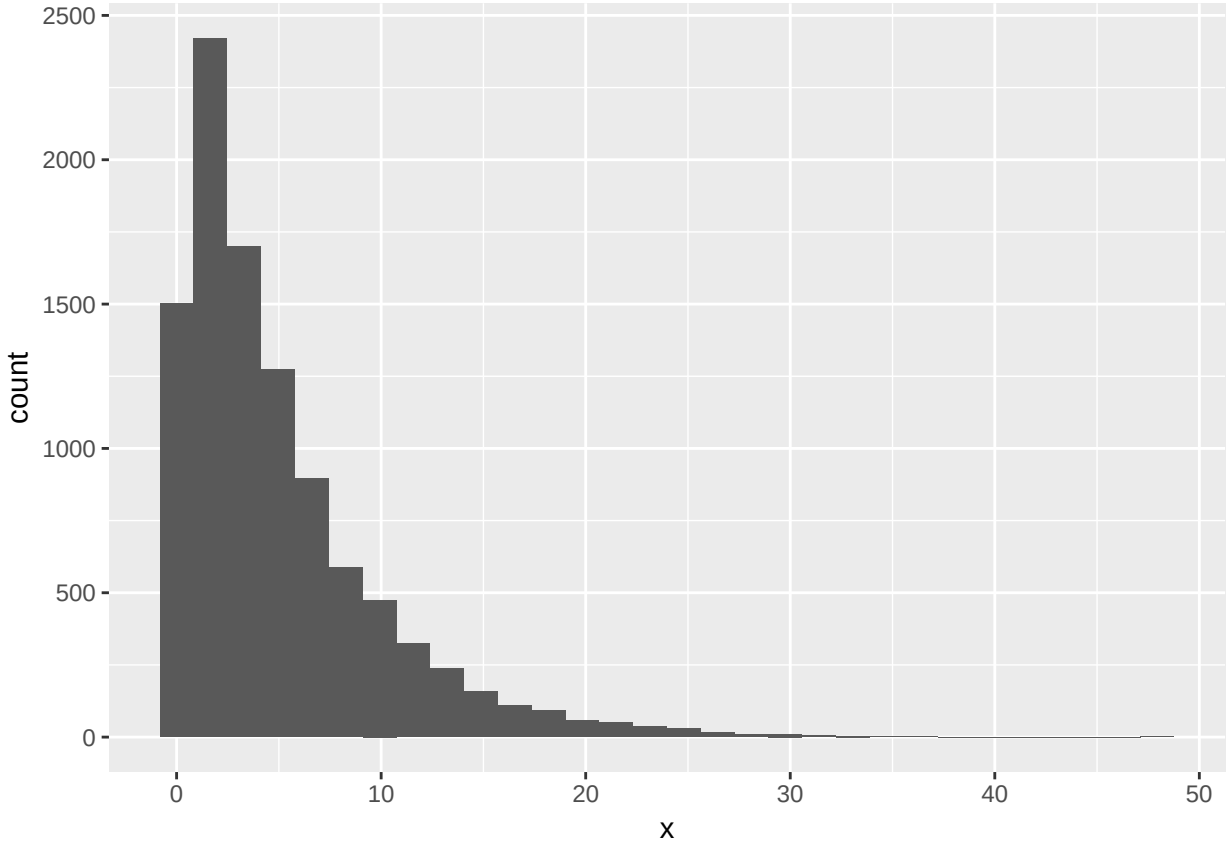


9.2.2 Histograms

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:

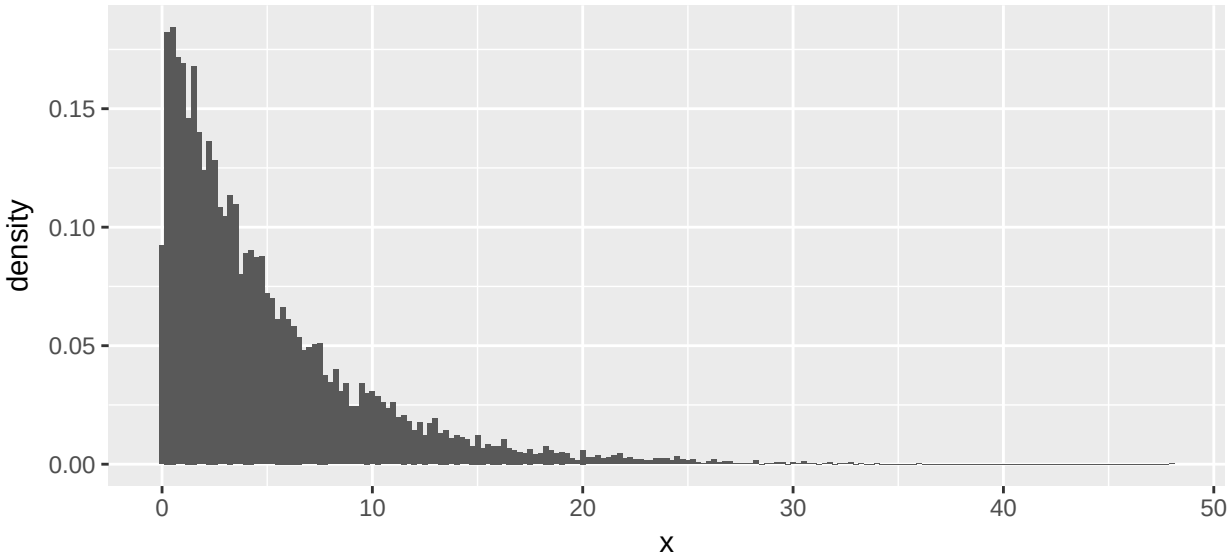
```
data <- data.frame(x=rexp(10000, rate=1/5))
ggplot(data, aes(x=x)) +
  geom_histogram()
```

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



Somewhat annoyingly, `ggplot2` does not by default use an intelligent choice for the number of bins. Instead we are stuck investigating different bin-widths by hand. To do this, we 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 (so that the area shaded has area 1), we just need to tell geom_histogram to have `y=..density..` instead of the default.

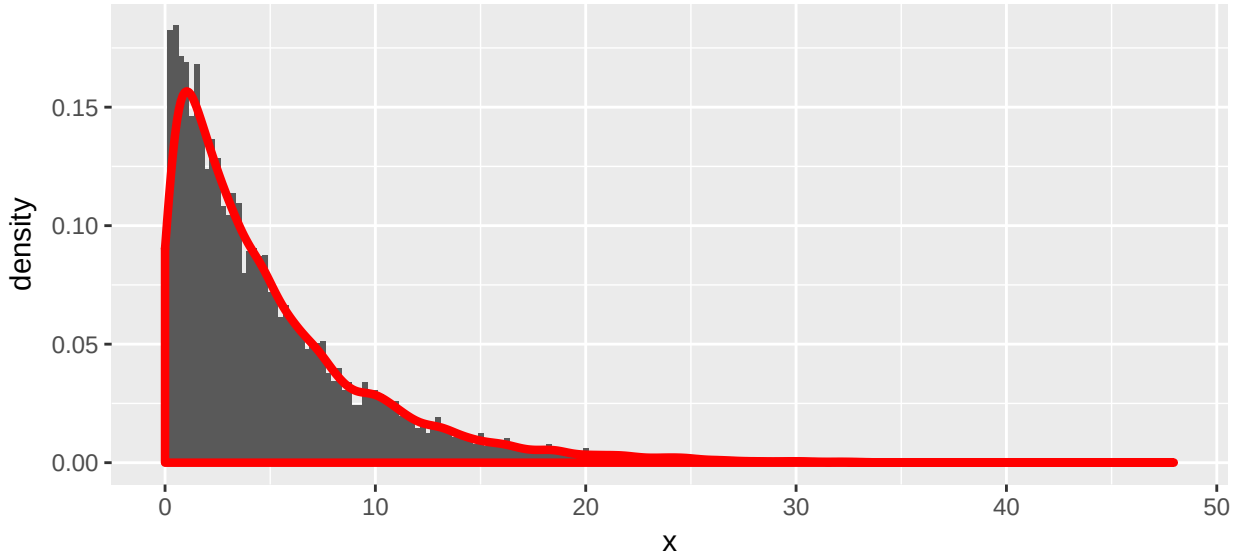
```
ggplot(data, aes(x=x, y=..density..)) +
  geom_histogram(binwidth=.25)
```



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.

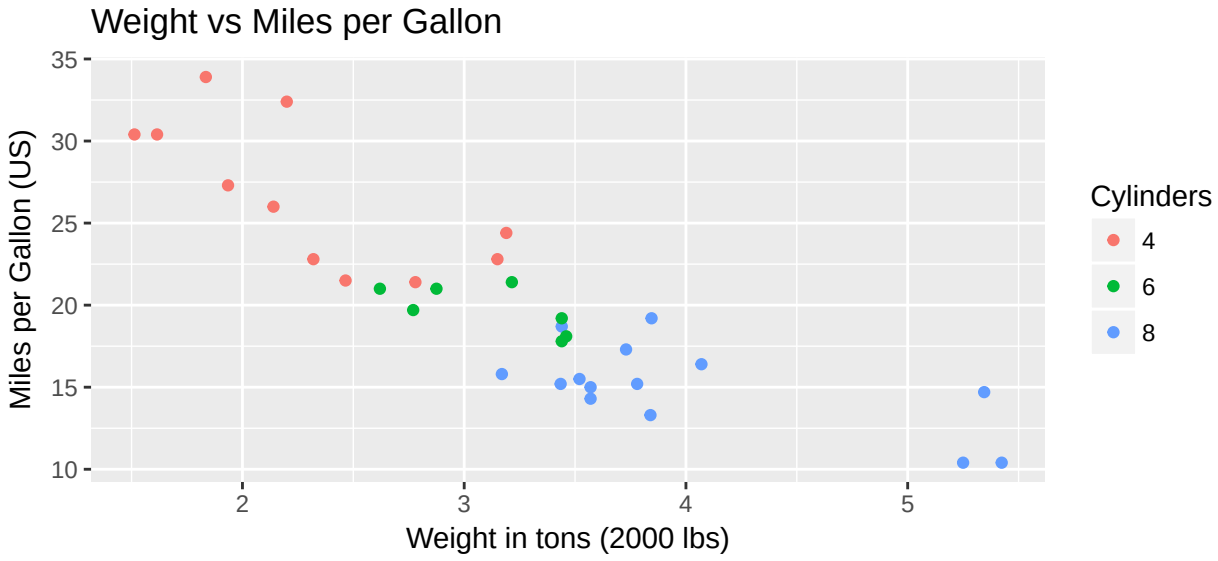
```
ggplot(data, aes(x=x, y=..density..)) +
  geom_histogram(binwidth=.25) +
  geom_density(color='red', size=1.5)
```



9.2.3 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")
```



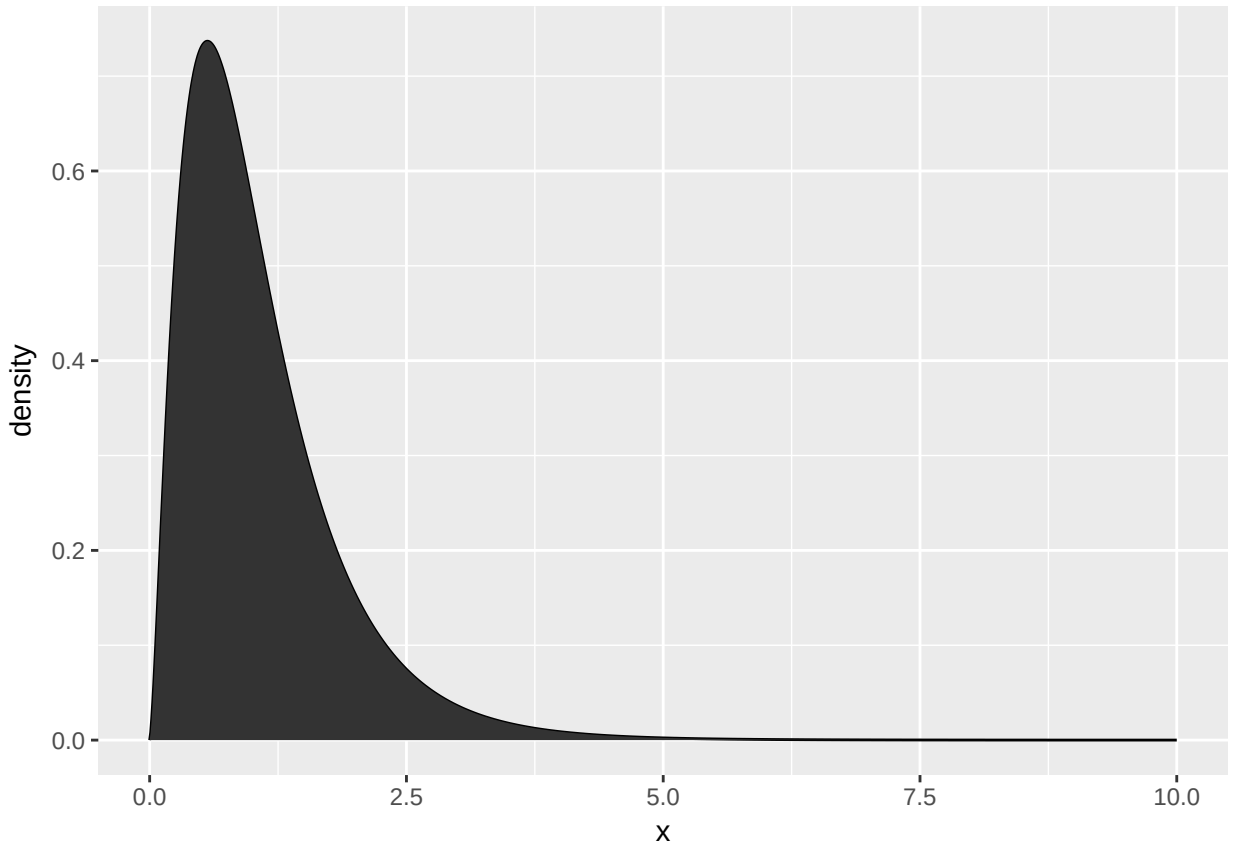
9.2.4 Plotting distributions

Often I need to plot a distribution and perhaps shade some area in. In this section we'll give a method for plotting continuous and discrete distributions using `ggplot2`.

9.2.4.1 Continuous distributions

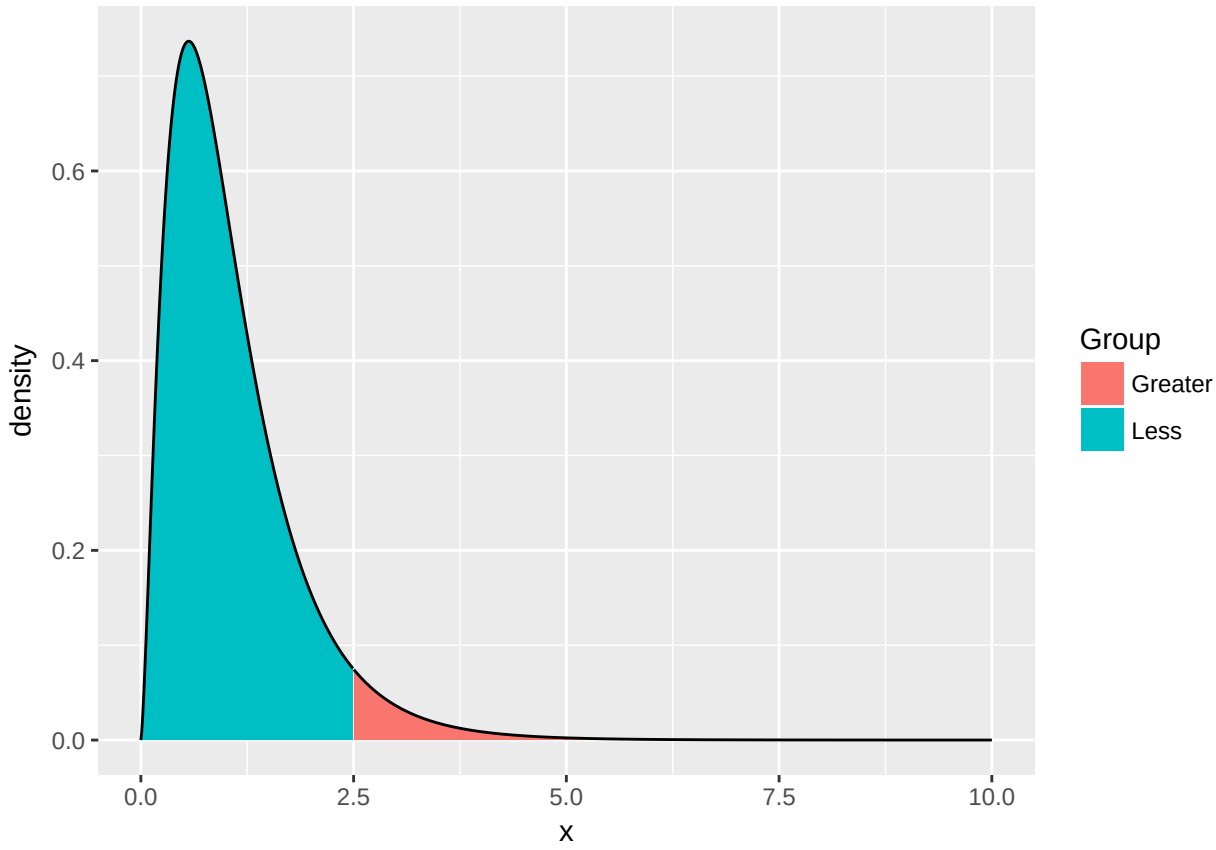
First we need to create a data.frame that contains a sequence of (x,y) pairs that we'll pass to our graphing program to draw the curve by connecting-the-dots, but because the dots will be very close together, the resulting curve looks smooth. For example, lets plot the F-distribution with parameters $\nu_1 = 5$ and $\nu_2 = 30$.

```
# define 1000 points to do a "connect-the-dots"
plot.data <- data.frame( x=seq(0,10, length=1000) ) %>%
  mutate( density = df(x, 5, 30) )

ggplot(plot.data, aes(x=x, y=density)) +
  geom_line()  +   # just a line
  geom_area()      # shade in the area under the line
```



This isn't too bad, but often we want to add some color to two different sections, perhaps we want different colors distinguishing between values ≥ 2.5 vs values < 2.5

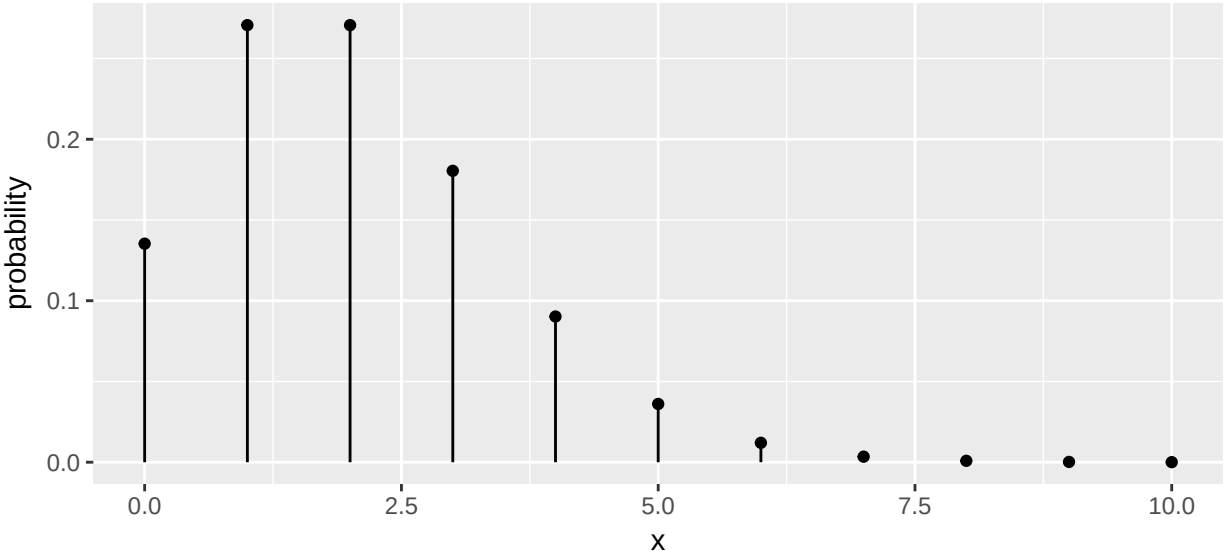
```
plot.data <- data.frame( x=seq(0,10, length=1000) ) %>%
  mutate( density = df(x, 5, 30),
          Group = ifelse(x <= 2.5, 'Less','Greater') )

ggplot(plot.data, aes(x=x, y=density, fill=Group)) +
  geom_area() +
  geom_line()
```



9.2.4.2 Discrete distributions

The idea for discrete distributions will be to draw points for the height and then add bars. Lets look at doing this for the poisson distribution with rate parameter $\lambda = 2$.

```
plot.data <- data.frame( x=seq(0,10) ) %>%
  mutate( probability = dpois(x, lambda=2) )

ggplot(plot.data, aes(x=x)) +
  geom_point( aes(y=probability) ) +
  geom_linerange(aes(ymax=probability), ymin=0)
```



The key trick here was to set the `ymin` value to always be zero.

9.3 Exercises

1. For the dataset trees, which should already be pre-loaded. Look at the help file using `?trees` for more information about this data set. We wish to build a scatterplot that compares the height and girth of these cherry trees to the volume of lumber that was produced.

   a) 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. Which do you think is a more intuitive representation?
   b) Add appropriate labels for the main title and the x and y axes.

2. Consider the following small dataset that represents the number of times per day my wife played "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.

```
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 an `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 an `x`, `ymin`, and `ymax` columns to be defined. For examples of using `geom_ribbon()` see the online documentation: [http://docs.ggplot2.org/current/geom_ribbon.html].

```
ggplot(Rosy, aes(x=day)) +
  geom_point(aes(y=times)) +
  geom_line( aes(y=yhat)) +
  geom_ribbon( aes(ymin=lwr, ymax=upr), fill='salmon')
```

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.

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

3. The R package `babynames` contains a single dataset that lists the number of children registered with Social Security with a particular name along with the proportion out of all children born in a given year. The dataset covers the from 1880 to the present. We want to plot the relative popularity of the names 'Elise' and 'Casey'.

   a) Load the package. If it is not found on your computer, download the package from CRAN.

   ```
   library(babynames)
   data("babynames")
   ```

   b) Read the help file for the data set `babynames` to get a sense of the columns

   c) Create a small dataset that only has the names 'Elise' and 'Casey'.

   d) Make a plot where the x-axis is the year and the y-axis is the proportion of babies given the names. Use a line to display this relationship and distinguish the two names by color. Notice this graph is a bit ugly because there is a lot of year-to-year variability that we should smooth over.

   e) We'll use dplyr to collapse the individual years into decades using the following code:

   ```
   small <- babynames %>%
     filter( name=='Elise' | name=='Casey') %>%
     mutate( decade = cut(year, breaks = seq(1869,2019,by=10) )) %>%
     group_by(name, decade) %>%
     summarise( prop = mean(prop),
                year = min(year))
   ```

   f) Now draw the same graph you had in part (d).

   g) Next we'll create an area plot where the height is the total proportion of the both names and the colors split up the proportion.

```
ggplot(small, aes(x=year, y=prop, fill=name)) +
   geom_area()
```

This is a pretty neat graph as it show the relative popularity of the name over time and can easily be expanded to many many names. In fact, there is a wonderful website that takes this same data and allows you select the names quite nicely: [http://www.babynamewizard.com/voyager]. My wife and I used this a lot while figuring out what to name our children. Notice that this site really uses the same graph type we just built but there are a few extra neat interactivity tricks.

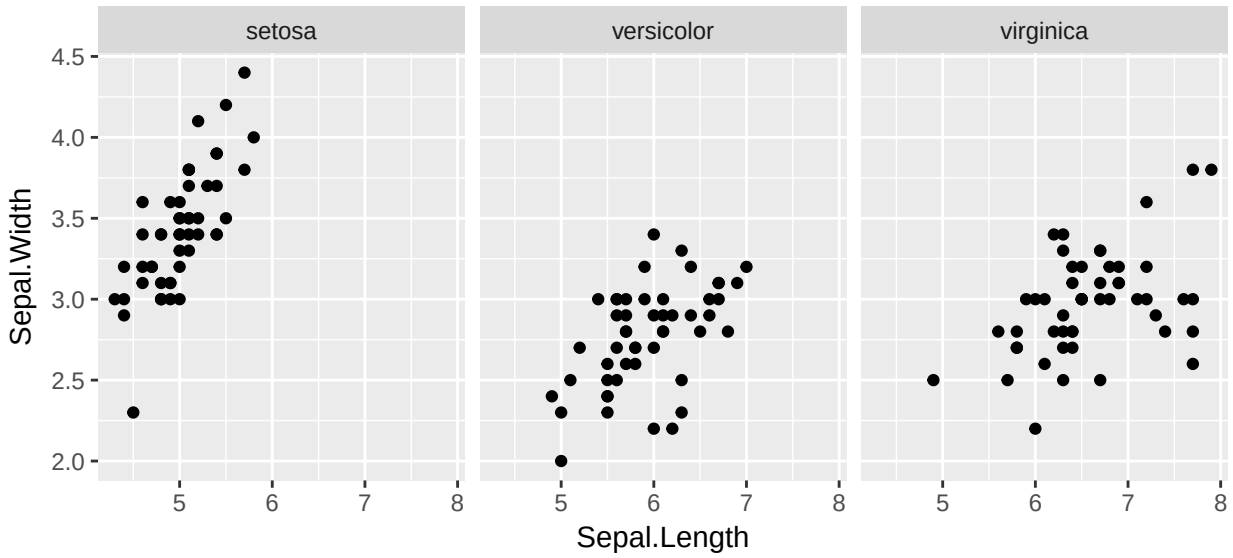
Chapter 10

More ggplot2

10.1 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 ~ .`.

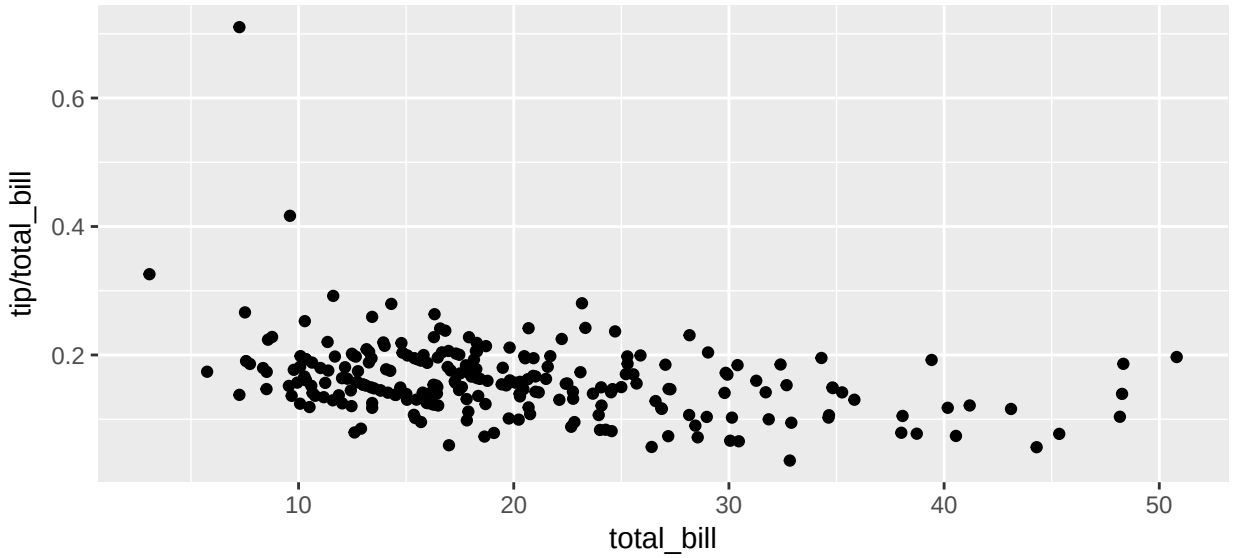
For a second example, we look at a dataset that examines the amount a waiter was tipped by 244 parties. Covariates that were measured include the day of the week, size of the party, total amount of the bill, amount tipped, whether there were smokers in the group and the gender of the person paying the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

```
data(tips, package='reshape')
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
```

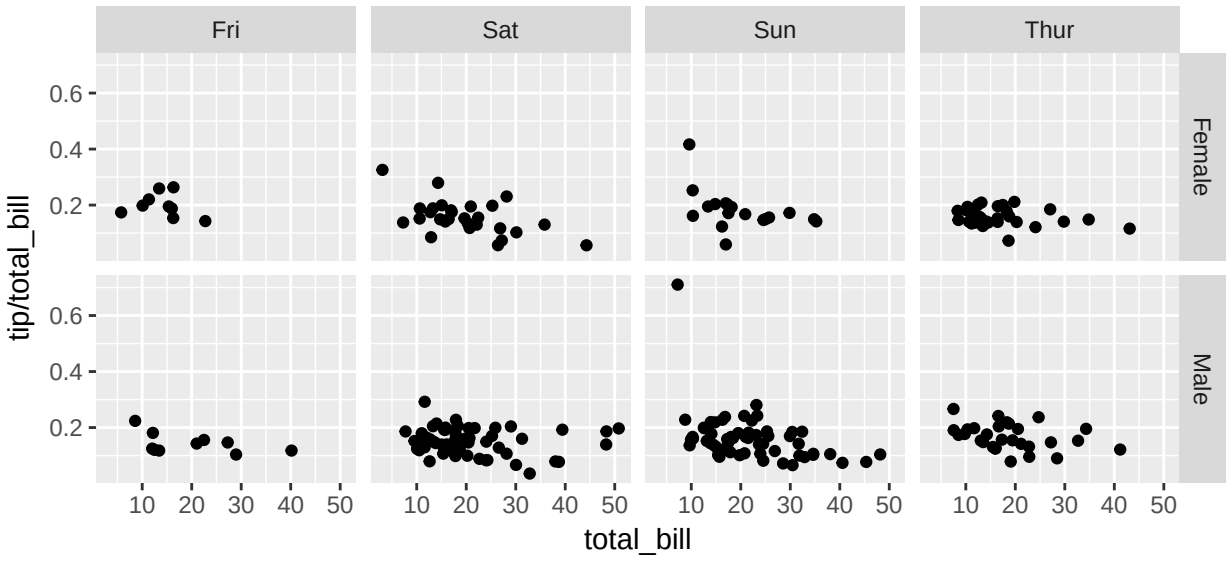
It is easy to look at the relationship between the size of the bill and the percent tipped.

```
ggplot(tips, aes(x = total_bill, y = tip / total_bill )) +
  geom_point()
```



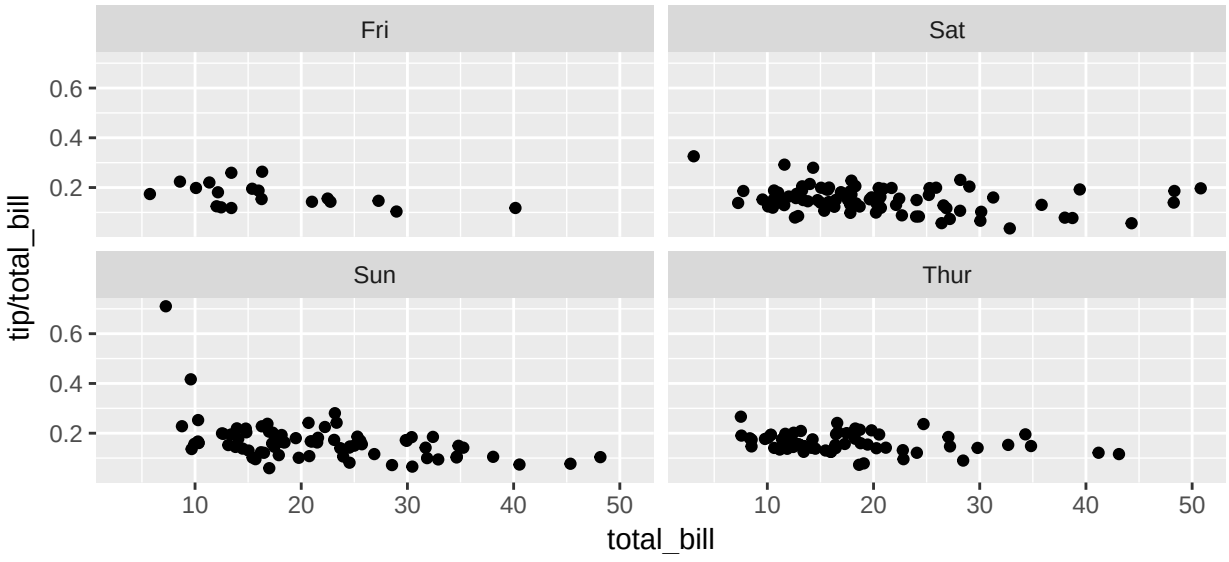
Next we ask if there is a difference in tipping percent based on gender or day of the week by plotting this relationship for each combination of gender and day.

```
ggplot(tips, aes(x = total_bill, y = tip / total_bill )) +
  geom_point() +
  facet_grid( sex ~ day )
```



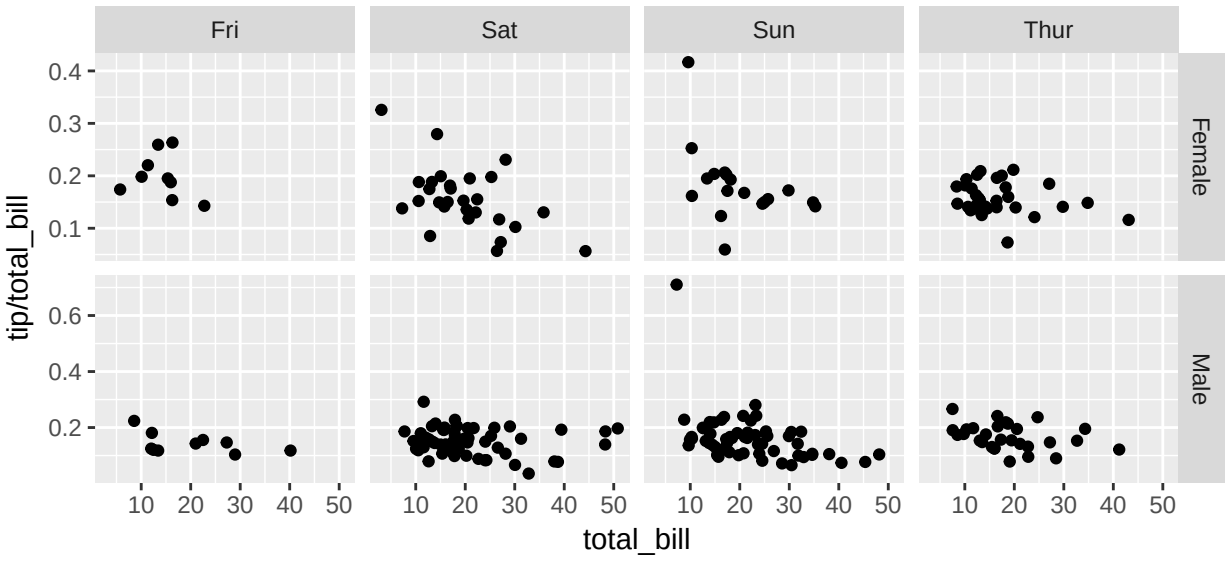
Sometimes we want multiple rows and columns of facets, but there is only one categorical variable with many levels. In that case we use facet_wrap which takes a one-sided formula.

```
ggplot(tips, aes(x = total_bill, y = tip / total_bill )) +
  geom_point() +
  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.

```
ggplot(tips, aes(x = total_bill, y = tip / total_bill )) +
  geom_point() +
  facet_grid( sex ~ day, scales="free_y" )
```



10.2 Modifying Scales

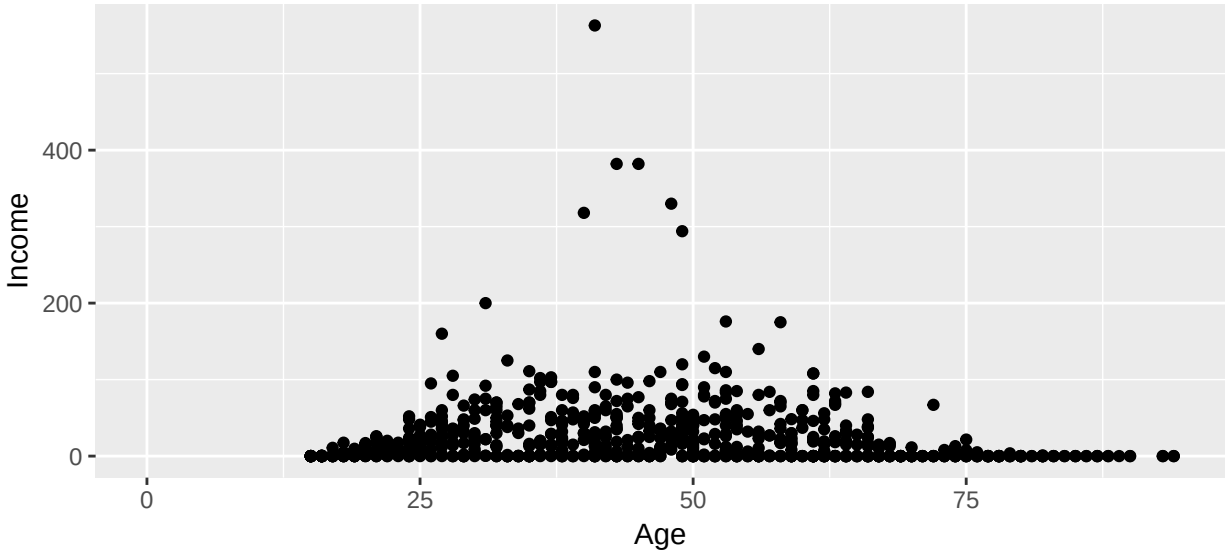
Often it is useful to modify the scales that we have on the x or y axis. In particular we might want to display some modified version of a variable.

10.2.1 Log scales

For this example, we'll use the `ACS` data from the `Lock5Data` package that has information about `Income` (in thousands of dollars) and `Age`. Lets make a scatterplot of the data.

```
library(Lock5Data)
data(ACS)
ggplot(ACS, aes(x=Age, y=Income)) +
  geom_point()
```

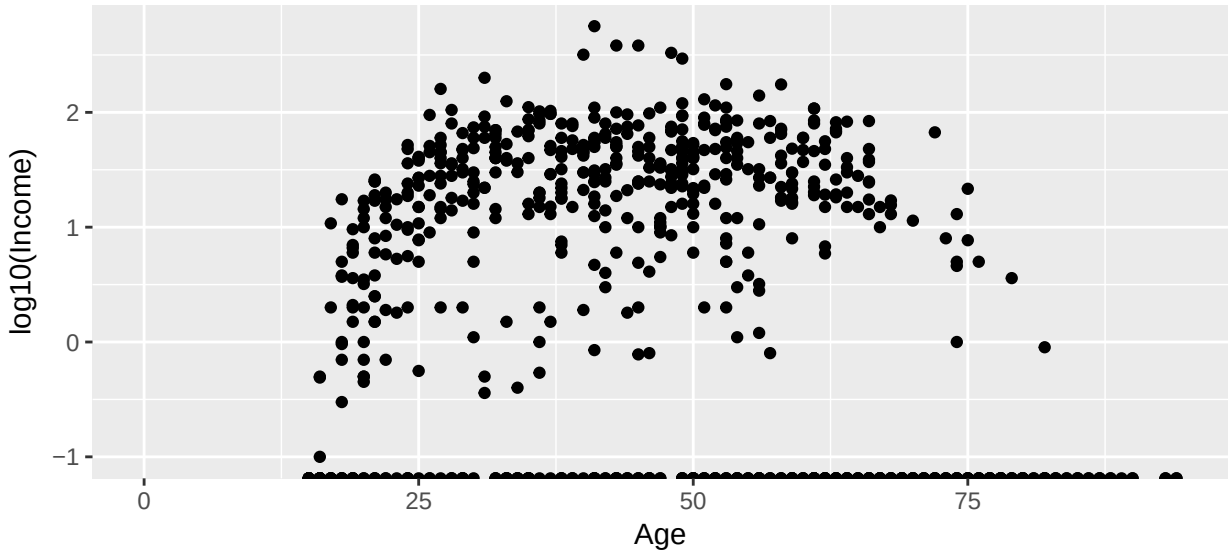
```
## Warning: Removed 175 rows containing missing values (geom_point).
```



This is an ugly graph because six observations dominate the graph and the bulk of the data (income < \$100,000) is squished together. One solution is to plot income on the $\log_{10}$ scale. There are a couple ways to do this. The simplest way is to just do a transformation on the column of data.

```
ggplot(ACS, aes(x=Age, y=log10(Income))) +
  geom_point()
```

```
## Warning: Removed 175 rows containing missing values (geom_point).
```

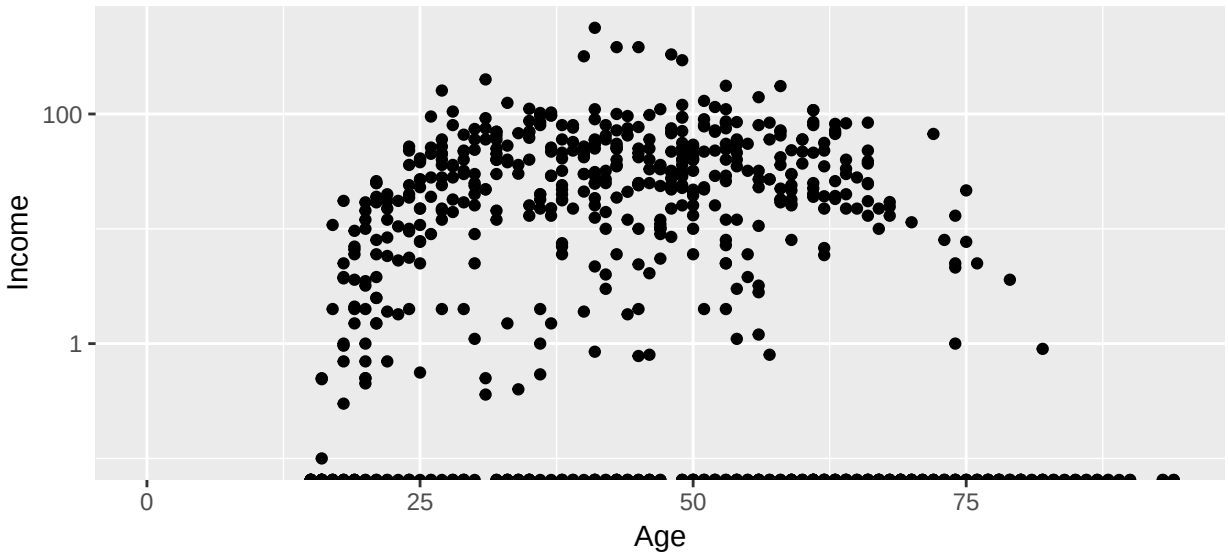


This works quite well to see the trend of peak earning happening in a persons 40s and 50s, but the scale is difficult for me to understand (what does $\log_{10}(X) = 1$ mean here? Oh right, that is $10^1 = X$ so that is the \$10,000 line). It would be really nice if we could do the transformation but have the labels on the original scale.

```
ggplot(ACS, aes(x=Age, y=Income)) +
  geom_point() +
  scale_y_log10()
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
## Warning: Removed 175 rows containing missing values (geom_point).
```

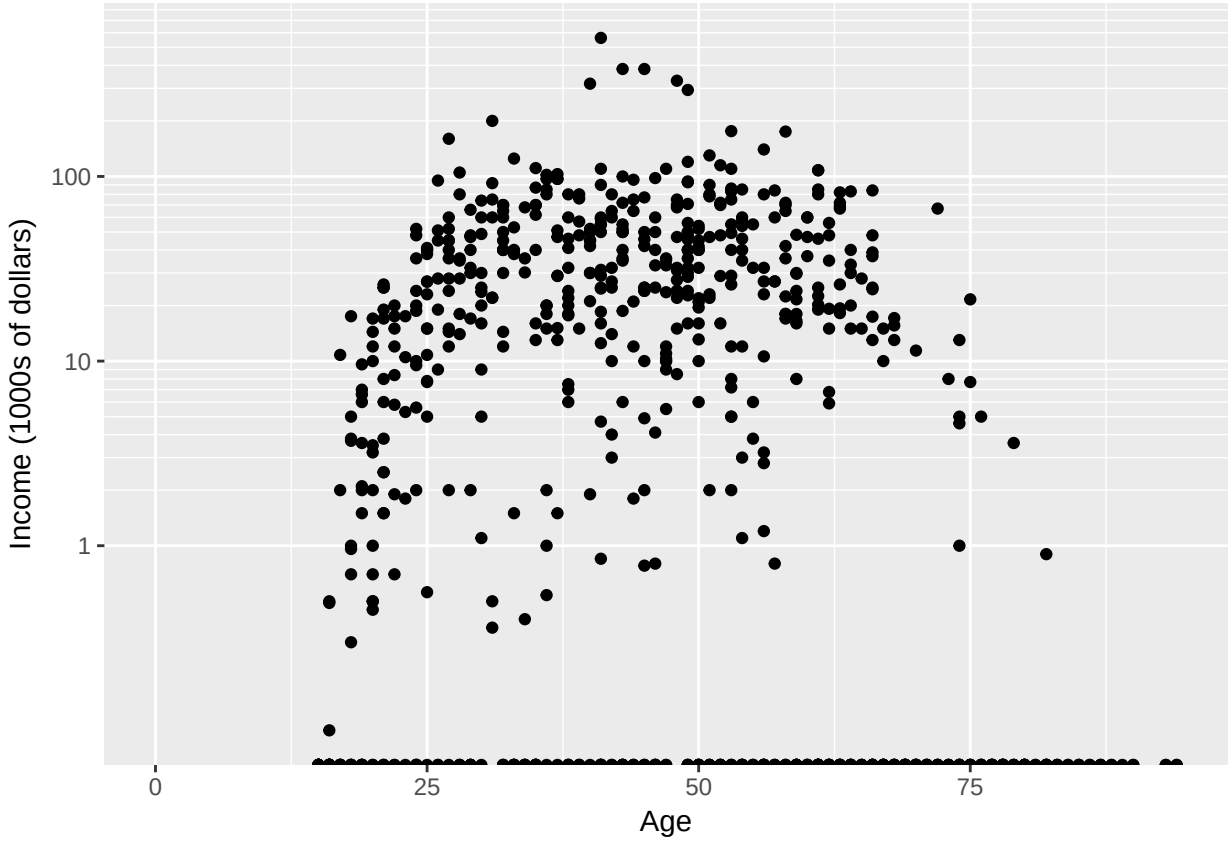


Now the y-axis is in the original units (thousands of dollars) but obnoxiously we only have two labeled values. Lets define the major break points (the white lines that have numerical labels) to be at 1,10,100 thousand dollars in salary. Likewise we will tell `ggplot2` to set minor break points at 1 to 10 thousand dollars (with steps of 1 thousand dollars) and then 10 thousand to 100 thousand but with step sizes of 10 thousand, and finally minor breaks above 100 thousand being in steps of 100 thousand.

```
ggplot(ACS, aes(x=Age, y=Income)) +
  geom_point() +
  scale_y_log10(breaks=c(1,10,100),
                minor=c(1:10,
                        seq( 10, 100,by=10 ),
                        seq(100,1000,by=100))) +
  ylab('Income (1000s of dollars)')
```

```
## Warning: Transformation introduced infinite values in continuous y-axis
```

```
## Warning: Removed 175 rows containing missing values (geom_point).
```



10.2.2 Arbitrary transformations

The function `scale_y_log10()` is actually just a wrapper to the `scale_y_continuous()` function with a predefined transformation. If you want to rescale function using some other function (say the inverse, or square-root, or $\log_2$) you can use the `scale_y_continuous()` function (for the x-axis there is a corresponding `scale_x_????`) family of functions. There is a whole list of transformations built into ggplot2 that work (transformations include "asn", "atanh", "boxcox", "exp", "identity", "log", "log10", "log1p", "log2", "logit", "probability", "probit", "reciprocal", "reverse" and "sqrt"). If you need a custom function, that can be done by defining a new transformation via the trans_new() function.

10.3 Multi-plot

There are times that you must create a graphic that is composed of several sub-graphs and think of it as one object. Unfortunately the mechanism that `ggplot2` gives for this is cumbersome and it is usually easier to use a function called `multiplot`. The explaination I've heard about why this function wasn't included in ggplot2 is that you should think about faceting first and only resort to `multiplot` if you have to. The function `multiplot` is included in a couple of packages, e.g. `Rmisc`, but I always just google 'ggplot2 multiplot' to get to the webpage [http://www.cookbook-r.com/Graphs/Multiple_graphs_on_one_page_(ggplot2)/]

```
# This example uses the ChickWeight dataset, which comes with ggplot2
# First plot
p1 <- ggplot(ChickWeight, aes(x=Time, y=weight, colour=Diet, group=Chick)) +
    geom_line() +
    ggtitle("Growth curve for individual chicks")
```

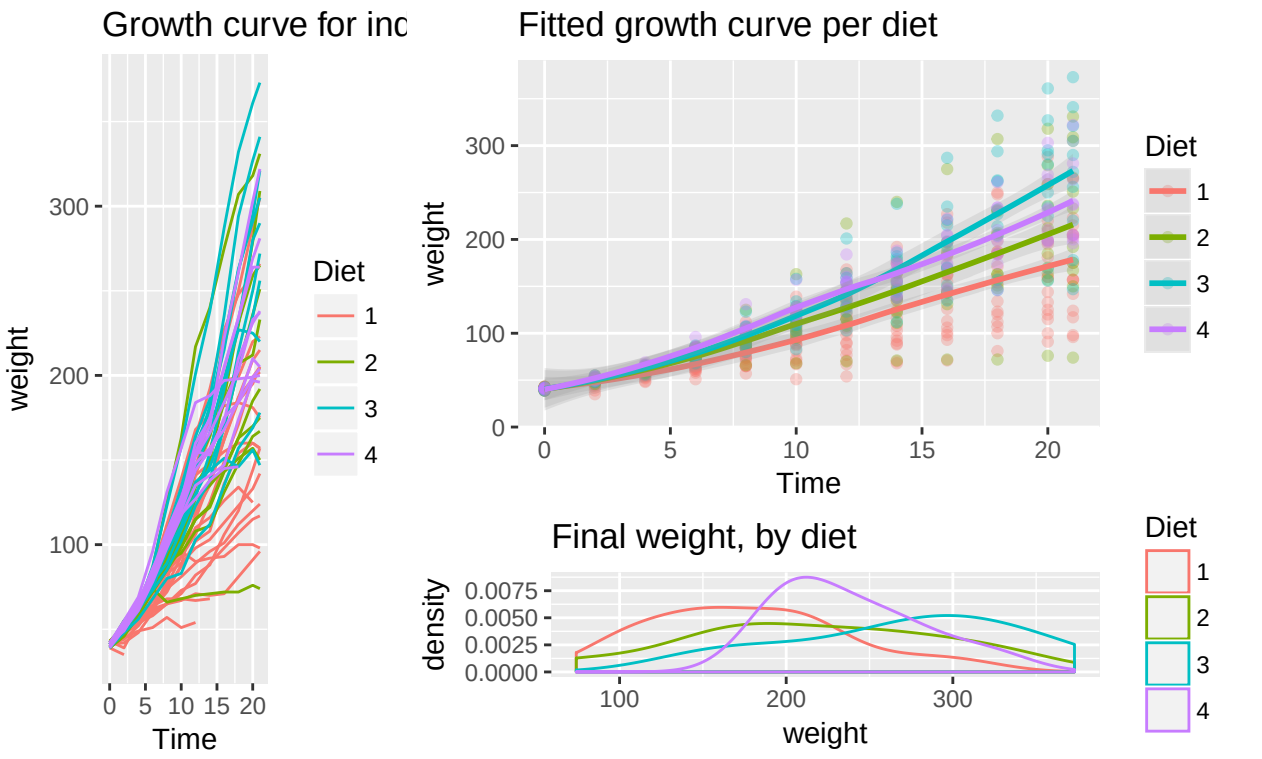
```
# Second plot
p2 <- ggplot(ChickWeight, aes(x=Time, y=weight, colour=Diet)) +
    geom_point(alpha=.3) +
    geom_smooth(alpha=.2, size=1) +
    ggtitle("Fitted growth curve per diet")

# Third plot
p3 <- ggplot(subset(ChickWeight, Time==21), aes(x=weight, colour=Diet)) +
    geom_density() +
    ggtitle("Final weight, by diet")
```

Suppose that I want to layout these three plots in an arrangement like so:

$$\text{layout} = \begin{bmatrix} 1 & 2 & 2 \\ 1 & 2 & 2 \\ 1 & 3 & 3 \end{bmatrix}$$

where plot 1 is a tall, skinny plot on the left, plot 2 is more squarish, and plot 3 is short on the bottom right. This sort of table arrangement can be quite flexible if you have many rows and many columns, but generally we can get by with something with only a couple rows/columns.

```
my.layout = cbind( c(1,1,1), c(2,2,3), c(2,2,3) )
Rmisc::multiplot( p1, p2, p3, layout=my.layout)  # Package::FunctionName
```

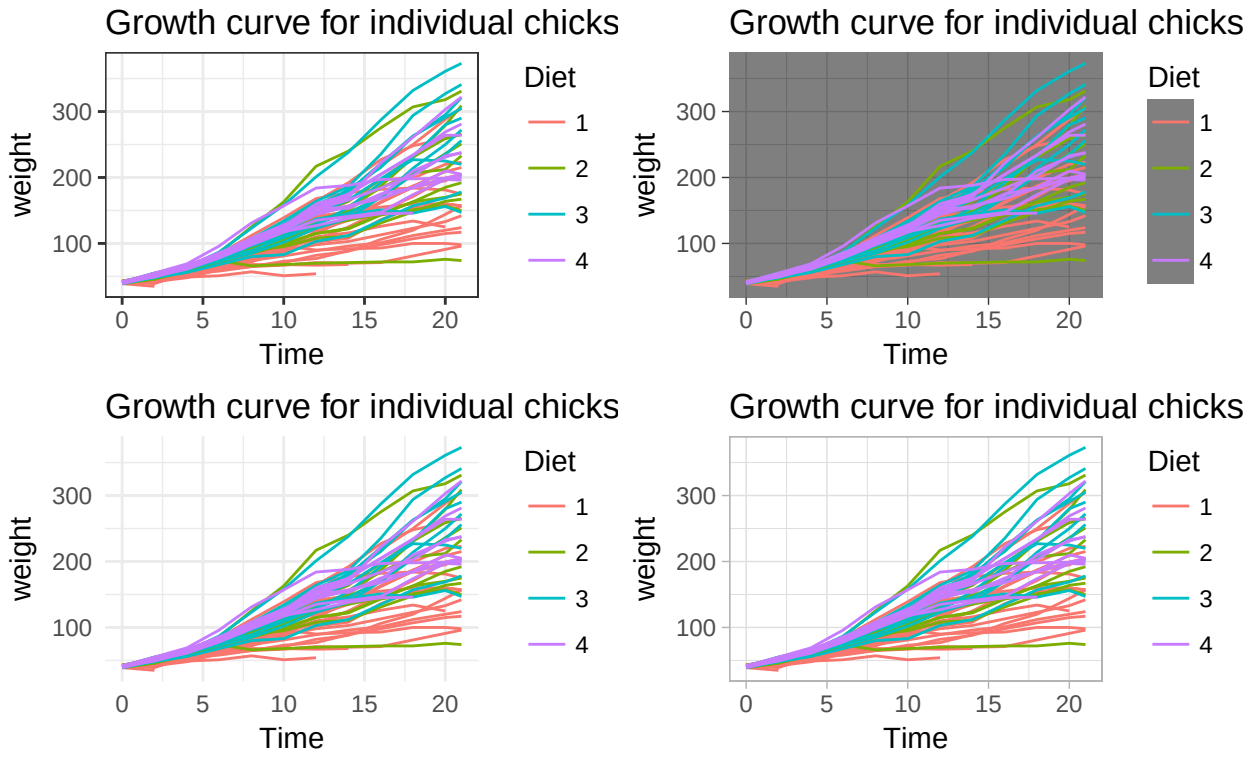


10.4 Themes

A great deal of thought went into the default settings of ggplot2 to maximize the visual clarity of the graphs. However some people believe the defaults for many of the tiny graphical settings are poor. You can modify

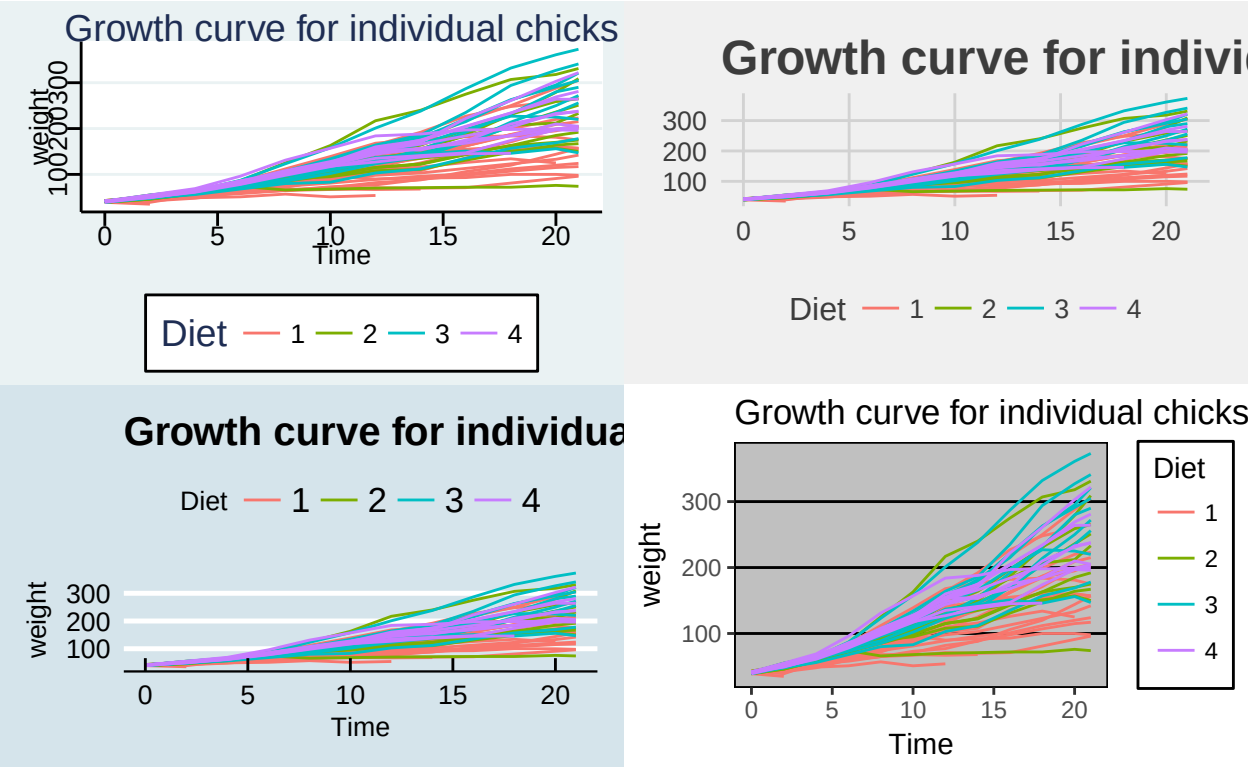
each of these but it is often easier to modify them all at once by selecting a different theme. The ggplot2 package includes several, `theme_bw()`, and `theme_minimal()` being the two that I use most often. Below are a few to examples:

```
Rmisc::multiplot( p1 + theme_bw(),          # Black and white
                  p1 + theme_minimal(),
                  p1 + theme_dark(),
                  p1 + theme_light(),
                  cols=2 )                        # two columns of graphs
```



There are more themes in the package `ggthemes`

```
library(ggthemes)
Rmisc::multiplot( p1 + theme_stata(),          # Black and white
                  p1 + theme_economist(),
                  p1 + theme_fivethirtyeight(),
                  p1 + theme_excel(),
                  cols=2 )                        # two columns of graphs
```



Almost everything you want to modify can be modified within the theme and you should check out the `ggplot2` documentation for more information and examples of how to modify different elements. [http://docs.ggplot2.org/current/theme.html]

10.5 Exercises

1. 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)
library(dplyr)
birthwt <- birthwt %>% mutate(
  race  = factor(race,  labels=c('White','Black','Other')),
  smoke = factor(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()` command.

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'`. To play with different colors that have names, check out the following: [http://www.stat.columbia.edu/~tzheng/files/Rcolor.pdf].

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?

2. 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.

Chapter 11

Flow Control

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        # can be many lines of code
}

# 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] 0
```

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

```
result
```

```
## [1] "Tail"
```

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] 0
```

```
# 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 if statement, got a Tail! "
```

```
result
```

```
## [1] "Tail"
```

Run this code several times until you get both cases several times.

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] "The second child was ignored"
```

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 $= 2 * P\left(T_{df} \leq t\right)$
- If the test statistic t is positive, then p-value $= 2 * P\left(T_{df} \geq t\right)$.

```
# 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] 1.769405e-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   # One line of R-code

# while loop with multiple lines to be repeated
while( logical ){
  expression1      # multiple lines of R code
  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*.

```
# Example of an infinite loop!  Do not Run!
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 )
  expression

for( index in vector ){
  expression1
  expression2
}
```

where the `index` variable 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)         # initialize a vector of zeros
F[1] <- 0               # F[1]  should be zero
F[2] <- 1               # F[2]  should be 1
cat('F = ', F, '\n')    # concatenate for pretty output; Just for show
```

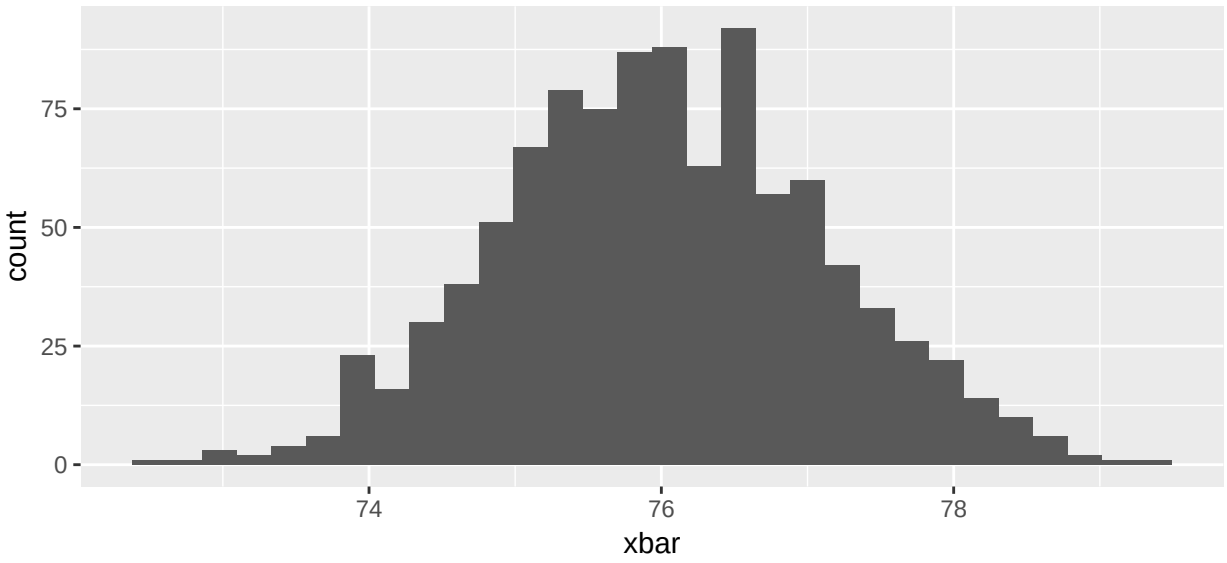
```
## F =  0 1 0 0 0 0 0 0 0 0
```

```
for( n in 3:10 ){
  F[n] <- F[n-1] + F[n-2] # define based on the prior two values
  cat('F = ', F, '\n')    # show the current step of the loop
}
```

```
## 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.

```
library(dplyr)
library(ggplot2)

SampDist <- data.frame() # Make a data frame to store the means
for( i in 1:1000 ){
  SampDist <- trees %>%
    sample_frac(replace=TRUE) %>%
    dplyr::summarise(xbar=mean(Height)) %>% # 1x1 data frame
    rbind( SampDist )
}

ggplot(SampDist, aes(x=xbar)) +
  geom_histogram()
```



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. 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. 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      # The min and max values we will use for this example
b <- 10     # Could be anything, but we need to pick something

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

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

```
## [1] 0.1666667
```

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. Run this code a few times and notice sometimes the result is 0 and sometimes it is $1/(10-4) = 0.16666667$.

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

```
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.

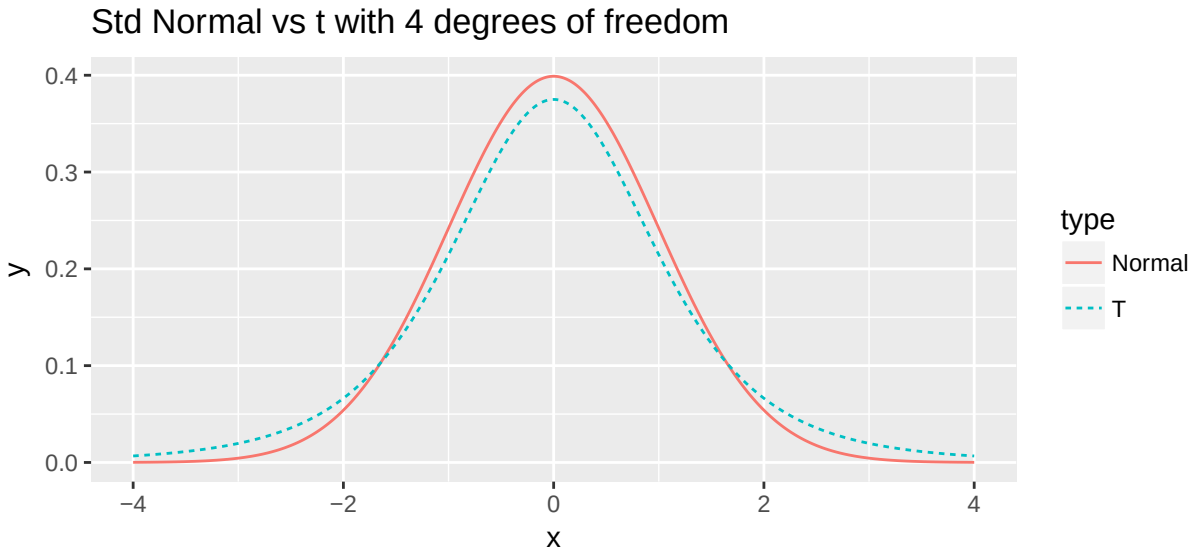
i.
```
x <- runif(n=1, 0,10)  # one random value between 0 and 10
if( (a<=x) & (x<=b) ){
  result <- 1/(b-a)
}else{
  result <- 0
}
print(paste('x=',round(x,digits=3), '  result=', round(result,digits=3)))
```

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)
}
print(paste('x=',round(x,digits=3), '  result=', round(result,digits=3)))
```

iii.
```
x <- runif(n=1, 0,10)  # one random value between 0 and 10
result <- ifelse( a<x & x<b, ???, ??? )
print(paste('x=',round(x,digits=3), '  result=', round(result,digits=3)))
```

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){
  statement1
  statement2
}
```

where `arg1` is the first argument passed to the function and `arg2` is the second.

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

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 string.
  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)
one.sample.t.test( test.data, mu0=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.

```
# 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)
}
```

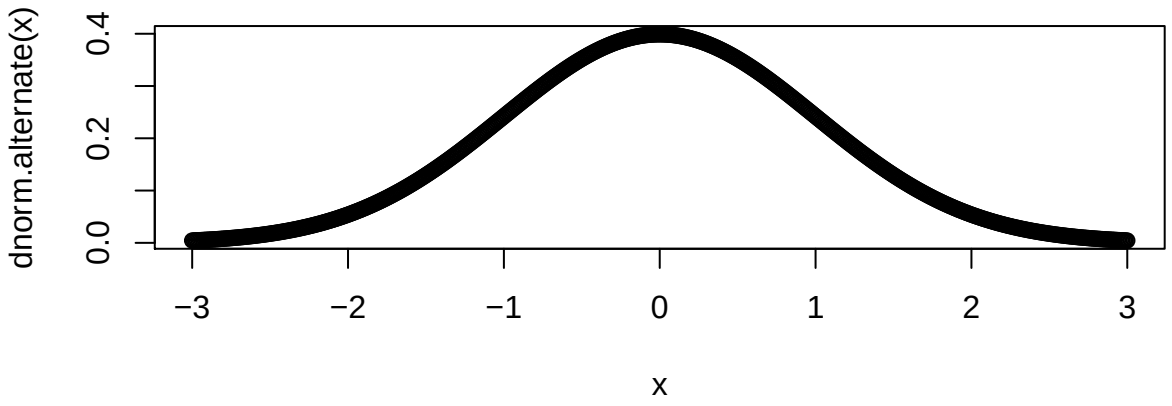
```
# test the function to see if it works
dnorm.alternate(1)
```

```
## [1] 0.2419707
```

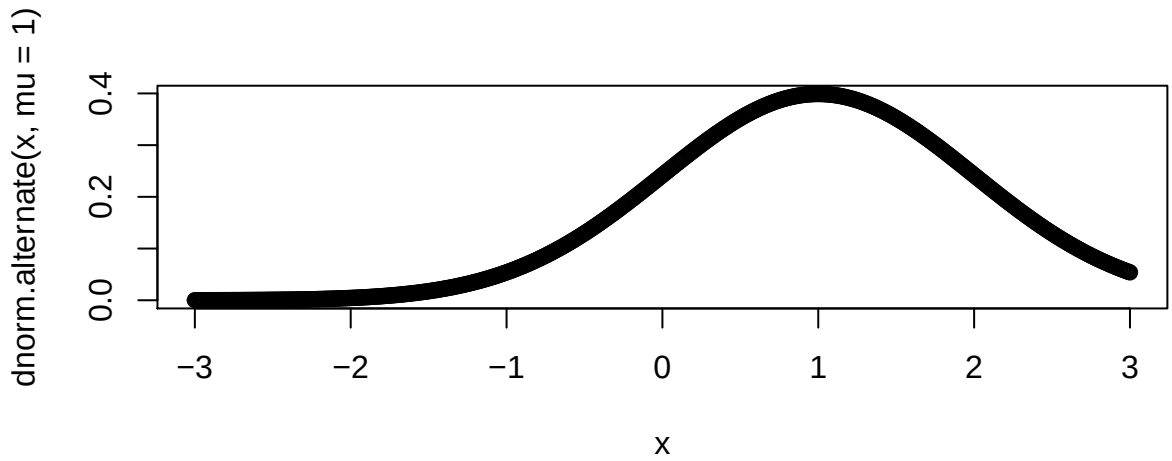
```
dnorm.alternate(1, mu=1)
```

```
## [1] 0.3989423
```

```
# 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`.

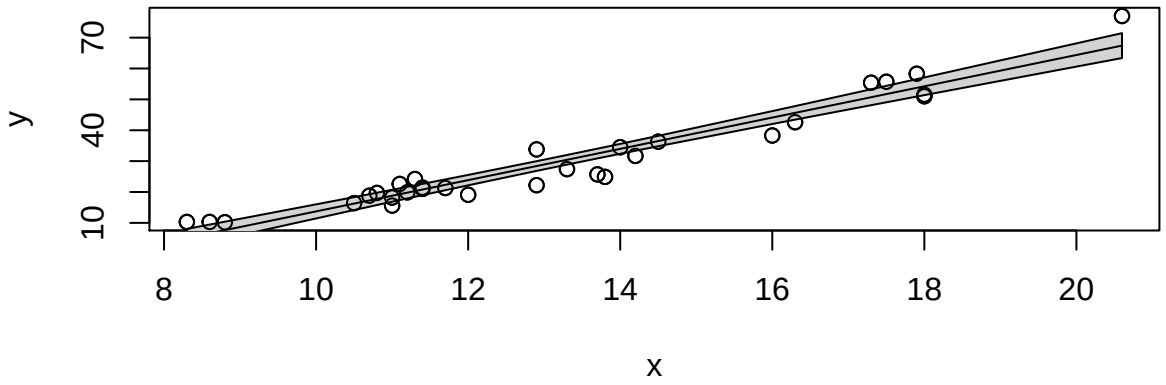
12.3 Ellipses

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.

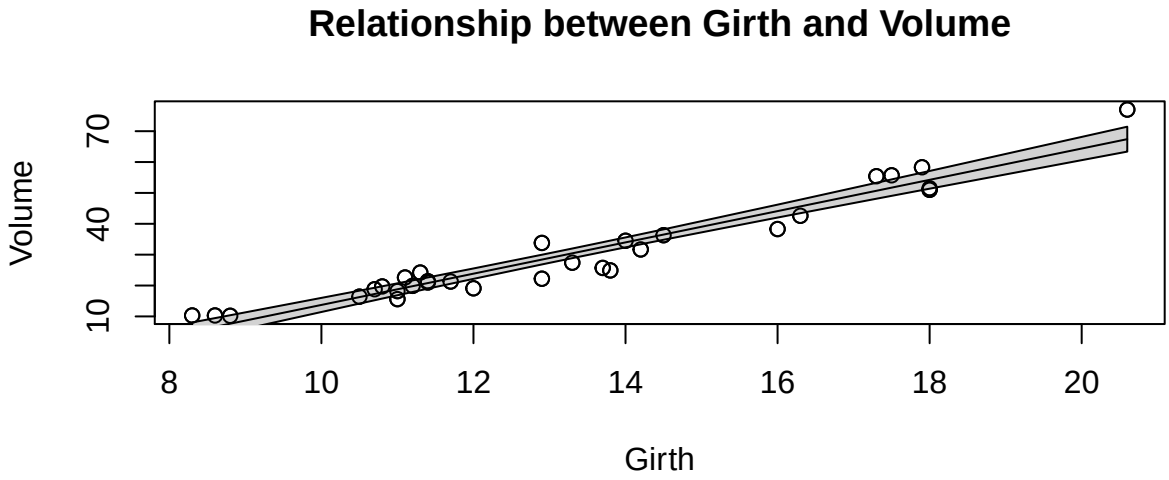
```
# a function that draws the regression line and confidence interval
# notice it doesn't return anything... all it does is draw a plot
show.lm <- function(m, interval.type='confidence', fill.col='light grey', ...){
  x <- m$model[,2]       # extract the predictor variable
  y <- m$model[,1]       # 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.

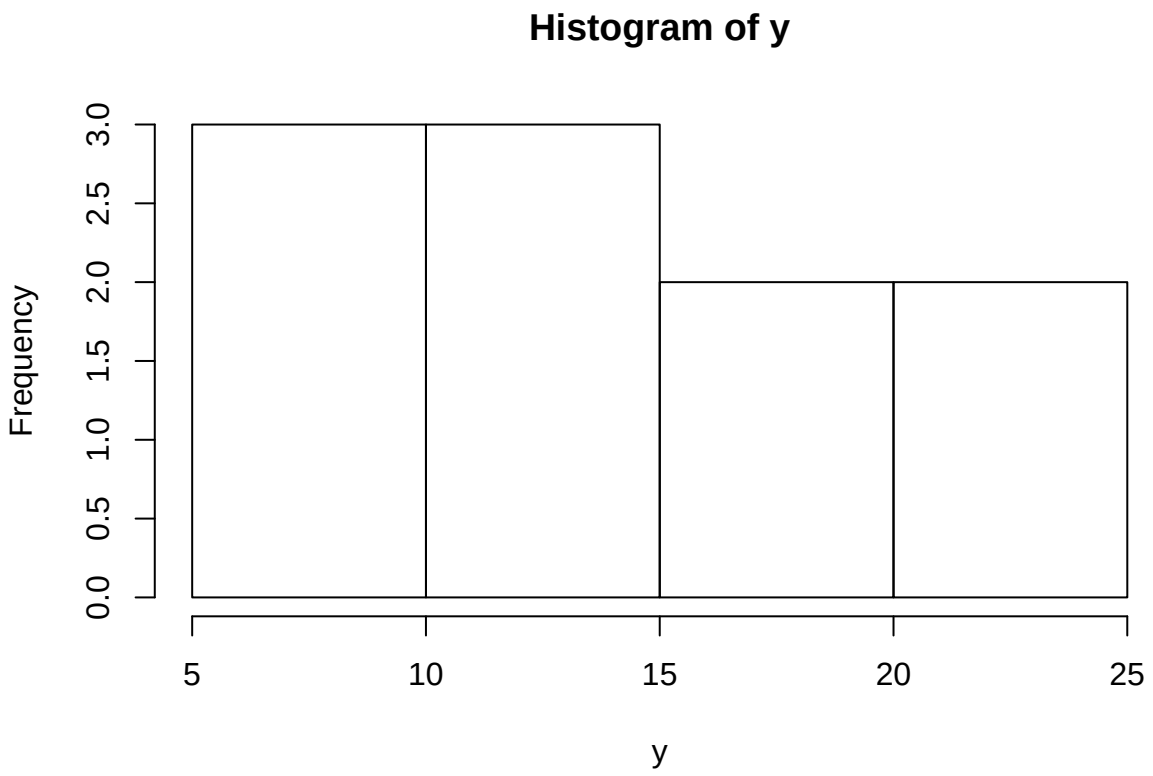
12.4 Function Overloading

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 exists a `resid.lm()` function, 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.

```
# Define a function for the trimmed mean
# x: vector of values to be averaged
# k: the number of elements to trim on either side
trimmed.mean <- function(x, k=0){
  x <- sort(x)       # arrange the input according magnitude
  n <- length(x)     # n = how many observations
  if( k > 0){
    x <- x[c(-1*(1:k), -1*((n-k+1):n))]  # remove first k, last k
  }
  tm <- sum(x) / length(x)  # mean of the remaining observations
  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. 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. 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.

```
# a horribly defined function that has no parameters
# but still accesses something called "x"
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 )    # data to trim
k <- 2

trimmed.mean()  # amazingly this still works
```

```
## [1] 6
```

```
# but what if k wasn't defined?
rm(k)           # remove k
trimmed.mean()  # now the function can't find anything named k and throws and error.
```

```
## Error in trimmed.mean(): object 'k' not found
```

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. 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.

2. 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

String Manipulation

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

1.1.1 `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

Function	Description
str_sub()	extract a substring
str_trim()	remove leading and trailing whitespace
str_pad()	pad a string with empty space to make it a certain length

13.2.1 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_c( ..., 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_c() 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_c( first.names, last.names, sep='.', collapse=' : ')
```

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

13.2.2 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.

13.2.3 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"

13.2.4 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"
```

13.2.5 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 input string
`str_locate()` `str_locate_all()`	Locates the first (or all) positions 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 substring(s) with a new pattern
`str_split()` `str_split_fixed()`	Splits the input string based on the inputed 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.

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')
```

13.3.1 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.

13.3.2 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.

```
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()`.

13.3.3 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"
```

13.3.4 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).

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 with the `n=` argument), 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

The next section will introduce using regular expressions. 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.

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. 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
 S123   P2    C10 2012    06  21   21     34     22
  S10   P1     C1 2012    06  22   05     01     48
 S187   P2     C2 2012    07  02   02     35     01
```

Hint: Convert all the dashes to periods and then split on the dots. After that you'll have to further tear apart the date and time columns using str_sub().

Chapter 14

Dates and Times

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. 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	Uncommon Orders
`ymd()` Year Month Day	`dym()` Day Year Month
`mdy()` Month Day Year	`myd()` Month Year Day
`dmy()` Day Month Year	`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:

```
library( lubridate )
mdy( 'June 26, 1997', 'Jun 26 97', '6-26-97', '6-26-1997', '6/26/97', '6-26/97' )
```

```
## [1] "1997-06-26" "1997-06-26" "1997-06-26" "1997-06-26" "1997-06-26"
```

```
## [6] "1997-06-26"
```

Unfortunately `lubridate()` is inconsistency recognizing the two digit year as either 97 or 1997. 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"
```

```
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

```
mdy_hm('Sept 18, 2010 5:30 PM', '9-18-2010 17:30')
```

```
## [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
```

```
## Warning in as.POSIXct.POSIXlt(lt): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(ct): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(x, tz): unknown timezone 'default/America/
## Phoenix'
```

```
## [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
```

```
## Warning in as.POSIXct.POSIXlt(lt): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(ct): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXct.POSIXlt(dlt): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(dct): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(x, tz): unknown timezone 'default/America/
## Phoenix'
```

```
## [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.

```
mdy_hm('9-18-2010 17:30', tz='US/Arizona') # US Arizona time
```

```
## Warning in as.POSIXct.POSIXlt(lt): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(ct): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(x, tz): unknown timezone 'default/America/
## Phoenix'
```

```
## [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 [http://en.wikipedia.org/wiki/List_of_tz_database_time_zones||http://en.wikipedia.org/wiki/List_of_tz_database_time_zones].

14.2 Extracting information

The `lubridate` package provides many functions for extracting information from the date. Suppose we have defined

```
# Derek's wedding!
x <- mdy_hm('9-18-2010 17:30', tz='US/Mountain') # US Mountain time
```

```
## Warning in as.POSIXct.POSIXlt(lt): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(ct): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXct.POSIXlt(dlt): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(dct): unknown timezone 'default/America/
## Phoenix'
```

Command	Ouput	Description
`year(x)`	2010	Year
`month(x)`	9	Month
`day(x)`	18	Day
`hour(x)`	17	Hour of the day
`minute(x)`	30	Minute of the hour
`second(x)`	0	Seconds
`wday(x)`	7	Day of the week (Sunday = 1)
`mday(x)`	18	Day of the month

Command	Ouput	Description
`yday(x)`	261	Day of the year

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	Ouput
`wday(x, label=TRUE)`	Sat
`month(x, label=TRUE)`	Sep

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
```

```
## Warning in as.POSIXlt.POSIXct(x): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(x, tz = tz(x)): unknown timezone 'default/
## America/Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(date): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXct.POSIXlt(lt): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(ct): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXct.POSIXlt(new): unknown timezone 'default/America/
## Phoenix'
```

```
x
```

```
## Warning in as.POSIXlt.POSIXct(x, tz): unknown timezone 'default/America/
## Phoenix'
```

```
## [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')
```

```
## Warning in as.POSIXct.POSIXlt(lt): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(ct): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXct.POSIXlt(dlt): unknown timezone 'default/America/
## Phoenix'
```

```
## Warning in as.POSIXlt.POSIXct(dct): unknown timezone 'default/America/
## Phoenix'
```

```
with_tz(GoT, tz='US/Arizona')
```

```
## Warning in as.POSIXlt.POSIXct(x, tz): unknown timezone 'default/America/
## Phoenix'
```

```
## [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.

```
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)  # Just add two to the year
```

```
## [1] "2013-02-21"
```

```
x + dyears(2) # Add 2*365 days; 2012 was a leap year
```

```
## [1] "2013-02-20"
```

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?

```
birthday <- c(
  'September 13, 1978',
  'Sept 13, 1978',
  'Sep 13, 1978',
  '9-13-78',
  '9/13/78')
```

2. 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?

3. It turns out there is some interesting periodicity regarding the number of births on particular days of the year.

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.

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(mosaicData)
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.

Chapter 15

Speeding up R

```
library(microbenchmark)  # for measuring how long stuff takes

library(doMC)       # do multi-core stuff
library(foreach)    # parallelizable for loops

library(ggplot2)
library(dplyr)

library(faraway)    # some examples
library(boot)
library(caret)
library(glmnet)
```

Eventually if you have large enough data sets, an R user eventually writes code that is slow to execute and needs to be sped up. This chapter tries to lay out common problems and bad habits and shows how to correct them. However, the correctness and maintainability of code should take precendence over speed. Too often, misguided attempts to obtain efficient code results in an unmaintainable mess that is no faster that the initial code.

Hadley Wickham has a book aimed at advanced R user that describes many of the finer details about R. One section in the book describes his process for building fast, maintainable software projects and if you have the time, I highly suggest reading the on-line version, Advanced R.

First we need some way of measuring how long our code took to run. For this we will use the package `microbenchmark`. The idea is that we want to evaluate two or three expressions that solve a problem.

```
x <- runif(1000)
microbenchmark(
  sqrt(x),          # First expression to compare
  x^(0.5)           # second expression to compare
) %>% print(digits=3)
```

```
## Unit: microseconds
##     expr   min    lq  mean median    uq   max neval cld
##  sqrt(x)  2.58  2.71  3.69    2.9  4.13  18.9   100  a
##  x^(0.5) 29.66 30.00 33.52   30.2 31.25 139.8   100   b
```

What `microbenchmark` does is run the two expressions a number of times and then produces the 5-number summary of those times. By running it multiple times, we account for the randomness associated with a operating system that is also running at the same time.

15.1 Faster for loops?

Often we need to perform some simple action repeatedly. It is natural to write a `for` loop to do the action and we wish to speed the up. In this first case, we will consider having to do the action millions of times and each chunk of computation within the `for` takes very little time.

Consider frame of 4 columns, and for each of n rows, we wish to know which column has the largest value.

```
make.data <- function(n){
  data <- cbind(
    rnorm(n, mean=5, sd=2),
    rpois(n, lambda = 5),
    rgamma(n, shape = 2, scale = 3),
    rexp(n, rate = 1/5))
  data <- data.frame(data)
  return(data)
}

data <- make.data(100)
```

The way that you might first think about solving this problem is to write a for loop and, for each row, figure it out.

```
f1 <- function( input ){
  output <- NULL
  for( i in 1:nrow(input) ){
    output[i] <- which.max( input[i,] )
  }
  return(output)
}
```

We might consider that there are two ways to return a value from a function (using the `return` function and just printing it). In fact, I've always heard that using the `return` statment is a touch slower.

```
f2.noReturn <- function( input ){
  output <- NULL
  for( i in 1:nrow(input) ){
    output[i] <- which.max( input[i,] )
  }
  output
}
```

```
data <- make.data(100)
microbenchmark(
  f1(data),
  f2.noReturn(data)
) %>% print(digits=3)
```

```
## Unit: milliseconds
##               expr  min   lq mean median   uq  max neval cld
##           f1(data) 3.57 3.96 4.39   4.16 4.51 7.86   100   a
##  f2.noReturn(data) 3.56 3.86 4.32   4.06 4.38 8.79   100   a
```

In fact, it looks like it is a touch slower, but not massively compared to the run-to-run variability. I prefer to use the `return` statement for readability, but if we agree have the last line of code in the function be whatever needs to be returned, readability isn't strongly effected.

We next consider whether it would be faster to allocate the output vector once we figure out the number of

rows needed, or just build it on the fly?

```
f3.AllocOutput <- function( input ){
  n <- nrow(input)
  output <- rep(NULL, n)
  for( i in 1:nrow(input) ){
    output[i] <- which.max( input[i,] )
  }
  return(output)
}
```

```
microbenchmark(
  f1(data),
  f3.AllocOutput(data)
) %>% print(digits=3)
```

```
## Unit: milliseconds
##                   expr  min   lq mean median   uq   max neval cld
##              f1(data) 3.58 3.73 4.01   3.82 4.06  7.03   100   a
##  f3.AllocOutput(data) 3.58 3.75 4.24   3.89 4.20 13.88   100   a
```

If anything, allocating the size of output first was slower. So given this, we shouldn't feel to bad being lazy and using `output <- NULL` to initiallize things.

15.2 Vectorizing loops

In general, `for` loops in R are very slow and we want to avoid them as much as possible. The `apply` family of functions can be quite helpful for applying a function to each row or column of a matrix or data.frame or to each element of a list.

To test this, instead of a `for` loop, we will use `apply`.

```
f4.apply <- function( input ){
  output <- apply(input, 1, which.max)
  return(output)
}
```

```
microbenchmark(
  f1(data),
  f4.apply(data)
) %>% print(digits=3)
```

```
## Unit: microseconds
##            expr  min   lq mean median   uq  max neval cld
##        f1(data) 3535 3673 4086   3819 4243 6409   100   b
##  f4.apply(data)  284  303  350    334  365  585   100  a
```

This is the type of speed up that matters. We have a 10-fold speed up in execution time and particularly the maximum time has dropped impressively.

Unfortunately, I have always found the `apply` functions a little cumbersome and I prefer to use `dplyr` instead strictly for readability.

```
f5.dplyr <- function( input ){
  output <- input %>%
    mutate( max.col=which.max( c(X1, X2, X3, X4) ) )
```

```
  return(output$max.col)
}
```

```
microbenchmark(
  f4.apply(data),
  f5.dplyr(data)
) %>% print(digits=3)
```

```
## Unit: microseconds
##            expr  min   lq mean median   uq  max neval cld
##  f4.apply(data)  312  351  410    377  404 2710   100  a
##  f5.dplyr(data) 2163 2286 2452   2368 2516 3809   100   b
```

Unfortunately `dplyr` is a lot slower than `apply` in this case. I wonder if the dynamics would change with a larger `n`?

```
data <- make.data(10000)
microbenchmark(
  f4.apply(data),
  f5.dplyr(data)
) %>% print(digits=3)
```

```
## Unit: milliseconds
##            expr   min    lq  mean median    uq   max neval cld
##  f4.apply(data) 25.49 28.55 31.73  29.93 32.31 73.01   100   b
##  f5.dplyr(data)  2.26  2.59  3.09   2.77  3.05  8.54   100  a
```

```
data <- make.data(100000)
microbenchmark(
  f4.apply(data),
  f5.dplyr(data)
) %>% print(digits=3)
```

```
## Unit: milliseconds
##            expr    min     lq  mean median     uq max neval cld
##  f4.apply(data) 301.40 374.17 456.8  451.4 521.47 724   100   b
##  f5.dplyr(data)   3.56   4.19  11.4    4.4   4.76 203   100  a
```

What just happened? The package `dplyr` is designed to work well for large data sets, and utilizes a modified structure, called a `tibble`, which provides massive benefits for large tables, but at the small scale, the overhead of converting the `data.frame` to a `tibble` overwhelms any speed up. But because the small sample case is already fast enough to not be noticable, we don't really care about the small `n` case.

15.3 Parallel Processing

Most modern computers have multiple computing cores, and can run muliple processes at the same time. Sometimes this means that you can run multiple programs and switch back and forth easily without lag, but we are now interested in using as many cores as possible to get our statistical calculations completed by using muliple processing cores at the same time. This is referred to as running the process "in parallel" and there are many tasks in modern statistical computing that are "embarrasingly easily parallelized". In particular bootstrapping and cross validation techniques are extremely easy to implement in a parallel fashion.

However, running commands in parallel incurs some overhead cost in set up computation, as well as all the message passing from core to core. For example, to have 5 cores all perform an analysis on a set of data, all 5 cores must have access to the data, and not overwrite any of it. So parallelizing code only makes sense if

the individual steps that we pass to each core is of sufficient size that the overhead incurred is substantially less than the time to run the job.

We should think of executing code in parallel as having three major steps: 1. Tell R that there are multiple computing cores available and to set up a useable cluster to which we can pass jobs to. 2. Decide what 'computational chunk' should be sent to each core and distribute all necessary data, libraries, etc to each core. 3. Combine the results of each core back into a unified object.

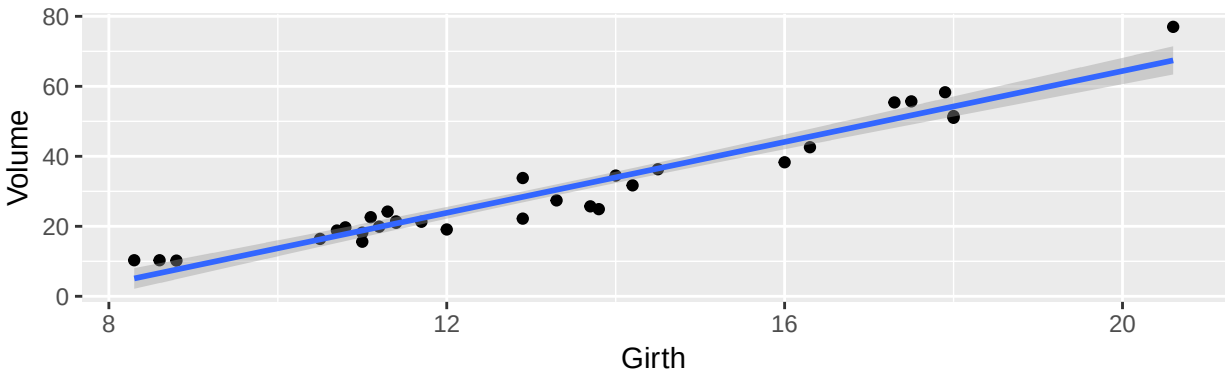
15.4 Parallelizing for loops

There are a number of packages that allow you to tell R how many cores you have access to. One of the easiest ways to parallelize a for loop is using a package called `foreach`. The registration of multiple cores is actually pretty easy.

```
doMC::registerDoMC(cores = 2)  # my laptop only has two cores.
```

We will consider an example that is common in modern statistics. We will examine parallel computing utilizing a bootstrap example where we create bootstrap samples for calculating confidence intervals for regression coefficients.

```
ggplot(trees, aes(x=Girth, y=Volume)) + geom_point() + geom_smooth(method='lm')
```




```
model <- lm( Volume ~ Girth, data=trees)
```

This is how we would do this previously.

```
# f is a formula
# df is the input data frame
# M is the number of bootstrap iterations
boot.for <- function( f, df, M=999){
  output <- list()
  for( i in 1:100 ){
    # Do stuff
    model.star <- lm( f, data=df %>% sample_frac(1, replace=TRUE) )
    output[[i]] <- model.star$coefficients
  }

  # use rbind to put the list of results together into a data.frame
  output <- sapply(output, rbind) %>% t() %>% data.frame()
  return(output)
}
```

We will first ask about how to do the same thing using the function `foreach`

```
# f is a formula
# df is the input data frame
# M is the number of bootstrap iterations
boot.foreach <- function(f, df, M=999){
  output <- foreach( i=1:100 ) %dopar% {
    # Do stuff
    model.star <- lm( f, data=df %>% sample_frac(1, replace=TRUE) )
    model.star$coefficients
  }

  # use rbind to put the list of results together into a data.frame
  output <- sapply(output, rbind) %>% t() %>% data.frame()
  return(output)
}
```

Not much has changed in our code. Lets see which is faster.

```
microbenchmark(
  boot.for( Volume~Girth, trees ),
  boot.foreach( Volume~Girth, trees )
) %>% print(digits=3)
```

```
## Unit: milliseconds
##                                 expr min  lq mean median  uq  max neval
##      boot.for(Volume ~ Girth, trees) 244 257  387    297 324 4416   100
##  boot.foreach(Volume ~ Girth, trees) 349 372  454    381 439 3263   100
##  cld
##    a
##    a
```

In this case, the overhead associated with splitting the job across two cores, copying the data over, and then combining the results back together was more than we saved by using both cores. If the nugget of computation within each pass of the `for` loop was larger, then it would pay to use both cores.

```
# massiveTrees has 31000 observations
massiveTrees <- NULL
for( i in 1:1000 ){
  massiveTrees <- rbind(massiveTrees, trees)
}
microbenchmark(
  boot.for( Volume~Girth, massiveTrees )  ,
  boot.foreach( Volume~Girth, massiveTrees )
) %>% print(digits=3)
```

```
## Unit: seconds
##                                      expr  min   lq mean median   uq
##      boot.for(Volume ~ Girth, massiveTrees) 4.15 4.38 4.78   4.50 4.61
##  boot.foreach(Volume ~ Girth, massiveTrees) 2.42 2.46 2.70   2.48 2.55
##    max neval cld
##  11.47   100   b
##   4.33   100  a
```

Because we often generate a bunch of results that we want to see as a data.frame, the `foreach` function includes and option to do it for us.

```
output <- foreach( i=1:100, .combine=data.frame ) %dopar% {
  # Do stuff
```

```
  model.star <- lm( Volume ~ Girth, data= trees %>% sample_frac(1, replace=TRUE) )
  model$coefficients
}
```

It is important to recognize that the data.frame `trees` was utilized inside the `foreach` loop. So when we called the `foreach` loop and distributed the workload across the cores, it was smart enough to distribute the data to each core. However, if there were functions that we utilized inside the foor loop that came from a packege, we need to tell each core to load the function.

```
output <- foreach( i=1:1000, .combine=data.frame, .packages='dplyr' ) %dopar% {
  # Do stuff
  model.star <- lm( Volume ~ Girth, data= trees %>% sample_frac(1, replace=TRUE) )
  model.star$coefficients
}
```

15.5 Parallel Aware Functions

There are many packages that address problems that are "embarassingly easily parallelized" and they will happily work with multiple cores. Methods that rely on resampling certainly fit into this category.

15.5.1 `boot::boot`

Bootstrapping relys on resampling the dataset and calculating test statistics from each resample. In R, the most common way to do this is using the package `boot` and we just need to tell the `boot` function, to use the multiple cores available. (Note, we have to have registered the cores first!)

```
model <- lm( Volume ~ Girth, data=trees)
my.fun <- function(df, index){
  model.star <- lm( Volume ~ Girth, data= trees[index,] )
  model.star$coefficients
}
microbenchmark(
  serial   = boot::boot( trees, my.fun, R=1000 ),
  parallel = boot::boot( trees, my.fun, R=1000,
                         parallel='multicore', ncpus=2 )
) %>% print(digits=3)
```

```
## Unit: milliseconds
##      expr min  lq mean median  uq  max neval cld
##    serial 713 737  864    797 828 2637   100   b
##  parallel 625 643  721    663 683 2461   100  a
```

In this case, we had a bit of a spead up, but not a factor of 2. This is due to the overhead of splitting the job across both cores.

15.5.2 `caret::train`

The statistical learning package `caret` also handles all the work to do cross validation in a parallel computing environment. The functions in `caret` have an option `allowParallel` which by default is TRUE, which controls if we should use all the cores. Assuming we have already registered the number of cores, then by default `caret` will use them all.

```
library(faraway)
library(caret)
ctrl.serial <- trainControl( method='repeatedcv', number=5, repeats=4,
                      preProcOptions = c('center','scale'),
                      allowParallel = FALSE)
ctrl.parallel <- trainControl( method='repeatedcv', number=5, repeats=4,
                      preProcOptions = c('center','scale'),
                      allowParallel = TRUE)
grid <- data.frame(
  alpha  = 1,  # 1 => Lasso Regression
  lambda = exp(seq(-6, 1, length=50)))

microbenchmark(
  model <- train( lpsa ~ ., data=prostate, method='glmnet',
                  trControl=ctrl.serial, tuneGrid=grid,
                  lambda = grid$lambda ),
  model <- train( lpsa ~ ., data=prostate, method='glmnet',
                  trControl=ctrl.parallel, tuneGrid=grid,
                  lambda = grid$lambda )
) %>% print(digits=3)
```

```
## Unit: seconds
##                                                                                                  expr
##   model <- train(lpsa ~ ., data = prostate, method = "glmnet",     trControl = ctrl.serial, tuneGrid = grid
##  model <- train(lpsa ~ ., data = prostate, method = "glmnet",    trControl = ctrl.parallel, tuneGrid = grid
##    min   lq mean median   uq  max neval cld
##   1.08 1.11 1.21   1.12 1.15 2.94   100   a
##   1.11 1.14 1.23   1.14 1.17 2.93   100   a
```

Again, we saw only moderate gains by using both cores, however it didn't really cost us anything. Because the `caret` package by default allows parallel processing, it doesn't hurt to just load the `doMC` package and register the number of cores. Even in just the two core case, it is a good habit to get into so that when you port your code to a huge computer with many cores, the only thing to change is how many cores you have access to.

Chapter 16

Rmarkdown Tricks

We have been using RMarkdown files to combine the analysis and discussion into one nice document that contains all the analysis steps so that your research is reproducible.

There are many resources on the web about Markdown and the variant that RStudio uses (called RMarkdown), but the easiest reference is to just use the RStudio help tab to access the help. I particular like `Help -> Cheatsheets -> RMarkdown Reference Guide` because it gives me the standard Markdown information but also a bunch of information about the options I can use to customize the behavior of individual R code chunks.

Two topics that aren't covered in the RStudio help files are how to insert mathematical text symbols and how to produce decent looking tables without too much fuss.

Most of what is presented here isn't primarily about how to use R, but rather how to work with tools in RMarkdown so that the final product is neat and tidy. While you could print out your RMarkdown file and then clean it up in MS Word, sometimes there is a good to want as nice a starting point as possible.

16.1 Mathematical expressions

The primary way to insert a mathematical expression is to use a markup language called LaTeX. This is a very powerful system and it is what most Mathematicians use to write their documents. The downside is that there is a lot to learn. However, you can get most of what you need pretty easily.

For RMarkdown to recognize you are writing math using LaTeX, you need to enclose the LaTeX with dollar signs ($). Some examples of common LaTeX patterns are given below:

Goal	LaTeX	Output	LaTeX	Output
power	`$x^2$`	x^2	`$y^{0.95}$`	$y^{0.95}$
Subscript	`$x_i$`	x_i	`$t_{24}$`	t_{24}
Greek	`$\alpha$ $\beta$`	α β	`$\theta$ $\Theta$`	θ Θ
Bar	`$\bar{x}$`	$\bar{x}$	`$\bar{mu}_i$`	$\bar{\mu}_i$
Hat	`$\hat{mu}$`	$\hat{\mu}$	`$\hat{y}_i$`	$\hat{y}_i$
Star	`$y^*$`	y^*	`$\hat{\mu}^*_i$`	$\hat{\mu}^*_i$
Centered Dot	`$\cdot$`	$\cdot$	`$\bar{y}_{i\cdot}$`	$\bar{y}_{i\cdot}$
Sum	`$\sum x_i$`	$\sum x_i$	`$\sum_{i=0}^N x_i$`	$\sum_{i=0}^{N} x_i$

Goal	LaTeX	Output	LaTeX	Output
Square Root	`$\sqrt{a}$`	$\sqrt{a}$	`$\sqrt{a^2 + b^2}$`	$\sqrt{a^2 + b^2}$
Fractions	`$\frac{a}{b}$`	$\frac{a}{b}$	`$\frac{x_i - \bar{x}}{s/\sqrt{n}}$`	$\frac{x_i - \bar{x}}{s/\sqrt{n}}$

Within your RMarkdown document, you can include LaTeX code by enclosing it with dollar signs. So you might write `$\alpha=0.05$` in your text, but after it is knitted to a pdf, html, or Word, you'll see $\alpha = 0.05$. If you want your mathematical equation to be on its own line, all by itself, enclose it with double dollar signs. So

```
$$z_i = \frac{z_i-\bar{x}}{\sigma / \sqrt{n}}$$
```

would be displayed as

$$z_i = \frac{x_i - \bar{X}}{\sigma/\sqrt{n}}$$

Unfortunately RMarkdown is a little picky about spaces near the $ and $$ signs and you can't have any spaces between them and the LaTeX command. For a more information about all the different symbols you can use, google 'LaTeX math symbols'.

16.2 Tables

For the following descriptions of the simple, grid, and pipe tables, I've shamelessly stolen from the Pandoc documentation. [http://pandoc.org/README.html#tables]

One way to print a table is to just print in in R and have the table presented in the code chunk. For example, suppose I want to print out the first 4 rows of the trees dataset.

```
data <- trees[1:4, ]
data
```

```
##   Girth Height Volume
## 1   8.3     70   10.3
## 2   8.6     65   10.3
## 3   8.8     63   10.2
## 4  10.5     72   16.4
```

Usually this is sufficient, but suppose you want something a bit nicer because you are generating tables regularly and you don't want to have to clean them up by hand. Tables in RMarkdown follow the table conventions from the Markdown class with a few minor exceptions. Markdown provides 4 ways to define a table and RMarkdown supports 3 of those.

16.2.1 Simple Tables

Simple tables look like this (Notice I don't wrap these dollar signs or anything, just a blank line above and below the table):

```
Right   Left     Center   Default
------- ------ ---------- -------
     12 12        hmmm        12
```

```
    123 123         123         123
      1 1             1           1
```

and would be rendered like this:

Right	Left	Center	Default
12	12	hmmm	12
123	123	123	123
1	1	1	1

The headers and table rows must each fit on one line. Column alignments are determined by the position of the header text relative to the dashed line below it.

If the dashed line is flush with the header text on the right side but extends beyond it on the left, the column is right-aligned. If the dashed line is flush with the header text on the left side but extends beyond it on the right, the column is left-aligned. If the dashed line extends beyond the header text on both sides, the column is centered. If the dashed line is flush with the header text on both sides, the default alignment is used (in most cases, this will be left). The table must end with a blank line, or a line of dashes followed by a blank line.

16.2.2 Grid Tables

Grid tables are a little more flexible and each cell can take an arbitrary Markdown block elements (such as lists).

```
+---------------+---------------+--------------------+
| Fruit         | Price         | Advantages         |
+===============+===============+====================+
| Bananas       | $1.34         | - built-in wrapper |
|               |               | - bright color     |
+---------------+---------------+--------------------+
| Oranges       | $2.10         | - cures scurvy     |
|               |               | - tasty            |
+---------------+---------------+--------------------+
```

which is rendered as the following:

Fruit	Price	Advantages
Bananas	$1.34	• built-in wrapper • bright color
Oranges	$2.10	• cures scurvy • tasty

Grid table doesn't support Left/Center/Right alignment. Both Simple tables and Grid tables require you to format the blocks nicely inside the RMarkdown file and that can be a bit annoying if something changes and you have to fix the spacing in the rest of the table. Both Simple and Grid tables don't require column headers.

16.2.3 Pipe Tables

Pipe tables look quite similar to grid tables but Markdown isn't as picky about the pipes lining up. However, it does require a header row (which you could leave the elements blank in).

```
| Right | Left | Default | Center |
|------:|:-----|---------|:------:|
|   12  |  12  |    12   |    12  |
|  123  |  123 |   123   |   123  |
|    1  |    1 |     1   |     1  |
```

which will render as the following:

Right	Left	Default	Center
12	12	12	12
123	123	123	123
1	1	1	1

In general I prefer to use the pipe tables because it seems a little less picky about getting everything correct. However it is still pretty annoying to get the table laid out correctly.

In all of these tables, you can use the regular RMarkdown formatting tricks for italicizing and bolding. So I could have a table such as the following:

```
|   Source    |  df  |   Sum of Sq   |    Mean Sq    |    F    |  $Pr(>F_{1,29})$    |
|:------------|-----:|--------------:|--------------:|--------:|--------------------:|
|  Girth      |  *1* |  7581.8       |  7581.8       | 419.26  |  **< 2.2e-16**      |
|  Residual   |  29  |  524.3        |   18.1        |         |                     |
```

and have it look like this:

Source	df	Sum of Sq	Mean Sq	F	$Pr(>F_{1,29})$
Girth	*1*	7581.8	7581.8	419.26	$<$ **2.2e-16**
Residual	29	524.3	18.1		

The problem with all of this is that I don't want to create these by hand. Instead I would like functions that take a data frame or matrix and spit out the RMarkdown code for the table.

16.3 R functions to produce table code.

There are a couple of different packages that convert a data frame to simple/grid/pipe table. We will explore a couple of these, starting with the most basic and moving to the more complicated. The general idea is that we'll produce the appropriate simple/grid/pipe table syntax in R, and when it gets knitted, then RMarkdown will turn our simple/grid/pipe table into something pretty.

16.3.1 `knitr::kable`

The `knitr` package includes a function that produces simple tables. It doesn't have much customizability, but it gets the job done.

```
# in this code chunk, I've used the "results='hold'" option to prevent
# the RMarkdown processor from turning this into something pretty
knitr::kable( data )
```

Girth	Height	Volume
8.3	70	10.3
8.6	65	10.3
8.8	63	10.2
10.5	72	16.4

which, if I don't prevent the RMarkdown processor from doing its job, will get rendered as such:

```
knitr::kable( data )
```

Girth	Height	Volume
8.3	70	10.3
8.6	65	10.3
8.8	63	10.2
10.5	72	16.4

16.3.2 Package `pander`

The package `pander` seems to be a nice compromise between customization and not having to learn too much. It is relatively powerful in that it will take `summary()` and `anova()` output and produce tables for them. By default `pander` will produce simple tables, but you can ask for Grid or Pipe tables.

```
library(pander)
pander( data, style='rmarkdown' )   # style is pipe tables...
```

Girth	Height	Volume
8.3	70	10.3
8.6	65	10.3
8.8	63	10.2
10.5	72	16.4

The `pander` package deals with summary and anova tables from a variety of different analyses. So you can simply ask for a nice looking version using the following:

```
model <- lm( Volume ~ Girth, data=trees )    # a simple regression
pander( summary(model) )    # my usual summary table
```

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	-36.94	3.365	-10.98	7.621e-12
Girth	5.066	0.2474	20.48	8.644e-19

Table 16.8: Fitting linear model: Volume ~ Girth

Observations	Residual Std. Error	R^2	Adjusted R^2
31	4.252	0.9353	0.9331

```
pander( anova( model ) )     # my usual anova table
```

Table 16.9: Analysis of Variance Table

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Girth	1	7582	7582	419.4	8.644e-19
Residuals	29	524.3	18.08	NA	NA

Bibliography