

Notes for Teaching an Undergraduate Statistics Using fastR

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Preface

This book is based on the notes I distribute to my students as part of a one semester course on probability and statistics. I have used these notes for 3 semesters and so they have seen multiple revisions. This notes are based on using the first addition of Prium's book Foundations and Applications of Statistics: An Introduction Using R (2011). I have selected this book because its cost is reasonable and it does a great job balancing mathematical rigor with computational skills. I also like the way that R is woven within the text to include the examples and problems.

0.1 Who is this book for?

I designed these notes for the instructor who wants to adopt a course that combines elements of a traditional mathematical statistics course with more computational and programming emphasis. My subsequent course is a machine learning course and this course has provided my students with a solid foundation to approach that next course. I think these notes will aid any instructor in getting a course with Prium's book up and running in a short amount of time.

0.2 Book Structure and How to Use It

In Appendix A, I have provided my syllabus as an example of how to use the notes. This syllabus is based on 40 lessons each of 53 minutes long. Obviously this will have to altered based on the length of course you want to run.

I aligned these notes with the chapters in Prium's textbook. Within each chapter there are subsections for each lesson. These match the lessons in the syllabus in Appendix A.

Every lesson starts with administrative tasks to cover topics such as upcoming exams, points from previous class that need clarification, and homework questions. For example, in one lesson I reviewed an RMarkdown cheat sheet, answered one homework questions, and answered a question on running swirl. In the notes I have excluded the admin section but be aware that I have one for each lesson.

I have shortened chapter 5 to allow a brief introduction to linear regression in chapter 6. The speed of the course is fast and I have had to make some difficult decisions about what to include and exclude.

I typically include 4 exams in addition to a final. I leave the lesson before the exam as a review and catch-up day. Thus the 4 exams and 4 review lessons take 8 lessons. The course is fast so I don't mind putting these extra lessons into the design.

I also include a project I have used in Appendix B.



Figure 1:



Figure 2:

0.3 Prerequisites

To take my course, students are expected to have completed calculus up through and including multivariate calculus. I don't assume they have any programming experience and thus I have used the swirl package to help them get started in R. I have the students load and run R locally on their personal computers and we also use Rstudio as the IDE for our work.

These notes make use of the following packages in R **knitr** (Xie, 2017b), **rmarkdown** (Allaire et al., 2017), **fastR** (Pruim, 2017), **Hmisc** (Harrell, 2018), **lattice** (Sarkar, 2017), **vcd** (Meyer et al., 2017), **ggplot2** (Wickham and Chang, 2016), **MASS** (Ripley, 2017), **TeachingDemos** (Snow, 2016), **Stat2Data** (Lock, 2013), **car** (Fox and Weisberg, 2017), **DT** (Xie, 2016).

0.4 Acknowledgements

I have been lucky to work with many faculty on this project but would like to thank Stephanie Bruce and Ken Horton for the willingness to use and experiment with these notes and for the sound feedback they have provided.

This book was written using the excellent **bookdown** package (Xie, 2017a).

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Chapter 1

Summarizing Data

The first chapter is completed in three lessons. The first lesson is an introduction to the course. We make sure that R is installed correctly. We cover the syllabus and expectations for the course. The next two lessons break chapter one into two parts, univariate and multivariate data. What follows are the lesson plans.

1.1 Admin and Course Introduction

1.1.1 Objectives

1. Introduce the course
2. Understand classroom expectations
3. Use R for some basic computations

Material discussed in class:

Why stats and probability?

Math 377 course and purpose

Look at syllabus and due dates

1.1.2 In Class Work

Load and use swirl

Demo R

Load a library and explain installing versus loading:

```
library(fastrR)
```

Look at the structure of a dataframe.

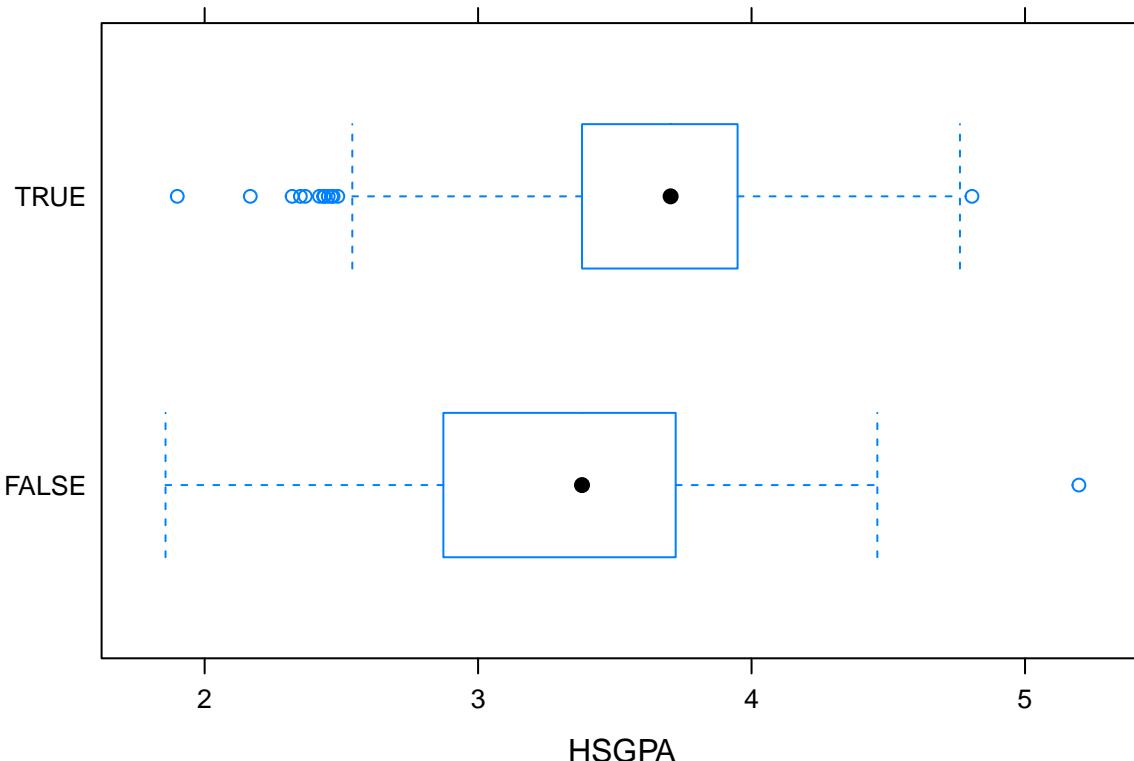
```
str(students)
```

```
## 'data.frame':    1000 obs. of  6 variables:  
##   $ ACT      : int  30 20 23 30 21 NA 23 25 30 21 ...  
##   $ SAT      : int  NA NA 1060 1420 1010 730 NA NA NA NA ...  
##   $ Grad     : logi  TRUE TRUE TRUE TRUE TRUE ...
```

```
## $ GradGPA: num 3.61 2.99 3.58 3.51 2.7 ...
## $ HSGPA : num 3.74 2.97 3.51 3.99 3.25 ...
## $ Cohort : int 2002 2004 2002 2005 2005 2001 2003 2005 2003 2003 ...
```

Create a simple plot and comments.

```
bwplot(Grad~HSGPA, students)
```



```
# This is a great plot
```

1.2 Summarizing Univariate Data

1.2.1 Objectives

1. Create univariate summaries, both numerical and graphical
2. Understand and use data structures (e.g. str, head, \$)
3. Learn definitions of new terms such as mean, median, standard deviation, and p-quantile.

1.2.2 Intro Material

This class is based on empirical deductive reasoning. We have a question or conjecture and then we collect data and see if it supports or refutes the conjecture. Often we have only a sample from a population and thus must you probability to help in the decision.

With the development of powerful computers, we are now also able to perform empirical inductive reasoning. This is what occurs in the areas of data mining and machine learning. Math 378 will emphasize these ideas.

Data is the heart of both methods.

1.2.3 Data Collection

We don't really have a hypothesis at this point just an observation that this class of Math 377 has some tall people in it. Let's collect the data and summarize.

It is often easier to enter data in a CSV, comma separated values, in Excel. We will then read the data into a data frame in R. This is done using the import tab in RStudio.

Open a new RMarkdown file to store our work.

Now that we have the data and before we start, let's practice some of the ideas in Sections 1.1 and 1.2 of the book.

1.2.4 Background

Load libraries.

```
library('fastR')
library(Hmisc)
library(lattice)
```

Look at available data sets. Use the command.

```
data()
```

Let's use the data set students in the fastR package. Before we start, let's get a feel for the data.

The `str` function gives the structure of the data

```
str(students)
```

```
## 'data.frame': 1000 obs. of 6 variables:
## $ ACT      : int 30 20 23 30 21 NA 23 25 30 21 ...
## $ SAT      : int NA NA 1060 1420 1010 730 NA NA NA NA ...
## $ Grad     : logi TRUE TRUE TRUE TRUE TRUE TRUE ...
## $ GradGPA: num 3.61 2.99 3.58 3.51 2.7 ...
## $ HSGPA   : num 3.74 2.97 3.51 3.99 3.25 ...
## $ Cohort  : int 2002 2004 2002 2005 2005 2001 2003 2005 2003 ...
```

To look at the first few rows

```
head(students)
```

```
##   ACT  SAT Grad GradGPA HSGPA Cohort
## 1  30    NA  TRUE    3.613 3.743  2002
## 2  20    NA  TRUE    2.993 2.968  2004
## 3  23  1060  TRUE    3.582 3.507  2002
## 4  30  1420  TRUE    3.513 3.990  2005
## 5  21  1010  TRUE    2.703 3.253  2005
## 6   NA   730  TRUE    3.360 2.621  2001
```

If you want a nice output when you knit into an html or pdf file

```
knitr::kable(
  head(students)
)
```

ACT	SAT	Grad	GradGPA	HSGPA	Cohort
30	NA	TRUE	3.613	3.743	2002
20	NA	TRUE	2.993	2.968	2004
23	1060	TRUE	3.582	3.507	2002
30	1420	TRUE	3.513	3.990	2005
21	1010	TRUE	2.703	3.253	2005
NA	730	TRUE	3.360	2.621	2001

```
summary(students)
```

```
##          ACT             SAT            Grad           GradGPA
##  Min.   :14.00   Min.   :730   Mode :logical  Min.   :2.075
##  1st Qu.:23.00  1st Qu.:1080  FALSE:268    1st Qu.:3.033
##  Median :26.00  Median :1180   TRUE :732    Median :3.389
##  Mean   :25.94  Mean   :1199                    Mean   :3.322
##  3rd Qu.:29.00 3rd Qu.:1310                    3rd Qu.:3.657
##  Max.   :36.00  Max.   :1590                    Max.   :4.000
##  NA's   :169    NA's   :636    NA's   :268
##          HSGPA          Cohort
##  Min.   :1.857   Min.   :2001
##  1st Qu.:3.252  1st Qu.:2002
##  Median :3.635  Median :2003
##  Mean   :3.546  Mean   :2003
##  3rd Qu.:3.912  3rd Qu.:2004
##  Max.   :5.197  Max.   :2005
##  NA's   :16
```

You can also use the help menu to find out more about the data, `?students`

Some basic summaries of the data. Since `Grad` is discrete we summarize with a table.

```
table(students$Grad)
```

```
##
## FALSE  TRUE
##    268    732
```

The variable `HSGPA` is more like a continuous variable.

```
mean(students$HSGPA,na.rm=TRUE)
```

```
## [1] 3.545669
```

```
median(students$HSGPA,na.rm=TRUE)
```

```
## [1] 3.6345
```

```
quantile(students$HSGPA,na.rm = TRUE)
```

```
##      0%      25%      50%      75%     100%
## 1.85700 3.25250 3.63450 3.91225 5.19700
```

The calculation of quantiles can be confusing, but the book does a nice job explaining how it is done. We can also get help on the function using `?quantile`.

Notice that if we did remove missing values, we would get an `NA`.

```
mean(students$HSGPA)
```

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

For dispersion, we can summarize with variance and standard deviation.

```
sd(~GradGPA,data=students,na.rm=T)
```

```
## [1] 0.4220109
```

```
sd(students$GradGPA,na.rm=T)
```

```
## [1] 0.4220109
```

```
var(students$GradGPA,na.rm=T)
```

```
## [1] 0.1780932
```

A useful function in the mosaic package is favstats.

```
favstats(~HSGPA,data=students)
```

```
##   min      Q1 median      Q3 max      mean      sd n missing
## 1.857 3.2525 3.6345 3.91225 5.197 3.545669 0.4793097 984      16
```

Notice we used the R formula notation discussed in the book.

Breaking it down by year group.

```
favstats(HSGPA~Cohort,data=students)
```

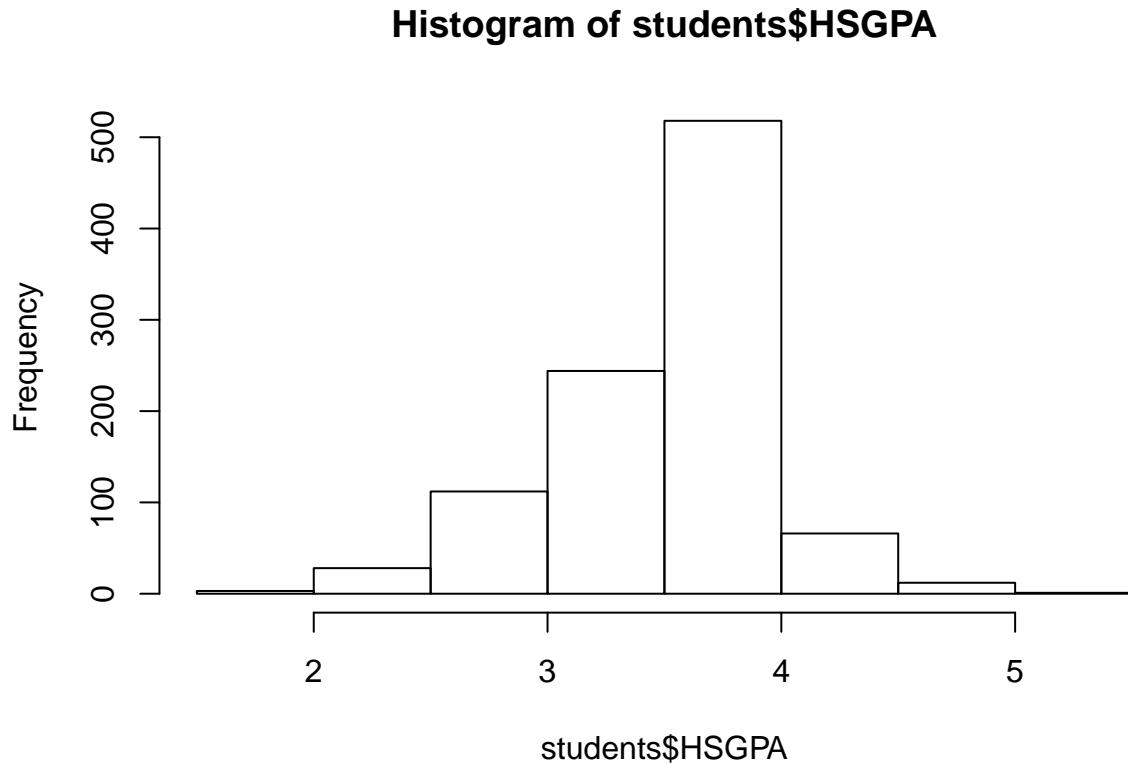
```
##   Cohort min      Q1 median      Q3 max      mean      sd n missing
## 1 2001 2.167 3.16350 3.6195 3.88575 5.197 3.502119 0.5393179 194      6
## 2 2002 2.320 3.34325 3.6940 3.92825 4.705 3.600908 0.4266389 218      3
## 3 2003 1.857 3.25100 3.6905 3.90925 4.762 3.563235 0.4829192 200      4
## 4 2004 2.160 3.28400 3.6200 3.90600 4.806 3.544259 0.4631015 185      2
## 5 2005 1.900 3.24950 3.5650 3.92600 4.337 3.509059 0.4807082 187      1
```

```
summary(HSGPA~Grad,data=students,fun=favstats)
```

```
## HSGPA      N= 984 , 16 Missing
##
## +-----+-----+-----+-----+-----+-----+-----+-----+
## |      |N|min|Q1|median|Q3|max|mean|sd|n|missing|
## +-----+-----+-----+-----+-----+-----+-----+-----+
## |Grad|No|263|1.857|2.8730|3.3800|3.72250|5.197|3.307817|0.5373946|263|0|
## |    |Yes|721|1.900|3.3800|3.7040|3.94900|4.806|3.632430|0.4246933|721|0|
## +-----+-----+-----+-----+-----+-----+-----+-----+
## |Overall|  |984|1.857|3.2525|3.6345|3.91225|5.197|3.545669|0.4793097|984|0|
## +-----+-----+-----+-----+-----+-----+-----+-----+
```

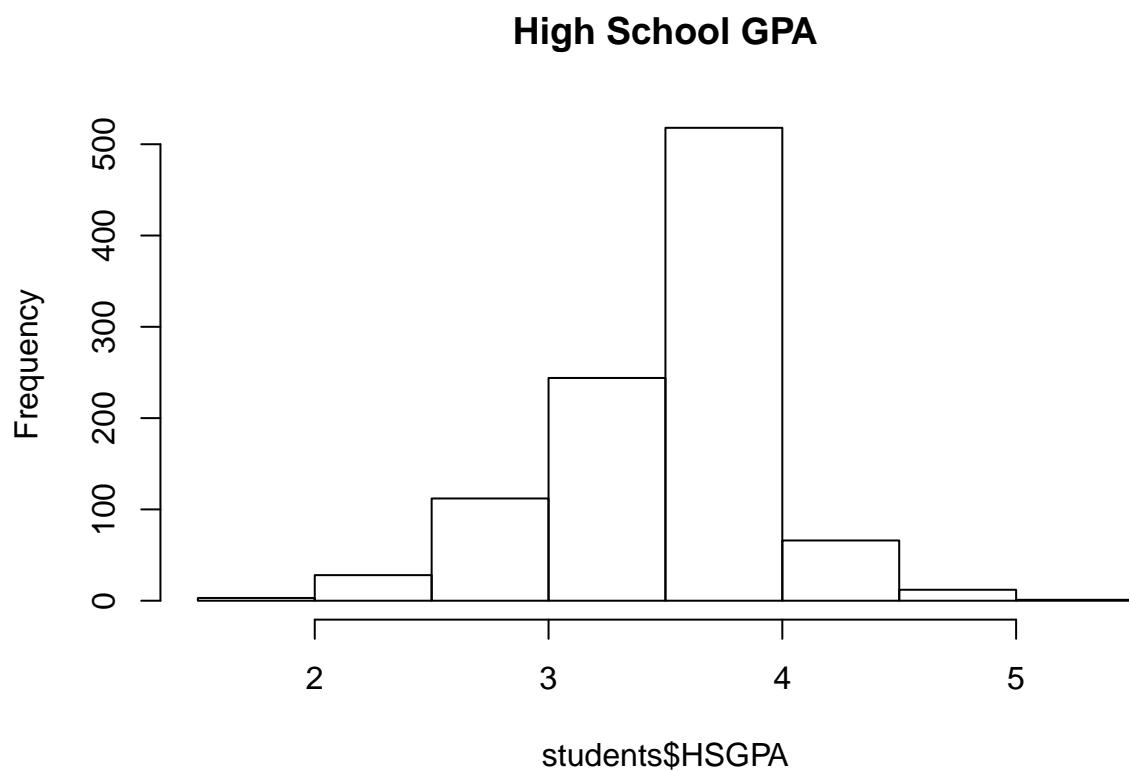
Visual summaries. The command `hist` is in the base package while `histogram` is in lattice.

```
hist(students$HSGPA)
```



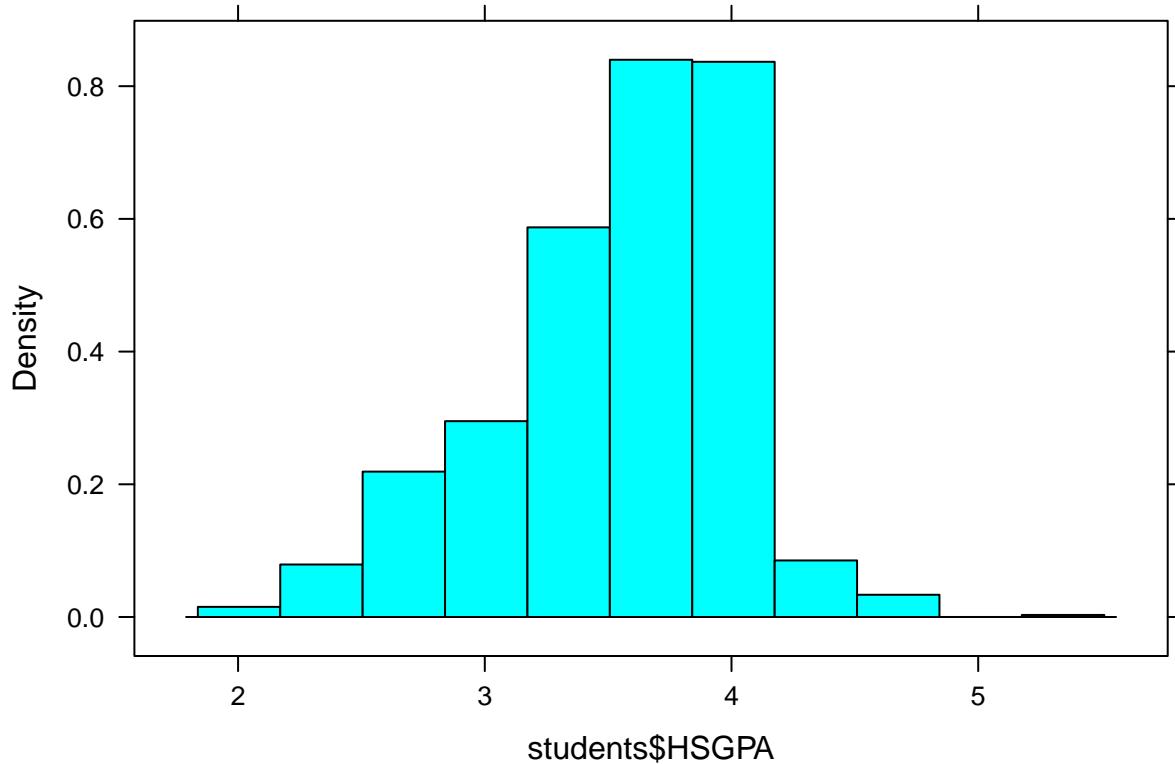
With a title.

```
hist(students$HSGPA,main="High School GPA")
```

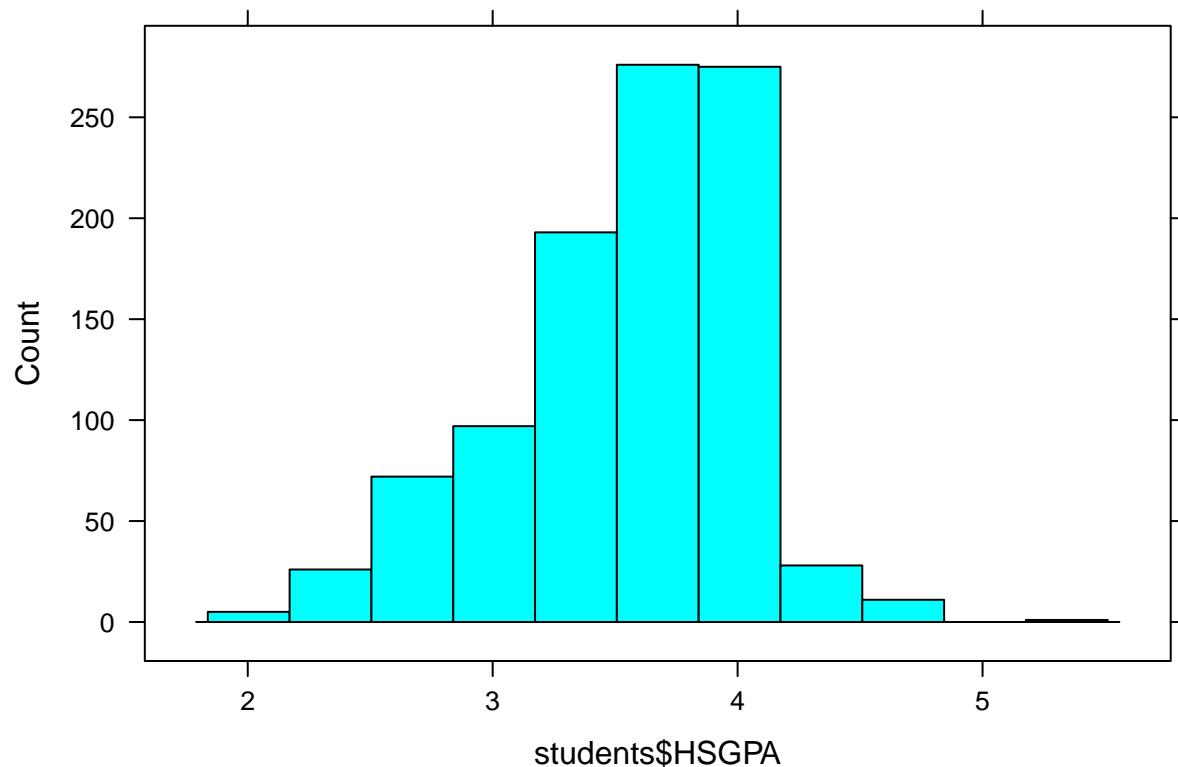


The command `histogram` has more options.

```
histogram(students$HSGPA)
```

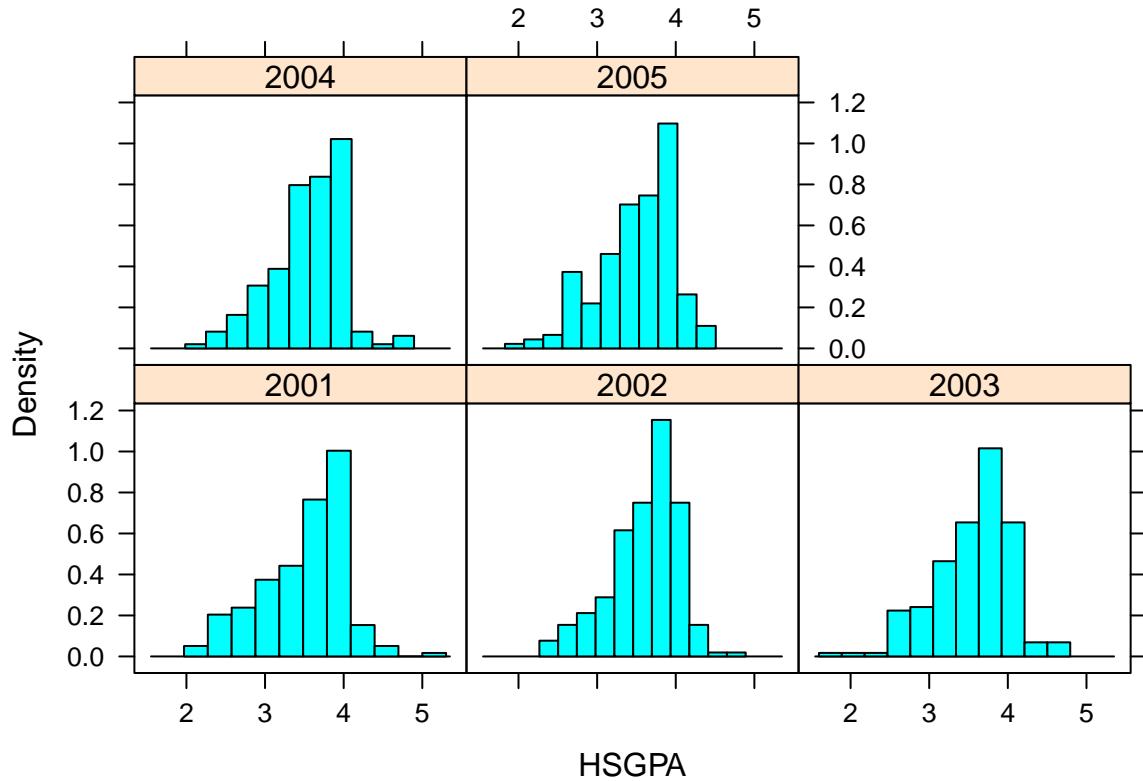


```
histogram(students$HSGPA, type="count")
```



A panel display to show histograms next to each other.

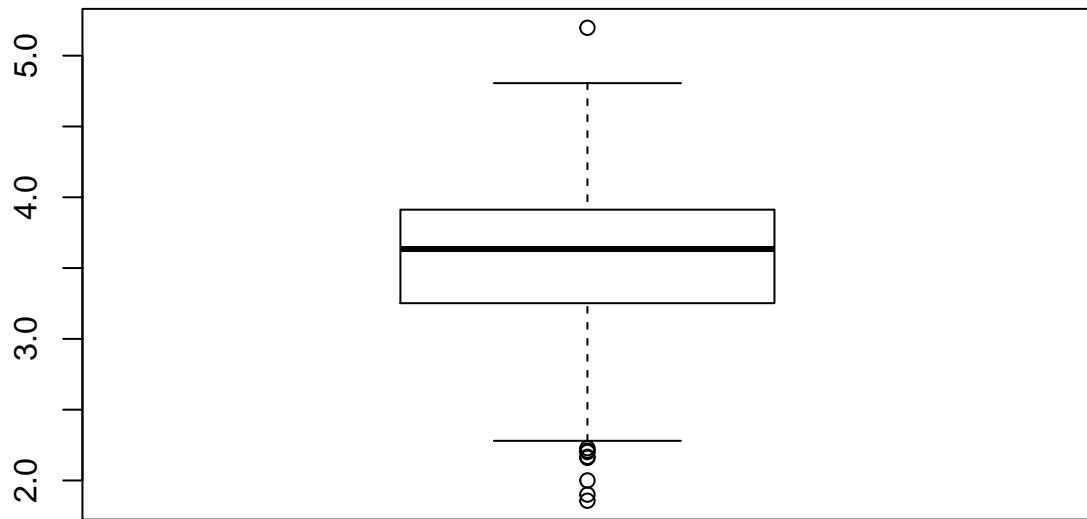
```
histogram(~HSGPA | factor(Cohort), data=students)
```



Another type of plot is the box and whiskers plot.

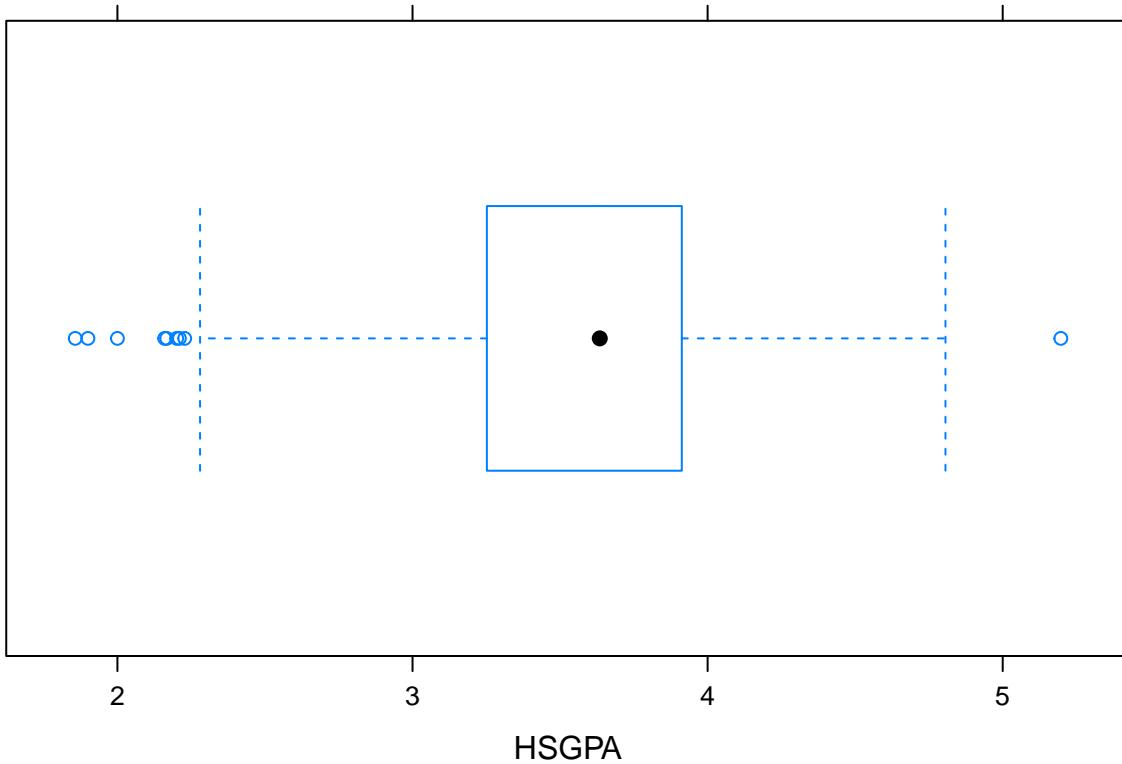
From the base package.

```
boxplot(students$HSGPA)
```

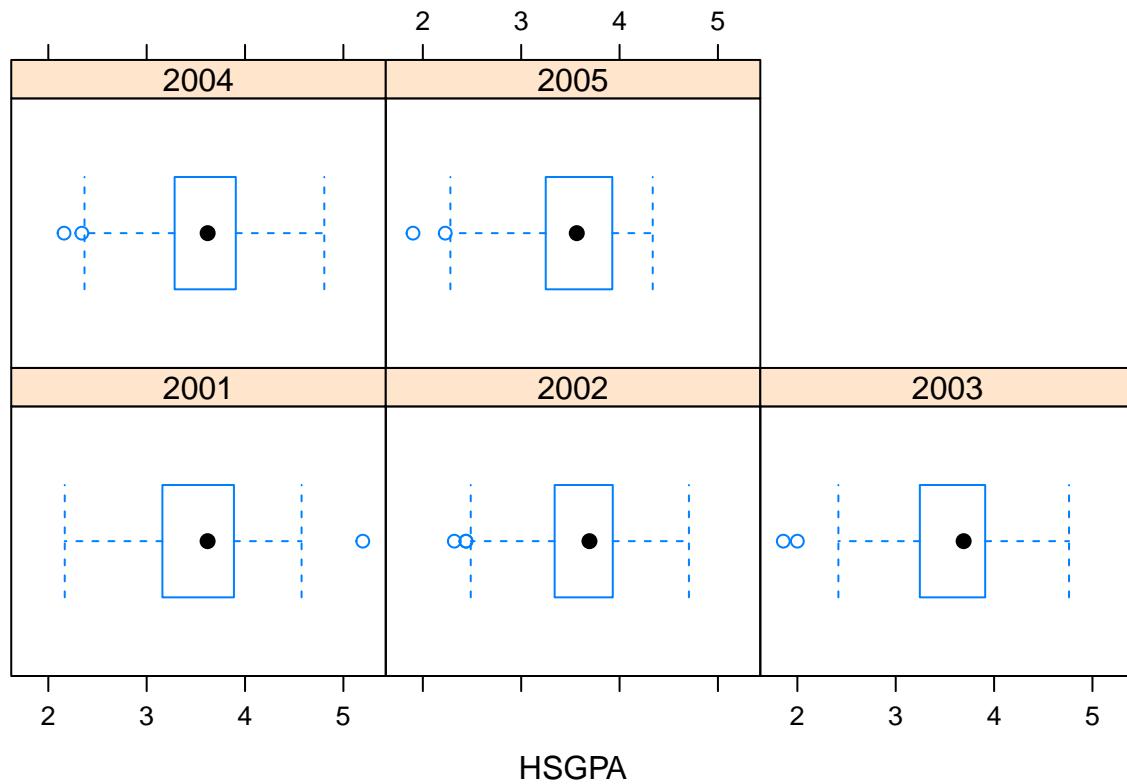


And from lattice.

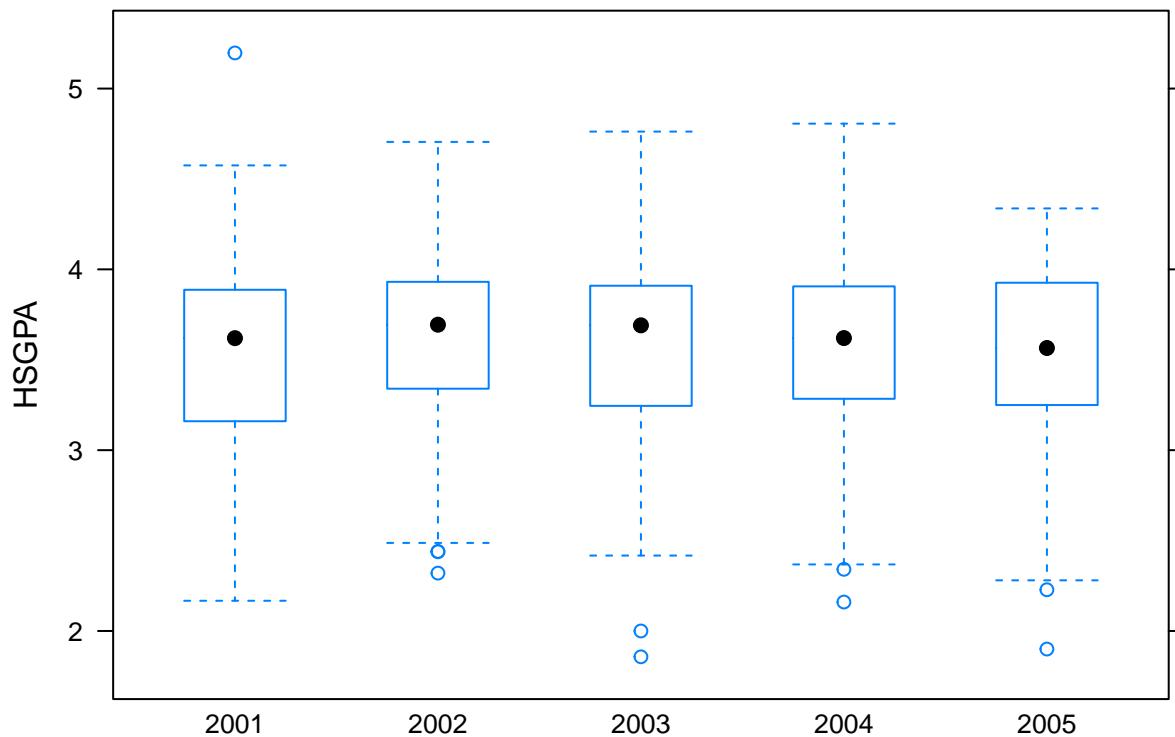
```
bwplot(~HSGPA, students)
```



```
bwplot(~HSGPA|factor(Cohort),students)
```

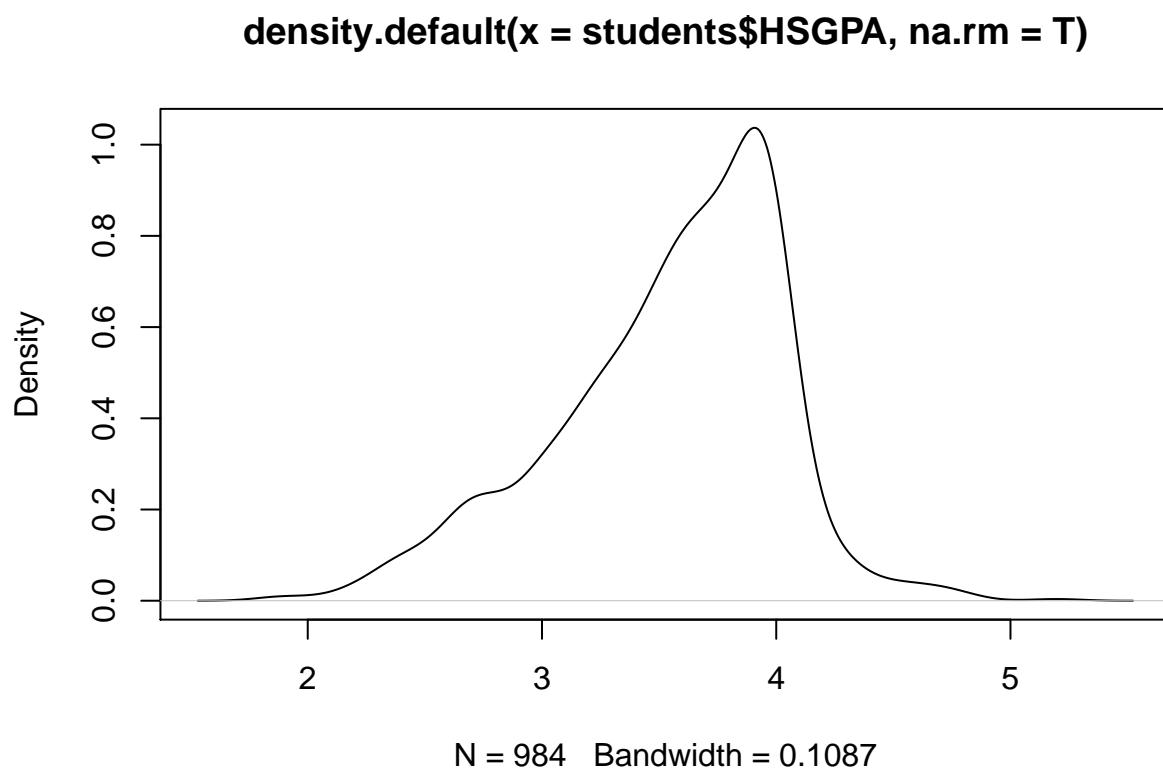


```
bwplot(HSGPA~factor(Cohort),students)
```



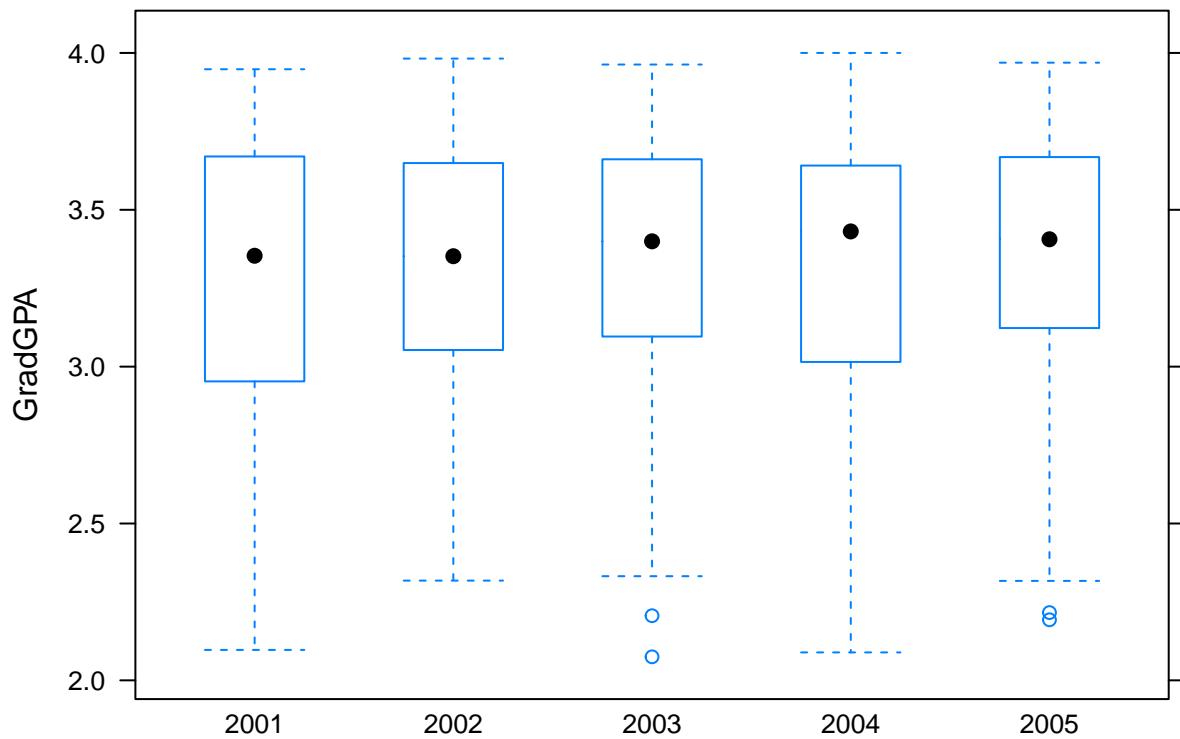
Histograms are notoriously sensitive to the parameters used to build them such as number of bins and location of bins. A better method is to use a density plot.

```
plot(density(students$HSGPA,na.rm=T))
```



And for interest, another variable.

```
bwplot(GradGPA~factor(Cohort), students)
```



Now you investigate the height data we took in class.

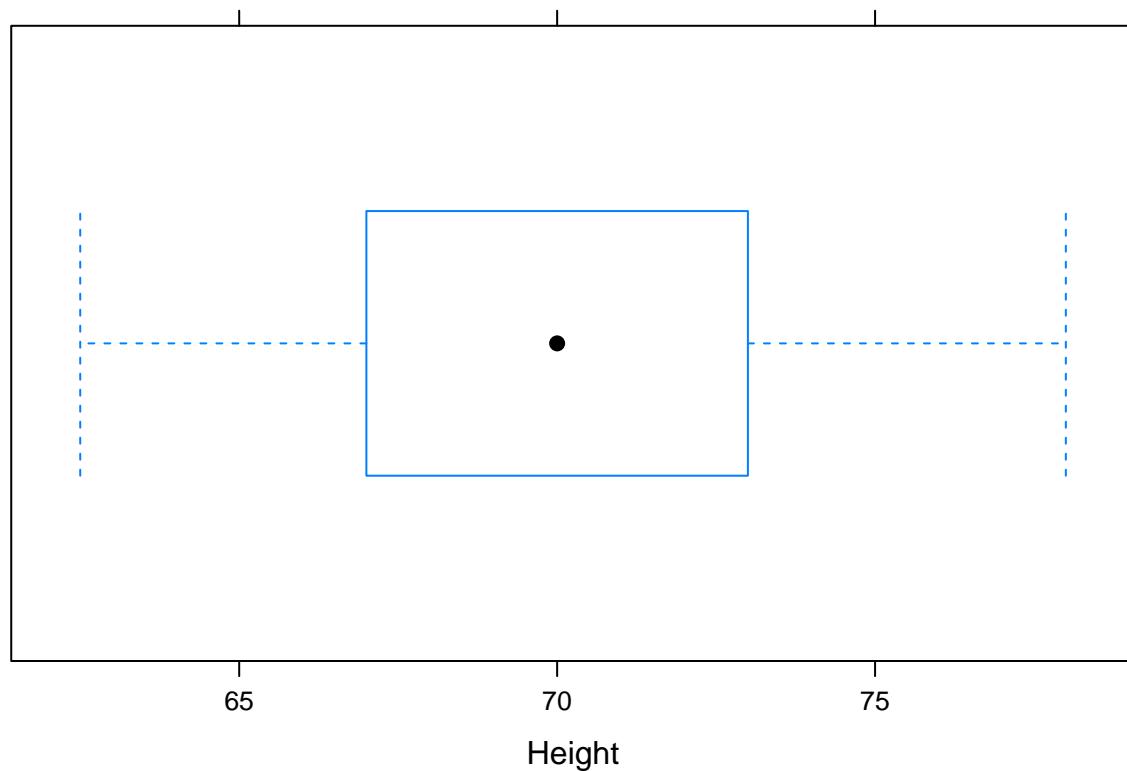
```
Lesson2_Data <- read.csv("Lesson2_Height.csv")
```

```
str(Lesson2_Data)
```

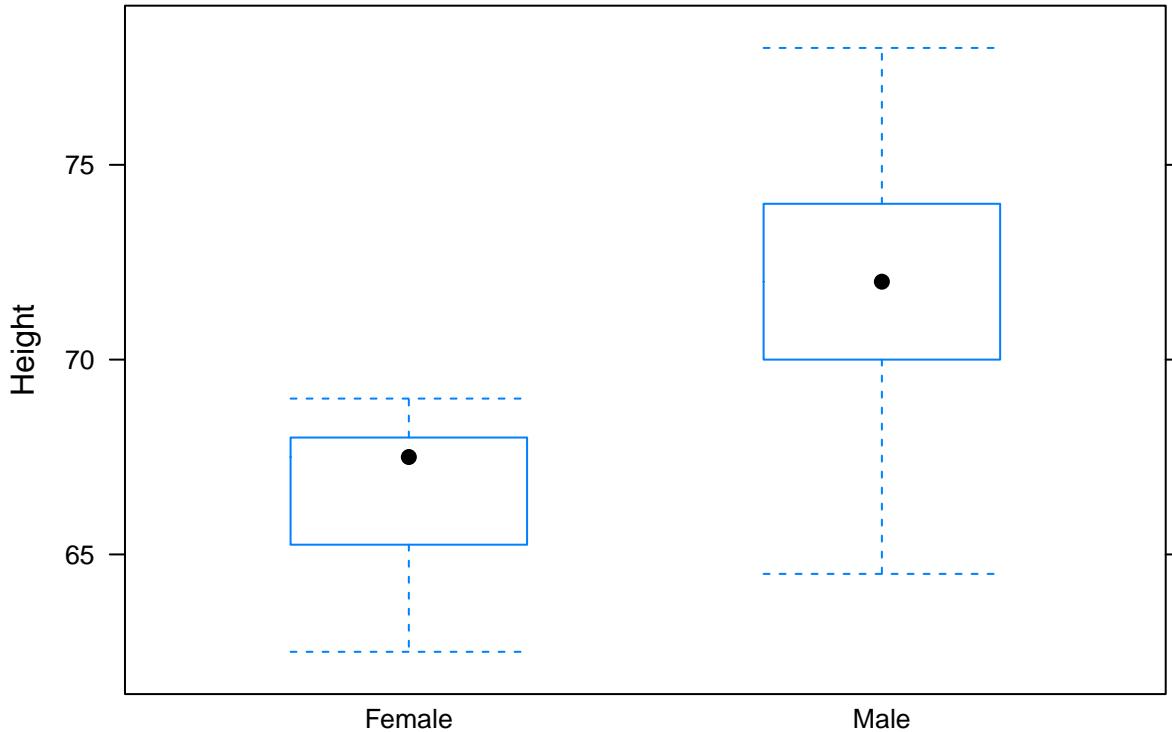
```
## 'data.frame': 25 obs. of 2 variables:
## $ Gender: Factor w/ 2 levels "Female","Male": 2 2 2 2 2 2 2 2 2 ...
## $ Height: num 69 78 77 64.5 67 72 72 67 75 77 ...
summary(Lesson2_Data)
```

```
##      Gender      Height
## Female: 8   Min.   :62.50
## Male  :17   1st Qu.:67.00
##                  Median :70.00
##                  Mean   :70.14
##                  3rd Qu.:73.00
##                  Max.   :78.00
```

```
bwplot(~Height,Lesson2_Data)
```



```
bwplot(Height~Gender,Lesson2_Data)
```



```
summary(Height~Gender,data=Lesson2_Data,fun=favstats)
```

```
## Height      N= 25
##
## +-----+-----+-----+-----+-----+-----+-----+
## |       |N |min |Q1   |median |Q3   |max   |mean    |sd      |n |missing |
## +-----+-----+-----+-----+-----+-----+-----+-----+
## |Gender |Female| 8|62.5|65.875|67.5| 68|69| 66.62500|2.248015| 8|0|
## |       |Male  |17|64.5|70.000|72.0| 74|78| 71.79412|3.804023|17|0|
## +-----+-----+-----+-----+-----+-----+-----+-----+
## |Overall|      |25|62.5|67.000|70.0| 73|78| 70.14000|4.144575|25|0|
## +-----+-----+-----+-----+-----+-----+-----+-----+
```

1.3 Summarizing Multivariate Data

1.3.1 Objectives

1. Understand model notation by using in R
2. Distinguish between variable types (nominal, ordinal, and continuous) and give examples
3. Develop a framework and use to create numeric and visual summaries of bivariate data
4. Explain lurking variable

1.3.2 Ideas from last lesson

In 1.2 we discussed the idea of symmetry. Symmetry and the idea on equality of mean and median depend on definition of symmetric. Some basic definitions of symmetry are simply that the mean and median are equal. However, page 22 of the book has a different definition of symmetry. This second definition is more accurate and will be easier to understand when we introduce probability density functions.

Using the second definition, if a distribution is symmetric, then the mean and median are equal. However, if the mean and median are equal, then the distribution does not have to be symmetric.

Consider the following data set:

```
Les3_ex<-c(-2,4,5,8,10)
```

```
summary(Les3_ex)
```

```
##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.
##    -2      4      5      5      8     10
```

From last class, what would be the difference between

```
bwplot(Height~Gender,Lesson2_Data)
```

and

```
bwplot(~Height|Gender,Lesson2_Data)
```

Is class year qualitative or quantitative?

Homework 1.10 Try it.

1.3.3 Bivariate Data

Load libraries

```
library('fastR')
library(Hmisc)
library(lattice)
library(vcd)
```

Bivariate data means that we have two variables. There are three possibilities, in the next chapter will cover the idea of counting but here we are sampling with replacement and order does not matter. We could have two qualitative variables, one qualitative and one quantitative, and finally two quantitative.

Qualitative variables are often the most difficult to look at. Last lesson we looked at one variable being qualitative and the other being quantitative. We created side-by-side plots and summary statistics by categories of the qualitative variable.

Now, let's look at two qualitative variables. Use the data set airlineArrival for this analysis.

```
str(airlineArrival)
```

```
## 'data.frame': 11000 obs. of 3 variables:
## $ Airport: Factor w/ 5 levels "LosAngeles","Phoenix",...: 2 4 4 4 2 1 2 2 5 5 ...
## $ Result : Factor w/ 2 levels "Delayed","OnTime": 2 2 2 2 2 2 2 2 2 ...
## $ Airline: Factor w/ 2 levels "Alaska","AmericaWest": 2 1 1 1 2 1 2 2 1 1 ...
```

Summarize in a table

```
xtabs(~Result+Airline,data=airlineArrival)
```

```
##          Airline
## Result    Alaska AmericaWest
## Delayed    501      787
## OnTime     3274     6438
```

Often you can do things several ways in R

```
table(airlineArrival[,2:3])
```

```
##          Airline
## Result    Alaska AmericaWest
## Delayed    501      787
## OnTime     3274     6438
table(airlineArrival$Result,airlineArrival$Airline)
```

```
##
##          Alaska AmericaWest
## Delayed    501      787
## OnTime     3274     6438
```

If we want proportion, we can use

```
prop.table(table(airlineArrival[,2:3]),2)
```

```
##          Airline
## Result    Alaska AmericaWest
## Delayed  0.1327152  0.1089273
## OnTime   0.8672848  0.8910727
```

Why not the following?

```
prop.table(table(airlineArrival[,2:3])) #not what we want
```

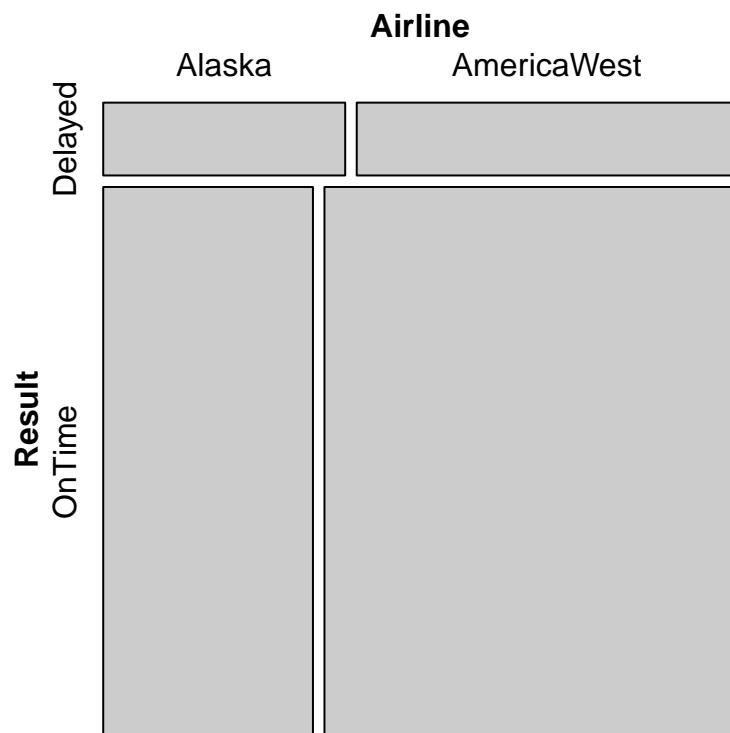
```
##          Airline
## Result    Alaska AmericaWest
## Delayed  0.04554545  0.07154545
## OnTime   0.29763636  0.58527273
```

In this problem we can look at the variable result depending on the airline. Thus we summarize the data differently than if both variables were thought of being independent. We will see this more in chapter 4.

There is a plot method called `mosaic`. Be careful using this because it uses areas and we are not good at visually comparing areas, thus avoid pie charts. The function is in the `vcd` package.

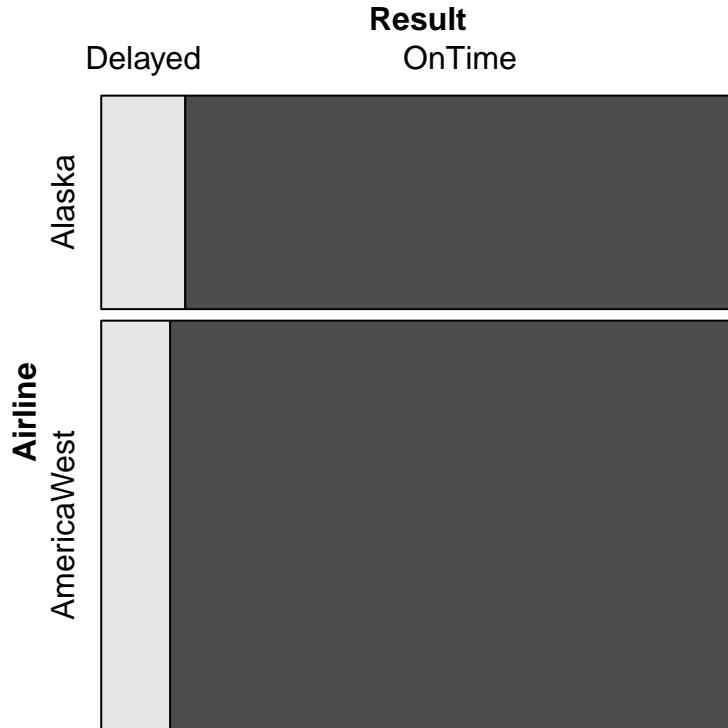
```
require(vcd)
```

```
mosaic(~Result+Airline,airlineArrival) # This is the wrong plot why?
```



Better plot is

```
mosaic(Result~Airline,airlineArrival)
```



Looks like AmericaWest is the better airline because it has a higher proportion of the planes arrive on time. But wait.

Let's break it down by airport.

```
structable(~Result+Airline+Airport,airlineArrival)
```

```
##                               Airline Alaska AmericaWest
## Result    Airport
## Delayed   LosAngeles      62     117
##           Phoenix        12     415
##           SanDiego       20      65
##           SanFrancisco  102    129
##           Seattle        305     61
## OnTime    LosAngeles    497    694
##           Phoenix       221   4840
##           SanDiego      212    383
##           SanFrancisco  503    320
##           Seattle       1841   201
```

This is too hard to read, so look at this result:

```
prop.table(table(airlineArrival),c(1,3))
```

```
## , , Airline = Alaska
##
##             Result
## Airport          Delayed      OnTime
##   LosAngeles  0.11091234  0.88908766
```

```

##   Phoenix      0.05150215 0.94849785
##   SanDiego     0.08620690 0.91379310
##   SanFrancisco 0.16859504 0.83140496
##   Seattle      0.14212488 0.85787512
##
## , , Airline = AmericaWest
##
##           Result
## Airport      Delayed    OnTime
## LosAngeles   0.14426634 0.85573366
## Phoenix      0.07897241 0.92102759
## SanDiego     0.14508929 0.85491071
## SanFrancisco 0.28730512 0.71269488
## Seattle      0.23282443 0.76717557

```

It looks like for every airport, Alaska has a better on time rate than AmericaWest. How come AmericaWest has the overall better on time rate?

See this site for another example of Simpson's Paradox and the idea of a lurking variable.

The following is a plot but I don't like it as much as a table.

```
mosaic(Result~Airline+Airport,airlineArrival)
```



Bivariate with both quantitative leads to the familiar scatterplot. The book's example on the iris data set is good.

In that case they add a third qualitative variable and use color via the groups option to visualize.

Some more examples

```
names(students)

## [1] "ACT"      "SAT"      "Grad"     "GradGPA"   "HSGPA"    "Cohort"

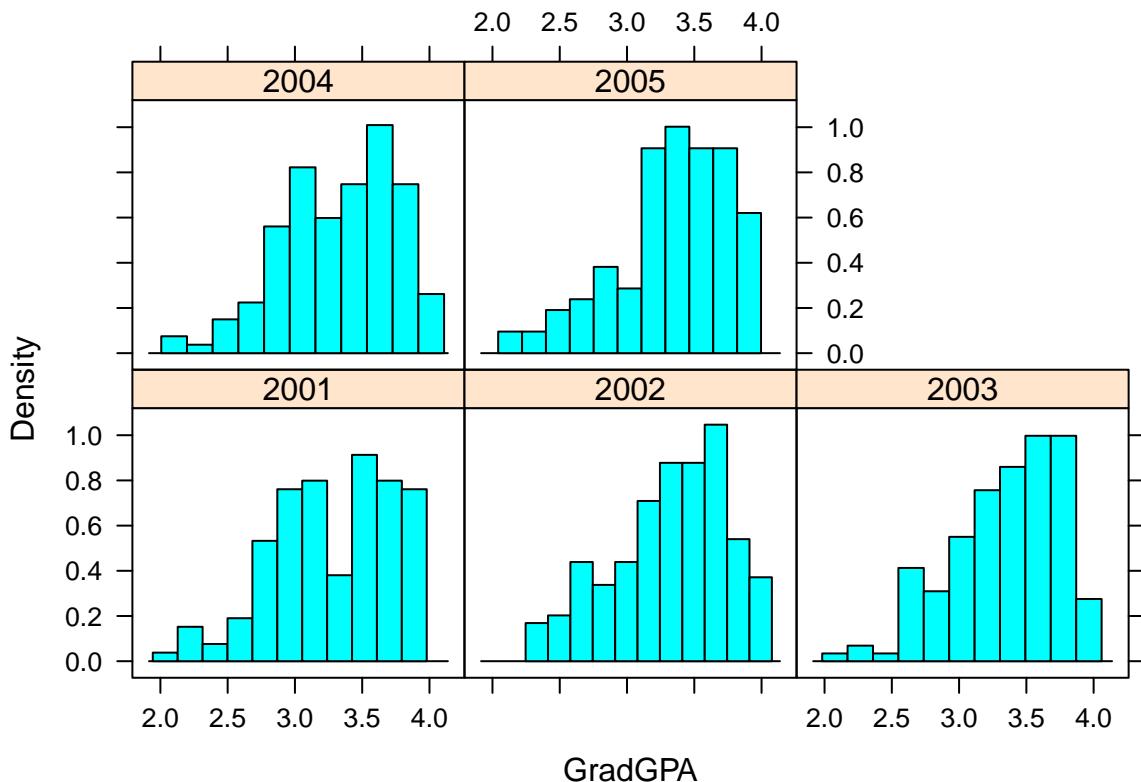
table(students$Cohort,students$Grad)

##
##          FALSE  TRUE
## 2001      58 142
## 2002      43 178
## 2003      50 154
## 2004      47 140
## 2005      70 118

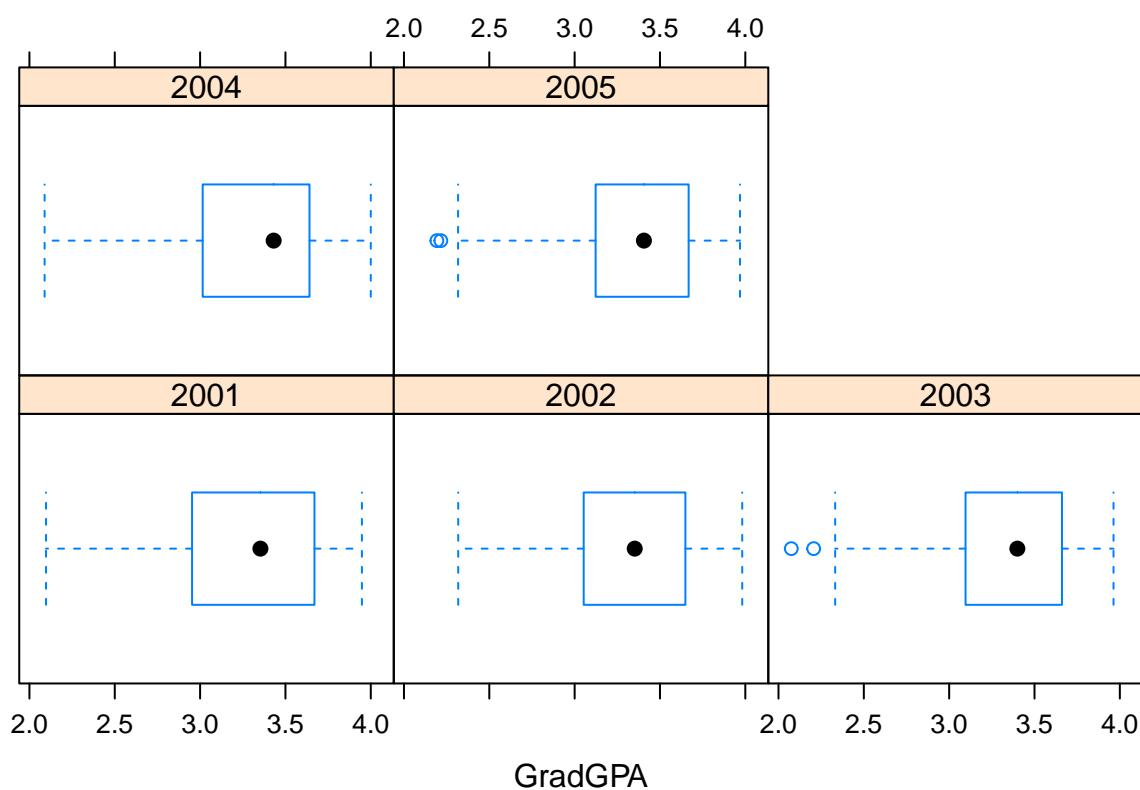
xtabs(~Cohort+Grad,students)

##          Grad
## Cohort FALSE  TRUE
## 2001      58 142
## 2002      43 178
## 2003      50 154
## 2004      47 140
## 2005      70 118

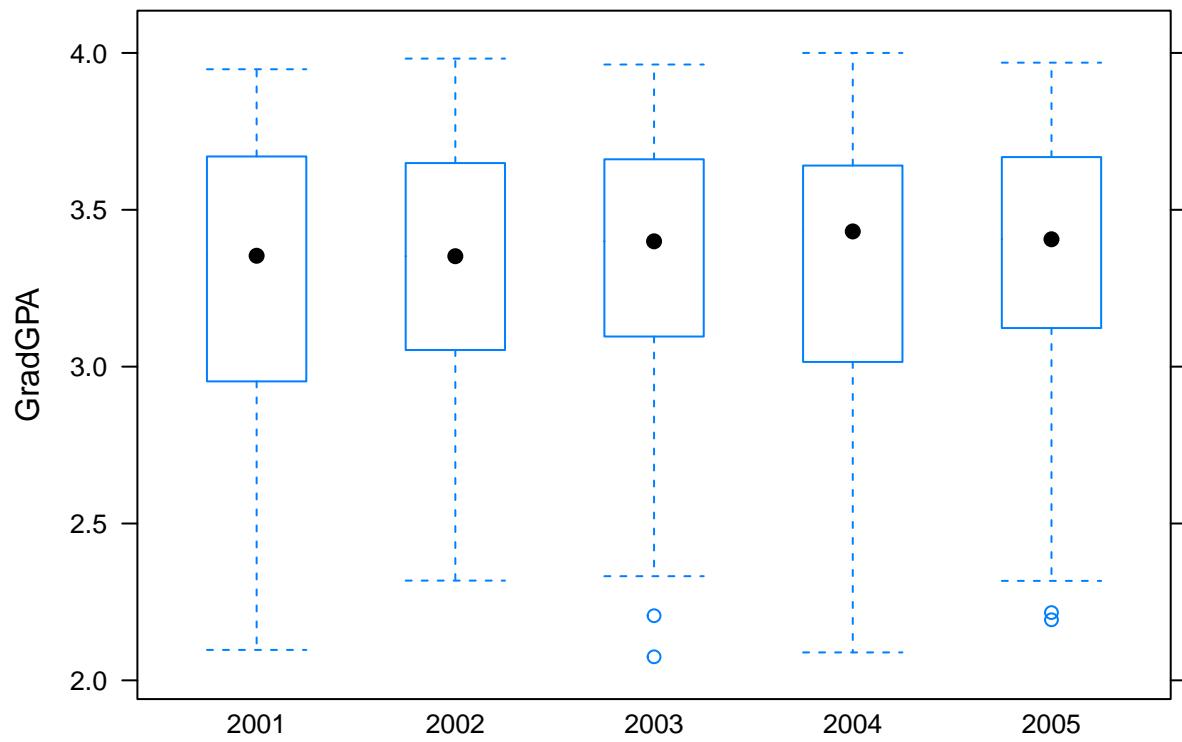
histogram(~GradGPA|factor(Cohort),students)
```



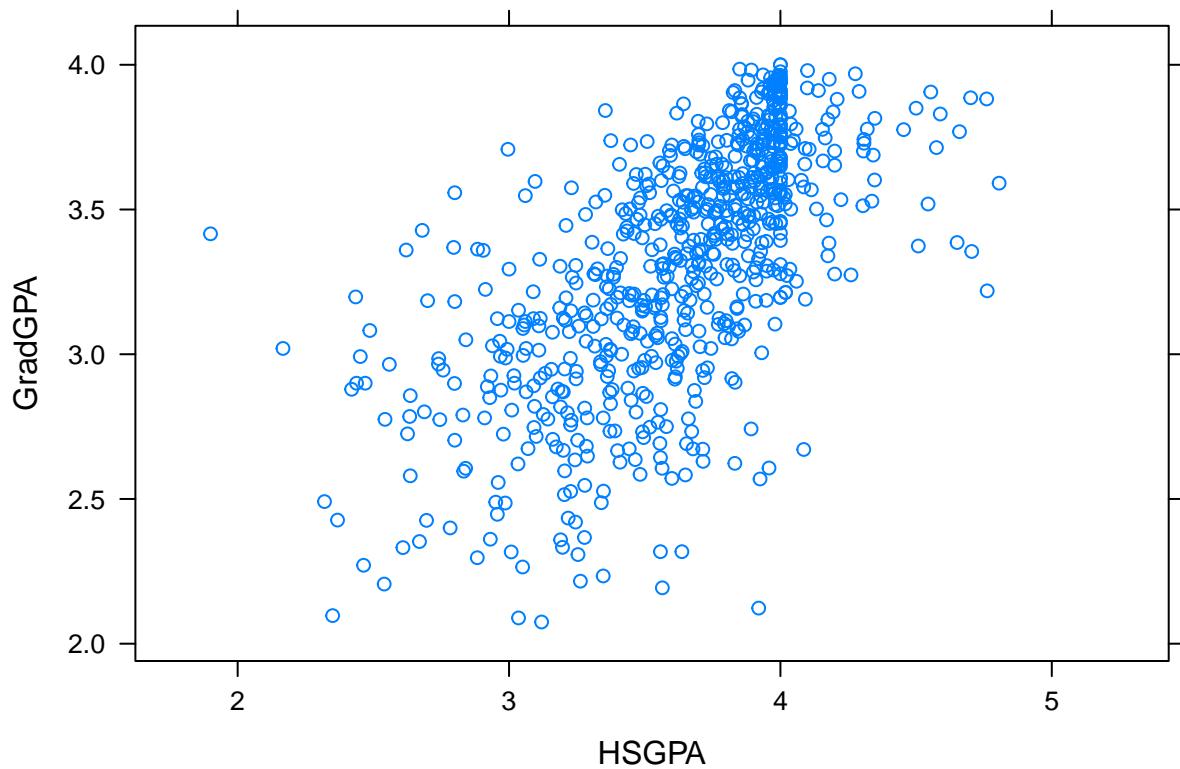
```
bwplot(~GradGPA|factor(Cohort),students)
```



```
bwplot(GradGPA~factor(Cohort),students)
```

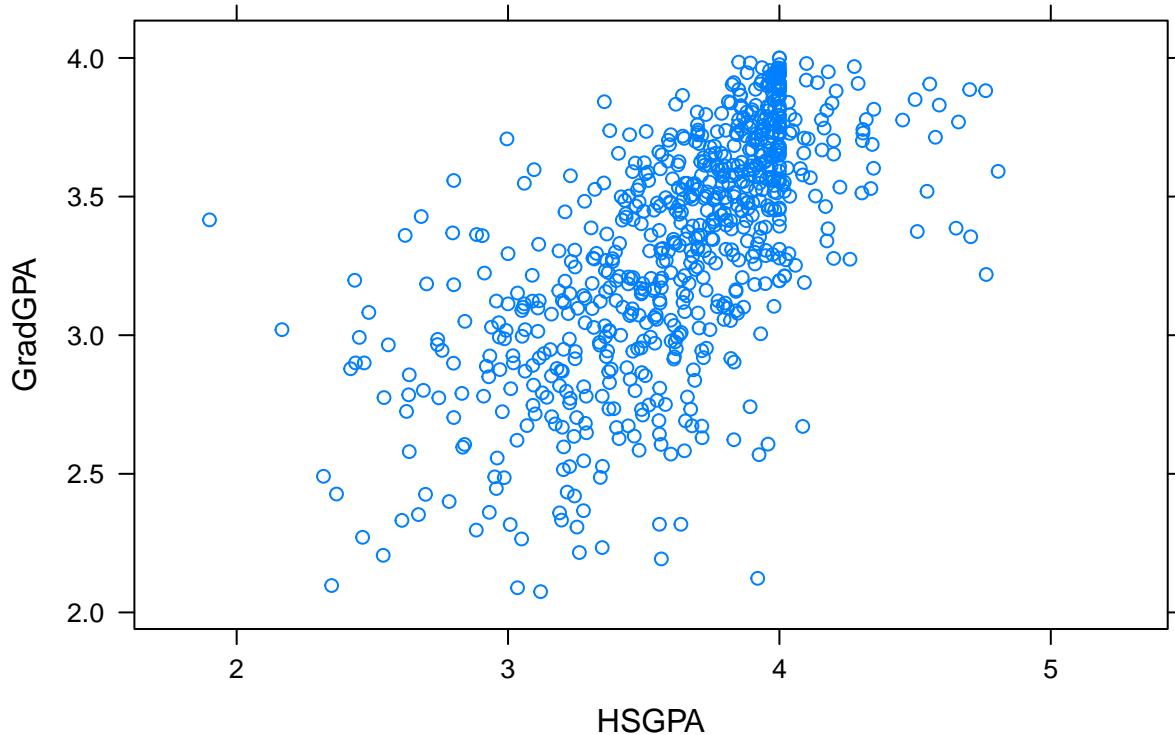


```
xyplot(GradGPA~HSGPA,students)
```

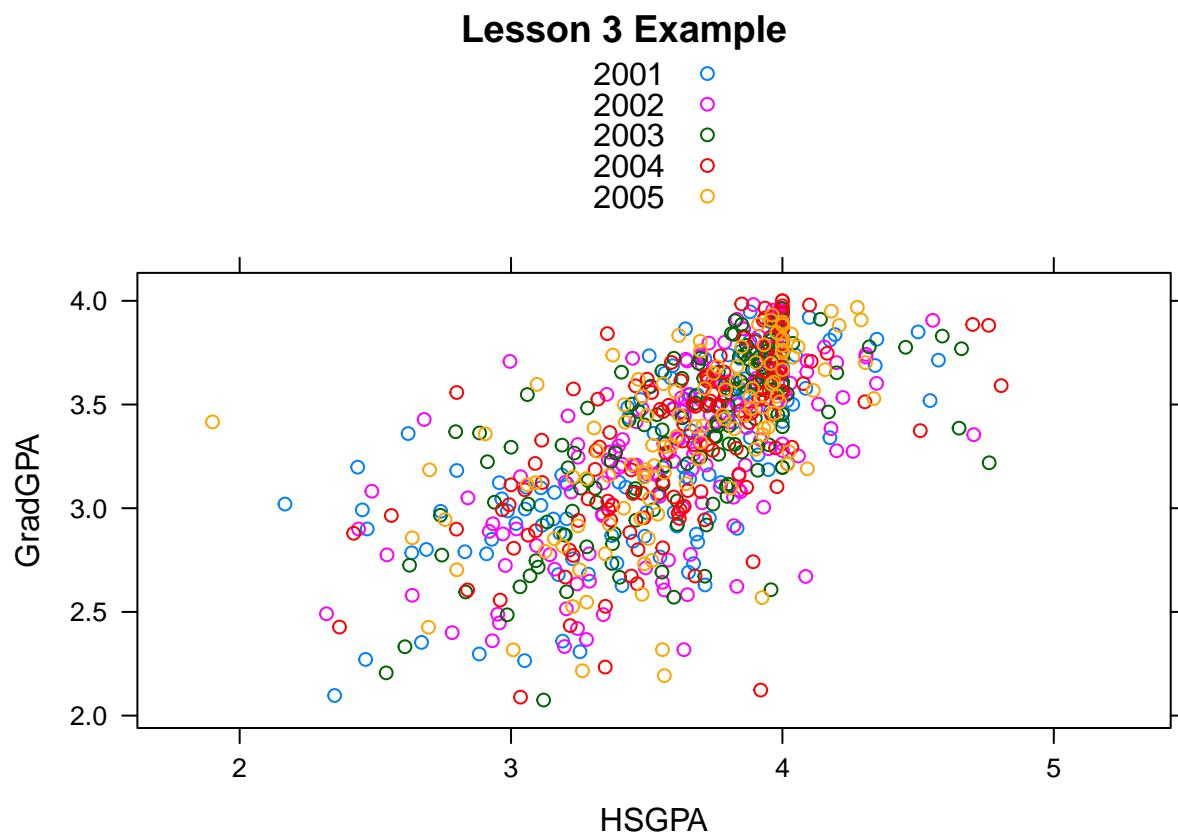


```
xyplot(GradGPA~HSGPA,students,main="Lesson 3 Example")
```

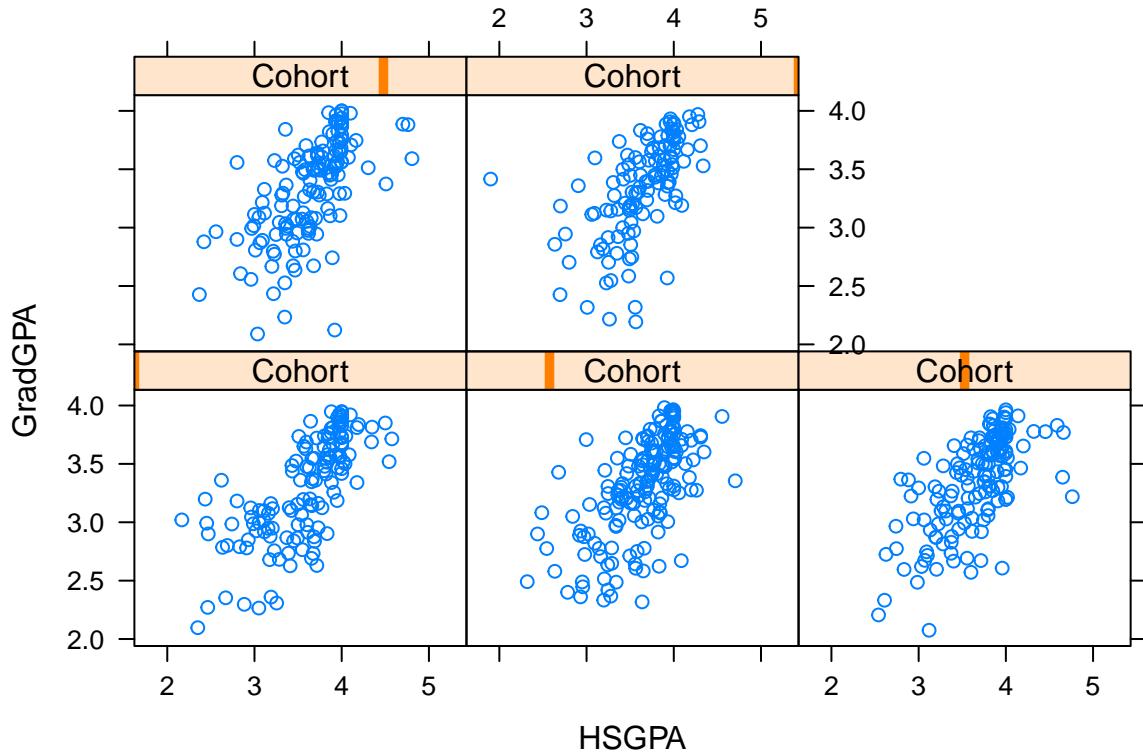
Lesson 3 Example



```
xypplot(GradGPA~HSGPA,group=Cohort,students,main="Lesson 3 Example",auto.key=T)
```

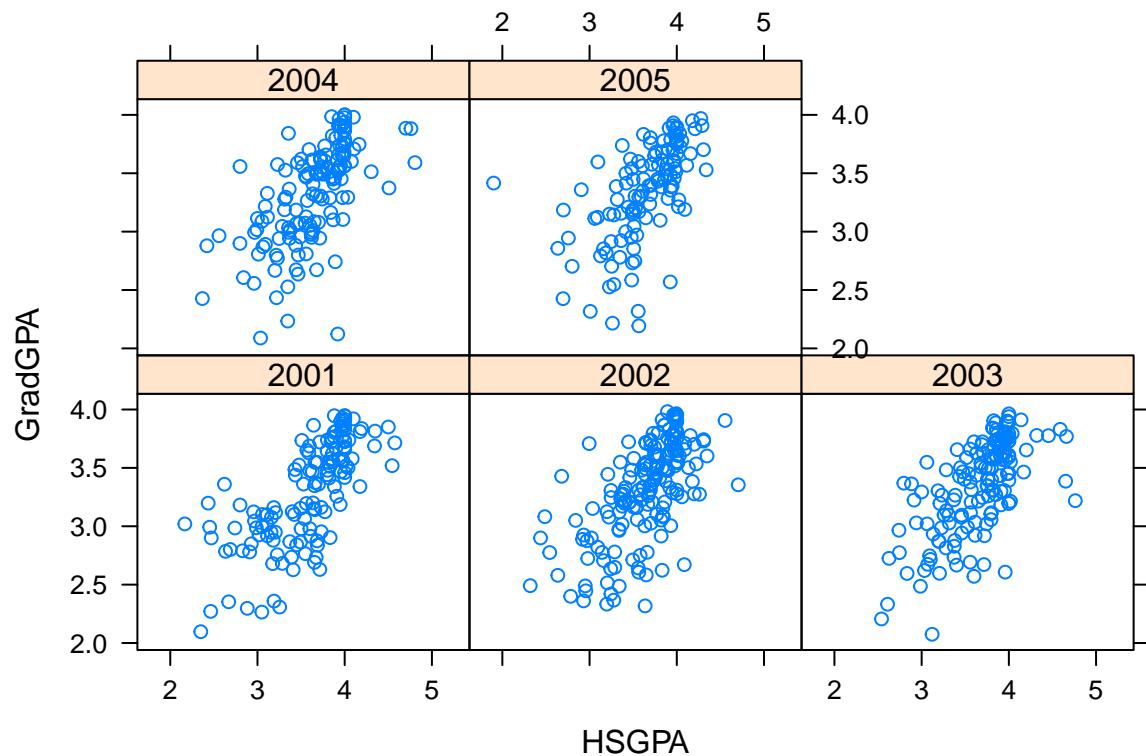


Lesson 3 Example

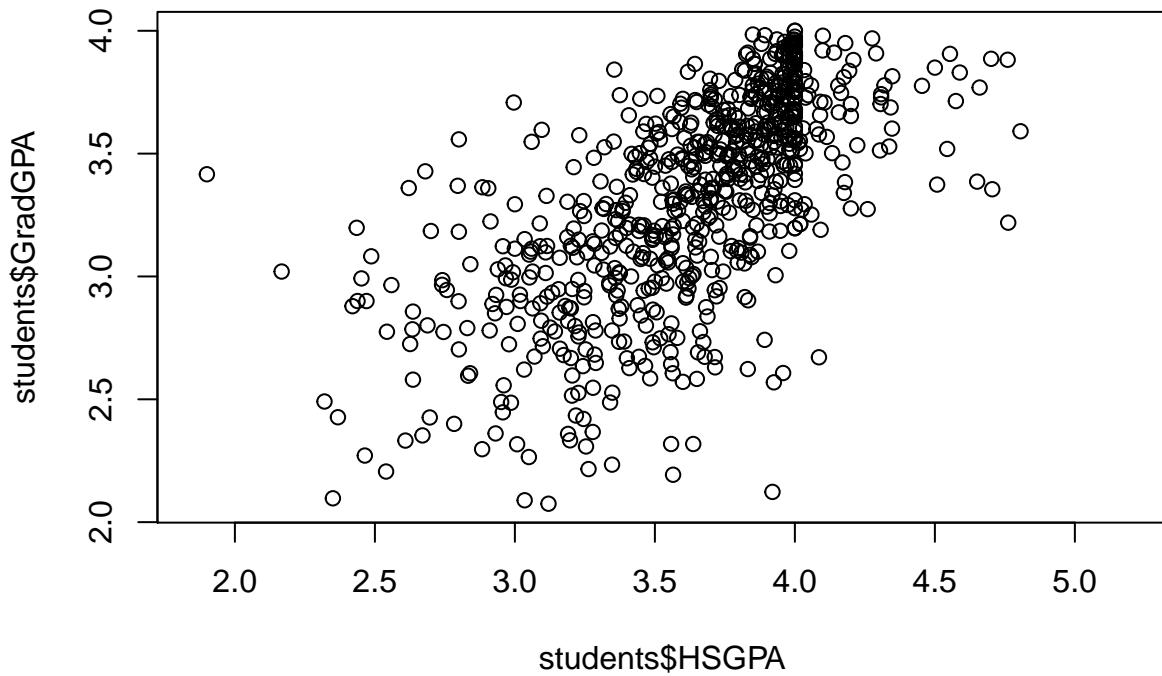


```
xyplot(GradGPA~HSGPA|factor(Cohort),students,main="Lesson 3 Example")
```

Lesson 3 Example



```
plot(students$HSGPA,students$GradGPA)
```

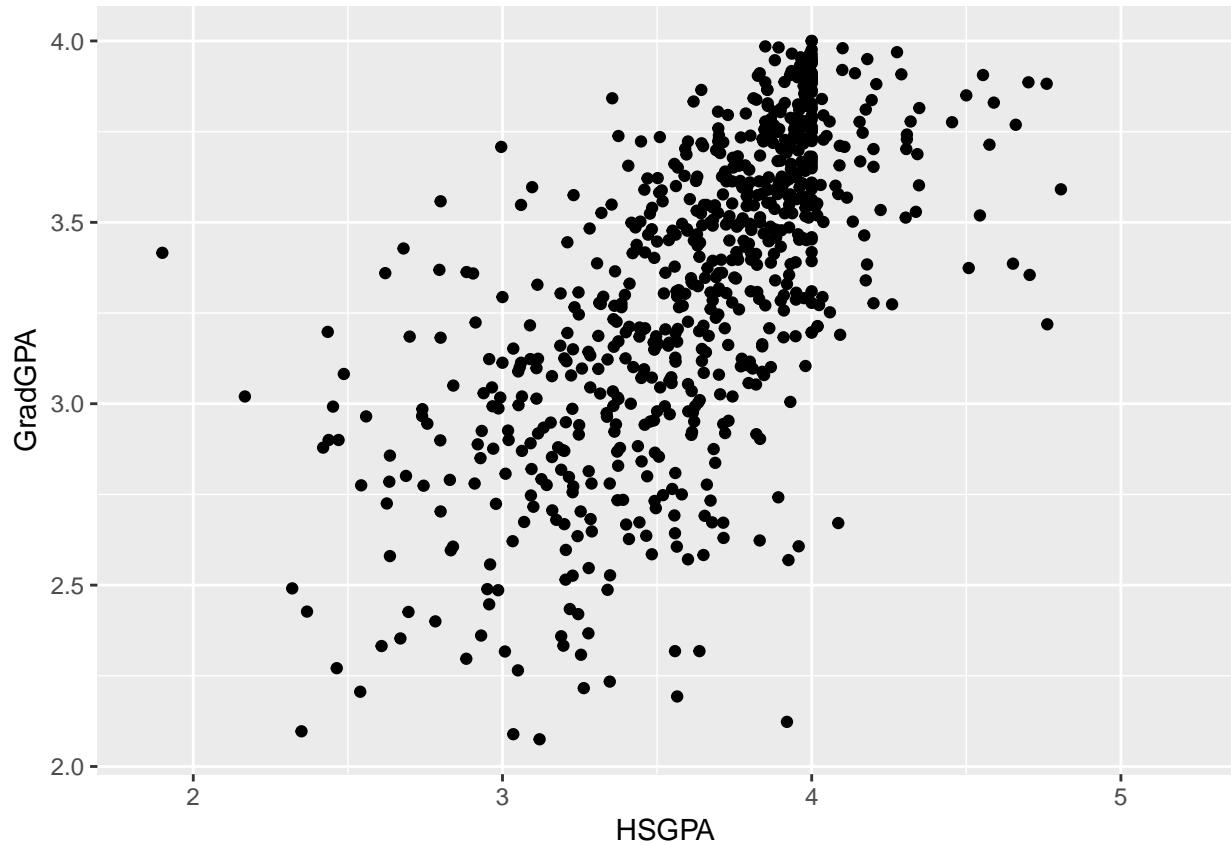


Another plotting program that is one of the most popular is ggplot.

```
require(ggplot2)
```

```
qplot(HSGPA, GradGPA, data=students)
```

```
## Warning: Removed 279 rows containing missing values (geom_point).
```



The example from the book.

```
xtabs(~Defendant+Penalty,deathPenalty)
```

```
##           Penalty
## Defendant Death Not
##     Black      17 149
##     White      19 141
```

```
prop.table(xtabs(~Defendant+Penalty,deathPenalty),2)
```

```
##           Penalty
## Defendant    Death      Not
##     Black 0.4722222 0.5137931
##     White 0.5277778 0.4862069
```

```
xtabs(~Defendant+Victim+Penalty,deathPenalty)
```

```
## , , Penalty = Death
##
##           Victim
## Defendant Black White
##     Black      6     11
##     White      0     19
##
## , , Penalty = Not
##
##           Victim
```

```
## Defendant Black White
##      Black     97     52
##      White      9    132
```

Chapter 2

Probability and Random Variables

The second chapter is completed in eight lessons. Section 2.2 of the book has been historically difficult for the students so I have broken it into two lessons. Also in the first lesson, I have added material from section B of the book as some students are deficient in this knowledge.

2.1 Random Variables

2.1.1 Objectives

1. Know definitions introduced in the section, of particular importance is Random Variable
2. Use set notation

2.1.2 Terminology

Probability and randomness are difficult and deep philosophical questions. We will make it easier by looking at repeatable random process. A process has to have more than one possible outcome.

Some new terms

Outcome

Event

Sample space Probability

Random Variable

If set notation is new, read Appendix B.

We can have deductive probabilities, mostly what we do in this class, and inductive empirical probabilities.

Do Problem 2.1

Do Problem B-1

Summation and product notation is difficult

Do 1.10

2.2 Probability Rules

2.2.1 Objectives

1. Solve counting problems using bijection, multiplication, complement, division, and inclusion-exclusion rules
2. Use proper notation
3. Find probabilities using counting rules

2.2.2 Probability: General

We will be using the deductive notion of probability, theoretical probability, in this section. That is, we make use of the axioms on page 31 and results derived from them.

Technically, probability is a space, but we will make it easier by thinking of it as a function from the sample space to a real number in $[0, 1]$. Often the sample space is a random variable.

The big issue for students when first working with probability is confusing the algebra of sets with the algebra of numbers. So the following are all valid for some event E :

$$\begin{aligned} E \cup E^c \\ P(E \cup E^c) \\ P(E) + P(E^c) = 1 \end{aligned}$$

So from the axioms, we get:

$$\begin{aligned} E \cup E^c &= S \\ P(E \cup E^c) &= P(S) \end{aligned}$$

because E and E^c are mutually exclusive:

$$\begin{aligned} P(E) + P(E^c) &= 1 \\ P(E) &= 1 - P(E^c) \end{aligned}$$

Notice that the following are nonsensical:

$$\begin{aligned} P(E) \cup P(E^c) \\ E + E^c \end{aligned}$$

2.2.3 Counting

We will be making indirect use of the bijection principle as we are always mapping from objects to numbers. In addition, in using counting, we are making use of the equally likely rule. This is an assumption and we must always be aware of the assumptions and whether they apply.

In our counting problems we have to determine if we are sampling with replacement or not and whether order matters or not. Determining if order matters is difficult and takes practice. To set up these four possibilities we will use a simple case of 3 balls and 10 people, this is an example from the book. All of these methods make use of the multiplication principle.

Problem 1: We have three different colored balls that we will give to 10 people. A person can get more than one ball. How many ways can we distribute the balls?

We can think of the ten people as the numbers, this is the bijection rule. Since each person can get more than one ball, we are sampling with replacement. Since the balls are different colors, then order matters. For example, if Billy gets the blue and green ball, and Sally gets the red ball. This is different from Billy getting the red and blue, and Sally getting the green. To solve this problem, we use the multiplication rule. There are 10 choices of people to give the first ball to. There are 10 for the second ball and 10 for the third. Thus there are 10^3 or 1000 ways.

Problem 2: Same problem but now each person can get at most one ball. In this case order matters but we sample without replacement. Thus we have 10 choices for the first ball, 9 for the second, and 8 for the third. This is called a permutation. Let's write our own function for this.

```
perm<-function(n,r){
  result<-prod(n:(n-r+1))
  return(result)
}
```

For our problem

```
perm(10,3)
```

```
## [1] 720
```

The notation for a permutation is $_nP_k$ and the formula is

$$\frac{n!}{(n - k)!}$$

Note that we must define $0!=1$ to make this work.

Problem 3: Let's do problem 2 but this time the balls are all the same color. In this case the order does not matter. To understand what to do, make the problem simpler and enumerate. Let's say we have three people {Billy, Sally, Tommy} and two red balls. If ordered mattered we could enumerate the permutations using tuples. The first position represents ball 1 and the second ball 2. Thus we have 6 possibilities:

```
perm(3,2)
```

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

(Billy, Sally), (Billy, Tommy), (Sally, Tommy), (Sally, Billy), (Tommy, Sally), (Tommy, Billy).

But since the balls are identical (Billy, Sally) is the same as (Sally, Billy). So we need the division rule to remove redundant outcomes. Each outcome has two possibilities thus we have $2!$ ways that are equivalent. This is a combination and has the notation $_nC_k$ and the formulas:

$$\binom{n}{k} = \frac{n!}{(n - k)!k!}$$

which is the permutation divided by $k!$.

R has the function `choose` to find the values for us.

```
choose(10,3)
```

```
## [1] 120
```

Problem 4: Now this is a difficult one and that is when order does not matter and we sample with replacement. This is the most difficult and is what is being done in Example 2.2.14 in the book. Let's look at the simple case of three people and two identical balls. We have the following results (Billy, Billy), (Billy, Sally), (Billy, Tommy), (Sally, Sally), (Sally, Tommy), and (Tommy, Tommy). There are six ways to do this. This is equivalent to solving the problem of finding the number of solutions to

$$x_1 + x_2 + x_3 = 3$$

Where x_1 is the number of balls Billy is given, etc. This is the bijection rule.

This problem is solved by thinking of vertical lines representing the numbers of balls someone is given and the plus signs between the vertical lines. Thus one outcome is Billy receives all three balls. This would be $|||++$. If each person were given a ball, this would look like $|+|+$. Thus we have k vertical lines and $n - 1$ plus signs. Using this bijection, the number of solutions is

$$\binom{n+k-1}{k} = \frac{(n+k-1)!}{(n-1)!k!}$$

For the problem with 3 people and 2 identical balls.

```
choose((3+2-1), 2)
```

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

And for the problem with 10 people and 3 identical balls.

```
choose((10+3-1), 3)
```

```
## [1] 220
```

We can combine these ideas with the multiplication rule. The question of order is the most difficult part. For example, if we roll two dice and record the values on the faces, how many possibilities are there?

2.2.4 Probability: Equally Likely Events

For equally likely events, we find the probability by dividing the number of ways of the event by the number of ways in the sample space.

Drawing five cards from a deck of cards, what is the probability that at least two cards have the same face value?

The denominator is ${}_{52}C_5$

```
choose(52, 5)
```

```
## [1] 2598960
```

For the numerator we will use the complement rule. Thus we need to select 5 face card values of different values. We select 5 face card values from 13 without replacement. Order does not matter. Then for each face value we have 4 suits. Thus the numerator is:

```
choose(13, 5)*4^5
```

```
## [1] 1317888
```

By the division rule, we have the probability as

```
(choose(13, 5)*4^5)/choose(52, 5)
```

```
## [1] 0.5070828
```

And the probability we want is

```
1-(choose(13, 5)*4^5)/choose(52, 5)
```

```
## [1] 0.4929172
```

How about the probability that all the cards come from the same suit, a flush?

```
(choose(13, 5)*choose(4, 1))/choose(52, 5)
```

```
## [1] 0.001980792
```

Homework 2.6 and 2.7

Note that

$${}_{13}P_2 = {}_{13}C_1 * {}_{12}C_1$$

2.3 Inclusion-Exclusion, Conditional Probability

2.3.1 Objectives

1. Using definitions, calculate conditioning probabilities
2. Determine if events are independent, or if events are independent find joint probabilities
3. Use Bayes theorem to find conditional probabilities

2.3.2 Definitions

Know these

$$P(A \cup B) = P(A) + P(B) - P(A \cap B)$$

Iff A and B are independent

$$P(A \cap B) = P(A)P(B)$$

or equivalently

$$P(A|B) = P(A)$$

If A and B are mutually exclusive

$$P(A \cap B) = 0$$

Finally, conditional probability which takes practice to master and understand

$$P(A|B) = \frac{P(A \cap B)}{P(B)}$$

Other relationships can be derived from drawing Venn diagrams. For example:

$$P(A) = P((A \cap B) \cup (A \cap B^c)) = P(A \cap B) + P(A \cap B^c)$$

Independence is difficult to visualize on a Venn diagram since it is a ratio of areas and humans do not perceive difference in areas very well.

In many problems we need to find $P(A \cap B)$. There are many ways to do this but the most common using conditional probability.

$$P(A \cap B) = P(A|B)P(B) = P(B|A)P(A)$$

Another confusion is with the given part of the conditional probability. The given event is not random, it did happen. Thus the sample space is reduced, this is why division by the probability of the given event is happening. The book does a nice example with Example 2.2.15.

The second most common way to find $P(A \cap B)$ is with independence so that

$$P(A \cap B) = P(A)P(B)$$

2.3.3 Problems

1. We shuffle a deck of cards and turn the top card over. It is an Ace. What is the probability the second card is an Ace?

Let A - face value on first card is an Ace and B - face value on the second card is an Ace

we want $P(B|A)$. Given that the first card is an Ace we have 51 cards left and 3 are Aces.

2. We shuffle a deck of cards and turn the top cards over. What is the probability we have two Aces?

Let A - face value on first card is an Ace and B - face value on the second card is an Ace

We want $P(A \cap B)$. Using conditional probability

$$P(A \cap B) = P(A)P(B|A) = \frac{4}{52} \frac{3}{51}$$

3. We shuffle a deck of cards and set the first card to the side without revealing it. What is the probability the second card is an Ace?

Intuitively we know the answer is $\frac{4}{52}$ but let's use our probability rules to find it.

Let A - face value on first card is an Ace and B - face value on the second card is an Ace

We want $P(B)$

Now

$$P(B) = P(A \cap B) + P(A^c \cap B)$$

where now

$$P(A \cap B) = P(B|A)P(A) = \frac{4}{52} \frac{3}{51}$$

and

$$P(A^c \cap B) = P(B|A^c)P(A^c) = \frac{48}{52} \frac{4}{51}$$

Finally

$$\begin{aligned} P(B) &= P(A \cap B) + P(A^c \cap B) = \frac{4}{52} \frac{3}{51} + \frac{48}{52} \frac{4}{51} \\ &= \frac{4}{52} \left(\frac{3}{51} + \frac{48}{51} \right) = \frac{4}{52} \end{aligned}$$

4. We shuffle a deck of cards and set the first card to the side without revealing it. The second card is an Ace, what is the probability the first card is an Ace?

Let A - face value on first card is an Ace and B - face value on the second card is an Ace

We want $P(A|B)$

From the definition of conditional probability, we have

$$P(A|B) = \frac{P(A \cap B)}{P(B)} = \frac{P(B|A)P(A)}{P(B)} = \frac{P(B|A)P(A)}{P(A \cap B) + P(A^c \cap B)} = \frac{P(B|A)P(A)}{P(B|A)P(A) + P(B|A^c)P(A^c)}$$

This is Bayes Rule and comes from the definition of conditional probability.

The answer is

$$\begin{aligned} P(A|B) &= \frac{\frac{4}{52} \frac{3}{51}}{\frac{4}{52} \frac{3}{51} + \frac{48}{52} \frac{4}{51}} \\ &= \frac{\frac{3}{51}}{\frac{3}{51} + \frac{48}{51}} = \frac{3}{51} \end{aligned}$$

2.3.4 Bayes Rule

From Example 2.2.22:

Suppose a test correctly identifies diseased people 98% of the time and correctly identifies healthy people 99% of the time. Furthermore assume that in a certain population, one person in 1000 has the disease. If a random person is tested and the test comes back positive, what is the probability that the person has the disease?

This problem can be done as a tree and many of you may have seen this approach. However, we will use numbers instead of proportions. It is more difficult for us to understand and interpret proportions as compared to numbers. Let's proceed using numbers.

Suppose we have 100,000 people. 100 will be diseased and 99900 will be healthy. Of those that are diseased, 2 will test negative and 98 positive. Of those that are healthy, 999 will test positive and 97902 will test negative. Now of those that test positive, how many will be diseased?

$$P(D|+) = \frac{98}{98 + 999} = 0.08933455$$

Practice Exam Question

My birthday is March 26, what is the probability at least one of my 23 students in class will have the same birthday?

2.4 Discrete Distributions

2.4.1 Objectives

1. Use, including proper notations, terms and definitions such as probability mass function, cumulative distribution functions, etc.
2. Solve probability problems, including the use of R, for binomial and negative binomial random variables.
3. Explain the assumptions of the binomial and negative binomial distributions.

2.4.2 Definitions

Again, you must learn and know the definitions in this section. The pmf and cdf are confusing to students when first learning but think of the pmf as a function that maps from the random variable to a probability. We know that probabilities have to be in $[0, 1]$ and the sum of all the probabilities must be 1.

The cdf, cumulative distribution function is simply $P(X \leq x)$. The capital notation is for a random variable and the lower for a value of the random variable.

2.4.3 Practice

You flip a coin two times where the probability of heads is 0.51.

1. Write the sample space
2. Create a random variable for this scenario
3. Write the probability mass function

4. Write the cdf

5. Use R to find

i. $P(X = 2)$

ii. $P(X = 0 \cup X = 2)$

6. Is this a binomial?

Do Problem 2.43

2.5 Introduction to Hypothesis Testing

2.5.1 Objectives

1. Correctly use all new terminology and definitions to include: statistic, test statistic, p-value, Type I error, Type II error, power, null hypothesis, and alternative hypothesis
2. Conduct a statistical hypothesis test using the four steps introduced in the book
3. Conduct a power analysis

2.5.2 Hypotheses Testing

Hypothesis testing is difficult to understand and requires thought and practice. The examples in the book are good and detailed. I am going to simplify the example here to help learn the definitions, but you must then wrestle with the examples in the book. I am going to use a simple hypothesis where as the book is using a complex.

I am going to generate a random sample from a binomial where the number of trials is 100. The probability of success is either .45 or .5 and your job is empirically test which value you think I used based on the data. First let's practice the command `rbinom`. To get sample I could do the following commands, I set the seed to make sure I can repeat the results.

```
(temp<-rbinom(100,1,.45))

## [1] 0 0 0 0 0 0 1 0 1 0 0 1 1 1 1 1 0 1 1 1 0 1 0 0 1 0 0 1 1 0 0 1 0 0 0
## [36] 1 0 0 1 0 1 1 1 1 0 1 0 0 1 0 0 0 1 1 1 0 1 0 0 0 0 1 0 0 0 1 1 0 0
## [71] 0 0 1 0 0 0 1 0 0 0 0 1 0 0 0 1 1 0 0 0 1 0 0 1 0 1 0 0 1 1
```

```
sum(temp)
```

```
## [1] 41
```

Note: A success is a 1 and a failure is a 0.

Thus in this random process, I had 41 successes out of 100 trials. This is a binomial because each trial is independent, the probability of success is constant, the trial are fixed, and each trial has two outcomes.

I could have also done

```
rbinom(1,100,.45)
```

```
## [1] 38
```

For interest what would `rbinom(10, 100, .45)` give you?

I will generate a sample with the probability of success as either .45 or .50. You must decide which you think it is.

2.5.2.1 Step 1: State the null and alternative hypotheses

State the null and alternative hypothesis. In practice, the alternative is set to the condition that you want to demonstrate. This is similar to a criminal trial where you are the prosecutor and you want to show that the accused is guilty. The null is that the accused is innocent and the alternative is that they are guilty.

For this artificial problem, it is not clear what the alternative should be. Thus we will select the alternative as the probability of success is 0.5. The hypotheses are:

$$H_o : \pi = 0.45$$

$$H_a : \pi = 0.50$$

Here π is the unknown population parameter probability of success.

2.5.2.2 Step 2: Calculate a test statistic

We run 100 trials and get

```
## [1] 49
```

successes.

The estimate of the probability of success $49/100$ or 0.49 . We will learn more about these types of estimates. They are called point estimates.

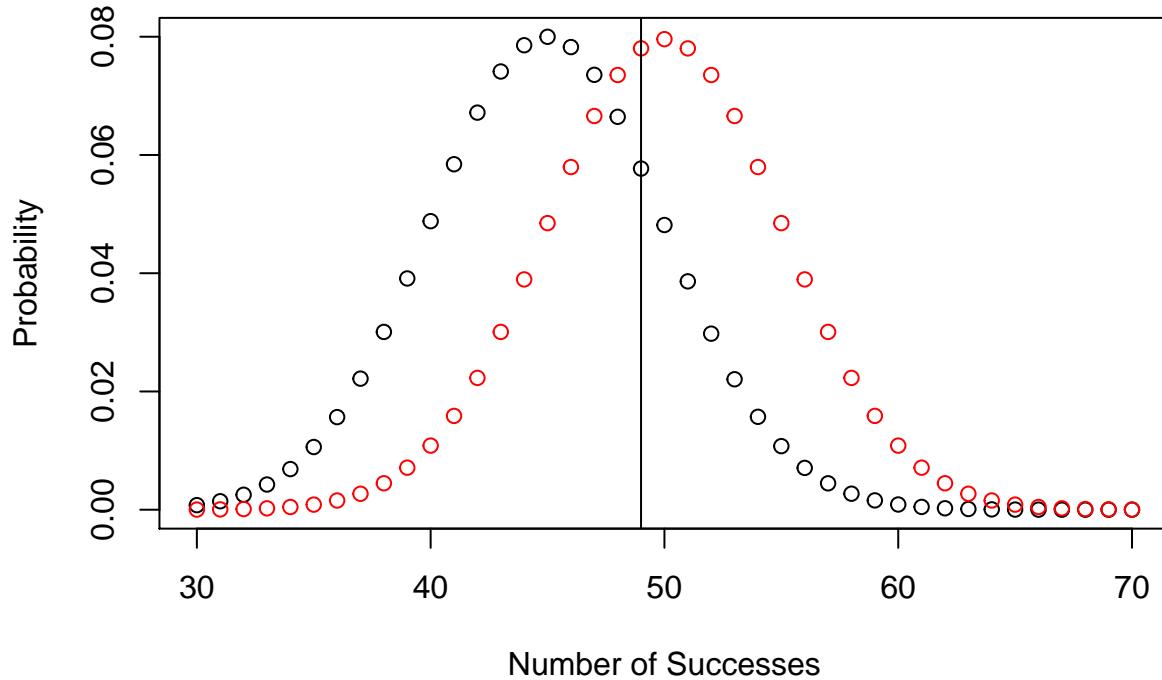
We could have many different test statistics and the choice is important for analysis. We will discuss properties later in the course. But two examples of test statistics are the proportion of success 0.49 and the number of success 49 . We will use the number of successes. The statistic is the number of successes, a random variable, and the test statistic is 49 .

2.5.2.3 Step 3: Compute the p-value

The definition of p-value is a conditional probability. Given that null hypothesis is true, what is the probability of the data or more extreme. The difficult part is what is meant by more extreme. Our statistic is the number of successes out of 100 trials. It is a binomial.

Before we calculate the p-value, let's think about how we could decide whether we believe that the data comes with the probability of success equal to $.45$ or $.50$. It seems that since $.49$ is closer that we think it should be $.50$. Let's plot the probability mass function for each case.

```
plot((30:70),dbinom((30:70),100,.45),type="p",xlab="Number of Successes",ylab="Probability")
points((30:70),dbinom((30:70),100,.5),type="p",col=2)
abline(v=49)
```



Notice the use of `dbinom` in this code.

One way to decide is to pick a rejection region where the probability of that number of successes is higher under each different value of the probability of success. We can find these by creating a table.

```
prob_table<-rbind(dbinom((40:60),100,.45),dbinom((40:60),100,.5))
colnames(prob_table)<-(40:60)
row.names(prob_table)<-c("Prob = 0.45","Prob = 0.50")
prob_table

##          40      41      42      43      44
## Prob = 0.45 0.04880290 0.05843363 0.06716073 0.07411819 0.07855915
## Prob = 0.50 0.01084387 0.01586907 0.02229227 0.03006864 0.03895256
##          45      46      47      48      49
## Prob = 0.45 0.0799875 0.07824864 0.07355675 0.06645184 0.05769844
## Prob = 0.50 0.0484743 0.05795840 0.06659050 0.07352701 0.07802866
##          50      51      52      53      54
## Prob = 0.45 0.04815197 0.03862458 0.02977874 0.02206589 0.01571359
## Prob = 0.50 0.07958924 0.07802866 0.07352701 0.06659050 0.05795840
##          55      56      57      58      59
## Prob = 0.45 0.01075277 0.007069597 0.004465009 0.002708399 0.001577465
## Prob = 0.50 0.04847430 0.038952560 0.030068643 0.022292270 0.015869073
##          60
## Prob = 0.45 0.0008819463
## Prob = 0.50 0.0108438667
```

Based on this table, if we have 47 or less successes, we should fail to reject that $\pi = 0.45$ while 48 or more means we reject H_0 in favor of H_a . We use the fail to reject instead of accept just like we use not guilty

instead of innocent. This idea of finding a cutpoint number is called the rejection region. Using the test statistic of 49, which is greater than 47, we would reject $H_o : \pi = 0.45$ in favor of $H_a : \pi = 0.50$.

Another, and more common, method to determine the rejection region is to find the quantile associated with a small probability. This probability is called the significance level and is usually set to 0.05. It turns out it is the probability of rejecting when the null is true. In this case we want to find the number of successes such that having that value or more extreme leads to a probability of 0.05. Why 0.05? This is unusual enough that we think that if it happens we conclude the null is not true. It is a sort of empirical proof by contradiction. Since we will reject $H_o : \pi = 0.45$ in favor of $H_a : \pi = 0.50$ only if the number of success is larger than the rejection value, we want the 0.05 probability to be in the upper tail. Thus we can use `qbinom`.

```
qbinom(.95, 100, .45)
```

```
## [1] 53
```

Just to check

```
1-pbinom(52:53, 100, .45)
```

```
## [1] 0.06617290 0.04410701
```

Since the distribution is discrete, we cannot find a quantile that will give us exactly 0.05 in the upper tail. We have a choice. If we reject when the number of successes is 53 or greater then percentile is 0.066. Likewise if we use 54 or greater, then the percentile is 0.044. I will go with the second because it is conservative. This choice has to do with a Type I error, which we will discuss shortly.

Based on this rejection region and the data, we fail to reject $H_o : \pi = 0.45$ in favor of $H_a : \pi = 0.50$.

The p-value is a similar idea but takes the context of the problem out of the decision. Under the null hypothesis, the probability of success is 0.45. To find the p-value, we calculate the probability of the data or more extreme under the null hypothesis. More extreme means further from the null and more towards the alternative. Thus for us we want to find $P(X \geq 49)$ which using R is

```
1-pbinom(48, 100, .45)
```

```
## [1] 0.2404266
```

```
pbinom(48, 100, .45, lower=FALSE)
```

```
## [1] 0.2404266
```

Since this is larger than our significance level of 0.05, we fail to reject $H_o : \pi = 0.45$ in favor of $H_a : \pi = 0.50$.

Which test is better, one rejected and the other did not? It is beyond the scope of this course, but is based on the idea of finding uniformly most powerful tests.

2.5.2.4 Draw a conclusion

Based on our data of 49 successes in 100 tries, under the null that the probability of heads is 0.45 we found the probability of 49 or more heads is 0.2404 which is greater than 0.05. Thus we fail to reject $H_o : \pi = 0.45$ in favor of $H_a : \pi = 0.50$.

2.5.3 More terms - Errors

We can make two types of error. We can reject when the null is true. This is a type I error. The probability of this is the significance level, usually called α . Formally, the probability of a type I error is $P(\text{reject} | \text{null hypothesis is true})$. We pick this value as part of the test design. This is why we put what we are trying to show in the alternative because we are trying to reject the null and we can control the type I error.

The second type of error is called the type II error, yes these are poor names. Sometimes type I error is called a false positive, and type II a false negative. The type II error is when we fail to reject but the alternative is true. In practice this is difficult to calculate because the alternative is often a complex hypothesis and we don't have a value for the parameter under the alternative. But because I chose a simple alternative, we can easily find the probability of a type II error. The probability of a type II error is $P(\text{Fail to reject} | \text{Alternative hypothesis is true})$. Based on the work we did above, we reject when the number of successes is 54 or greater. The probability of a type II error thus is

```
pbinom(53, 100, .5)
```

```
## [1] 0.7579408
```

For our problem, since we failed to reject, the probability of a type II error is large. Typically we want it at 0.2 or smaller. For this problem that means a larger sample size is required. The calculation of sample size should have been done prior to the test.

The complement of a type II error is called power and it is the probability we reject given the alternative is true. Again, since we are setting up in the hopes of rejecting, power is a useful metric. For this problem, power is

```
1-pbinom(53, 100, .5)
```

```
## [1] 0.2420592
```

2.5.4 Sample Size

Instead of 100 trials how many should we have done? Using an α of 0.05, this is my type II error and a power of at least 0.80. Let's find the number. As a start, say the sample size is 200. Then the rejection region is

```
qbinom(.95, 200, .45)
```

```
## [1] 102
```

And the power is

```
1-pbinom(102, 200, .5)
```

```
## [1] 0.3618855
```

We are going to need a large sample. Next let's try 800 trials.

```
qbinom(.95, 800, .45)
```

```
## [1] 383
```

And the power is

```
1-pbinom(383, 800, .5)
```

```
## [1] 0.8783484
```

That is more like it. I think we can write a function to help us.

```
simple_sample_size<-function(n=100){1-pbinom(qbinom(.95,n,.45),n,.5)}
```

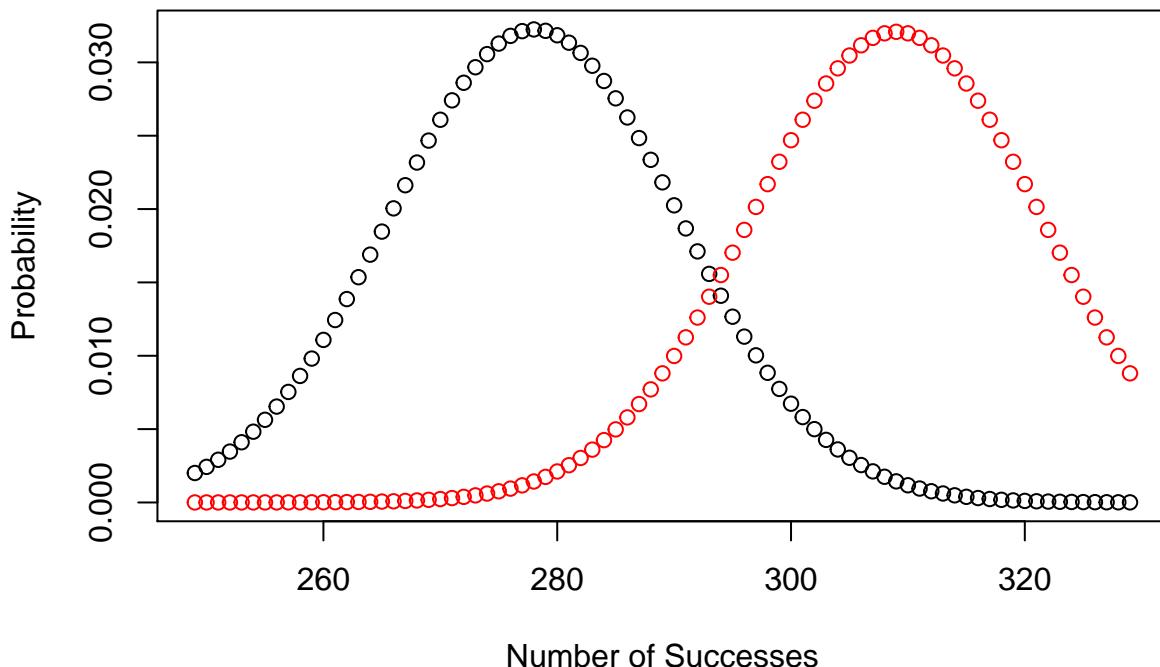
Now for a range of values

```
temp<-sapply((600:625),simple_sample_size)
names(temp)<-(600:625)
temp
```

```
##      600      601      602      603      604      605      606
## 0.7810158 0.7685830 0.7806348 0.7922992 0.7802553 0.7919132 0.7798774
##      607      608      609      610      611      612      613
## 0.7915286 0.7795009 0.7911456 0.7791259 0.7907640 0.7787524 0.7903839
##      614      615      616      617      618      619      620
## 0.7783803 0.7900052 0.7780097 0.7896280 0.8008639 0.7892522 0.8004829
##      621      622      623      624      625
## 0.7888779 0.8001033 0.7885049 0.7997251 0.7881334
```

So it looks like around 618 trials would work for use. Let's plot

```
plot((249:329),dbinom((249:329),618,.45),type="p",xlab="Number of Successes",ylab="Probability")
points((249:329),dbinom((249:329),618,.5),type="p",col=2)
```



2.5.5 Complex Hypothesis

The book goes through an example so we will keep it short here. Suppose our hypotheses were

$$H_o : \pi = .45$$

$$H_a : \pi \neq .45$$

The alternative is complex because it takes on many values. This particular test is two-sided and is the most common. A one-sided test can only be done if apriori you have knowledge that the parameter will be on one side of the null hypothesized value.

To conduct this test, we can use the function `binom.test`.

```
binom.test(49,100,p=.45,conf.level = .05)

##
##
##
## data: 49 out of 100
## number of successes = 49, number of trials = 100, p-value = 0.4235
## alternative hypothesis: true probability of success is not equal to 0.45
## 5 percent confidence interval:
## 0.4819244 0.4981442
## sample estimates:
## probability of success
## 0.49
```

Again, we fail to reject.

To find power, you need a specified difference or size of effect that you think is practically important, usually from a subject matter expert. Let's say that expert wants to detect a difference of 0.05, this is called the effect size. We now need a value for the alternative. We could pick either 0.40 or 0.50. Let's go with 0.50. You could do both and report the two power calculations back to the decision maker.

Since it is a two-sided test, we need to split the significance level between both tails. Thus the critical values, the values that define the rejection region are.

```
qbinom(.975,100,.45)
```

```
## [1] 55
qbinom(.025,100,.45)
```

```
## [1] 35
```

Again, since the distribution is discrete, it is unlikely that these values will give us the exact probabilities we want. Let's check and decide what we want to use.

```
1-pbinom(54:56,100,.45)
```

```
## [1] 0.02839342 0.01764065 0.01057105
pbinom(34:36,100,.45)
```

```
## [1] 0.01663269 0.02723630 0.04290071
```

If we reject when we have 34 or fewer heads and 56 or greater heads then the probability of a type I error is

```
1-(pbinom(55,100,.45)-pbinom(34,100,.45))
```

```
## [1] 0.03427334
```

This is conservative and less than 0.05. We could adjust a little

```
1-(pbinom(55,100,.45)-pbinom(35,100,.45))
```

```
## [1] 0.04487694
```

It is up to you to decide. Let's go with the second set. We reject if we have 35 or fewer or 56 and greater heads. Now to find power, we calculate the probability of rejecting given that the alternative is true, which we have selected as 0.05.

```
1-(pbinom(55,100,.5)-pbinom(35,100,.5))
```

```
## [1] 0.1373853
```

The power is small and thus to detect a difference of 0.05, we need a larger sample size than 100.

For interest, let's check the power if the alternative were 0.40.

```
1-(pbinom(55,100,.4)-pbinom(35,100,.4))
```

```
## [1] 0.1803512
```

2.6 Mean and Variance of Discrete Random Variable

2.6.1 Objectives

1. Know and use definitions and properties of $E(X)$ and $V(X)$
2. Find the pmf of the transformation of a random variable
3. Know $E(X)$ and $V(X)$ for common distributions

2.6.2 Review

Definitions you should know cold:

p-value: Probability of the observed data or more extreme given the null hypothesis is true
 Level of significance (α): The probability of rejecting given the null hypothesis is true

Power: The probability of rejecting given that the alternative hypothesis is true

β : 1 - Power, the probability of failing to reject given that the alternative hypothesis is true

2.6.2.1 Practice problems

1. We are testing if a die is fair by rolling it 30 time and recording the number of times one appears. The hypothesis is

$$H_o : \pi = \frac{1}{6}$$

$$H_a : \pi \neq \frac{1}{6}$$

The test statistic is 2. Using a significance level of $\alpha = 0.05$. Find the power of the test using an alternative probability of success of 0.20.

2. Let $X \sim Binom(15, .25)$ Find $P(X = 2), P(X < 7), P(X \geq 8)$, and $P(5 < X \leq 9)$

2.6.3 Problem

A random process flips a fair coin four times. Find the pmf for the random variable $Z =$ the difference between the number of heads and the number of tails.

The values that Z can take are -4, -2, 0, 2, and 4. The pmf will be the same as the pmf for a binomial of four flips. Thus

```
dbinom(0:4,4,.5)
```

```
## [1] 0.0625 0.2500 0.3750 0.2500 0.0625
```

If I install the MASS library, I can make these fractions.

```
library(MASS)

fractions(dbinom(0:4,4,.5))

## [1] 1/16 1/4 3/8 1/4 1/16
```

1. Find $E(Z)$

By definition $E(Z) = \sum_z z f(z)$

```
seq(-4,4,2)*fractions(dbinom(0:4,4,.5))

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

sum(seq(-4,4,2)*fractions(dbinom(0:4,4,.5)))

## [1] 0
```

The expected value, the average value of the population, is zero.

2. Now a transformation, let $Y = |Z|$. Find the pmf of Y and $E(Y)$.

This is an important definition:

Let X be a random variable and $t : \mathbb{R} \rightarrow \mathbb{R}$, then $E(t(X))$ is $E(t(X)) = \sum_x t(x)f(x)$

The pmf is

```
temp<-fractions(c(dbinom(2,4,.5),(dbinom(1,4,.5)+dbinom(3,4,.5)),dbinom(0,4,.5)+dbinom(0,4,.5)))
names(temp)<-c(0,2,4)
temp

## 0 2 4
## 3/8 1/2 1/8
```

The expected value is

```
sum(c(0,2,4)*temp)

## [1] 3/2

or

fractions(sum(abs(seq(-4,4,2))*dbinom(0:4,4,.5)))

## [1] 3/2
```

3. Find $E(Z^2)$

The pmf is

```
temp<-fractions(c(dbinom(2,4,.5),(dbinom(1,4,.5)+dbinom(3,4,.5)),dbinom(0,4,.5)+dbinom(0,4,.5)))
names(temp)<-c(0,4,16)
temp

## 0 4 16
## 3/8 1/2 1/8
```

The expected value is

```
sum(c(0,4,16)*temp)

## [1] 4
```

or

```
fractions(sum((seq(-4,4,2)^2)*dbinom(0:4,4,.5)))  
## [1] 4
```

4. Variance is just an expected value and is defined as

$$\text{Var}(X) = E((X - E(X))^2)$$

where $E(X)$ is sometimes denoted as μ

by definition:

$$E((X - E(X))^2) = E((X - \mu)^2) = \sum_x t(x)f(x) = \sum_x (x - \mu)^2 f(x)$$

find $\text{Var}(Z)$

```
(seq(-4,4,2)-0)^2*fractions(dbinom(0:4,4,.5))  
## [1] 1 1 0 1 1  
sum((seq(-4,4,2)-0)^2*fractions(dbinom(0:4,4,.5)))  
## [1] 4
```

You can also find variance using

$$\text{Var}(X) = E(X^2) - E(X)^2$$

5. Other properties

$$E(aX + b) = aE(X) + b$$

$$\text{Var}(aX + b) = a^2 \text{Var}(X)$$

Do Homework problem 2.64

2.7 Discrete Joint Distributions

2.7.1 Objectives

1. Know and use definitions such as joint pmf, conditional distribution, marginal distribution, independence, covariance, and correlation coefficient
2. Find the various probability mass functions (joint, marginal, and conditional)
3. Know and use properties of $E(X), V(X)$, and $\text{Cov}(X,Y)$ for sums and products of random variables

2.7.2 Example

Consider a contrived example of three random variables X, Y, and Z. The following is the joint probability mass function

```
library(MASS)
```

```
fractions(Les10ex<-array(c(3/64,9/64,9/64,27/64,2/64,6/64,2/64,6/64),dim=c(2,2,2),dimnames = list(c(0,1,
```

```

## , , 0
##
##   0      1
## 0  3/64  9/64
## 1  9/64 27/64
##
## , , 1
##
##   0      1
## 0  1/32  1/32
## 1  3/32  3/32

```

This might be easier to look at:

```
Les10exa<-data.frame(X=c(rep(0,16),rep(1,48)),Y=c(0,0,0,rep(1,9),rep(c(0,1),each=2),rep(0,9),rep(1,27),...
```

Now we have our pmf

```
fractions(prop.table(table(Les10exa)))
```

```

## , , Z = 0
##
##   Y
## X   0      1
## 0  3/64  9/64
## 1  9/64 27/64
##
## , , Z = 1
##
##   Y
## X   0      1
## 0  1/32  1/32
## 1  3/32  3/32

```

Notice this is a pmf since each value is between 0 and 1 and the sum is 1.

That is $\sum_{x,y,z} f_{XYZ}(x,y,z) = 1$.

```
sum(fractions(prop.table(table(Les10exa))))
```

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

2.7.3 Problem 1

- Find $P(X = 1, Y = 1, Z = 1)$ which is $f_{XYZ}(1, 1, 1)$. Notice that we are using a comma instead of the intersection symbol. This is to make the notation easier.

The answer is $6/64$. This is a joint probability.

- Find the marginal pmf of X.

```
fractions(apply(prop.table(table(Les10exa)), 1, sum))
```

```

##   0   1
## 1/4 3/4

```

- Find $E(X)$

```
sum(apply(fractions(prop.table(table(Les10exa))), 1, sum)*c(0, 1))
```

[1] 0.75

4. Find $f_{XY}(x, y)$.

```
fractions(apply(prop.table(table(Les10exa)), 1:2, sum))
```

```
##      Y
## X   0     1
##   0  5/64 11/64
##   1 15/64 33/64
```

5. Are X and Y independent?

We need to verify that $f_{XY}(x, y) = f_X(x)f_Y(y)$ for all x and y .

We need $f_X(x)$ and $f_Y(y)$

```
fractions(apply(prop.table(table(Les10exa)), 1, sum))
```

```
##   0   1
## 1/4 3/4
```

```
fractions(apply(prop.table(table(Les10exa)), 2, sum))
```

```
##   0   1
## 5/16 11/16
```

We could multiply these one at a time or use an outer product to make it easier

```
fractions(outer(apply(prop.table(table(Les10exa)), 1, sum), apply(prop.table(table(Les10exa)), 2, sum)))
```

```
##   0   1
## 0  5/64 11/64
## 1 15/64 33/64
```

The joint pmf is

```
fractions(apply(prop.table(table(Les10exa)), 1:2, sum))
```

```
##      Y
## X   0     1
##   0  5/64 11/64
##   1 15/64 33/64
```

They are equal so X and Y are independent.

5. How about X and Z ?

```
fractions(apply(prop.table(table(Les10exa)), 1, sum))
```

```
##   0   1
## 1/4 3/4
```

```
fractions(apply(prop.table(table(Les10exa)), 3, sum))
```

```
##   0   1
## 3/4 1/4
```

```
fractions(outer(apply(prop.table(table(Les10exa)), 1, sum), apply(prop.table(table(Les10exa)), 3, sum)))
```

```
##   0   1
```

```
## 0 3/16 1/16
## 1 9/16 3/16
```

The joint pmf is

```
fractions(apply(prop.table(table(Les10exa)),c(1,3),sum))
```

```
##      Z
## X 0    1
##   0 3/16 1/16
##   1 9/16 3/16
```

Thus X and Z are independent.

6. How about X , Y , and Z ?

If they are independent, then $f_{XYZ}(x, y, z) = f_X(x)f_Y(y)f_Z(z)$ for all x , y , and z .

```
fractions(apply(prop.table(table(Les10exa)),1,sum))
```

```
##      0    1
## 1/4 3/4

fractions(apply(prop.table(table(Les10exa)),2,sum))

##      0    1
## 5/16 11/16

fractions(apply(prop.table(table(Les10exa)),3,sum))

##      0    1
## 3/4 1/4
```

The product of the marginals is

```
fractions(outer(outer(apply(prop.table(table(Les10exa)),1,sum),apply(prop.table(table(Les10exa)),2,sum)))
```

```
## , , 0
##
##      0    1
## 0 15/256 33/256
## 1 45/256 99/256
##
## , , 1
##
##      0    1
## 0 5/256 11/256
## 1 15/256 33/256
```

The joint pmf is

```
fractions(prop.table(table(Les10exa)))
```

```
## , , Z = 0
##
##      Y
## X 0    1
##   0 3/64 9/64
##   1 9/64 27/64
##
## , , Z = 1
```

```
##      Y
## X   0     1
##   0 1/32 1/32
##   1 3/32 3/32
```

They are not independent.

In this problem we have pairwise independence but not independence.

7. Find $f_{X|Y=1}(x)$. This is a conditional pmf.

From the definition of conditional probability

$$f_{X|Y=1}(x) = \frac{f_{XY}(x,y)}{f_Y(y)}|_{y=1} = \frac{f_{XY}(x,1)}{f_Y(1)}$$

The joint pmf of X and Y is

```
fractions(apply(prop.table(table(Les10exa)), 1:2, sum))
```

```
##      Y
## X   0     1
##   0 5/64 11/64
##   1 15/64 33/64
```

and the marginal of Y is

```
fractions(apply(prop.table(table(Les10exa)), 2, sum))
```

```
##      0     1
## 5/16 11/16
```

Since $y = 1$ we want the second column of the joint

```
fractions(apply(prop.table(table(Les10exa)), 1:2, sum))[, 2]
```

```
##      0     1
## 11/64 33/64
```

divided by the second element of the marginal

```
fractions(apply(prop.table(table(Les10exa)), 2, sum))[2]
```

```
##      1
## 11/16
```

```
fractions(apply(prop.table(table(Les10exa)), 1:2, sum))[, 2] / fractions(apply(prop.table(table(Les10exa)), 2, sum))
##      0     1
## 1/4  3/4
```

Notice that since X and Y are independent, this is just the marginal of X

```
fractions(apply(prop.table(table(Les10exa)), 1, sum))
```

```
##      0     1
## 1/4  3/4
```

2.7.4 Problem 2

Let do a problem where the random variables are not independent.

```
Les10ex2<-data.frame(X=c(-1,0,0,1),Y=c(1,0,0,1))
```

Now we have our pmf

```
fractions(prop.table(table(Les10ex2)))
```

```
##      Y
## X   0   1
## -1  0 1/4
##  0 1/2  0
##  1  0 1/4
```

1. Are X and Y independent?

```
fractions(apply(prop.table(table(Les10ex2)),1,sum))
```

```
## -1  0   1
## 1/4 1/2 1/4
```

```
fractions(apply(prop.table(table(Les10ex2)),2,sum))
```

```
##  0   1
## 1/2 1/2
```

```
fractions(outer(fractions(apply(prop.table(table(Les10ex2)),1,sum)),fractions(apply(prop.table(table(Les10ex2)),2,sum))))
```

```
##      0   1
## -1 1/8 1/8
##  0 1/4 1/4
##  1 1/8 1/8
```

This is not equal to the joint pmf, so they are not independent.

2. Find $\text{Cov}(X,Y)$.

By definition, this is $E[(X - E(X))(Y - E(Y))]$.

Now $E(X)=0$ and $E(Y)=1/2$.

Now we can find the covariance, we do not need to write the product when the joint probability is zero since the product will be zero. Thus we have

$$(-1 - 0)(1 - 1/2)(1/4) + (0 - 0)(0 - 1/2)(1/2) + (1 - 0)(1 - 1/2)(1/4) = 0$$

The covariance is zero even though X and Y are dependent. That is because covariance measures a linear relationship. The relationship here is purely quadratic with no linear component.

3. Find $E(XY)$

We need the pmf of $W = XY$.

The random variable W can take on the values $-1, 0, 1$ with probabilities of $1/4, 1/2, 1/4$. Thus the expected value is $(1/4)(-1) + (1/2)(0) + (1/4)(1) = 0$

Notice that if random variables are independent, their covariance is zero. The converse is not true.

We have another formula for covariance

$$\text{Cov}(X, Y) = E(XY) - E(X)E(Y)$$

We also now have

$$\text{Var}(X, Y) = \text{Var}(X) + \text{Var}(Y) + 2\text{Cov}(X, Y)$$

2.7.5 Other

Make sure you know Thm 2.6.7, Lemma 2.6.13, and Lemma 2.6.14.

```
library(fastr)
```

For an example, let's use the airline data from a previous lessons. Let's assume this is the pmf and not empirical data.

```
prop.table(xtabs(~Airport+Airline+Result,airlineArrival))
```

```
## , , Result = Delayed
##
##          Airline
## Airport      Alaska AmericaWest
## LosAngeles  0.005636364 0.010636364
## Phoenix     0.001090909 0.037727273
## SanDiego    0.001818182 0.005909091
## SanFrancisco 0.009272727 0.011727273
## Seattle     0.027727273 0.005545455
##
## , , Result = OnTime
##
##          Airline
## Airport      Alaska AmericaWest
## LosAngeles  0.045181818 0.063090909
## Phoenix     0.020090909 0.440000000
## SanDiego    0.019272727 0.034818182
## SanFrancisco 0.045727273 0.029090909
## Seattle     0.167363636 0.018272727
```

Now you can do the same work of finding marginal pmf, checking for independence, finding conditional pmf, etc.

For example, the joint pmf for Airline and Result is:

```
apply(prop.table(xtabs(~Airport+Airline+Result,airlineArrival)),2:3,sum)
```

```
##          Result
## Airline      Delayed   OnTime
## Alaska     0.04554545 0.2976364
## AmericaWest 0.07154545 0.5852727
```

2.8 Other Discrete Distributions

2.8.1 Objectives

1. Know assumptions, parameters, $E(X)$, $V(X)$, and how to solve problems for Poisson and hypergeometric
2. Conduct hypothesis test using Fisher's exact test

2.8.2 Distributions

We have learned about the following distributions to this point:

1. Binomial: X the number of successes in n trials. The parameter is probability of success and the nuisance parameter is the number of successes. An example is the number of made free throws in 10 shots.
2. Negative Binomial: Y the number of failures until s successes. The parameter is probability of success and the nuisance parameter is number of successes. Note that in the binomial, the number of successes is random and the trials are fixed. In the negative binomial, the number of successes is fixed and the number of trials is random. An example is the number of free throws until I make 10.
3. Discrete Uniform. This was not directly mentioned in the book but used in several examples and homework problems. It is simply the case where each outcome has the same probability. An example is the number on a rolled die.

Two new distributions are:

4. Poisson: X is the number of occurrences in a fixed interval. The interval is fixed and is a measurement variable such as time or distance. The number of occurrences are random. An example is the number of people entering Chipotle in the next 45 minutes. The parameter for the Poisson is λ which is the average number of occurrences in the fixed interval. It is key to use the interval given in the problem.
5. Hypergeometric: X is the number of successes in a sample of size k where the population has m successes and n failures. An example is the number of girls on a 6 member team where we select from 7 girls and 5 boys. The hypergeometric is similar to the binomial except that we sample without replacement. Thus the probability of success is not constant and the trials are not independent.

2.8.3 Examples

On average, 45 cars enter the North Gate every hour. What is the probability that less than 20 cars will enter in the next 15 minutes.

The random variable is Y the number of cars entering the North Gate in 15 minutes. Thus λ is the average number of cars entering the gate in 15 minutes. It has the value of $45/4$. The answer is

```
ppois(19,45/4)
```

```
## [1] 0.9884122
```

The probability of exactly 20 cars in the next 15 minutes is

```
dpois(20,45/4)
```

```
## [1] 0.005637842
```

Changing the problem slightly, what is the probability of more than 30 cars in 45 minutes?

In this case λ is $45(3/4)$

```
1-ppois(30,45*3/4)
```

```
## [1] 0.7052313
```

For a hypergeometric, what is the probability of a 5 card hand having exactly two Kings?

We are sampling without replacement. We have two outcomes, King and not King. In the population we have 4 Kings and 48 non-Kings.

```
dhyper(x=2,m=4,n=48,k=5)
```

```
## [1] 0.03992982
```

2.8.4 Fisher's Exact Test

This test is used when we have two random variables each with two levels. It is checking for an association between the variables. In other words, it is checking for independence. The test is exact because we can use the hypergeometric distribution to find probabilities. We do not need approximations.

To illustrate the use of this test, I will work example 2.7.4 in different ways. This example uses the hypergeometric distribution and the built-in function `fisher.test` that uses the hypergeometric distribution for hypothesis testing.

As a reminder, the hypergeometric involves k trials where each trial has two outcomes. But in difference to the binomial, the hypergeometric has a finite population and samples without replacement, thus the probability of success is not constant and the trials are not independent. A generic hypergeometric random variable is

`X = the number of successes in k trials where the population has m successes and n failures.`

1. For this problem, I will alter the null and alternative hypothesis:

$$H_0 : \pi_d = \pi_m$$

$$H_a : \pi_d < \pi_m$$

Where π_d is the proportion of dizygotic twins where both had convictions. This hypothesis assumes that apriori we had information that indicated we thought dizygotic twins had a conviction percentage less than monozygotic. Somewhat questionable, but we will continue.

Next, enter the data into R:

```
convictions <- rbind(dizygotic=c(2,15), monozygotic=c(10,3))
colnames(convictions) <- c('convicted','not convicted')
convictions

##          convicted not convicted
## dizygotic           2            15
## monozygotic         10            3
```

Notice the marginal totals

```
colSums(convictions)

##      convicted not convicted
##             12            18

rowSums(convictions)

##      dizygotic monozygotic
##             17            13
```

These values, marginals, are assumed to be fixed. Testing the hypothesis we need to use one of the four cells from the table as a reference. By convention, the upper left cell is used in the `fisher.test` test. To find the p-value, we must find the probability of the data or more extreme given the null hypothesis is true. Using the upper left hand cell, more extreme means 2 or less dizygotic twins both have convictions, look at the alternative again. Assuming the null hypothesis being true, no difference between the dizygotic and monozygotic, means that we could trade entries in the cells. This leads to our test statistic:

`X = the number of dizygotic twins in 12 convicted twins where the population has 17 dizygotic twins and 13 monozygotic twins.`

This is a hypergeometric and the p-value is

$$P(X \leq 2 | H_0 \text{ is true}) =$$

```
phyper(2, 17, 13, 12)
```

```
## [1] 0.0004651809
```

Since the p-value is much less than 0.05, based on the data, we reject the hypothesis that dizygotic and monozygotic twins have the same mutual conviction proportion in favor of the hypothesis that dizygotic twins have a smaller mutual conviction proportion at the 0.05 significance level.

Notice that I could have also used the following equivalent analysis

```
X = the number of convicted twins in 17 dizygotic twins where the population has 12 convicted
twins and 18 not convicted twins.
```

This is a hypergeometric and the p-value is

```
 $P(X \leq 2 | H_0 \text{ is true}) =$ 
```

```
phyper(2, 12, 18, 17)
```

```
## [1] 0.0004651809
```

This is the same p-value.

We could have also used the function `fisher.test` to get the p-value:

```
fisher.test(convictions, alter="less")
```

```
##
## Fisher's Exact Test for Count Data
##
## data: convictions
## p-value = 0.0004652
## alternative hypothesis: true odds ratio is less than 1
## 95 percent confidence interval:
## 0.0000000 0.2849601
## sample estimates:
## odds ratio
## 0.04693661
```

2. I could have had the table come in this form, since the ordering of columns and rows is arbitrary:

```
convictions2 <- rbind(monozygotic=c(10, 3), dizygotic=c(2, 15))
colnames(convictions2) <- c('convicted', 'not convicted')
convictions2
```

```
##           convicted not convicted
## monozygotic      10            3
## dizygotic        2            15
```

Notice the marginal totals are the same:

```
colSums(convictions2)
```

```
##           convicted not convicted
##             12            18
```

```
rowSums(convictions2)
```

```
## monozygotic  dizygotic
##       13         17
```

Again, the upper left hand cell is the reference cell and we have the same hypotheses. To find the p-value for this arrangement the test statistic would be

X = the number of monozygotic twins in 12 convicted twins where the population has 17 dizygotic twins and 13 monozygotic twins.

$$P(X \geq 10 | H_O \text{ is true}) =$$

```
1-phyper(9, 13, 17, 12)
```

```
## [1] 0.0004651809
```

This is the same p-value. Using `fisher.test`

```
fisher.test(convictions2, alter="greater")
```

```
##
## Fisher's Exact Test for Count Data
##
## data: convictions2
## p-value = 0.0004652
## alternative hypothesis: true odds ratio is greater than 1
## 95 percent confidence interval:
## 3.509263      Inf
## sample estimates:
## odds ratio
## 21.30533
```

3. You try. For the following table, find the p-value for the

$$H_o : \pi_d = \pi_m$$

$$H_a : \pi_d < \pi_m$$

Where π_d is the proportion of dizygotic twins where both had convictions. This hypothesis assumes that apriori we had information that indicated we thought dizygotic twins had a double conviction percentage less than monozygotic. Somewhat questionable, but we will continue.

```
convictions3 <- rbind(monozygotic=c(3,10),dizygotic=c(15,2))
colnames(convictions3) <- c('not convicted','convicted')
convictions3
```

```
##           not convicted convicted
## monozygotic            3        10
## dizygotic              15        2
```

Let X = the number of monozygotic twins in 18 not convicted twins where the population has 17 dizygotic twins and 13 monozygotic twins.

```
phyper(3, 13, 17, 18)
```

```
## [1] 0.0004651809
```

```
fisher.test(convictions3, alternative = 'less')
```

```
##
## Fisher's Exact Test for Count Data
##
## data: convictions3
## p-value = 0.0004652
## alternative hypothesis: true odds ratio is less than 1
## 95 percent confidence interval:
## 0.0000000 0.2849601
## sample estimates:
```

```
## odds ratio  
## 0.04693661
```

Chapter 3

Continuous Distributions

The third chapter is completed in six lessons. Section 3.2 is small so it is combined in one lesson with the first part of section 3.3. Sections 3.5 and 3.6 are combined into one lessons.

3.1 Uniform and Exponential Distribution

3.1.1 Objectives

1. Know and confirm properties of pdf, use pdf to find cdf or vice versa.
2. Find transformations of random variables using cdf method.
3. Calculate probabilities for uniform and exponential distribution.

3.1.2 Probability Density Function

Probability density function is used with continuous random variables; the pdf is denoted $f(x)$ much like the probability mass function but has a much different interpretation. To get probabilities from a pdf you must integrate. It is the area under the pdf that is the probability. This is similar to the idea in physics where mass is considered a point or found by integrating density. The following figure illustrates the $P(a < X < b) = \int_a^b f(x)dx$.

Now using what we now about probability and calculus we know:

1. $f(x) \geq 0$
2. $\int_{-\infty}^{\infty} f(x)dx = 1$

Since probabilities are $[0,1]$, $f(x)$ has to be non-negative otherwise we would get negative probabilities. A common mistake is to think that $f(x)$ has to be less than or equal to one. That is not true. If you are doing this mistake, you are confusing probability with density. The area under the density curve, which is a probability, has to be less than or equal to one.

Use calculus knowledge to solve probability problems for continuous random variables.

For example $P(X = a) = \int_a^a f(x)dx = 0$.

The cumulative distribution function has the same definition

$$P(X \leq x) = \int_{-\infty}^x f(x)dx = F(x)$$

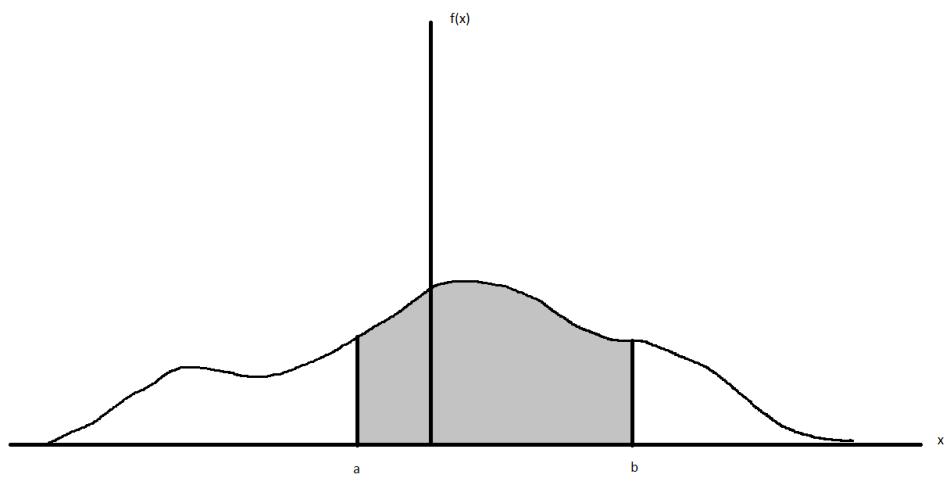


Figure 3.1: Figure 3.1a

The variable x in the integral is confusing to students but remember the variable in the integration is a dummy variable so we could have written it as

$$P(X \leq x) = \int_{-\infty}^x f(w)dw = F(x)$$

Using the fundamental theorem of calculus, we know the relationship between the pdf and cdf

$$f(x) = \frac{d}{dx} F(x)$$

Definition 3.1.5 in the book is important if you want to state that two random variables have the same distribution.

3.1.3 Work problem 3.1a including finding cdf.

Do this by hand. In R you can do the following:

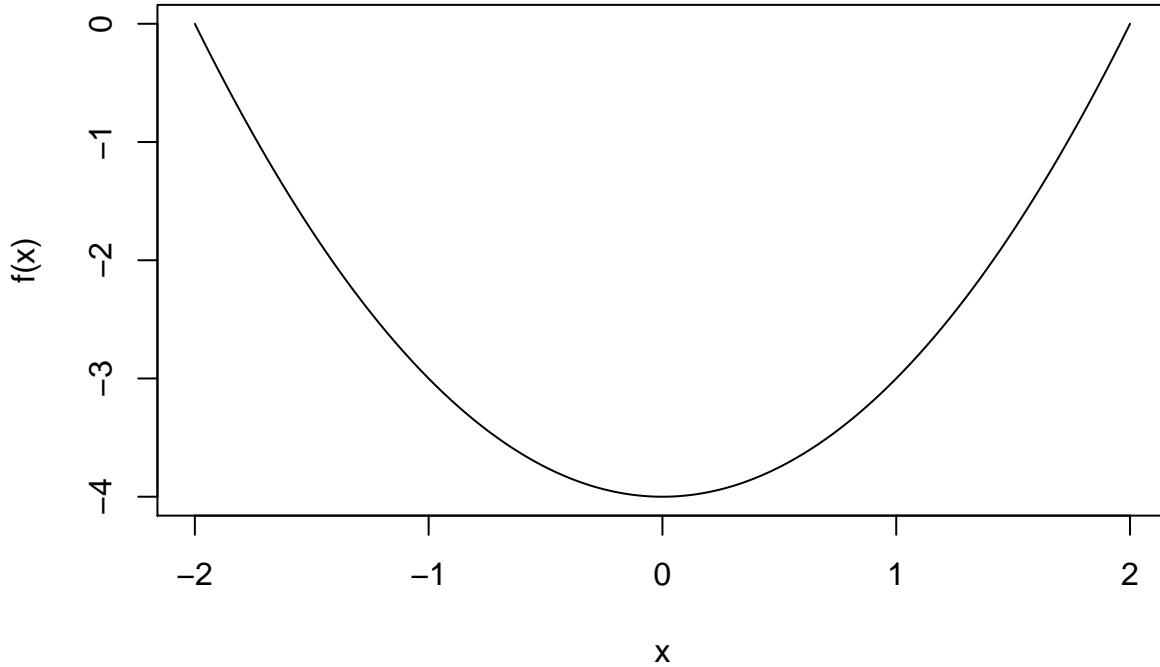
Define the kernel as a vectorized R function

```
f<-function(x){
  sapply(x,(function(x)((x-2)*(x+2)*{x>=-2&x<=2})))
}
```

Notice that I used a function inside the function. Since I did not give it a name it is often called an anonymous function.

A plot of the kernel

```
plot(seq(-2,2,.01),f(seq(-2,2,.01)),type="l",ylab="f(x)",xlab="x")
```



Notice this is not a pdf. We must find the scaling constant.

```
library(MASS)
fractions(integrate(f,-Inf,Inf)$value)
## [1] -32/3
```

Thus the pdf is

$$f(x) = \frac{-3}{32}(x-2)(x+2) \text{ for } -2 \leq x \leq 2$$

and

$$f(x) = 0 \text{ otherwise}$$

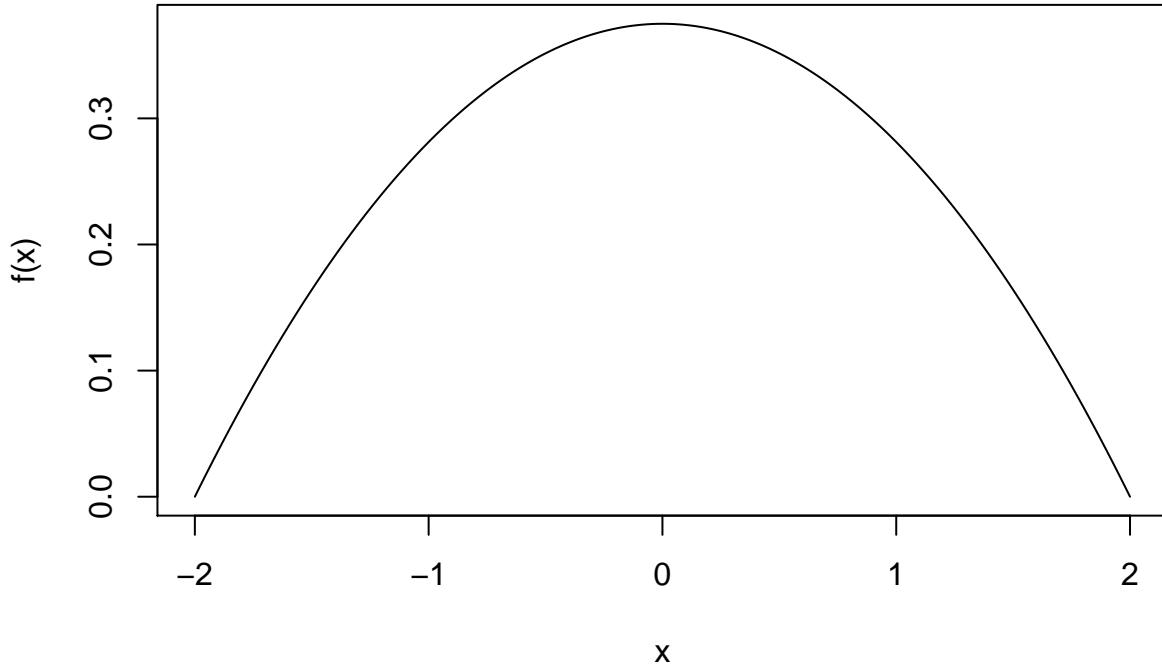
Let's see if we need to vectorize the function as the author suggested. Here is my pdf function

```
f3.1<-function(x)(-3/32*(x-2)*(x+2)*{x>=-2&x<=2})
```

This would be an R function that started with the letter d.

A plot of the pdf

```
plot(seq(-2,2,.01),f3.1(seq(-2,2,.01)),type="l",ylab="f(x)",xlab="x")
```



This is proper pdf since

$$f(x) \geq 0$$

and

$$\int_{-\infty}^{\infty} f(x)dx = 1$$

```
integrate(f3.1,-Inf,Inf)$value
```

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

It does not appear that we need to vectorize the function. Perhaps the logical statement is the function that is vectorizing the function for us.

By hand we get

$$\begin{aligned} \int_{-\infty}^{\infty} f(x)dx &= \int_{-\infty}^{-2} 0dx + \int_{-2}^2 \frac{-3}{32}(x-2)(x+2)dx + \int_2^{\infty} 0dx = \\ &\quad \left. \frac{-3}{32} \left(\frac{x^3}{3} - 4x \right) \right|_{-2}^2 = \\ &\quad \frac{-3}{32} \left(\frac{8}{3} - 8 - \left(\frac{-8}{3} + 8 \right) \right) = \\ &\quad \frac{-3}{32} * (16/3 - 16) = 1 \end{aligned}$$

The cdf is

$$F(x) = P(X \leq x) = \int_{-\infty}^x f(x)dx = \int_{-\infty}^{-2} 0dx + \int_{-2}^x \frac{-3}{32}(x-2)(x+2)dx =$$

$$-\frac{(x^3 - 12x - 16)}{32}$$

Thus the cdf is

$$\begin{aligned} & 0 \text{ for } x \leq -2 \\ & -\frac{(x^3 - 12x - 16)}{32} \text{ for } -2 \leq x \leq 2 \\ & 1 \text{ for } x > 2 \end{aligned}$$

As an R function

```
cdf3.1<-function(x){
  if (x < -2) {
    result=0
  } else if (x > 2) {
    result=1
  } else result = -(x^3-12*x-16)/32
return(result)
}
```

This would be an R function that started with the letter p.

As a check

```
fractions(cdf3.1(-1))

## [1] 5/32

fractions(integrate(f3.1,-Inf,-1)$value)
```

[1] 5/32

or equivalently

```
fractions(integrate(f3.1,-2,-1)$value)

## [1] 5/32
```

As an advanced problem, we can create our own q version of the function as well. This is where we find the quantiles. Here is my code

```
q3.1<-function(y)uniroot(function(x)cdf3.1(x)-y,c(-2,2))$root
```

I did not put any error checking in this function so I am assuming a knowledgeable user.

Let's test it.

```
q3.1(.5)

## [1] 0

q3.1(.75)

## [1] 0.6946066

q3.1(1)

## [1] 2

q3.1(0)

## [1] -2
```

Finally, I could write my R function as well.

```
r3.1<-function(n)sapply(runif(n),q3.1)
```

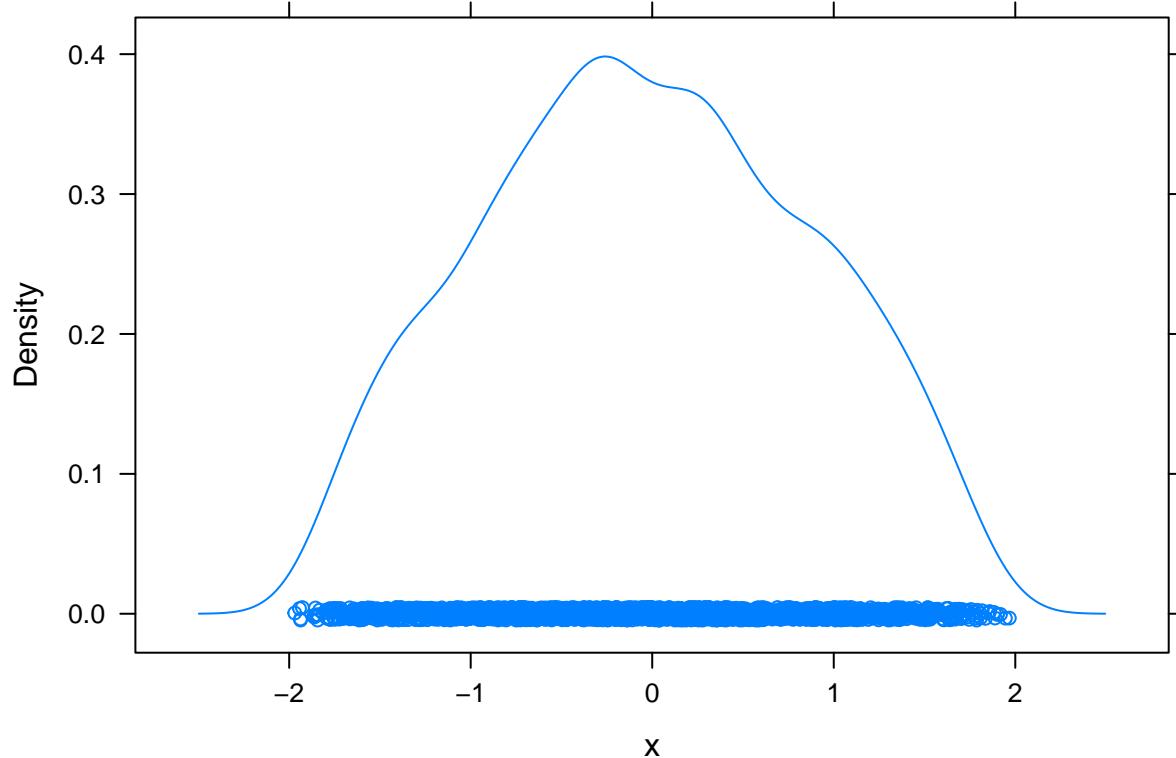
This is generating random samples from the distribution.

```
set.seed(2018)
r3.1(40)
```

```
## [1] -0.44421232 -0.09678344 -1.40086226 -0.85981410 -0.06853322
## [6] -0.54394904  0.28665737 -1.09649783  1.50998881  0.12509517
## [11] -0.28019423  0.44615514  1.68262229  0.48473231  0.87117150
## [16]  0.36177270 -0.63245071  0.14131294  0.65832434  0.94636589
## [21] -0.66414309  0.18280379 -1.01699362 -1.23849172  0.73101697
## [26]  0.09591294 -0.46749589  1.32583168  0.26369534 -1.37995268
## [31] -1.05390319  1.06862839 -1.55871257 -0.02612256  0.01648085
## [36]  0.73137964 -1.48148037 -1.44633673  0.21686676 -0.93427163
```

A plot of the sample is

```
library(lattice)
set.seed(2019)
densityplot(r3.1(2000),xlab="x")
```



This looks like our pdf.

3.1.4 Transformation Problem

For problem 3.1a, find the pdf of Y where $Y=X+2$.

Unlike the discrete case, we cannot simply substitute the transformation relationship into the pdf. However, since equality of distributions relies on the cdf we will use it.

We want to find the cdf of Y

$$F_Y(y) = P(Y \leq y) =$$

$$P(X + 2 \leq y) =$$

$$P(X \leq y - 2) =$$

$$F_X(y - 2)$$

This is the cdf of X which we know.

Thus the cdf of Y is

$$0 \text{ for } y \leq 0$$

$$-\frac{((y - 2)^3 - 12(y - 2) - 16)}{32} \text{ for } 0 \leq y \leq 4$$

$$1 \text{ for } y > 4$$

We find the domain of the cdf for Y by substituting in the domain values of X into the transformation relationship.

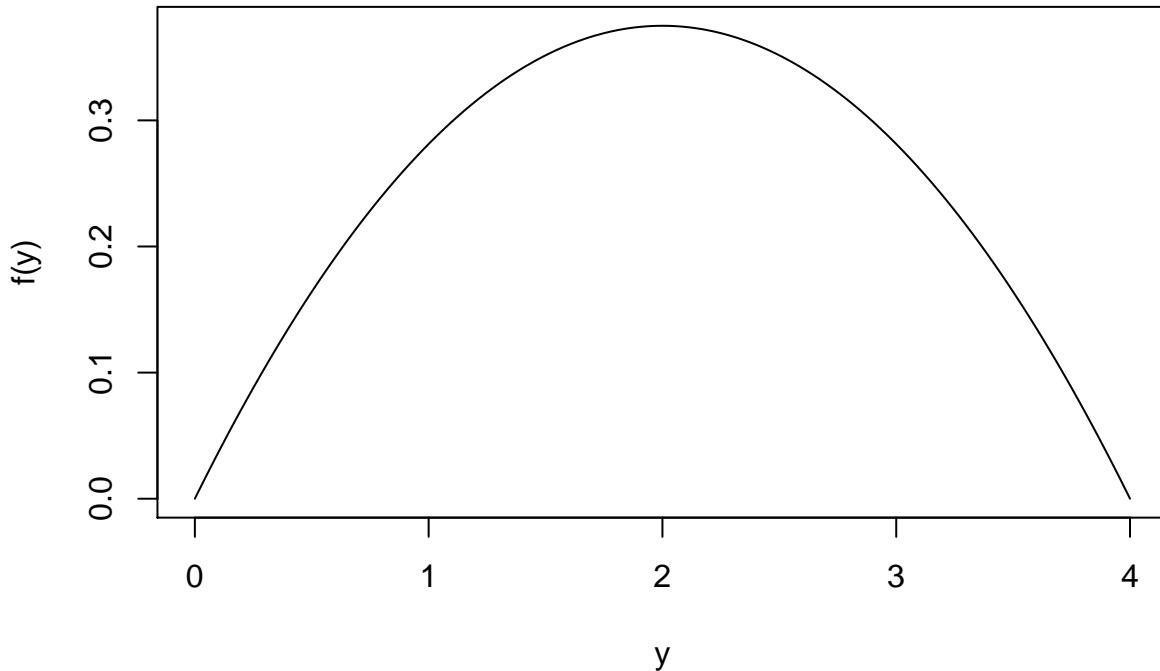
We have to be careful in this approach that the transformation is one-to-one and onto. If not, we have to divide the problem into regions where it is.

The pdf of Y is found by taking the derivative of the cdf.

$$f_Y(y) = -\frac{(3(y - 2)^2 - 12)}{32} \text{ for } 0 \leq y \leq 4$$

We should check that this is a pdf. I will use R to do the work for me.

```
f3.1a<-function(y)(-3/32*((y-2)^2-4)*{y>=0&y<=4})  
plot(seq(0,4,.01),f3.1a(seq(0,4,.01)),type="l",ylab="f(y)",xlab="y")
```



```
integrate(f3.1a,0,4)$value
## [1] 1
```

3.1.5 Named Continuous Random Variables: Uniform and Exponential

We introduce two named distributions, the uniform and exponential.

3.1.5.1 Uniform

Just as the name implies, for the uniform, the pdf is constant. It is typically written as $U(a, b)$. Using the properties of a pdf and the fact that it must be a constant, the pdf is

$$f(x) = \frac{1}{(b-a)} \text{ for } a \leq x \leq b$$

For a $U(1, 1.5)$ what is the pdf? Note that a pdf can be greater than one.

The pdf is $f(x) = 2$ for $1 \leq x \leq 1.5$.

Notice that you can use geometry to verify this is a proper pdf. Likewise, to find the cdf, you can use geometry.

3.1.5.2 Exponential

Exponential is the interval (time or distance) until next occurrence. Here the interval is random and the occurrences are fixed, as one. In the Poisson the occurrences are random and the interval is fixed. The exponential also uses λ for the parameter but now it has to be the average number of occurrences per unit time.

Let's work Prob 2.80a again using exponential.

$Y = \text{Time in minutes until the next customer arrives}$. We want $P(Y > 20)$ $\lambda = 6/60$ which is the average number of customer per minute.

```
1-pexp(20,1/10)
```

```
## [1] 0.1353353
```

or using Poisson to check

```
dpois(0,2)
```

```
## [1] 0.1353353
```

The distribution is called exponential because the pdf is an exponential function, $f(y) = \lambda e^{-\lambda y}$ for $y \geq 0$.

The exponential is often used for queuing models. It is also used in reliability models where we are looking for time to failure. It makes a strong assumption called the memory-less property. The probability of failure being greater than time $t_1 + t_2$ given the item has already lasted time t_1 is simply the probability an item last more than time t_2 . This is a strong assumption and often not realistic.

3.1.6 Additional Homework Problems

1. Let the probability density function of X be exponential with $\lambda = 1$. Find the probability density function of Y where $y = \sqrt{X}$.
2. The average number of cars that enter the North Gate is 48 per hour. What is the probability that no cars enter the gate in the next 5 minutes?

3.2 Moments

3.2.1 Objectives

1. Use Lemma 3.2.2 to find any k th moment about the mean or origin.
2. Interpret coefficient of skewness and coefficient of kurtosis.

3.2.2 Review

Solve problem 2.80a both as a Poisson and an Exponential. Write the random variable in each case.

3.2.2.1 Solution Poisson:

$X = \text{The number of customers in 20 minutes}$. We get an average of 6 customers per hour so λ is 2. We want $P(X = 0)$. Using R

```
dpois(0,2)
```

```
## [1] 0.1353353
```

3.2.2.2 Solution Exponential:

As an exponential, the random variable is $Y = \text{the time in minutes until the next customer arrives}$. Here the parameter is the average number of customer per minute, $\lambda = \frac{1}{10}$. The probability statement is $P(Y > 20)$. using R

```
1-pexp(20, 1/10)
```

```
## [1] 0.1353353
```

Or if you wanted to use $W = \text{the time in hours until the next customer arrives}$, $P(W > \frac{1}{3})$

```
1-pexp(1/3, 6)
```

```
## [1] 0.1353353
```

3.2.3 Definitions

1. The notation can be difficult as we now use μ to represent expected values, which are also called moments. In addition, the prime indicates a moment about the mean and the absence of a prime indicates a moment about the origin. Note that μ_1 is sometimes just called μ and μ'_2 is variance σ^2 .
2. Lemma 3.2.2 is the key basic idea.

$$E[t(X)] = \int_{-\infty}^{\infty} t(x)f(x)dx$$

3. Moments about the origin:

$$\mu_k = E(X^k) = \int_{-\infty}^{\infty} x^k f(x)dx$$

4. Moments about the mean:

$$\mu'_k = E[(X - E(X))^k] = \int_{-\infty}^{\infty} (x - \mu)^k f(x)dx$$

5. Practical: Moments are used to summarize/describe the data. The first moment about the origin is the mean and describes location. The second moment about the mean is variance and describes spread of the distribution. The third moment about the mean is used to calculate the coefficient of skewness which describes symmetry of the distribution. Finally, the fourth moment about the mean can be used to calculate the coefficient of kurtosis which describes if the data has a peak.

3.2.4 Practice

For $X \sim U(0,2)$, find $E(X), E(X^2), V(X), E(X^3), \mu'_3$, and γ_1 .

The pdf is $f(x) = \frac{1}{2}$ for $0 \leq x \leq 2$.

$$E(X) = \int_{-\infty}^{\infty} xf(x)dx = \int_0^2 \frac{1}{2} x dx = \frac{x^2}{4} \Big|_0^2 = 1$$

$$E(X^2) = \int_{-\infty}^{\infty} x^2 f(x)dx = \int_0^2 \frac{1}{2} x^2 dx = \frac{x^3}{6} \Big|_0^2 = \frac{4}{3}$$

Check using R

```
library(MASS)

fractions(integrate(function(x) 1/2*x*(x>=0 & x<=2), 0, 2)$value)

## [1] 1

fractions(integrate(function(x) 1/2*x^2*(x>=0 & x<=2), 0, 2)$value)

## [1] 4/3


$$V(X) = E[(X - \mu)^2] = E(X^2) - E(X)^2 = \frac{4}{3} - 1^2 = \frac{1}{3}$$


fractions(integrate(function(x) 1/2*(x-1)^2*(x>=0 & x<=2), 0, 2)$value)

## [1] 1/3


$$E(X^3) = \int_{-\infty}^{\infty} x^3 f(x) dx = \int_0^2 \frac{1}{2} x^3 dx = \frac{x^4}{8} \Big|_0^2 = 2$$


fractions(integrate(function(x) 1/2*x^3*(x>=0 & x<=2), 0, 2)$value)

## [1] 2
```

$$\mu'_3 = E[(X - \mu)^3] = \int_{-\infty}^{\infty} (x - 1)^3 f(x) dx = \int_0^2 \frac{1}{2} (x - 1)^3 dx$$

This is going to be difficult but can be done if we expand the polynomial. We could use R.

```
fractions(integrate(function(x) 1/2*(x-1)^3*(x>=0 & x<=2), 0, 2)$value)

## [1] 0
```

We could also use Lemma 3.3.2.

$$\mu'_3 = \mu_3 - 3\mu_2\mu + 2\mu^3 = 2 - 3 * \frac{4}{3} * 1 + 2 * 1^3 = 2 - 4 + 2 = 0$$

$$\gamma_1 = \frac{\mu'_3}{\sigma^3} = \frac{0}{\sigma^3} = 0$$

It is a symmetric distribution.

Do Homework 3.12

3.3 Generating Functions

3.3.1 Objectives

1. Given a pdf/pmf find the mgf, $M_X(t)$.
2. Find moments from a moment generating function.
3. Use moment generating function to find distributions of a transformation of a random variable, Thm 3.3.6.

3.3.2 Review

The Maclaurin series is a special case of the Taylor series. This is a power series representation of a function. We now have a fourth way to represent a function. One is a table, another is a formula, another is a graph, and now we can use an infinite sum. In general the Maclaurin series is

$$f(x) = f(0) + \frac{f'(0)x}{1!} + \frac{f''(0)x^2}{2!} + \frac{f^{(3)}(0)x^3}{3!} + \cdots + \frac{f^{(k)}(0)x^k}{k!} + \cdots$$

In Calculus we were interested in using the power series to represent function and one of the most common was

$$e^x = 1 + x + \frac{x^2}{2!} + \frac{x^3}{3!} + \cdots$$

We will use this expression.

Also remember that moments characterize a distribution. However, to find them we need to integrate. From last lesson we have

$$\mu_k = E(X^k) = \int_{-\infty}^{\infty} x^k f(x) dx$$

The key idea in this lesson is that we want to find a single function that summarizes, generates, all the moments of a distribution. Sounds like a crazy idea, but in fact it can be done. It is called the moment generating function. There are two advantages of the moment generating functions

- i) You use derivatives instead of integration to find moments, differentiation is often much easier than integration.
- ii) If you can recognize a moment generating function, a big if, then you can find the distribution of a linear transformation of a random variable or the linear combination of random variables. This is often easier than using the cdf method we learned earlier.

3.3.3 Moment Generating Functions

By definition the moment generating function is:

$$M_X(t) = E[e^{tX}] = \int_{-\infty}^{\infty} e^{tx} f(x) dx$$

for continuous random variables; for discrete random variables, replace the integration with a summation.

To find a the kth moment about the origin take the kth derivative of the moment generating function and evaluate at t = 0. That is

$$\mu_k = \left(\frac{d^k M_X(t)}{dt^k} \right)_{t=0}$$

Why would this work? The book gives a nice summary of the ideas. Along a similar thread, let's use the Maclaurin power series of $e^t x$:

$$e^{tx} = 1 + tx + t^2 x^2 / 2! + \cdots$$

Thus

$$M_X(t) = E[e^{tX}] = E[1 + tx + t^2x^2/2! + \dots] = 1 + tE[X] + t^2E[X^2] + \dots$$

Now taking the derivative with respect to t and then evaluating at $t = 0$ leads to the k th moment about the origin.

3.3.4 Practice

- Find the moment generating function for $U(0, 1)$.

$$E(e^{tX}) = \int_{-\infty}^{\infty} e^{tx} f(x) dx = \int_0^1 e^{tx} dx = \frac{1}{t} e^{tx} \Big|_0^1 = \frac{1}{t} [e^t - 1]$$

Note that this function is not defined at $t = 0$ but we can use our Macluarin again to help us.

$$M_X(t) = \frac{1}{t} [e^t - 1] = \frac{1}{t} \left[t + \frac{t^2}{2!} + \dots \right] = \left[1 + \frac{t}{2!} + \frac{t^2}{3!} + \dots \right]$$

Now you can take the derivative and evaluate at $t = 0$.

$$\frac{dM_X(t)}{dt} \Big|_{t=0} = \frac{1}{2}$$

- The moment generating function for the Poisson is $e^{-\lambda+\lambda e^t}$, find the mean and variance.

$$\frac{dM_X(t)}{dt} = (e^{-\lambda+\lambda e^t}) \lambda e^t$$

Evaluating at $t = 0$ yields

$$E(X) = (e^{-\lambda+\lambda e^0}) \lambda e^0 = (e^{-\lambda+\lambda}) \lambda = \lambda$$

$$E(X^2) = \mu_2 = \left(\frac{d^2 M_X(t)}{dt^2} \right)_{t=0}$$

$$\frac{d^2 M_X(t)}{dt^2} = (e^{-\lambda+\lambda e^t}) \lambda + (e^{-\lambda+\lambda e^t}) \lambda^2 e^{2t}$$

$$\left(\frac{d^2 M_X(t)}{dt^2} \right)_{t=0} = (e^{-\lambda+\lambda e^0}) \lambda + (e^{-\lambda+\lambda e^0}) \lambda^2 e^0 = \lambda + \lambda^2$$

Finally,

$$V(X) = E(X^2) - E(X)^2 = \lambda + \lambda^2 - (\lambda)^2 = \lambda$$

3.3.5 Transformations

There is no need to memorize the formulas in Theorem 3.3.6, you can derive them. For example, let $Y = aX$

$$M_Y(t) = E(e^{tY}) = E(e^{(ta)X}) = M_X(at)$$

The problem with this method is that we have to recognize the moment generating function. This is not necessarily easy.

3.3.6 Practice

Given $X \sim U(0, 1)$ find $Y = 2X + 3$ using Thm 3.3.6 and then the cdf method.

$$M_X(t) = \frac{1}{t} [e^t - 1]$$

$$M_Y(t) = E(e^{tY}) = E(e^{t(2X+3)}) = E(e^{2tx}e^{3t}) = e^{3t}E(e^{2tX}) = e^{3t}M_X(2t) =$$

$$e^{3t} \frac{1}{2t} [e^{2t} - 1] = \frac{1}{2t} [e^{5t} - e^{3t}]$$

Now we know

$$M_Y(t) = \frac{1}{2t} [e^{5t} - e^{3t}]$$

but the difficult part is that we have to recognize this. It turns out, if you look at the table in the back of the book, this is a uniform. Thus

$$Y \sim U(3, 5)$$

Using the cdf method

$$X \sim U(0, 1)$$

$$f(x) = 1$$

$$Y = 2X + 3$$

$$F_Y(y) = P(Y \leq y) = P(2X + 3 \leq y) = P\left(X \leq \frac{y-3}{2}\right) =$$

$$\int_0^{\frac{y-3}{2}} 1dx = \frac{y-3}{2}$$

$$f_Y(y) = \frac{dF_Y(y)}{dy} = \frac{1}{2} \text{ for } 0 \leq \frac{y-3}{2} \leq 1$$

Cleaning this up

$$f_Y(y) = \frac{1}{2} \text{ for } 3 \leq y \leq 5$$

This is a uniform.

3.4 Important Continuous Distributions

3.4.1 Objectives

1. Solve probability problems involving the normal, gamma, Weibull, and beta distributions.
2. Find distribution or mgf for transformations of known distributions.
3. Find quantiles of distributions.

3.4.2 Normal

Normal arises from the sum of random variables, common when errors are additive. The reading on this section is good, it brings in many ideas from previous sections and motivates why the standard normal is important.

The empirical rule is used for the normal. 68% of population within one standard deviation of the mean, 95% within 2, and 99.7 within 3. This is the idea behind the six sigma movement.

The normal has two parameters, the mean and the standard deviation. They completely specify the distribution. The notation is

$$X \sim N(\mu, \sigma)$$

The pdf for a normal is difficult to integrate and there is no closed form solution for the cdf. Software packages use a numerical method to find the cdf.

A common distribution is the standard normal $Z = \frac{x-\mu}{\sigma}$ where $X \sim N(\mu, \sigma)$

We can check these in R. Using a standard normal, the default in R

```
qnorm(.68+.16)
```

```
## [1] 0.9944579
```

```
qnorm(.16)
```

```
## [1] -0.9944579
```

So 68% is between -1 and 1, which is within one standard deviation of the mean. Or using pnorm

```
pnorm(1)-pnorm(-1)
```

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

Just to check, let's use a different Normal with μ 4 and σ of 3.

```
pnorm(7,4,3)-pnorm(1,4,3)
```

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

Likewise for two and three standard deviations

```
pnorm(2)-pnorm(-2)
```

```
## [1] 0.9544997
```

```
pnorm(3)-pnorm(-3)
```

```
## [1] 0.9973002
```

The normal will play an important role in hypothesis testing because of the Central Limit Theorem.

To bring some other ideas back in. The book claims that the moment generating function for $N(\mu, \sigma)$ is

$$M_X(t) = e^{\mu t + \frac{\sigma^2 t^2}{2}}$$

We can go from any Normal to the standard Normal using the following transformation, Z is used for the standard normal:

$$Z = \frac{X - \mu}{\sigma}$$

We know $E(X) = \mu$ so $E(Z) = E\left(\frac{X-\mu}{\sigma}\right) = \frac{1}{\sigma}E(x-\mu) = \frac{1}{\sigma}(E(x)-\mu) = 0$

To find the distribution of Z use the cdf method or the mgf method. We will use that later.

$$\begin{aligned} M_Z(t) &= E(e^{Zt}) = E \left[e^{\left(\frac{X-\mu}{\sigma} t \right)} \right] = \\ &e^{-\frac{\mu}{\sigma} t} E \left[e^{\left(\frac{X}{\sigma} t \right)} \right] = \\ &e^{-\frac{\mu}{\sigma} t} M_X \left(\frac{t}{\sigma} \right) = \\ &e^{-\frac{\mu}{\sigma} t} \left[e^{\mu \frac{t}{\sigma} + \frac{\sigma^2 t^2}{\sigma^2}} \right] = e^{-\frac{t^2}{2}} \end{aligned}$$

Now we must recognize this moment generating function, which is the Normal with $\mu = 0$ and $\sigma = 1$.

For a standard Normal, find $E(X^2)$.

$$\frac{d^2 M(t)}{dt^2} \Big|_{t=0} = \left(e^{-\frac{t^2}{2}} + \left(e^{-\frac{t^2}{2}} \right) t^2 \right) \Big|_{t=0} = 1$$

3.4.3 Gamma

The gamma distribution is for non-negative random variables. It is an extremely flexible distribution. It has been used in reliability analysis as well as medical fields for survival analysis. The gamma distribution has two parameters α called the shape parameter and λ called the rate. If α is an integer then the gamma is a generalization of the exponential and can represent the time until α occurrences. You can give R rate for the parameter or 1/rate, called scale, be careful. Look at the help menu.

The pdf has a gamma function in for the scaling constant. This function is implemented in R.

```
gamma(4)
```

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

```
gamma(.5)
```

```
## [1] 1.772454
```

3.4.4 Weibull

This distributions is also used to model failures where the entire system fails when the weakest link breaks. The Weibull has two parameters, α the shape parameter, and β the scale parameter.

3.4.5 Beta

The Beta generalizes the uniform and is used to model proportions. The beta distribution also has two parameters α and β . The bottom of page 143 has a nice summary of the impact of α and β on the shape of the distribution.

Note: Read the last three paragraphs on page 144.

3.4.6 Problems

- 1) The scores on an exam can be modeled as a normal with mean 75 and variance 100.
 - a) Find the probability of scoring more than 90.
 - b) Find the .8-quantile
 - c) Given that someone scored more than 50, what is the probability of scoring less than 90?

```
1-pnorm(90,75,10)
```

```
## [1] 0.0668072
```

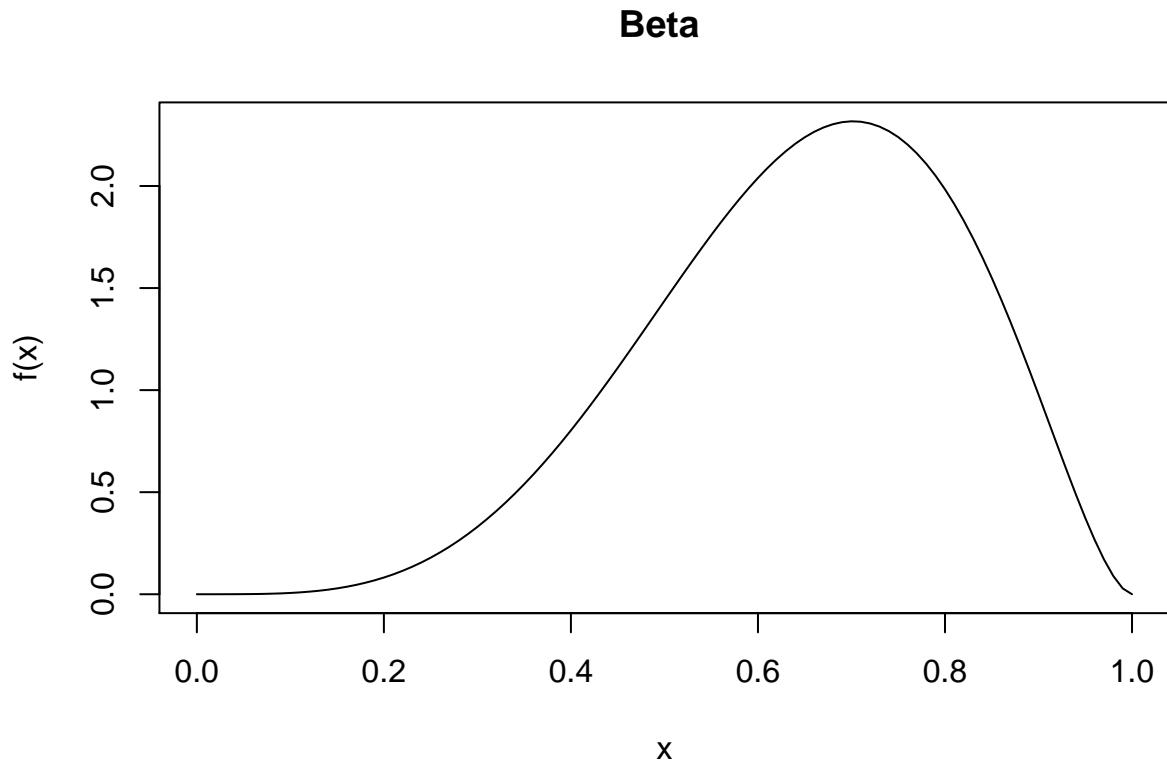
```
qnorm(.8,75,10)
```

```
## [1] 83.41621
```

```
(pnorm(90,75,10)-pnorm(50,75,10))/(1-pnorm(50,75,10))
```

```
## [1] 0.9327754
```

- 2) The percentages on an exam can be modeled with a Beta distribution with $\alpha = 5$ and $\beta = 2.7$. Here is a plot of the pdf.



- a) Find the probability of scoring more than .90.
- b) Find the .8-quantile
- c) Given that someone scored more than .50, what is the probability of scoring less than .90?

```
1-pbeta(0.9,5,2.7)
```

```
## [1] 0.04089716
```

```

qbeta(.8,5,2.7)

## [1] 0.7967842
(pbeta(.9,5,2.7)-pbeta(.5,5,2.7))/(1-pbeta(.5,5,2.7))

## [1] 0.9496102

3) The arrival of customers at a restaurant follows a Poisson process with 15 customers per hour on average.

a) Using a Poisson random variable, find the probability of 2 or less customers in 15 minutes.
b) Same probability question as part a, but using a Gamma with the random variable as time in minutes
until 3 customers arrive.

ppois(2,15/4)

## [1] 0.2770684
1-pgamma(15,3,1/4)

## [1] 0.2770684
1-pgamma(15,3,scale=4)

## [1] 0.2770684

```

3.5 Plots of Distributions

3.5.1 Objectives

1. Interpret normal-quantile plots and explain the types of departures from normality.
2. Generate quantile-quantile plots for any distribution.
3. Given data, generate density plots in R.

3.5.2 Review

The time to failure of an anchor chain in years follows a Weibull distribution with shape parameter 2 and scale parameter 10. What is the third quartile?

```
qweibull(.75,2,10)
```

```
## [1] 11.7741
```

3.5.3 Background

When we have data how do we estimate the pdf and/or determine if one of our known distributions is appropriate to use as a model? This is an empirical study question and can never be answered in certainty. This is the work of analysts and is difficult and a bit of an art.

3.5.4 Density Estimation

First, we will use data to estimate the probability density function. We actually did this before when we used a histogram, it is an estimate of the pdf, but we will look at more up-to-date and state-of-the-art methods. The idea of density estimation presented is similar to convolution and band-pass filters for the engineers. For the math and OR majors, we can think of it a running a window across the data and the shape of the window determines the weighting of the data. We are using data to develop a model of the population. This will be an important idea for the remainder of the semester.

To start, let's use the height data we collected earlier this semester.

```
Lesson2_Height <- read.csv("Lesson2_Height.csv")
```

```
summary(Lesson2_Height)
```

```
##      Gender      Height
##  Female: 8   Min.   :62.50
##  Male   :17   1st Qu.:67.00
##                  Median :70.00
##                  Mean   :70.14
##                  3rd Qu.:73.00
##                  Max.   :78.00
```

Now, let's use the author's code to explore the idea of density estimation.

```
library(fastR)
```

```
K1 <- function(x) { # rectangular
  return( as.numeric( -1 < x & x < 1 ) )
}
K2 <- function(x) { # triangular
  return( (1 - abs(x)) * as.numeric(abs(x) < 1) )
}

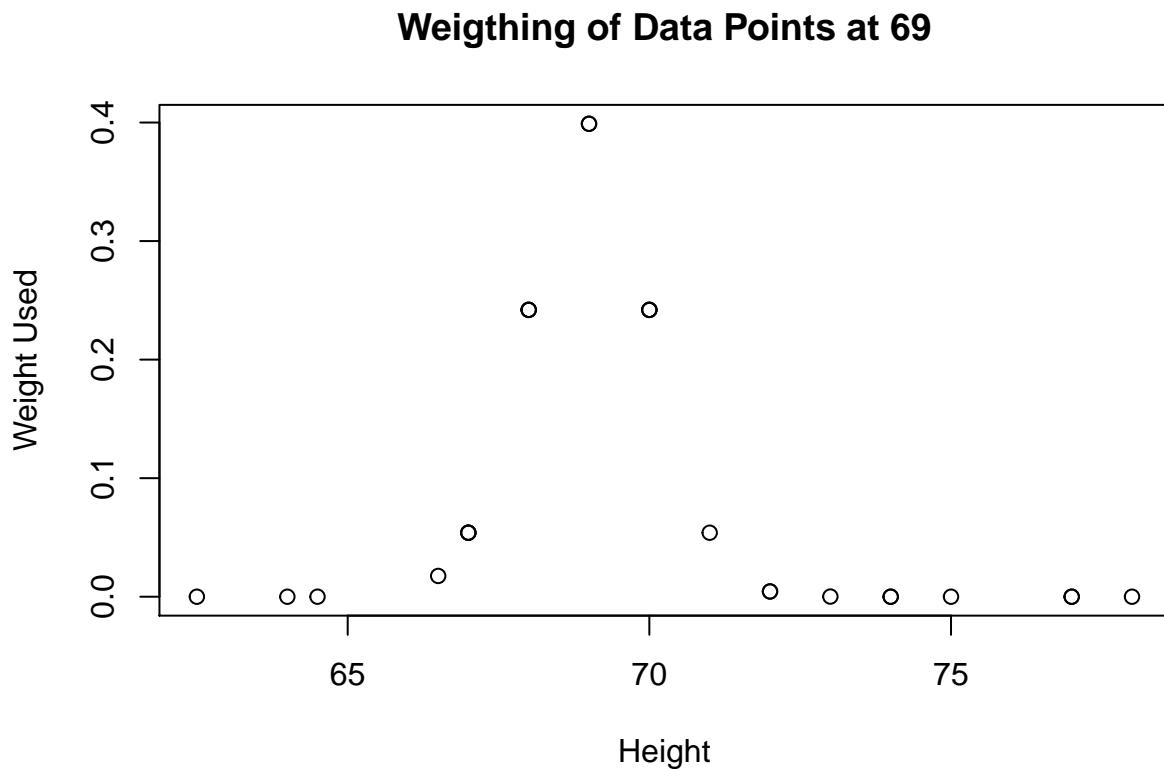
K3 <- function(x) {      # parabola / Epanechnikov
  return( (1 - x^2) * as.numeric(abs(x) < 1) )
}

K4 <- dnorm          # Gaussian

kde <- function(data,kernel=K1,...) {
  n <- length(data)
  scalingConstant=integrate(function(x){kernel(x,...)},-Inf,Inf)$value
  f <- function(x) {
    mat <- outer(x,data, FUN=function(x,data) {kernel(x-data,...)} )
    val <- apply(mat,1,sum)
    val <- val/(n*scalingConstant)
    return(val)
  }
  return(f)
}
```

Let's look at the kernel K4 at the point 69.

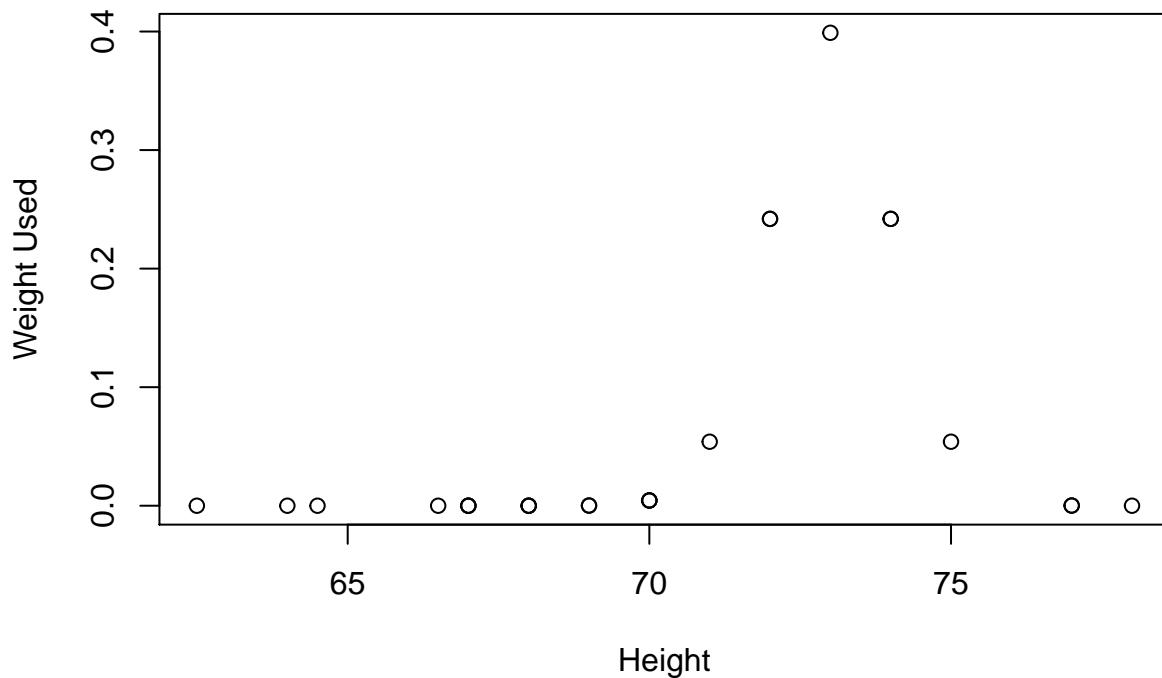
```
plot(Lesson2_Height$Height,K4(Lesson2_Height$Height-69),xlab="Height",ylab="Weight Used",main="Weigthing")
```



Likewise, here it is at the point 73.

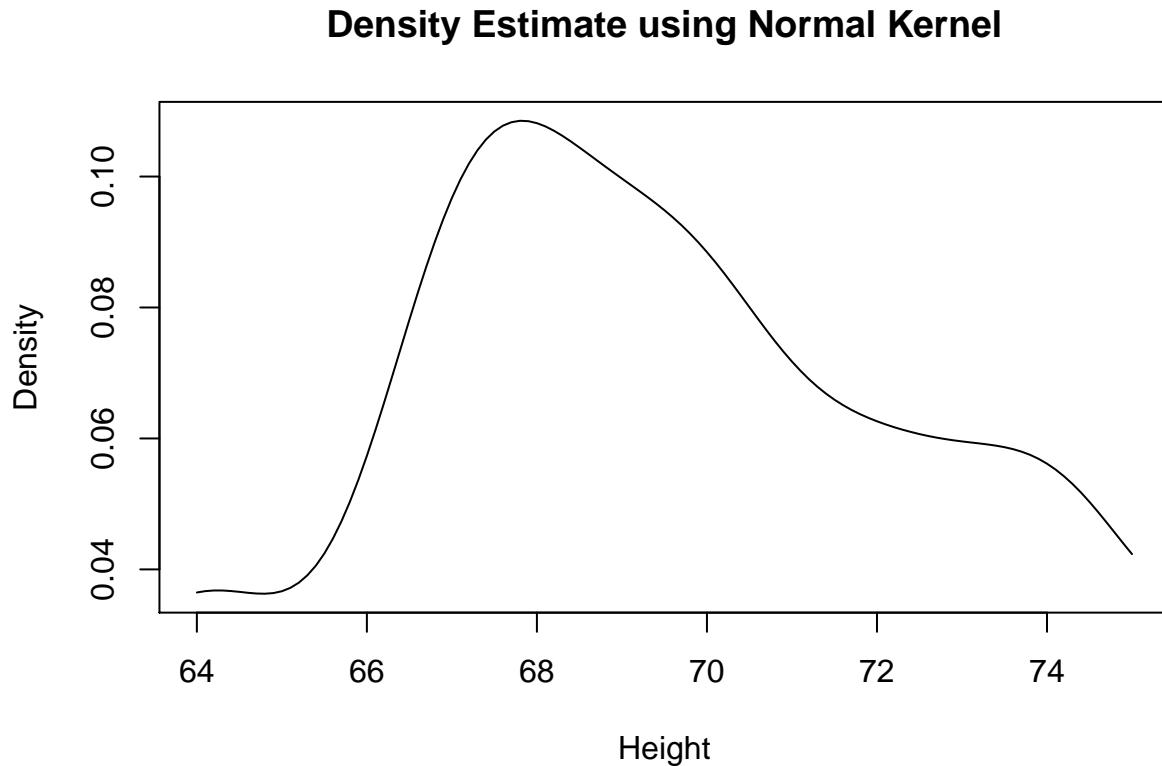
```
plot(Lesson2_Height$Height,K4(Lesson2_Height$Height-73),xlab="Height",ylab="Weight Used",main="Weigthing")
```

Weigthing of Data Points at 73



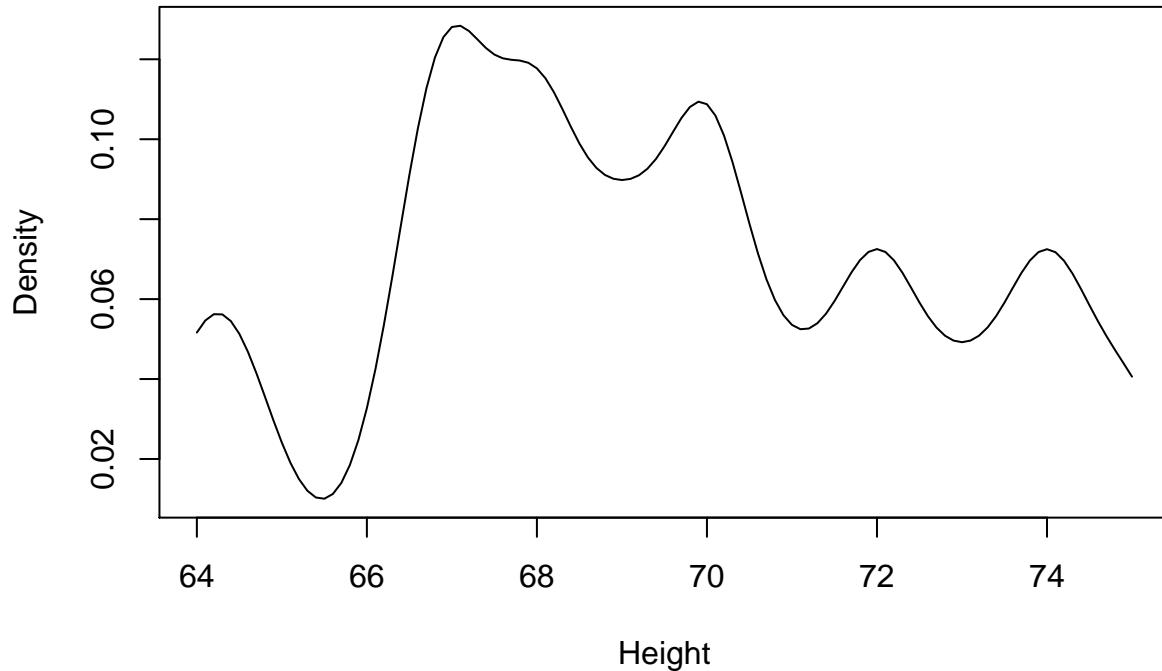
Now the kde function, applies the kernel in a moving window across the data. This gives an estimate of the pdf. For the height data, this is the estimate.

```
plot(seq(64,75,.1),kde(data=Lesson2_Height$Height,kernel = K4)(seq(64,75,.1)),type="l",xlab="Height",ylab="Density")
```



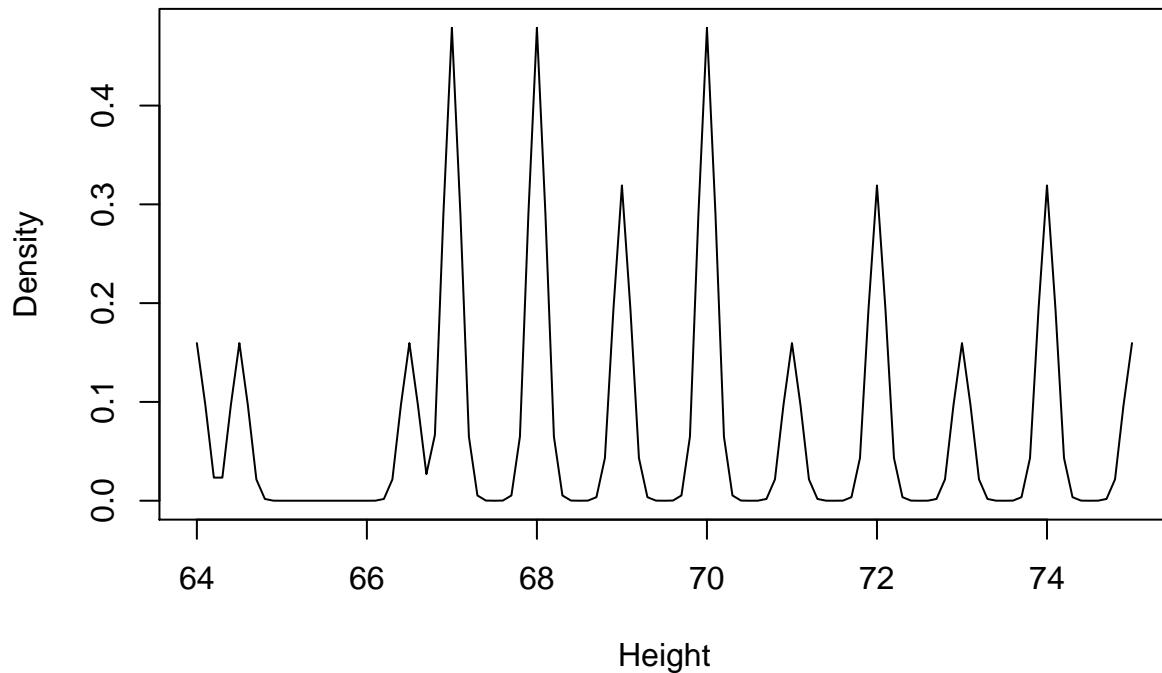
Now the width of the kernel will impact the estimate of the pdf. Let's change K4 to have a different width, standard deviation.

```
plot(seq(64,75,.1),kde(data=Lesson2_Height$Height,kernel = K4, sd=.5)(seq(64,75,.1)),type="l",xlab="Heig
```

Density Estimate using Normal Kernel SD=.5

This estimate is more sensitive to local data points. In the extreme we have

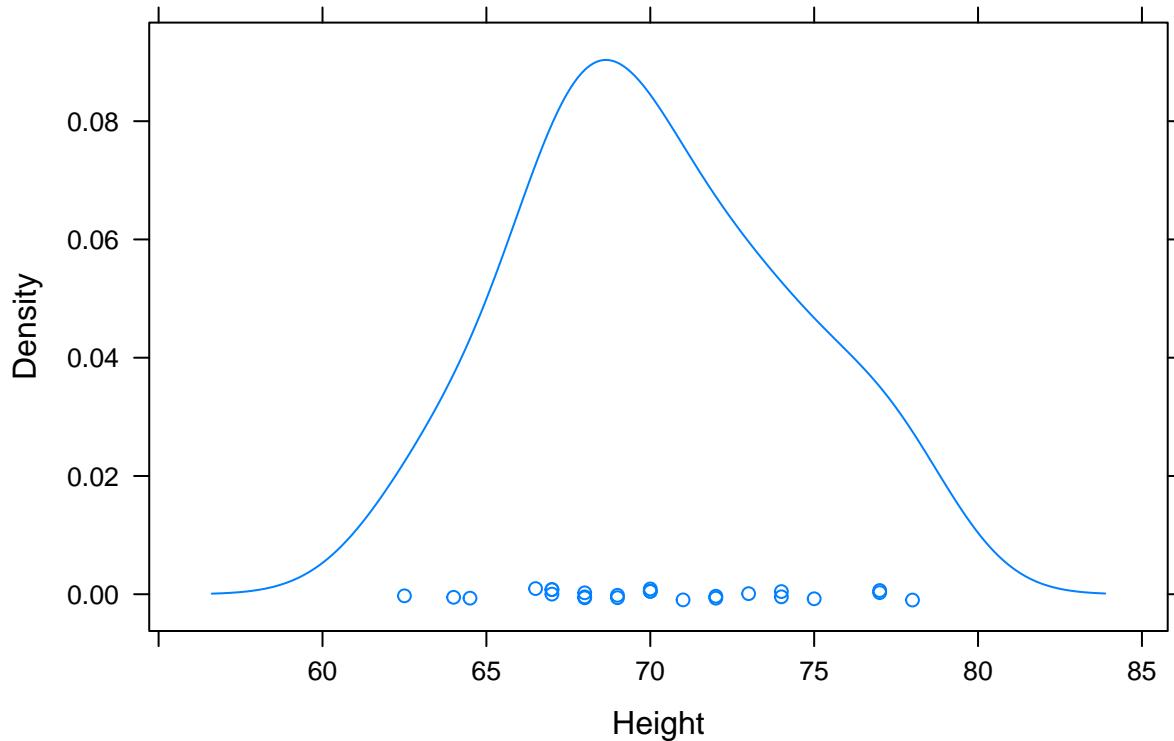
```
plot(seq(64,75,.1),kde(data=Lesson2_Height$Height,kernel = K4, sd=.1)(seq(64,75,.1)),type="l",xlab="Heig
```

Density Estimate using Normal Kernel SD=.1

The width of the kernel is a tuning parameter that we must choose. This requires an objective function. The book talks about using mean integrated square error. Luckily, R has a function that does this for us.

```
densityplot(Lesson2_Height$Height, xlab="Height", ylab="Density", main="Density Estimate using densityplot")
```

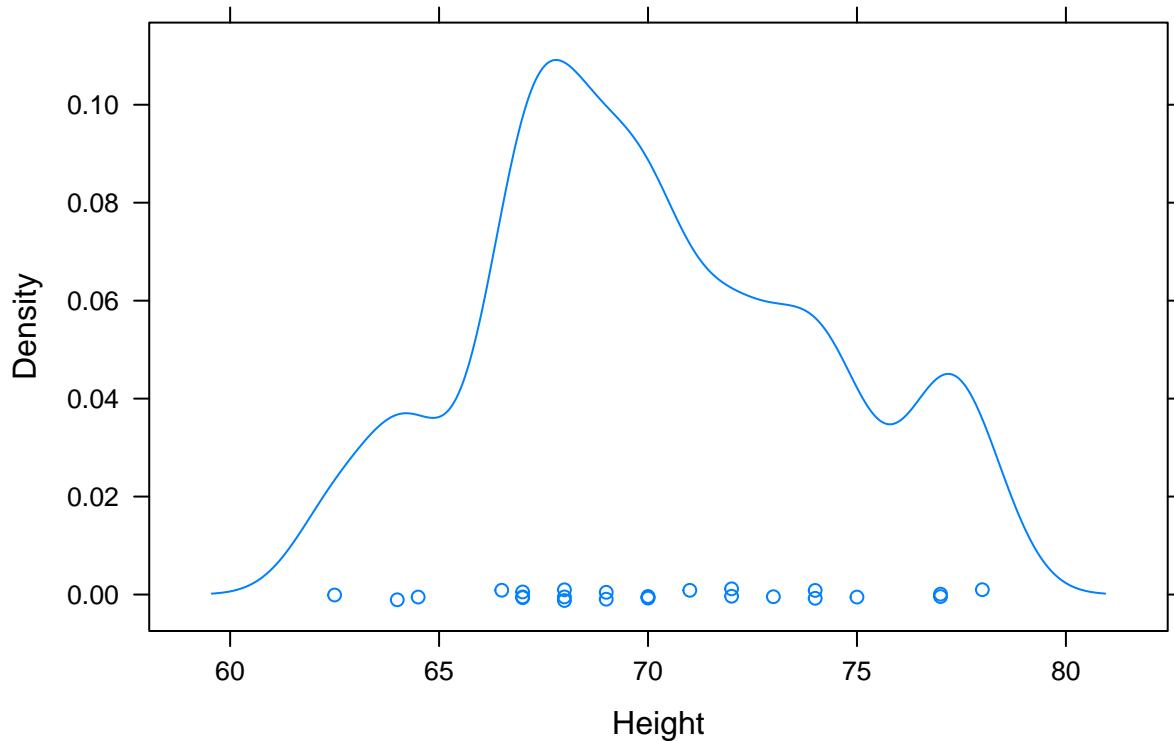
Density Estimate using densityplot



We can change the bandwidth directly or just scale the selected bandwidth using the `adjust` option.

```
densityplot(Lesson2_Height$Height, adjust=.5, xlab="Height", ylab="Density", main="Density Estimate using d")
```

Density Estimate using densityplot



3.5.5 Practice

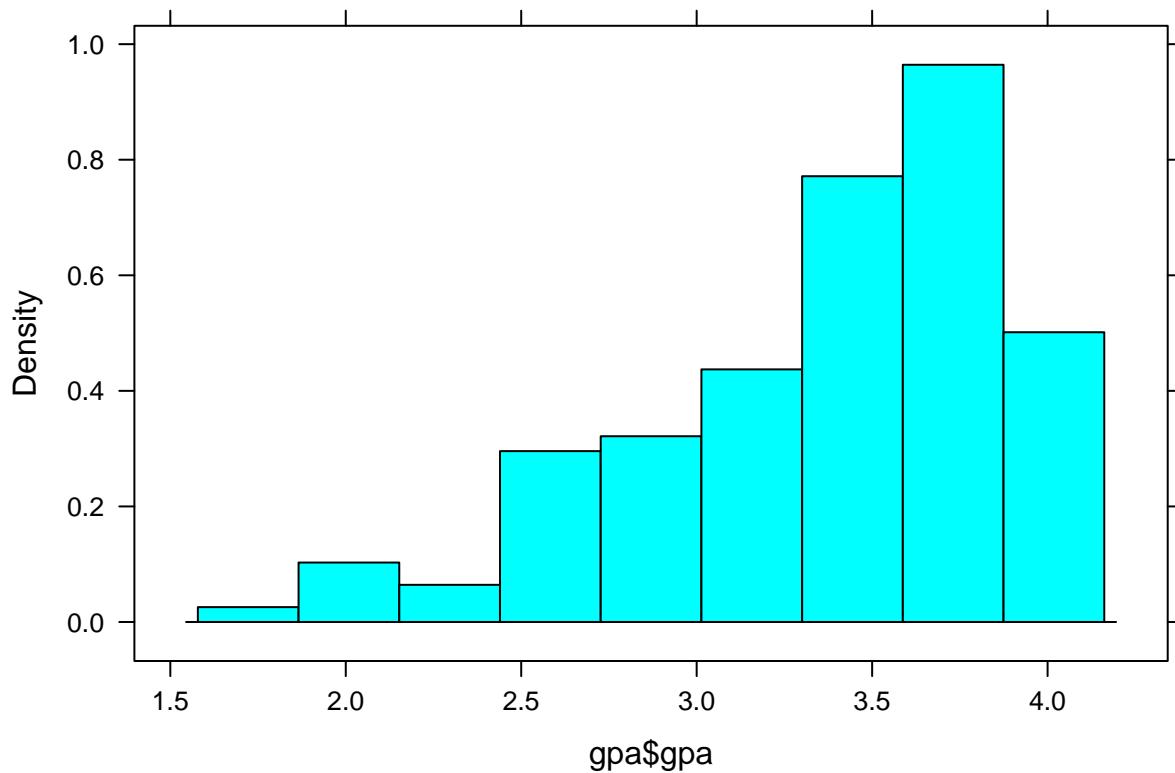
Let's work an example using the `gpa` data in `fastR`.

```
summary(gpa)
```

```
##      satm          satv          act          gpa
##  Min.   :370   Min.   :280.0   Min.   :15.0   Min.   :1.704
##  1st Qu.:560   1st Qu.:560.0   1st Qu.:25.0   1st Qu.:3.034
##  Median :630   Median :630.0   Median :28.0   Median :3.475
##  Mean    :623   Mean    :614.6   Mean    :27.7   Mean    :3.352
##  3rd Qu.:690   3rd Qu.:680.0   3rd Qu.:31.0   3rd Qu.:3.764
##  Max.    :800   Max.    :800.0   Max.    :35.0   Max.    :4.000
```

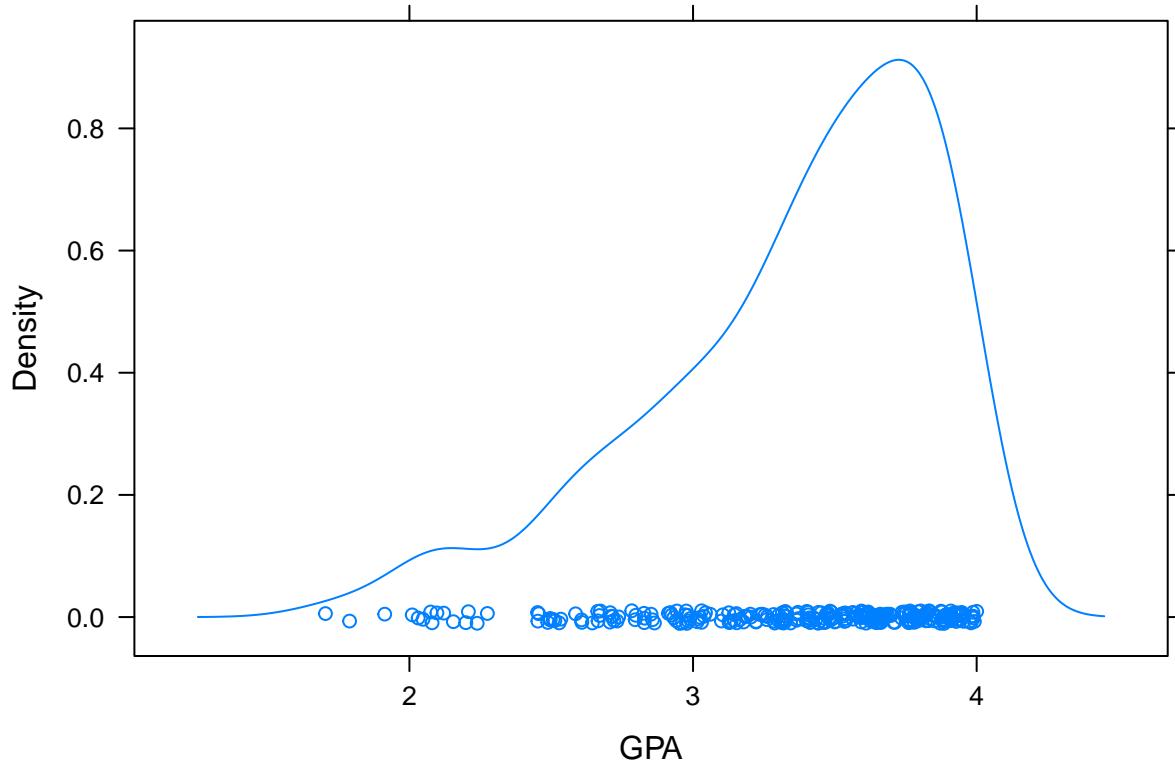
In Chapter 1 we made a histogram to summarize the data. For examples to summarize the `gpa`

```
histogram(gpa$gpa)
```



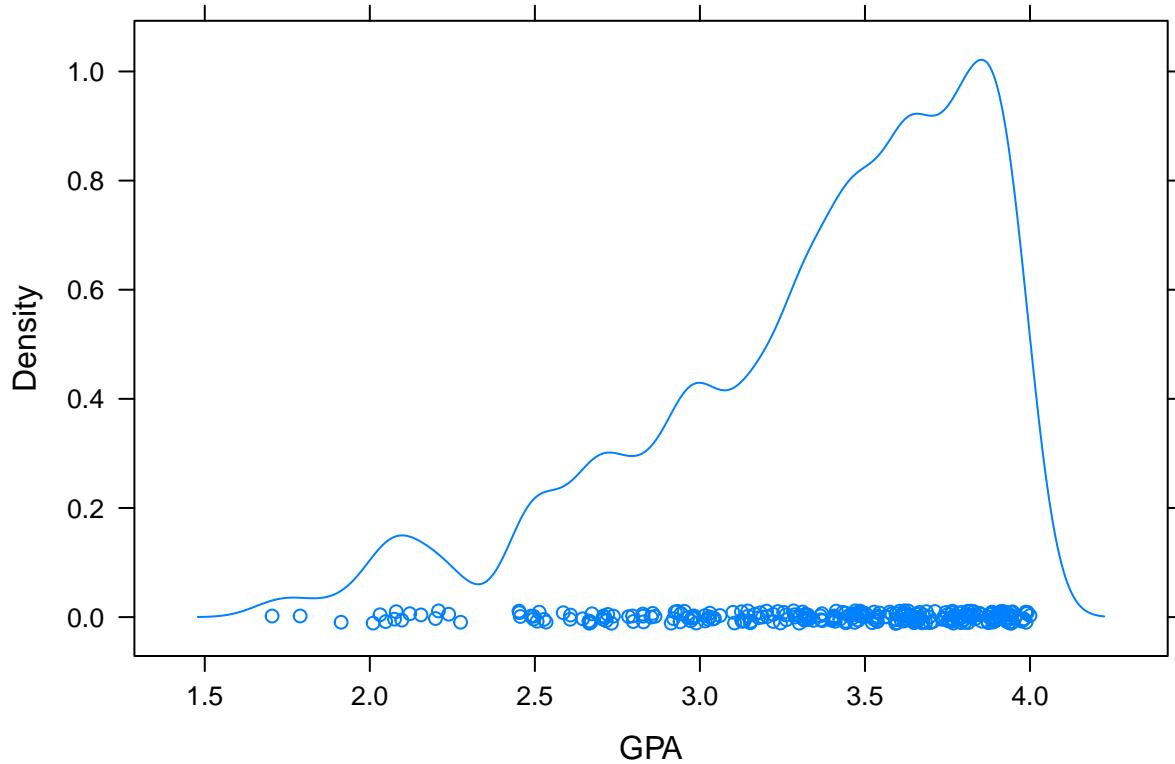
Now let's use a density plot:

```
densityplot(gpa$gpa,xlab="GPA")
```



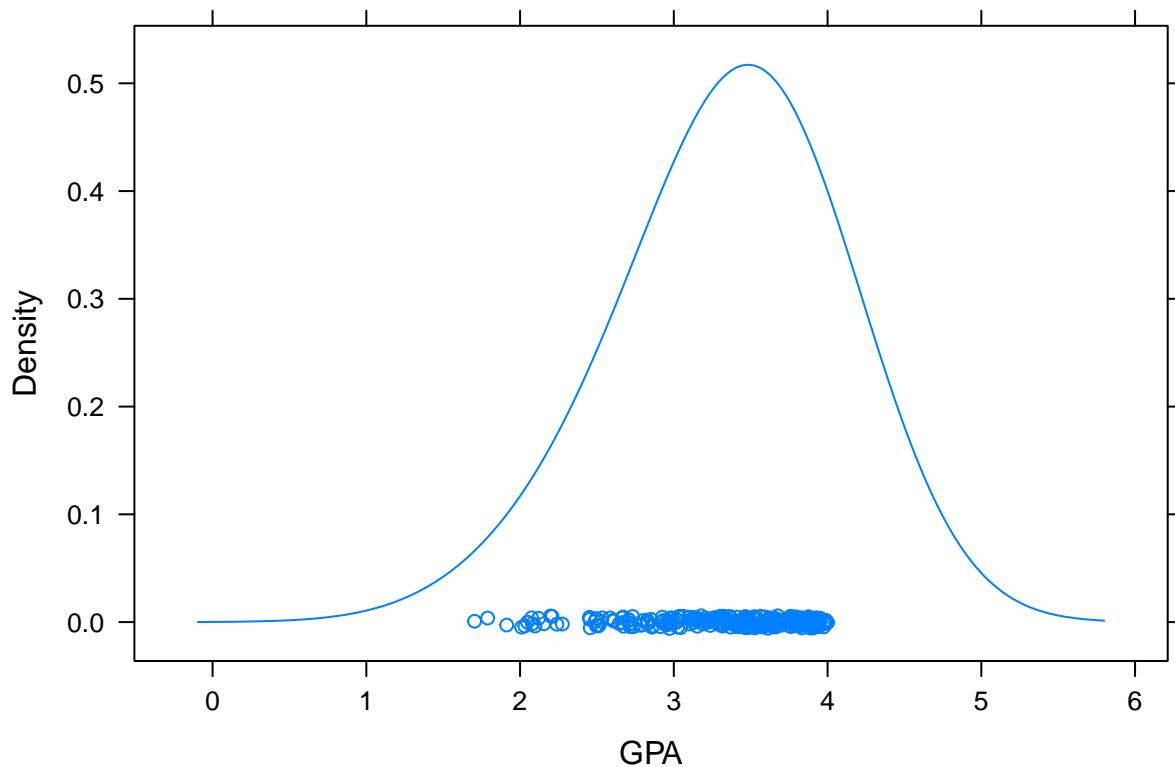
I think this gives a better representation of the data. Let's make the bandwidth 1/2 of the default.

```
densityplot(gpa$gpa,xlab="GPA",adjust=.5)
```



This is picking up more of the noise. Let's make the bandwidth larger which may cause too much smoothing.

```
densityplot(gpa$gpa,xlab="GPA",adjust=4)
```

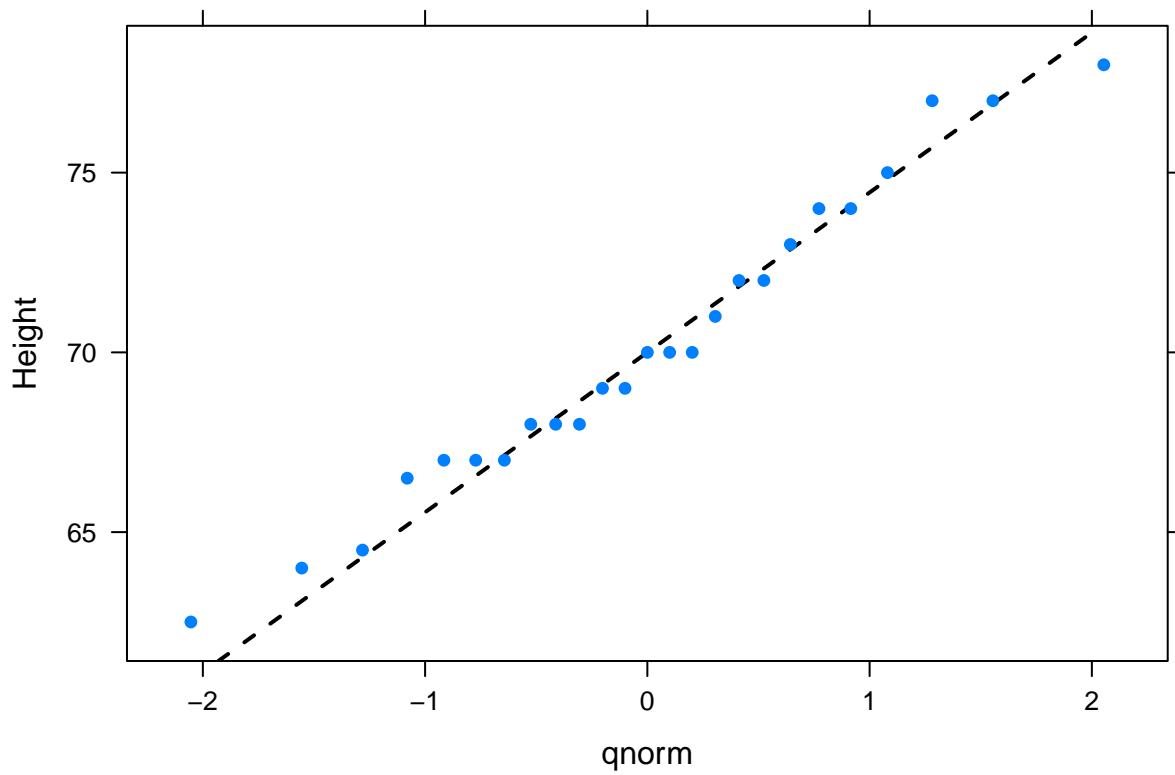


3.5.6 Q-Q Plots

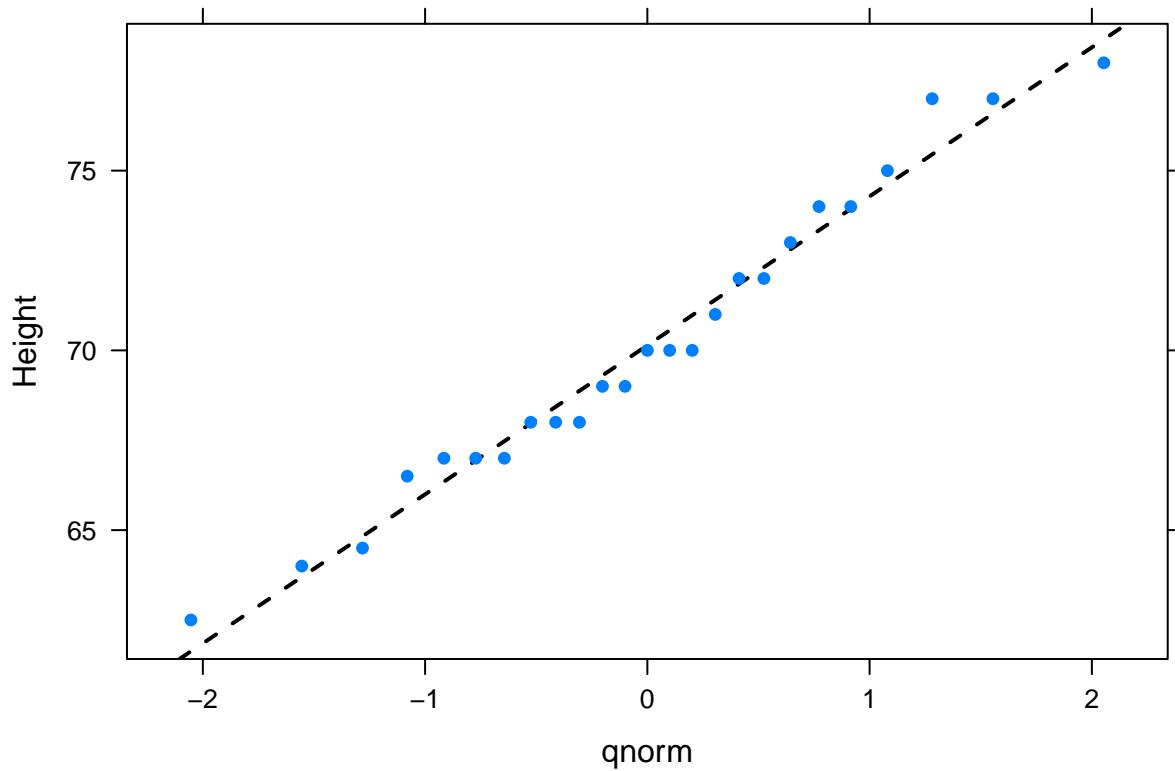
Next, we would like to be able to justify a certain distribution as a reasonable model for our data. For example, with the gpa data, you may be asked if it is valid to assume that the data is normally distributed. One way to answer this is by comparing the empirical quantiles from the data with the quantiles from the reference distribution. If it is a good match, the scatterplot will have the data points lying on a straight line. The function `xqqmath` in the `fastR` package makes this easy for us.

Let's start with the height data

```
xqqmath(~Height, data=Lesson2_Height)
```



```
xqqmath(~Height, data=Lesson2_Height, fitline=TRUE)
```



This plot is subjective. It is finding the empirical quantiles and then plotting these against the same quantiles from selected distribution, the normal by default. If the data comes from the selected distribution, the quantiles lie along a straight line. The data points will not be perfectly along the line, but as long as they are close, we feel comfortable with our assumption. As a follow-up, we can also check how sensitive our analysis is to the distributional assumption.

We can build our own q-q plot just to understand the process.

We have 25 data points that we will sort. The empirical quantiles are found by noticing that each data point is 1/25 or .04 of the data. We don't want to start or stop at 0 or 1, so let's split the .04 and start at .02 and end at .98. Thus the quantiles are

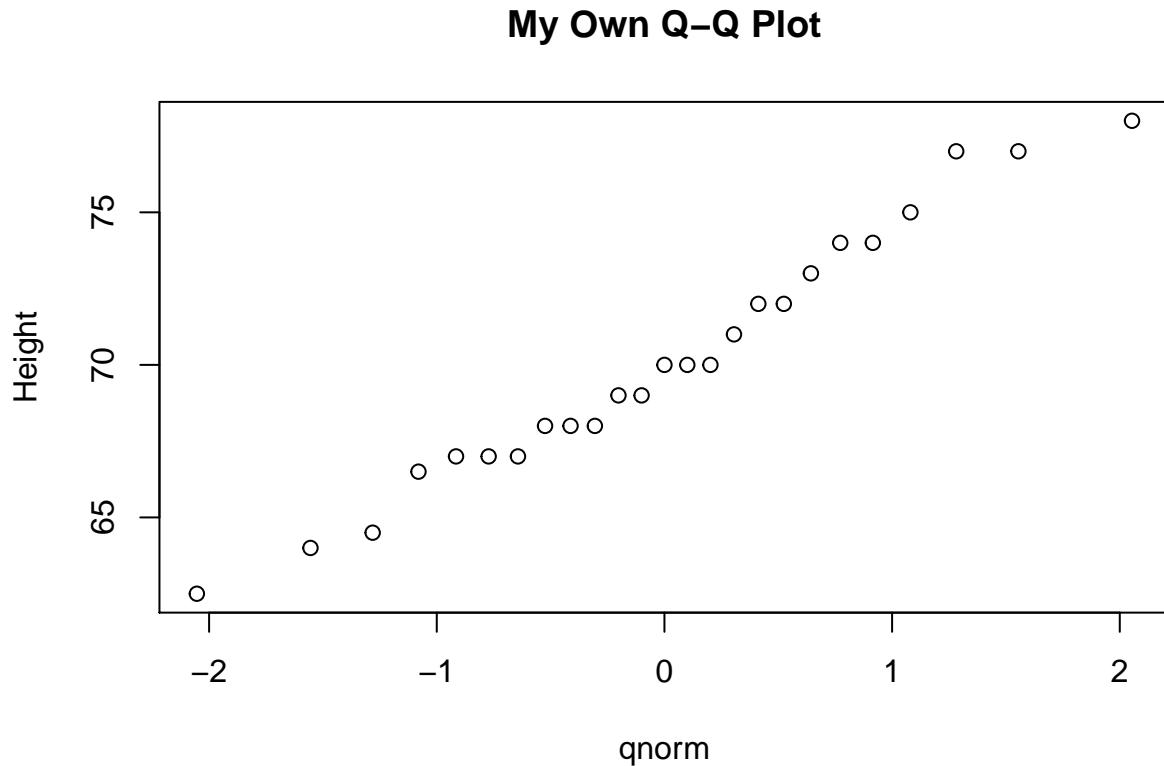
```
seq(.02, .98, .04)
```

```
## [1] 0.02 0.06 0.10 0.14 0.18 0.22 0.26 0.30 0.34 0.38 0.42 0.46 0.50 0.54
## [15] 0.58 0.62 0.66 0.70 0.74 0.78 0.82 0.86 0.90 0.94 0.98
```

Now, we must decide what to do with ties. We could just treat them as separate data points or we can accumulate all the probability at each point.

Here is the first method

```
plot(qnorm(seq(.02, .98, .04)), sort(Lesson2_Height$Height), xlab="qnorm", ylab="Height", main="My Own Q-Q Plot")
```



The second method is harder to do. I must table the numbers

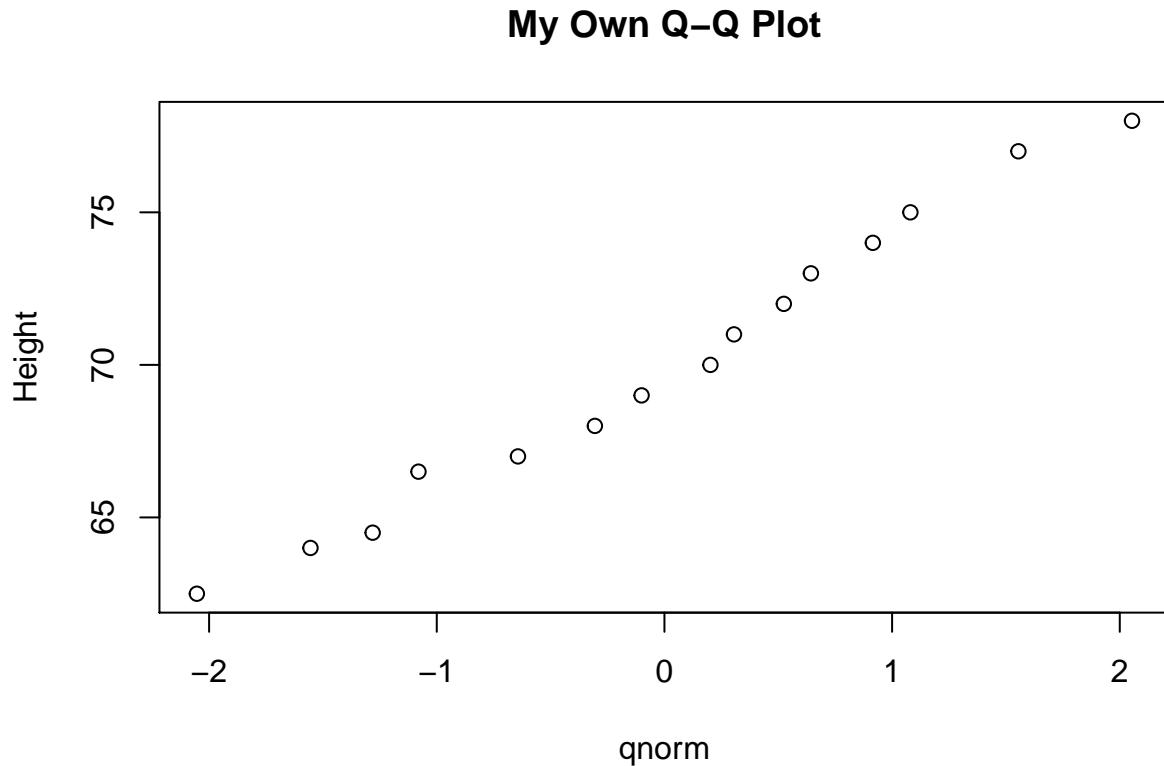
```
table(Lesson2_Height$Height)
```

```
##  
## 62.5   64  64.5  66.5   67   68   69   70   71   72   73   74   75   77   78  
##     1     1     1     1     3     3     2     3     1     2     1     2     1     2     1     1
```

So at 67, the quantile will jump by 0.12 instead of 0.04. Thus the empirical quantiles are

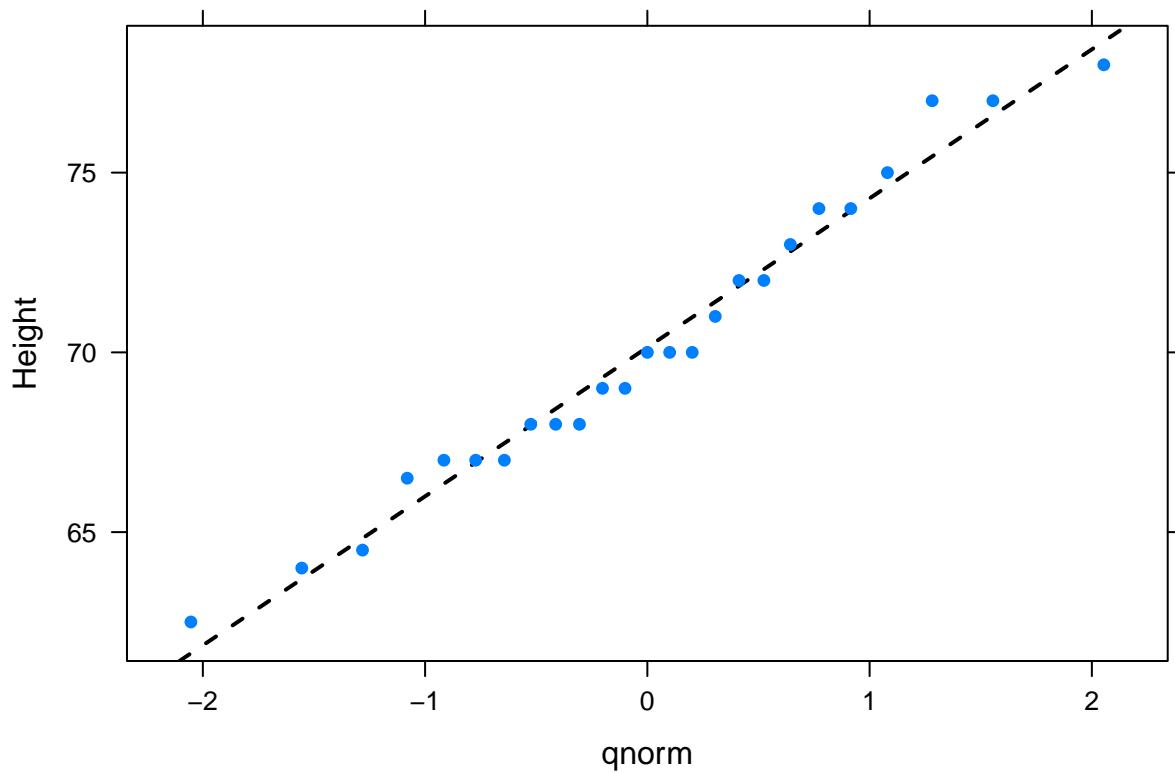
```
temp<-c(0.02,0.06,0.10,0.14,0.26,0.38,0.46,0.58,0.62,0.70,0.74,0.82,0.86,0.94,0.98)
```

```
plot(qnorm(temp),sort(unique(Lesson2_Height$Height)),xlab="qnorm",ylab="Height",main="My Own Q-Q Plot")
```



Back to `xqqmath`, the default method of inserting a line is to put it through the first and third quartiles. Another is the fit a line by estimating the mean and standard deviation. We will learn about these ideas later.

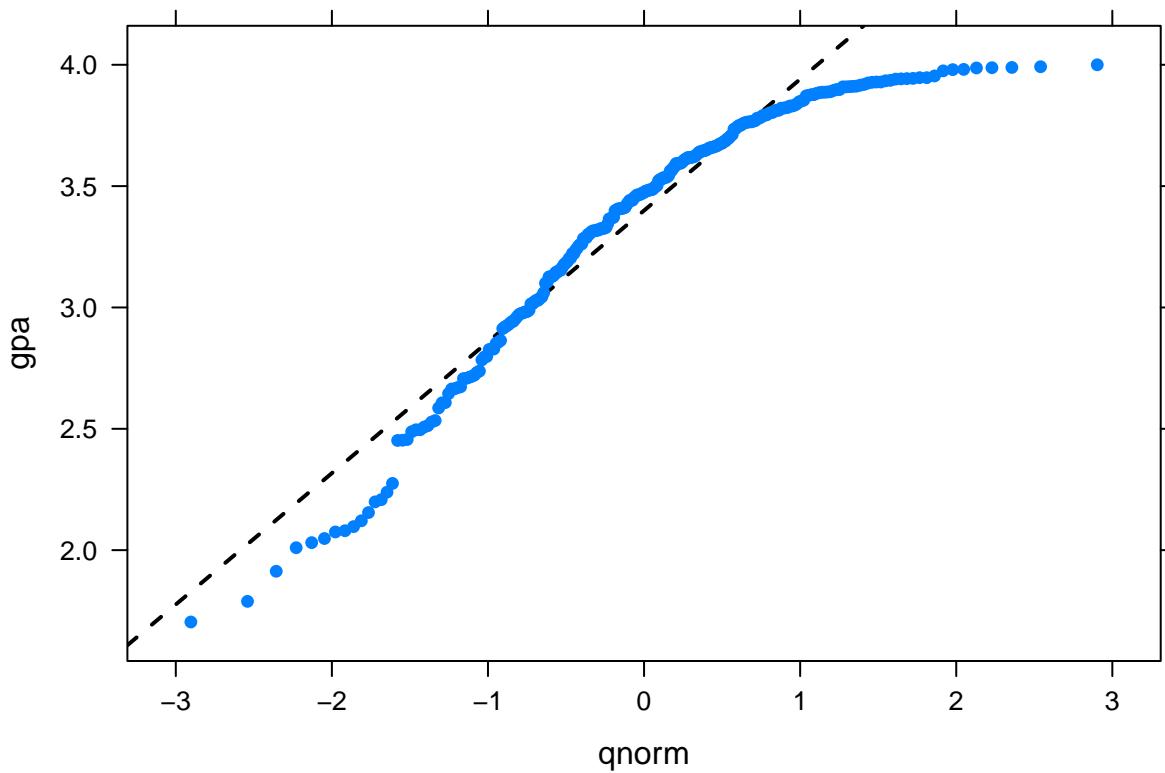
```
xqqmath(~Height, data=Lesson2_Height, fitline=TRUE)
```



From our data, the normal assumption is not bad.

Let's try it for the gpa data.

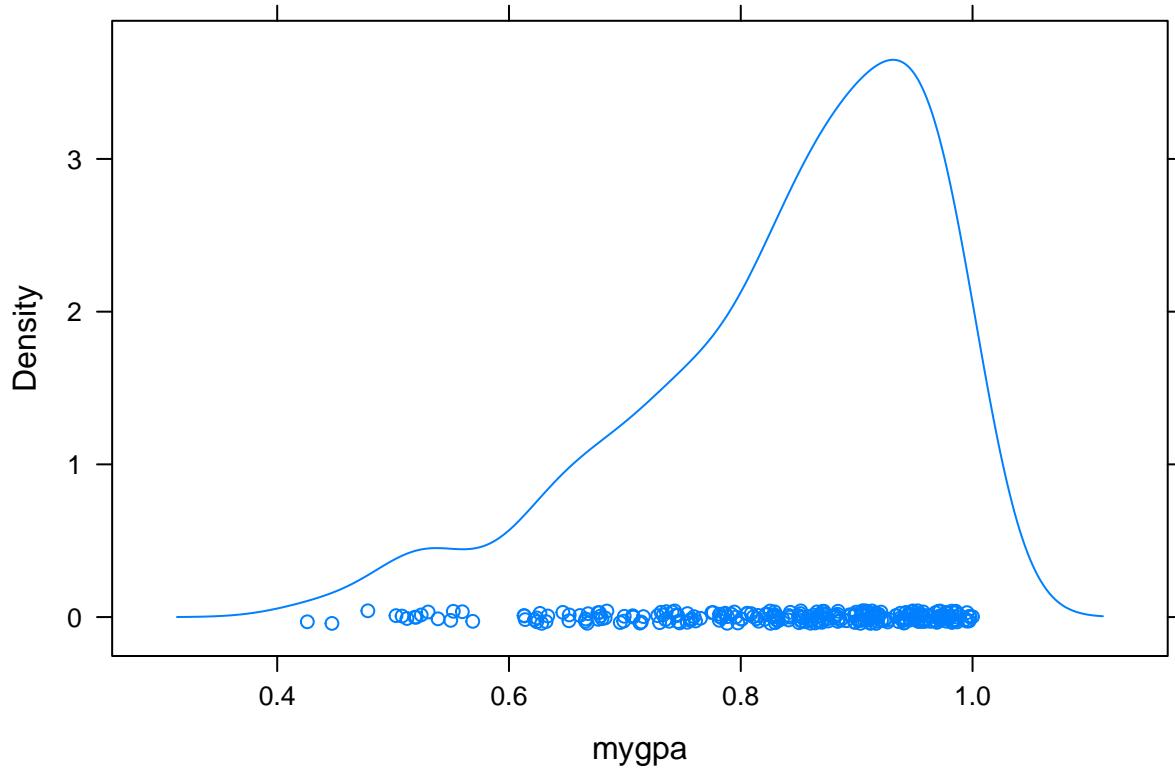
```
xqqmath(~gpa, data=gpa)
```



From this plot we can see that our data is skewed to the left compared with the normal distribution. Look at the right side of the figure, if the quantiles from the data increased as fast as those from the normal the points would fall along the line. Using a normal distribution for this data is not a good idea.

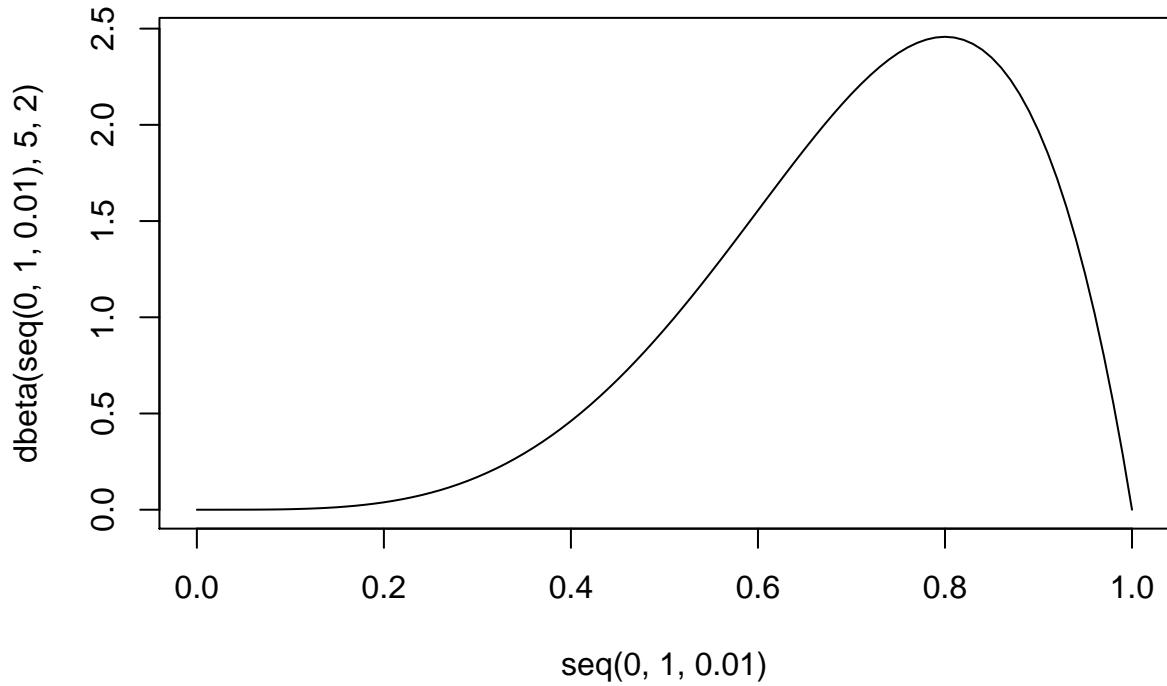
Maybe if we put gpa on a scale of 0 to 1 and then compare with a Beta, that is a better fit.

```
mygpa<-gpa$gpa/4  
densityplot(mygpa)
```

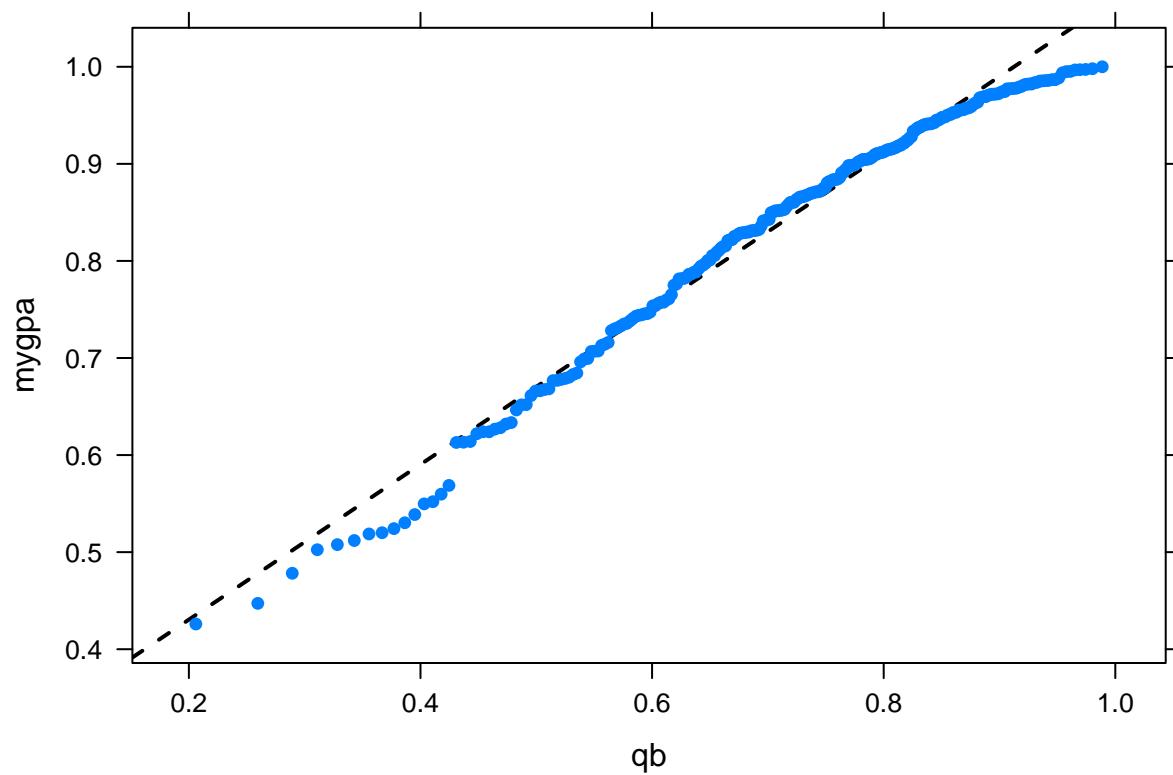


Next chapter we will look at estimating the parameters of a distributions; for now we will a Beta(5,2)

```
plot(seq(0,1,.01),dbeta(seq(0,1,.01),5,2),type="l")
```



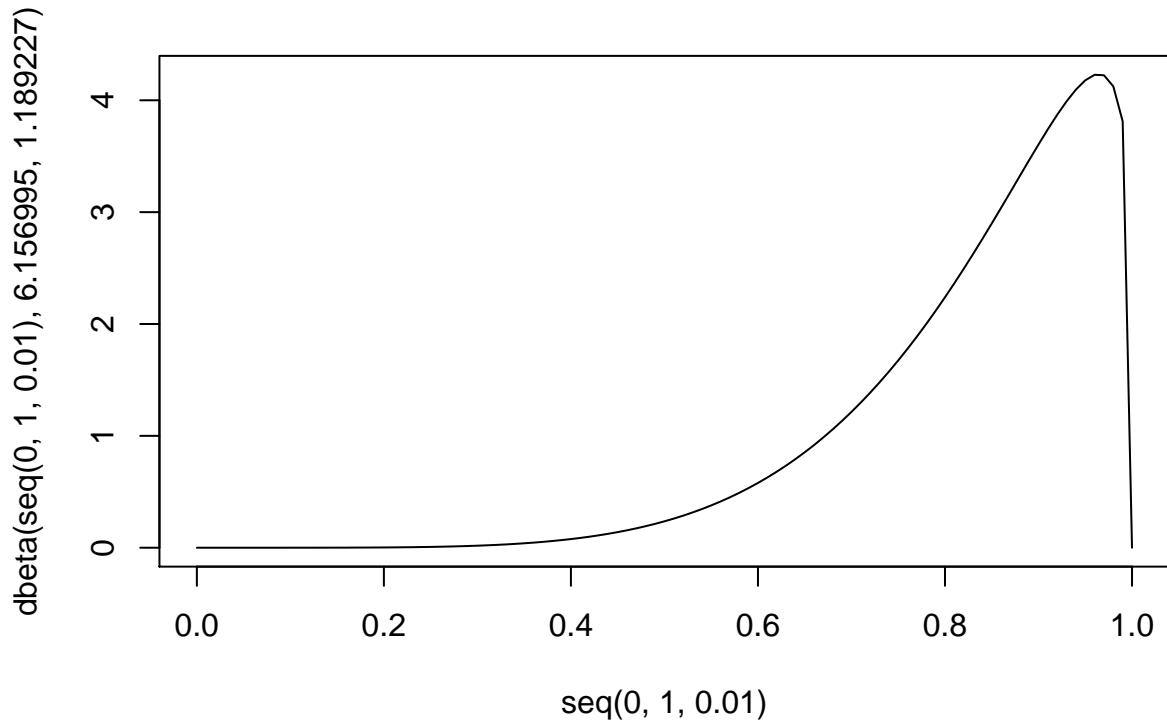
```
qb<-function(x){qbeta(x,5,2)}  
xqqmath(~mygpa,distribution=qb)
```



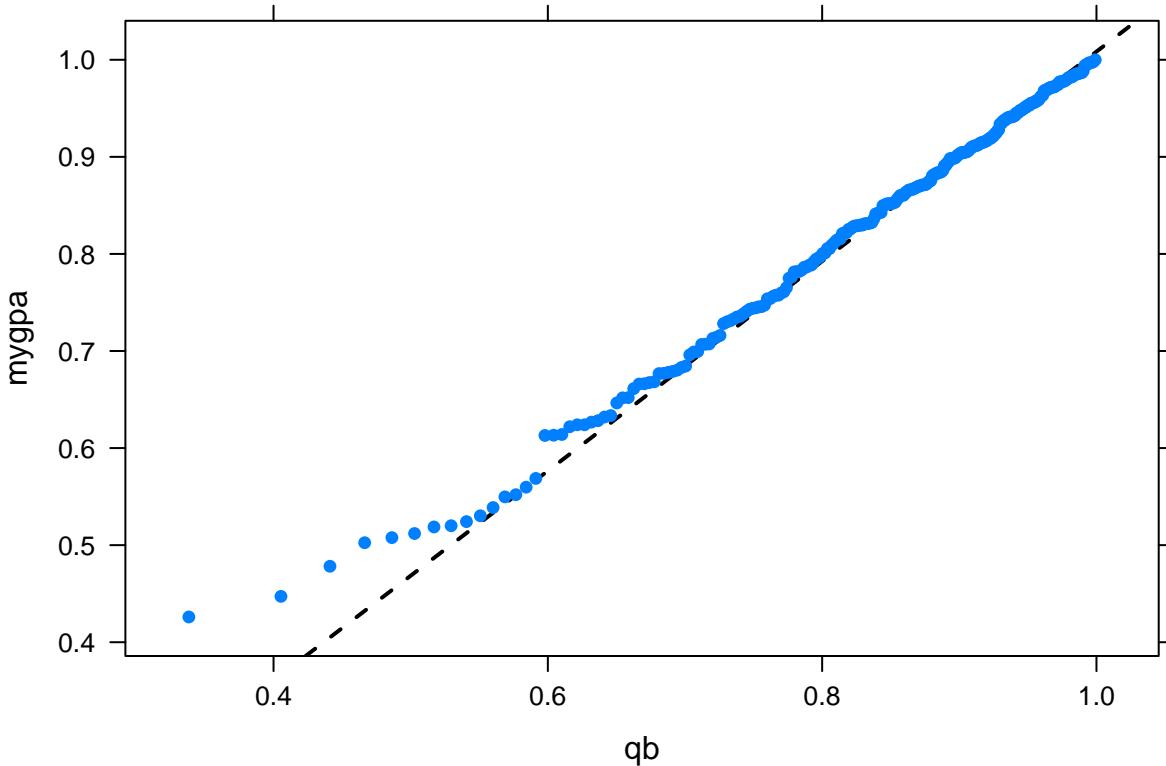
There are still some problems with the fit but it is better. The Beta has a longer tail to the right versus our data.

Finding the parameters using ideas from Chapter 4

```
plot(seq(0,1,.01),dbeta(seq(0,1,.01),6.156995,1.189227),type="l")
```



```
qb<-function(x){qbeta(x,6.156995,1.189227)}
xqqmath(~mygpa,distribution=qb)
```



Do Homework 3.38

3.6 Continuous Joint Distributions

3.6.1 Objectives

1. From a joint pdf find the marginal and conditional pdf
2. Calculate marginal, joint, and conditional probabilities using integration
3. Determine if two random variables are independent
4. Find the distribution of a sum of independent random variables, the most important case being normal random variables

3.6.2 Background

With continuous random variables, we use all the same ideas from joint distributions for discrete as well as the ideas from univariate continuous except

1. To find $P(X < x|Y = y)$ we need to find the conditional pdf $\frac{f_{X,Y}(x,y)}{f_Y(y)}|_{Y=y}$

2. Independence, iff $f_{X,Y}(x,y) = g(x)h(y)$ and the domain is rectangular $a \leq x \leq b$ and $c \leq y \leq d$ for real numbers a, b, c , and d .
3. Distribution of a sum of independent random variables, you can use the moment generating function and Thm 3.7.10.

Note: most of the problems in this section require Calc III ideas. Draw a picture of the domain to setup limits of integration. Also, for inequalities, set as an equality and then pick a point on one side of the line to check if it meets the condition of the inequality.

3.6.3 Practice

To make use of the ideas we will practice

1. Problem 3.45
 - a. Find joint pdf and verify it is a proper pdf
 - b. Find the probability that Alice and Bob arrive before 5:15
 - c. Find the probability that Alice arrives before Bob
 - d. Find the probability that Alice arrives before 5:30 given that Bob arrives before 5:30
 - e. Find the probability that Alice arrives before 5:30 given that Bob arrives at exactly 5:30
2. Change the problem to state that Alice will always arrive before Bob. Thus the domain is $5 \leq x < y \leq 6$. Assume the joint pdf is uniform.
 - a. Find joint pdf and verify it is a proper pdf
 - b. Find the probability that Alice and Bob arrive before 5:15
 - c. Find the probability that Alice arrives before Bob
 - d. Find the probability that Alice arrives before 5:30 given that Bob arrives before 5:45
 - e. Find the probability that Alice arrives before 5:30 given that Bob arrives at 5:45
 - f. Are X and Y independent?
3. Problem 3.51
4. If $X_i \stackrel{iid}{\sim} \text{Norm}(2, 3)$ what is the distribution of \bar{X} for a sample size of 10?

Here is some interesting code to perform multivariate integration.

```
f<-function(x,y)1/4*(x+2*y)
integrate(function(y){sapply(y,function(y){integrate(function(x)f(x,y),y,2$value)}),0,1)

## 0.7916667 with absolute error < 8.8e-15
integrate(function(y){sapply(y,function(y){integrate(function(x)f(x,y),0,2$value)}),0,1)

## 1 with absolute error < 1.1e-14
```


Chapter 4

Parameter Estimation and Testing

The fourth chapter is completed in seven lessons. Sections 4.1 and 4.2 are combined into one lesson. The same is true for sections 4.6 and 4.7 as well as 4.8 and 4.9. Section 4.6 tends to be technical and mathematical so we only require the students to know Lemma 4.6.1, Theorem 4.6.5, Definition 4.6.6, Lemma 4.6.7, Lemma 4.6.8, and Corollary 4.6.9.

4.1 Method of Moments

4.1.1 Objectives

1. Know and properly use the new terminology and notation to include but not limited to, sample moment, around origin and sample mean, parameter, and independent and identically distributed
2. Find parameter estimates, univariate and multivariate, using the method of moments, this may include using a root solver
3. Know the relationship between the second sample moment about the sample mean and the sample variance

4.1.2 Introduction

The book does a great job introducing the idea of statistical mathematical models. Typically in this class, we want to use them by using a sample and model of the population to make an inference about the population. In Math 378, we will start to use them to make predictions. We also see this a little at the end of this course when we introduce linear regression.

There are several issues that we have to handle. First we have to decide which model is appropriate. We already partially addressed this with the Q-Q plots of last chapter. The second issue is how to estimate parameters for the model. That is this lesson. Finally, we will have to address how to make inferences about the population parameter from the sample estimate.

4.1.3 Method of Moment Estimates

Once we have decided on a model for the population, we typically want to estimate parameters by using data from a sample. The idea that we will use is simply that we will equate sample moments to population moments and then try to solve for the parameter(s) of interest.

The book defines sample moments both around the origin and around the sample mean. See page 180. Do not confuse these with the population moments from Chapter 3, see page 126. Those are moments for the entire population and not just a sample.

As a comparison, here are the formulas for the k th sample moment about the origin and the k th moment about the origin.

$$\hat{\mu}_k = \frac{1}{n} \sum_{i=1}^n (x_i)^k$$

$$\mu_k = E(x^k)$$

Notice the `hat` on the sample moment. This notation is used to denote an estimate.

4.1.4 Example

Suppose I have some data

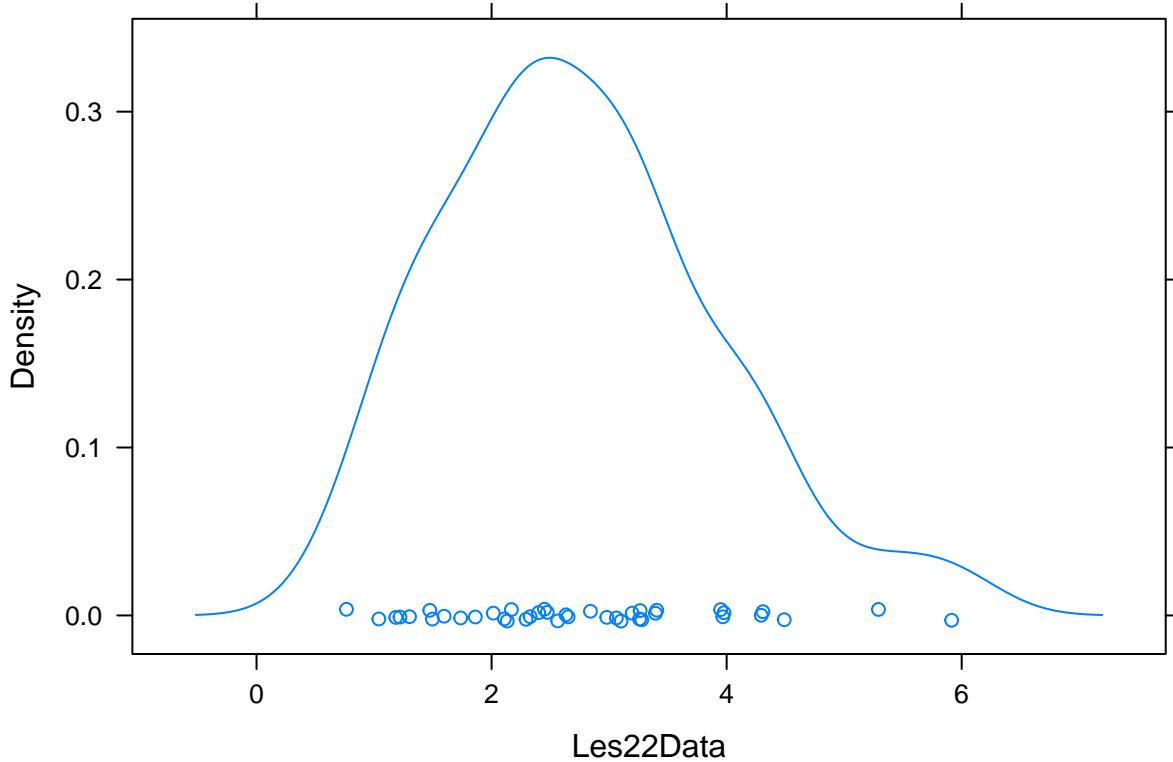
```
Les22Data
```

```
## [1] 3.1014985 1.7371363 5.2919977 1.4964655 2.6323325 2.8416648 2.1685008
## [8] 4.2943013 1.2207340 4.3090411 2.1333155 3.2770935 0.7652807 2.1089708
## [15] 2.5630758 3.3944054 3.2639452 3.9491399 1.4743717 1.0406365 2.2933009
## [22] 5.9144906 4.4901816 1.8617249 1.3017419 1.1851448 3.0619336 3.9773334
## [29] 1.5961078 2.3282182 2.9802030 2.4739417 3.2587091 2.4006987 2.0145723
## [36] 3.9677253 3.1962093 3.4056244 2.6510675 2.4499892
```

Let's plot it:

```
library(fastR)
```

```
densityplot(Les22Data)
```



I don't know the population mean, what would be a reasonable estimate? The sample mean is an obvious choice. Thus my estimate of $E(X)$ which is also called μ is $\hat{\mu}$.

Again, the key idea from this section is that the population moments are a function of the parameters of the distribution. Thus we can estimate those parameters by equating sample moments with population moments.

Here are the first sample moment about the origin and the second sample moment about the sample mean. Notice that the second sample moment about the sample mean is not the same as the sample variance. That is because one divides by n and the other by $n-1$.

```
(Les22Datamean<-mean(Les22Data))
```

```
## [1] 2.746821
sum((Les22Data-Les22Datamean)^2)/length(Les22Data)

## [1] 1.334194
var(Les22Data)

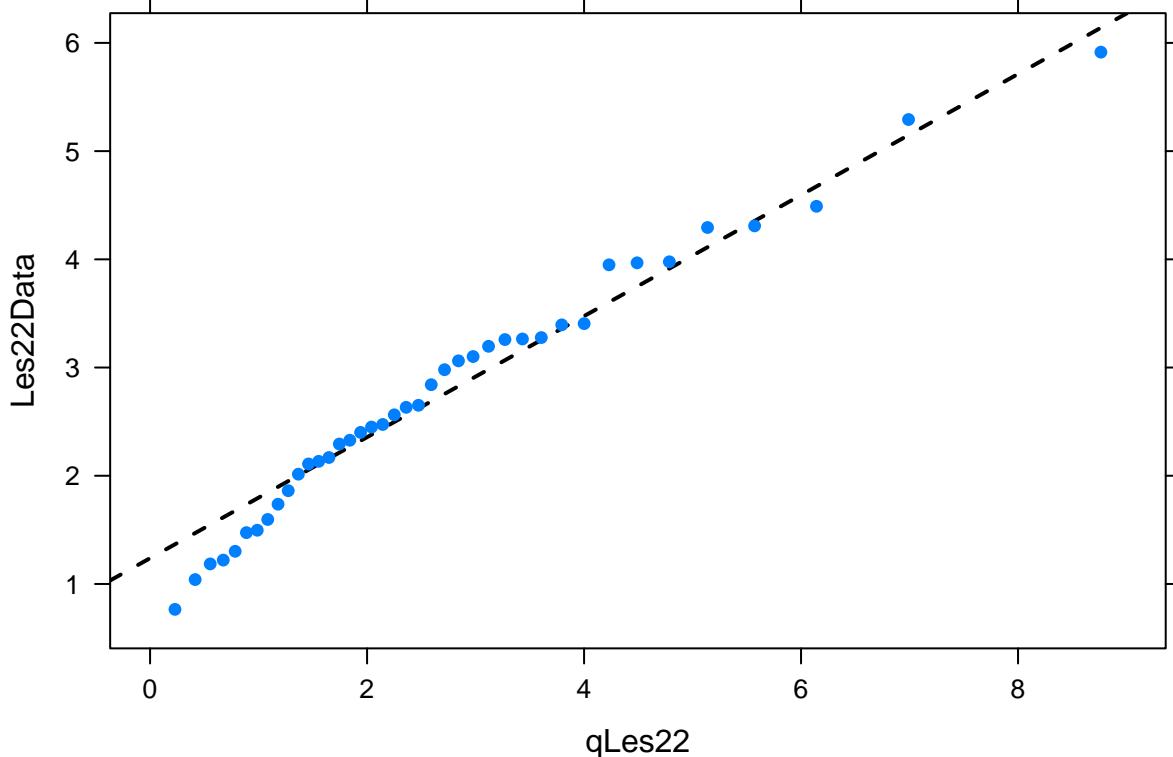
## [1] 1.368404
```

Now suppose we think the data comes from a gamma with $\alpha = 2$. Estimate λ .

From the back of the book, $E(X)$ for a gamma is $\frac{\alpha}{\lambda} = \frac{2}{\lambda}$. So $\bar{x} = \frac{2}{\lambda}$ and we have $\hat{\lambda} = \frac{2}{\bar{x}}$. Finally $\hat{\lambda} = 0.7281145$.

We could check using a q-q plot.

```
qLes22<-function(x){qgamma(x,2,rate=2/Les22Data$mean)}
xqmath(~Les22Data,distribution=qLes22)
```



This is not a good model, so we need to estimate both α and λ .

4.1.5 Practice

1. We think the data in this lesson comes from either an exponential or gamma. Use the method of moments to estimate the parameters of each model.
2. Homework 4.2
3. Homework 4.3 and 4.5

For the gamma

$$E(X) = \frac{\alpha}{\lambda}$$

$$V(X) = E(x - \mu)^2 = \mu'_2 = \frac{\alpha}{\lambda^2}$$

So

$$\hat{\mu}_1 = \bar{x} = \frac{\alpha}{\lambda}$$

$$\hat{\mu}'_2 = \frac{\alpha}{\lambda^2}$$

so

$$\hat{\lambda} = \frac{\hat{\mu}_1}{\hat{\mu}'_2}$$

$$\hat{\alpha} = \frac{\hat{\mu}_1^2}{\hat{\mu}'_2}$$

```
prob4.3<-function(n=6,theta=1){
  x<-runif(n,max=theta)
  return(as.numeric(2*mean(x)<max(x)))
}
sum(replicate(10000,prob4.3(6,1)))/10000

## [1] 0.2266
```

4.2 Estimates and Estimators

4.2.1 Objectives

1. Know and use notation and terminology such as estimate, estimator, simple random sample, independent and identically distributed sampling, unbiased estimator, consistent estimator, sequence of estimators, and the weak law of large numbers.
2. Determine if an estimator is unbiased and consistent by finding its mean and variance.
3. Know and apply Chebyshev's Inequality.
4. Use simulation in R to evaluate properties of estimators.

4.2.2 Background

This section is technical and only a small subset of estimator theory. The most important idea is to think of an estimator as a random variable. For example, the sample mean. If we have numbers, actual values, we could find the sample mean by adding all the numbers together and dividing by the total number. This will give us a single number, an estimate. However if we think of each value as a random variable, then the sample mean is a random variable. This is called an estimator. It will have a probability distribution, called the sampling distribution. We can then use this probability distribution to make inference decisions.

To compare estimators, we will use two ideas. Unbiased and consistency. There are many other ideas to compare estimators such as mean squared error (MSE) and minimum variance. However, we will only focus on the two in this class.

4.2.3 Estimator as a Random Variable

The abstraction in the sampling process and generation of an estimate is difficult to think about. That is because we are repeating the process of sampling over and over when in practice we only get one sample. Let's do a simulation to help us understand. The advantage of simulation is that we know the answer and can compare it with the sampling results from the simulation.

Let's simulate data from a gamma with parameters 5 and 2. Suppose we claim that we have data on the length of time in months until a light bulb fails. Here is the data:

```
Les23Data<-rgamma(40,5,2)
```

```
Les23Data
```

```
## [1] 1.8237222 1.4380527 2.5464852 4.4669474 1.9779904 2.7675456 2.6284489
## [8] 2.3932812 3.3676660 2.4363537 1.0743492 1.8020264 0.9286575 0.7292569
## [15] 3.0696257 5.0779691 2.5321907 4.5423615 1.1422669 1.4758949 2.7168385
## [22] 1.9717843 2.2220833 3.6738394 1.9764378 2.6641604 2.3605102 1.5289561
## [29] 1.2540347 1.6633310 1.8849037 1.9858505 3.5072801 2.0951056 1.3010411
## [36] 1.4997930 1.7766213 1.6700590 2.0199093 1.1035990
```

Suppose we think the distribution is an exponential. From this we calculated a method of moments estimate for an exponential distribution as

$$\hat{\lambda} = \frac{1}{\bar{x}}$$

For this data set, the estimate is

```
1/mean(Les23Data)
```

```
## [1] 0.4489477
```

Now suppose we could repeat this process with another data set. We would get another estimate of $\hat{\lambda}$.

```
Les23Data2<-rgamma(40,5,2)
```

```
Les23Data2
```

```
## [1] 2.5355098 0.9900852 6.0742837 2.6326927 1.6244409 1.9699979 2.4340282
## [8] 1.8101994 2.9695040 3.3516984 3.1451989 5.2537976 1.8012785 2.6318453
## [15] 2.8893933 2.2435369 2.7449025 3.0926211 2.1138304 3.1076069 2.1564097
## [22] 1.5444007 4.3389450 1.4993788 2.1243461 0.8083089 1.3913246 1.5392261
## [29] 4.2871195 0.9067133 3.8727659 4.1743425 3.2076029 2.9951832 2.0447721
## [36] 3.0208547 1.5488772 2.9257329 3.0873947 2.2799768
```

```
1/mean(Les23Data2)
```

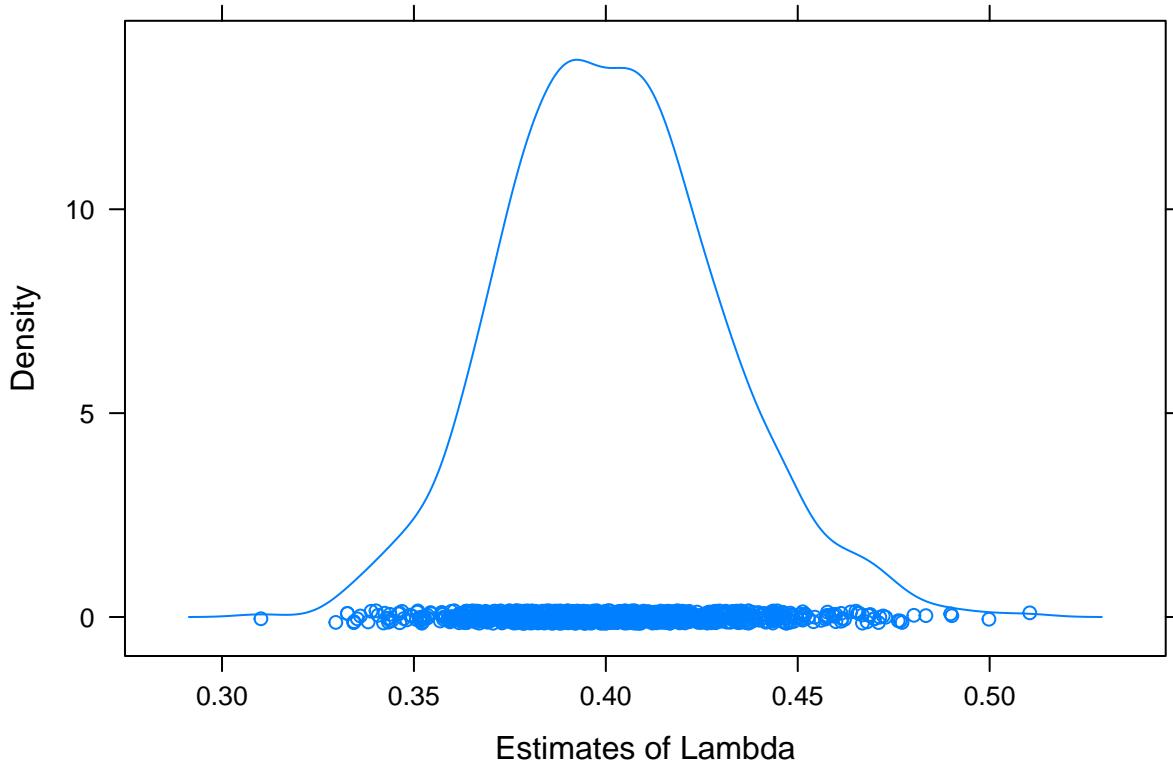
```
## [1] 0.3803361
```

Repeating this process many times, I start to get an idea of the distribution of $\hat{\lambda}$. Here is a density plot of 1000 estimates of λ . That is, I collected 40 data points, found the method of moment estimate and repeated 1000 times.

Load `fastR` and set the seed for repeatability.

```
library(fastR)
```

```
Les23DataMany<-replicate(1000,rgamma(40,5,2))
LambdaEstimator<-apply(Les23DataMany,2,function(x)(1/mean(x)))
```



This is just a simulation but this is the idea of thinking of an estimator as a random variable. It will vary from sample to sample and have a distribution. The distribution of the estimator is not necessarily the same as the distribution of the parent population. Since the estimator has a distribution, we can use ideas from previous sections such as moments, $E(X)$.

4.2.4 Properties of Estimators

Now that we have seen how to view estimators as random variables, let's look at some properties of estimators. We could understand properties of the distribution of estimators by using

1. Mathematical approach - this is general and abstract. We will do this with unbiased and consistent.
2. Repeat the experiment - this approach is the easiest but is way to costly in terms of time and money to be practical.
3. simulation - this is fast and easy but we must write programs and make assumptions about parent distribution and parameters.

The method of moments estimator uses the idea that the sample mean \bar{X} , as a random variable, is a good estimator of the population mean $E(x)$. What does good mean? There are many ways to answer this question but our book will only focus on two, unbiased and consistent. Note also that the book discusses two sampling methods, simple random sample and independent and identically distributed. In either case, these two methods don't change the two properties we want to discuss.

Let's explore these ideas using problem 4.1 as a reference. Here we flip a coin and record 0 if it is tails and 1 if it is heads. Thus X is a binomial random variable and is described as the number of heads in one flip of a coin. Now if we repeat this process n number of times, we have a sequence of random variables

$X_1, X_2, X_3, \dots, X_n$. These are independent and identically distributed. The method of moments estimator of the probability of heads is

$$\hat{\pi} = \bar{X}$$

As a example, suppose we repeat the flip 100 times. Here is a simulation of our data:

```
Les23flips<-rbinom(100,1,.5)
```

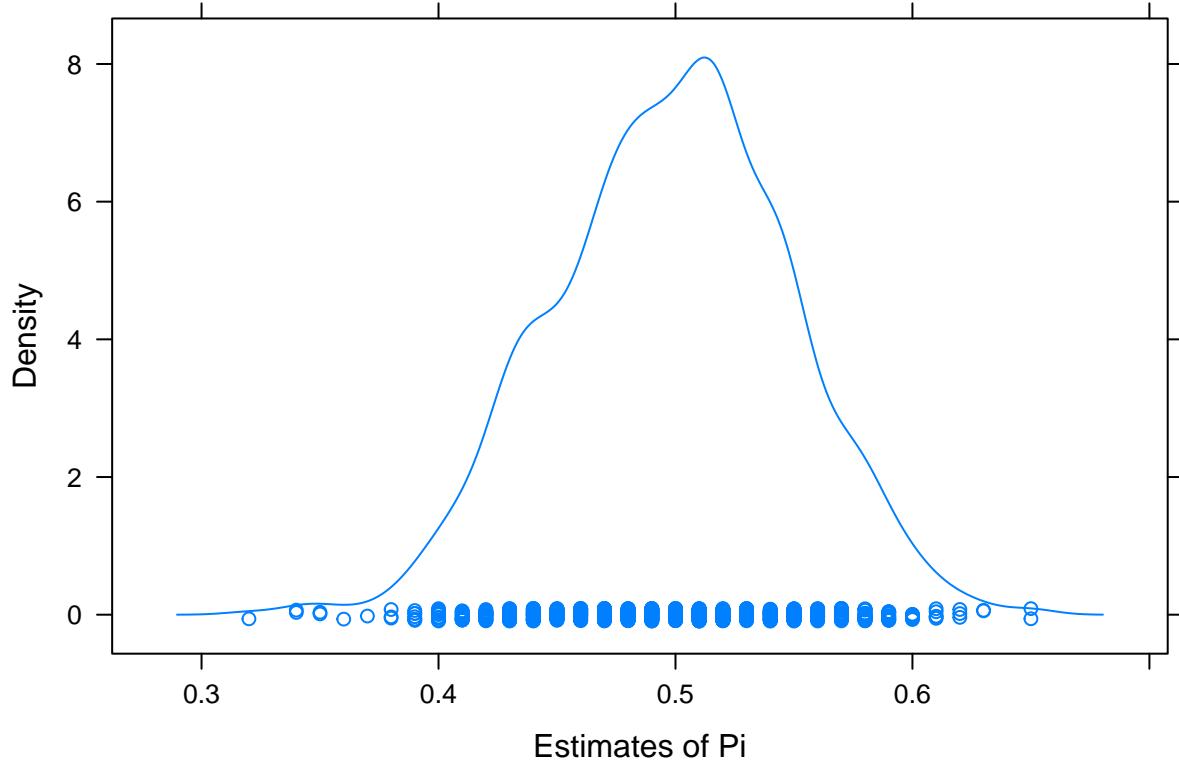
```
## [1] 0 0 1 1 0 1 1 0 0 0 0 0 1 1 1 1 1 1 0 0 0 0 0 0 1 0 0 0 0 1 1 0 1 0 1
## [36] 0 1 0 0 0 0 1 1 0 0 0 0 1 0 1 1 0 1 1 1 0 1 1 0 1 0 0 1 0 1 0 1 0 0 0 0
## [71] 0 1 1 0 1 0 0 1 0 0 1 0 0 1 1 1 0 1 0 1 1 1 1 0 0 1 0 1 0
```

We would estimate $\hat{\pi}$ as

```
## [1] 0.45
```

If we think of \bar{X} as estimator of π , then we could simulate its sampling distribution.

```
Les23FlipsMany<-replicate(1000,rbinom(100,1,.5))
PiEstimator<-apply(Les23FlipsMany,2,mean)
```



The two properties of estimators that we are interested in are

- 1) Unbiased, definition 4.3.4 and
- 2) Consistent, definition 4.3.6

Unbiased means

$$E(\hat{\pi}) = \pi$$

We have $X_i \stackrel{iid}{\sim} \text{binom}(1, \pi)$ and we know

$$E(X_i) = \pi$$

$$\text{Var}(X_i) = \pi(1 - \pi)$$

Our method of moments estimator is

$$\hat{\pi} = \bar{X}$$

and by definition

$$\bar{X} = \frac{\sum_{i=1}^n X_i}{n}$$

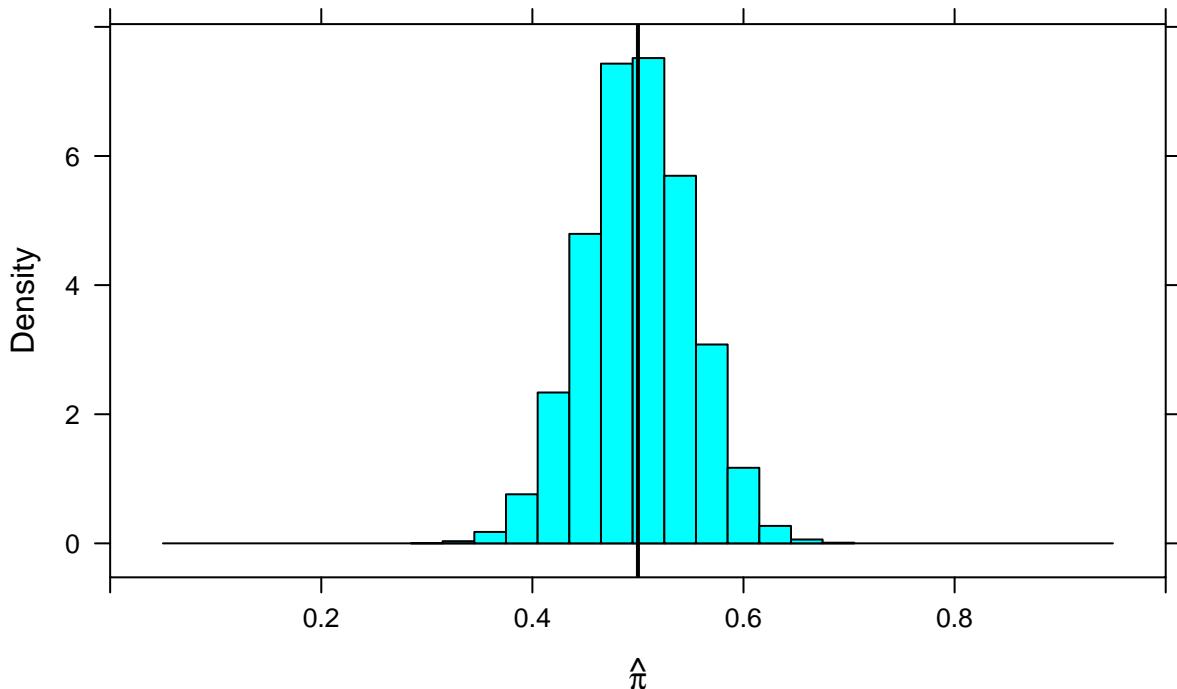
Thus

$$E(\bar{X}) = E\left(\frac{\sum_{i=1}^n X_i}{n}\right) = \frac{1}{n} E\left(\sum_{i=1}^n X_i\right) = \frac{1}{n} \sum_{i=1}^n E(X_i) = \frac{1}{n}(n\pi) = \pi$$

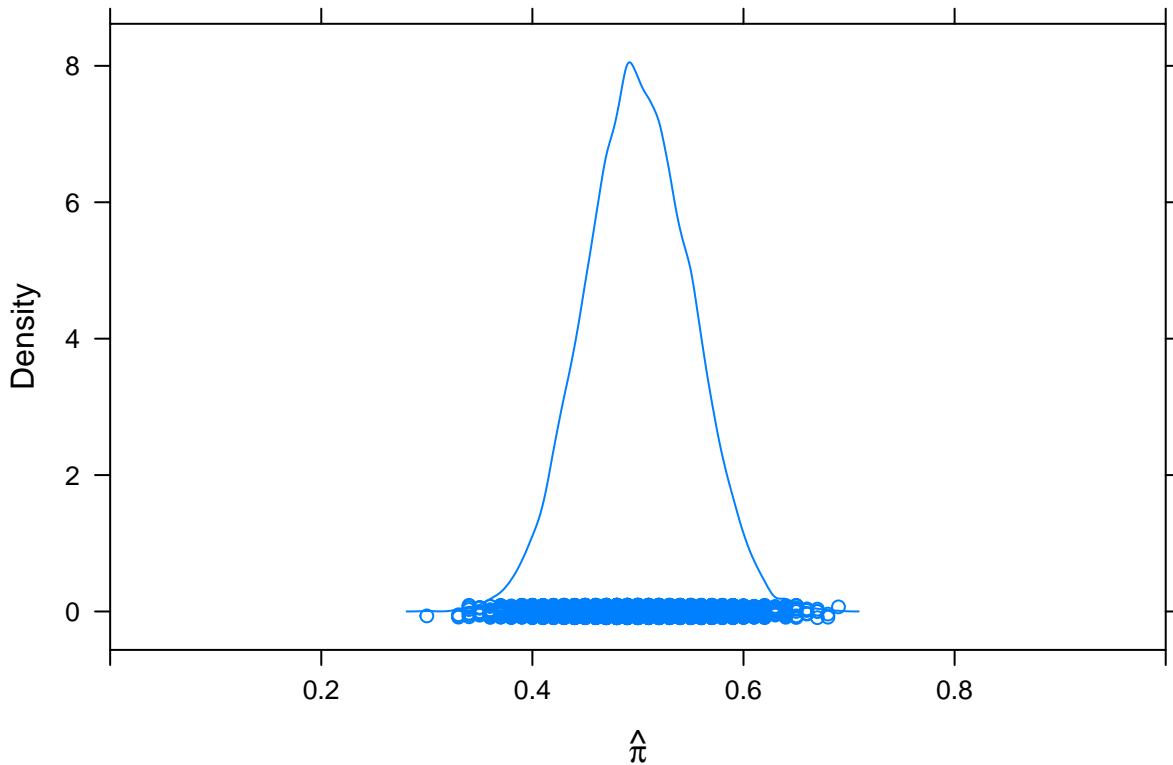
Thus we have an unbiased estimator. Let's simulate to get an idea

```
histogram(~replicate(10000, mean(rbinom(100, 1, 0.5))), v = 0.5, xlab = expression(hat(pi)),
  main = "Simulation of the Distribution of the Method of Moments Estimator \nfor Binom(0,.5), Sample",
  xlim = c(0, 1))
```

Simulation of the Distribution of the Method of Moments Estimator for Binom(0,.5), Sample Size 10



```
densityplot(~replicate(10000, mean(rbinom(100, 1, 0.5))), v = 0.5, xlim = c(0,
  1), xlab = expression(hat(pi)))
```



```
mean(replicate(10000, mean(rbinom(100, 1, 0.5))))
```

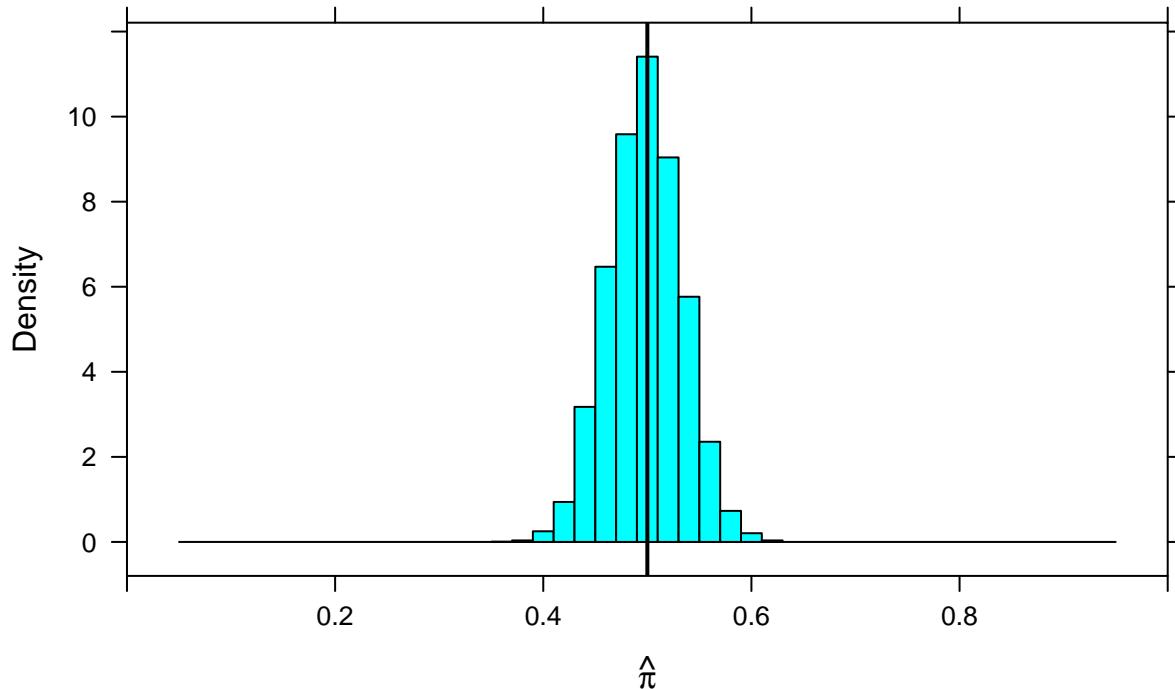
```
## [1] 0.499146
```

Notice that mean we calculated from the simulated sampling distribution is close to the true mean of 0.50.

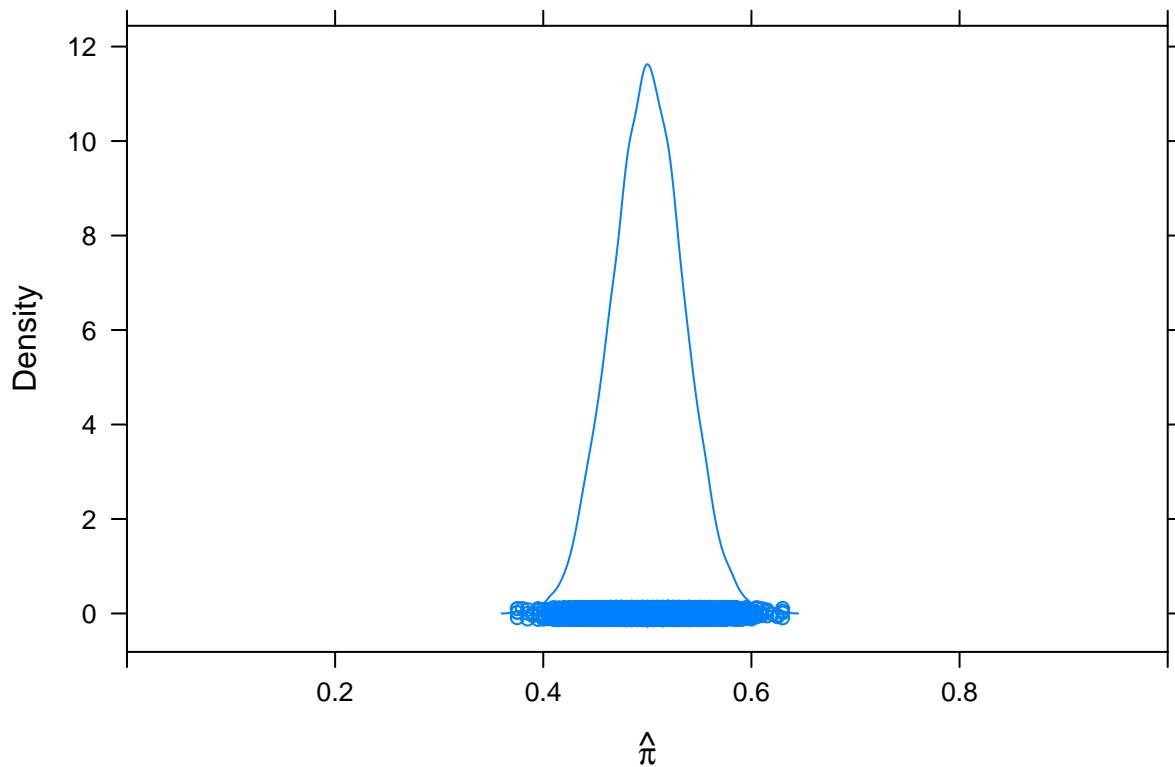
The idea of consistent is what happens as I make the sample size arbitrarily large. A desirable property is that as the sample size increases, the estimator gets arbitrarily close to the value being estimated. For us this means that the probability approaches one. We call this convergence in probability. There are many different types of convergence, convergence in distribution, convergence in mean, almost sure convergence, etc. To understand consistency, let's increase the sample size and see what happens in our simulation.

```
histogram(~replicate(10000, mean(rbinom(200, 1, 0.5))), v = 0.5, xlab = expression(hat(pi)),
main = "Simulation of the Distribution of the Method of Moments Estimator \nfor Binom(0,.5) Sample Size 200")
#> ## histogram is not currently available in R
#> ## Error: could not find function "histogram"
```

Simulation of the Distribution of the Method of Moments Estimator for Binom(0,.5) Sample Size 20

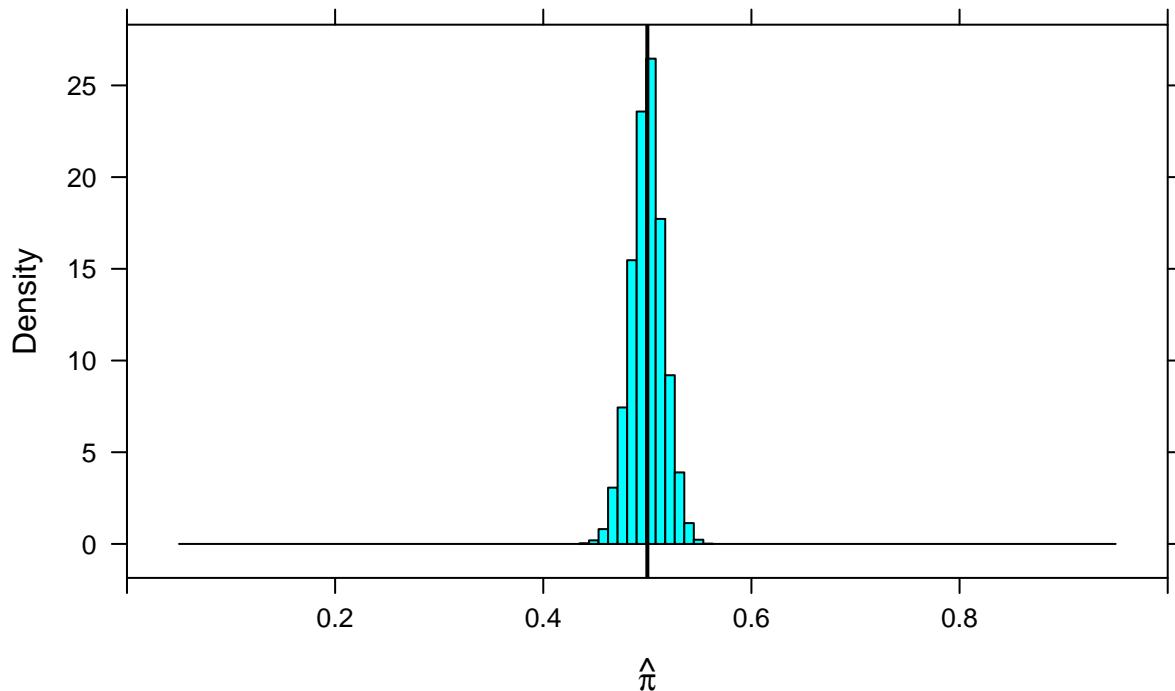


```
densityplot(~replicate(10000, mean(rbinom(200, 1, 0.5))), v = 0.5, xlim = c(0,
1), xlab = expression(hat(pi)))
```

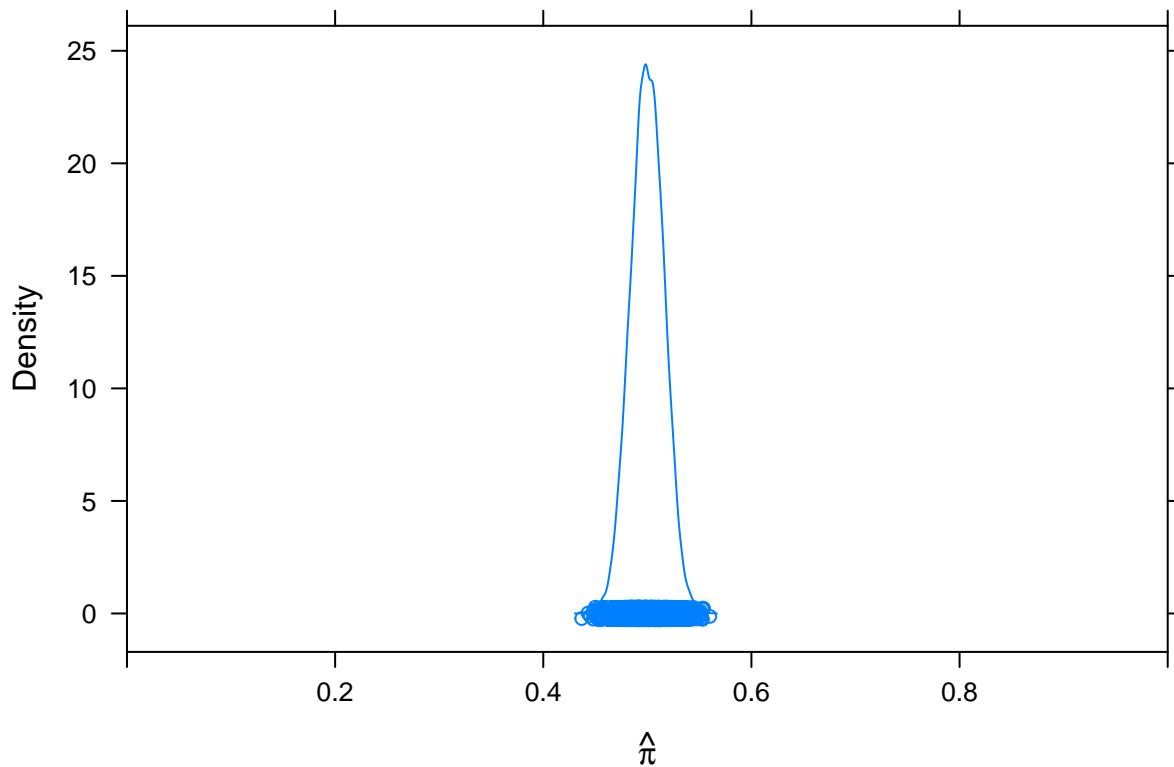


```
histogram(~replicate(10000, mean(rbinom(1000, 1, 0.5))), v = 0.5, xlab = expression(hat(pi)),
  main = "Simulation of the Distribution of the Method of Moments Estimator \nfor Binom(0,.5) Sample Size v = 0.5")
```

Simulation of the Distribution of the Method of Moments Estimator for Binom(0,.5) Sample Size 100

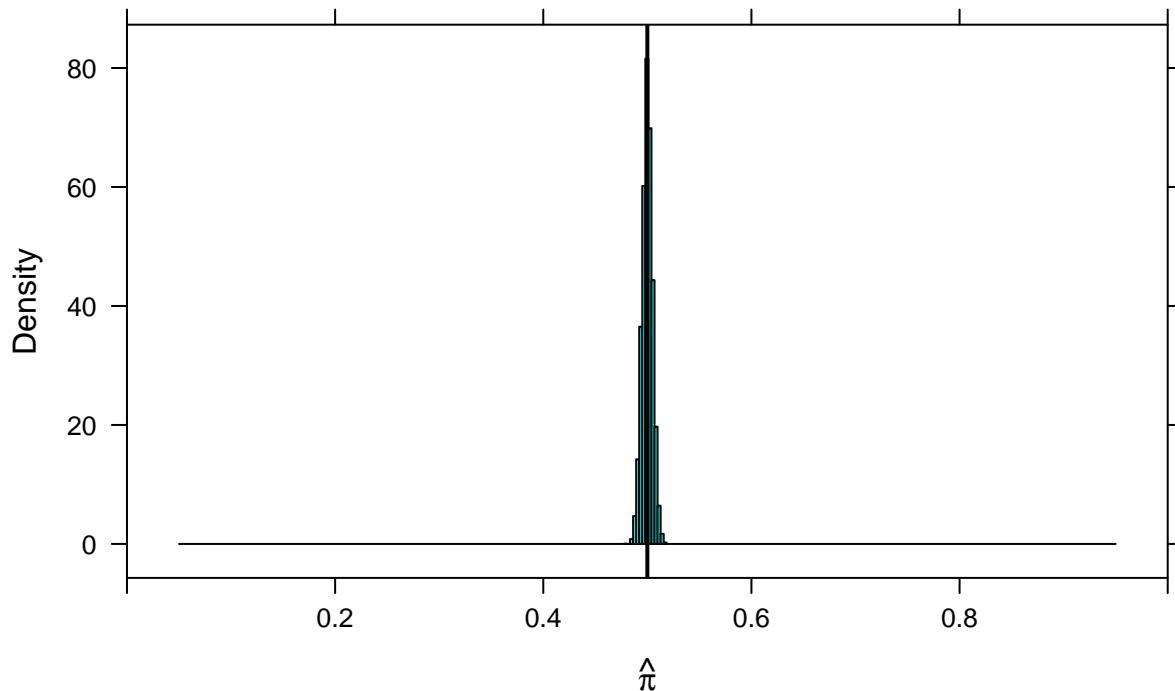


```
densityplot(~replicate(10000, mean(rbinom(1000, 1, 0.5))), v = 0.5, xlim = c(0,
1), xlab = expression(hat(pi)))
```

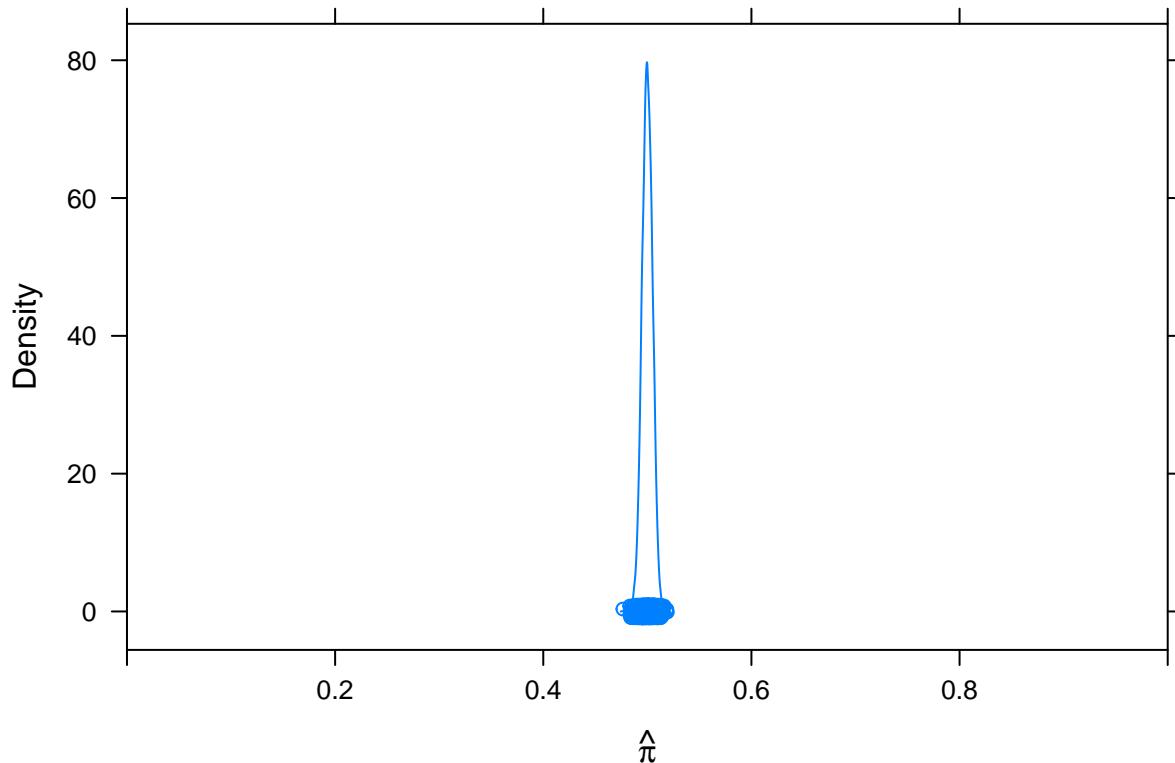


```
histogram(~replicate(10000, mean(rbinom(10000, 1, 0.5))), v = 0.5, xlab = expression(hat(pi)),
  main = "Simulation of the Distribution of the Method of Moments Estimator \nfor Binom(0,.5) Sample",
  xlim = c(0, 1))
```

Simulation of the Distribution of the Method of Moments Estimator for Binom(0,.5) Sample Size 100

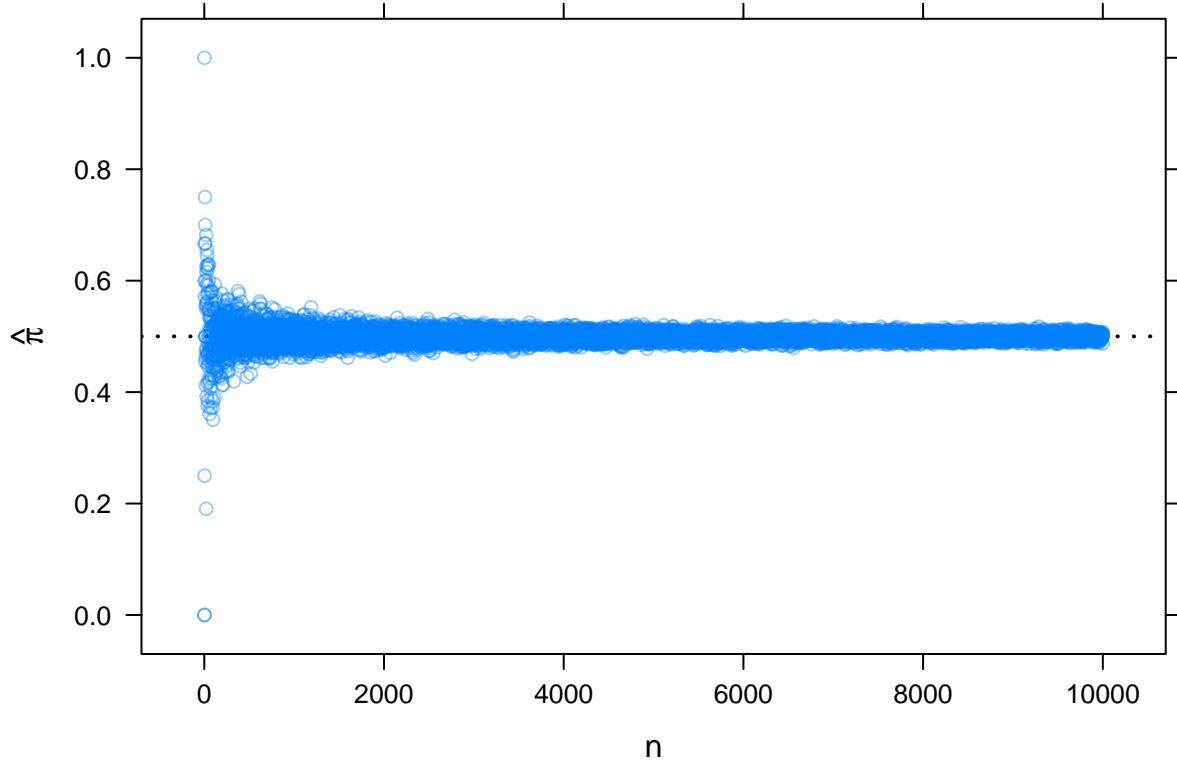


```
densityplot(~replicate(10000, mean(rbinom(10000, 1, 0.5))), v = 0.5, xlim = c(0,
1), xlab = expression(hat(pi)))
```



This is tiresome so let's write a function that will plot the behavior:

```
myrbinom<-function(n){rbinom(n,1,.5)}
xyplot(sapply(lapply(1:10000,myrbinom),mean)^-1:10000,xlab="n",ylab=expression(hat(pi)),alpha=.4,
       panel = function(...) {
         panel.abline(h=.5, lty = "dotted", col = "black",lwd=2)
         panel.xyplot(...)})
```



It looks like the sample mean is a consistent estimator of the probability of success. Mathematically we show this as

$$\text{Var}(\bar{X}) = \frac{1}{n^2} \sum_{i=1}^n \text{Var}(X_i) = \frac{1}{n^2} (n\pi(1-\pi)) = \frac{\pi(1-\pi)}{n}$$

We made use of independence in this argument.

Now

$$\lim_{n \rightarrow \infty} \frac{\pi(1-\pi)}{n} = 0$$

4.2.5 Chebyshev's Inequality

$$P(|X - \mu| \geq k\sigma) \leq \frac{1}{k^2}$$

4.2.6 Practice

Homework 4.11 and 4.13

4.3 Limit Theorems

4.3.1 Objectives

1. Find the distribution and solve probability questions for the sum of independent and identically distributed normal random variables.
2. Find the distribution and solve probability questions with and without the continuity correction, to include hypothesis testing, using the central limit theorem for the sum of independent and identically distributed binomial random variables.
3. Find the distribution and solve probability questions using the central limit theorem for the sum of independent and identically distributed random variables that are not normal.

4.3.2 Introduction

This section has the important result of the Central Limit Theorem. This idea has been and continues to be, at least for small sample inference, the corner stone of statistical inference. Its importance cannot be overstated.

From the previous two lessons, we have found a method to estimate parameters. It is called the method of moments. Assuming a sample is representative of the population, we set sample moments equal to population moments to find estimators of the population parameters.

Then we learned these estimators were random variables. We look at desirable properties based on the idea that these random variables have a distribution. The first property we found useful was unbiased. On average, the estimator should equal the true population parameter. This is $E(\hat{\theta}) = \theta$. The second idea was consistency. The estimator should get arbitrarily close to the parameter as the sample size increases. For an unbiased estimator, this means the variance of the estimator approaches 0 as the sample size becomes unbounded.

Without knowing the distribution of the estimator, we could use Chebyshev's equality to find probabilities on the sample mean as an estimator. In this section, we will try to find the distribution of the sample mean.

4.3.3 Parent Population is Normal

The sample mean is often used as an estimator of the population mean. We know it is unbiased and consistent. We could do more if we knew the distribution of the sample mean.

We know from previous work that if

$$X_i \stackrel{iid}{\sim} \text{Norm}(\mu, \sigma)$$

then

$$\sum_{i=1}^n X_i \sim \text{Norm}(n\mu, \sqrt{n}\sigma)$$

or the more well known results

$$\bar{X} = \sum_{i=1}^n \frac{X_i}{n} \sim \text{Norm}\left(\mu, \frac{\sigma}{\sqrt{n}}\right)$$

You should be able to prove this using moment generating functions. Try it!

Thus if the parent population is normal, then the sample mean is normal.

4.3.4 Parent Population is not Normal

The central limit theorem states that even if the parent population is not normal, a sum of iid random variables will be approximately normal.

$$\bar{X}_n \stackrel{\text{d}}{\sim} \text{Norm}\left(\mu, \frac{\sigma}{\sqrt{n}}\right)$$

This is called convergence in distribution.

Let's simulate the idea using the binomial from problem 4.1.

$$X_i \stackrel{iid}{\sim} \text{Binom}(1, \pi)$$

We found the method of moments estimator to be

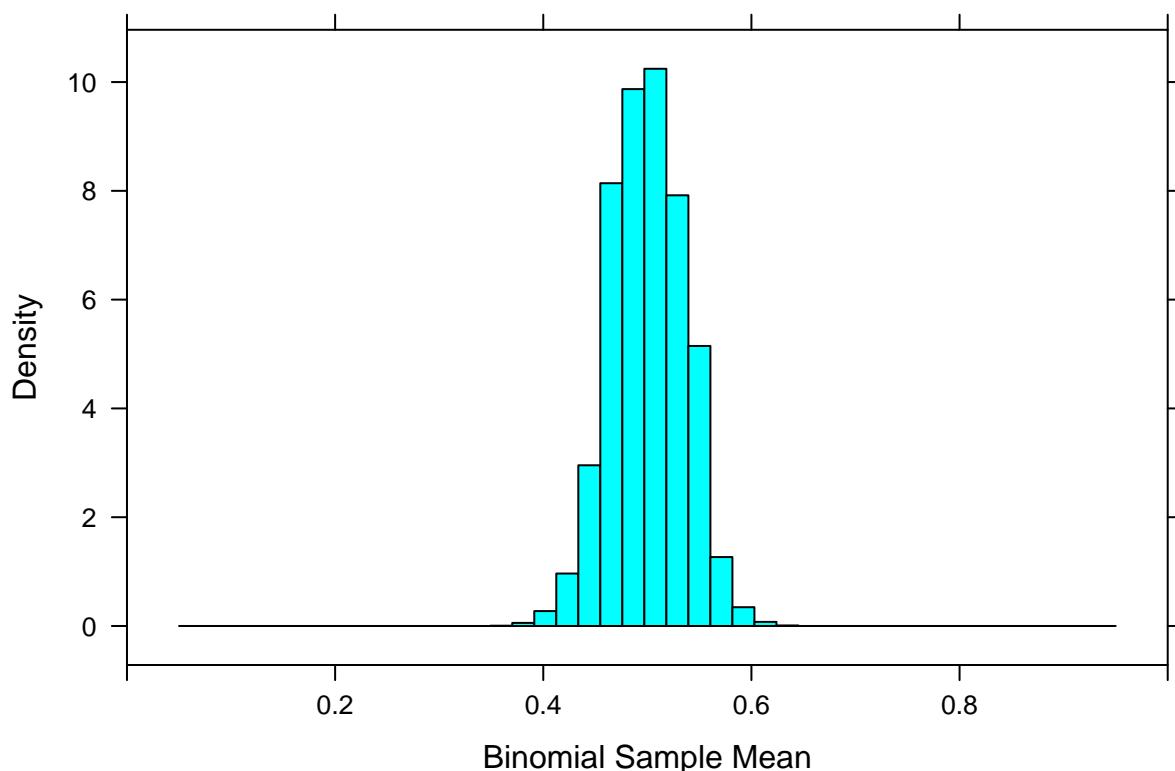
$$\hat{\pi} = \bar{X}$$

Using the central limit theorem the distribution of \bar{X} is

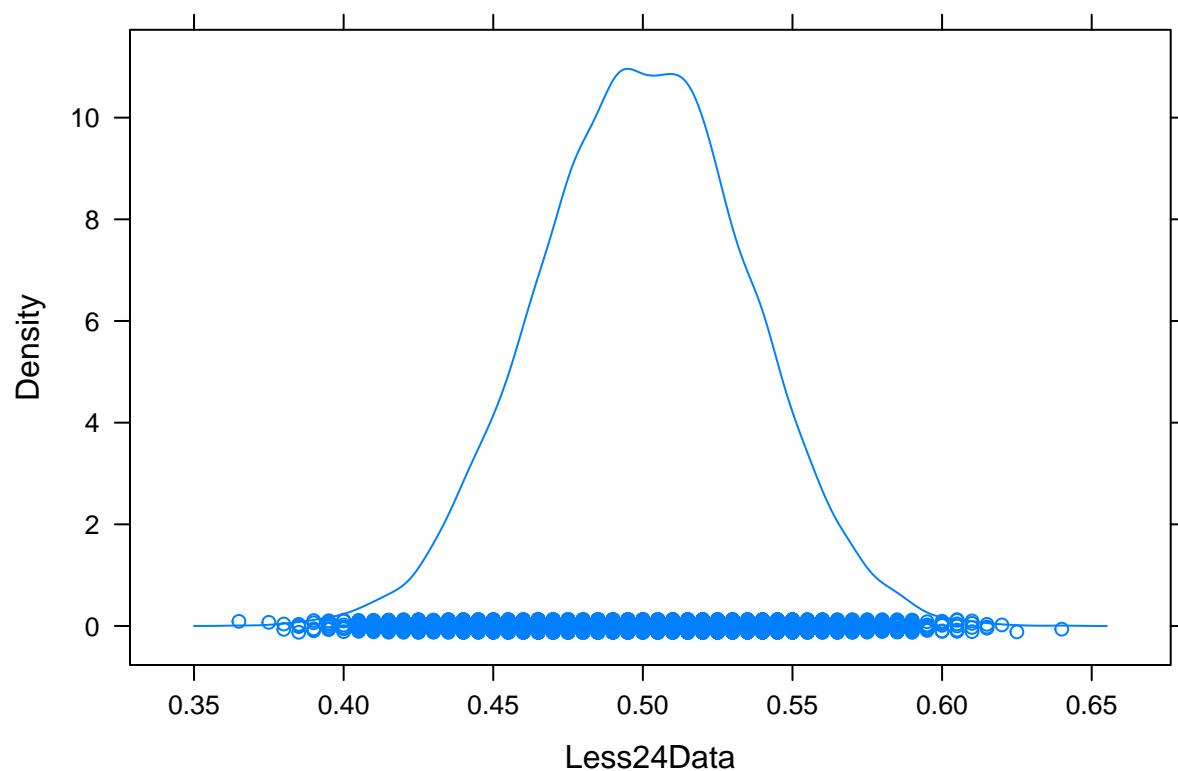
$$\bar{X}_n \stackrel{\text{d}}{\sim} \text{Norm}\left(\pi, \sqrt{\frac{\pi(1-\pi)}{n}}\right)$$

```
set.seed(6574)
library(fastr)
Less24Data<-apply(replicate(10000,rbinom(200,1,.5)),2,mean)
favstats(Less24Data)

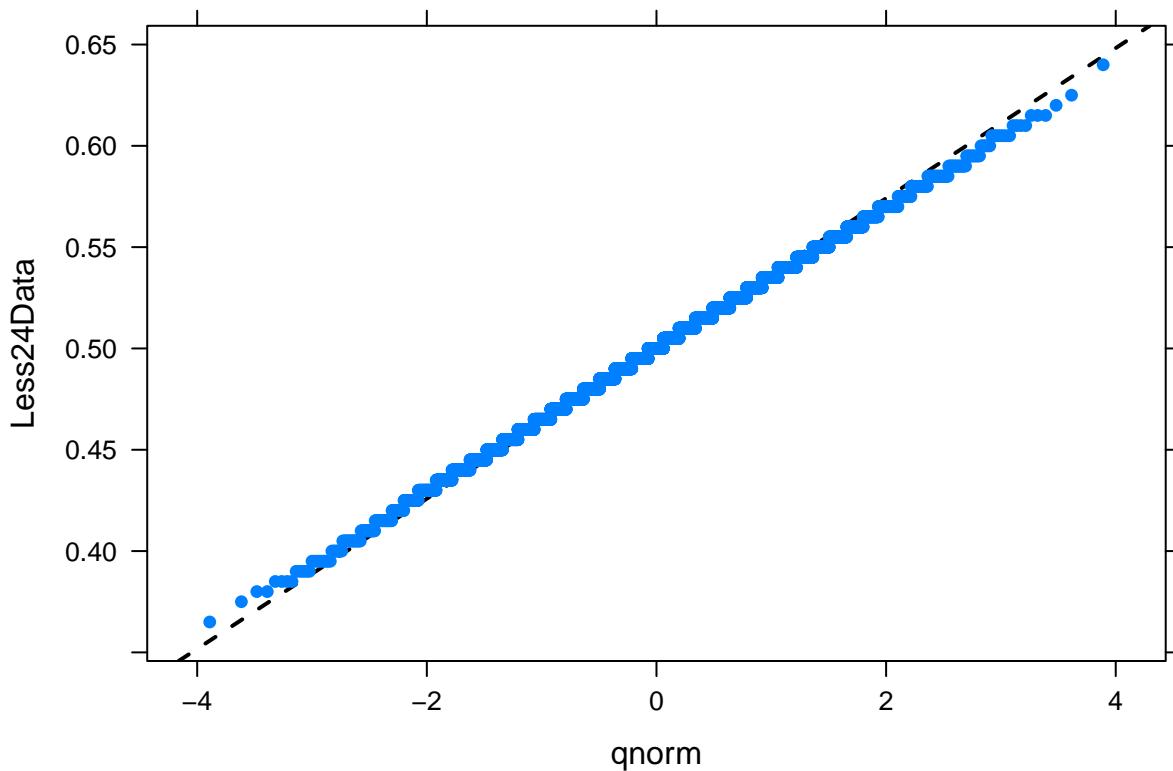
##      min     Q1 median     Q3    max      mean         sd      n missing
##  0.365 0.475    0.5 0.525 0.64 0.500005 0.03516857 10000       0
histogram(~Less24Data,xlab="Binomial Sample Mean",xlim=c(0,1))
```



```
densityplot(Less24Data)
```



```
xqqmath(~Less24Data)
```



There is some difficulty because the binomial is discrete while the normal is continuous. We will deal with that shortly.

There is also a question of how fast the convergence to the normal is. We will investigate that next with a simulation.

4.3.5 More examples of the CLT

Instead of using our own code, the package `TeachingDemos` has a function built-in that will help.

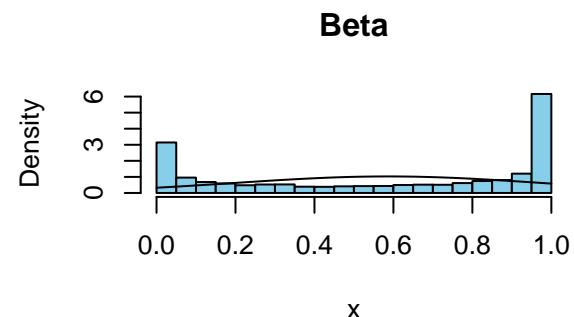
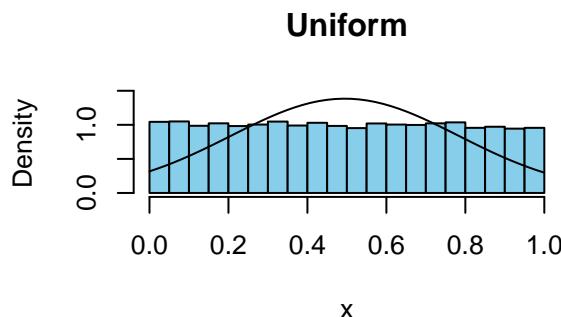
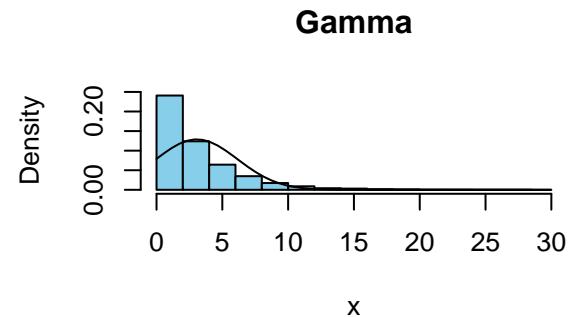
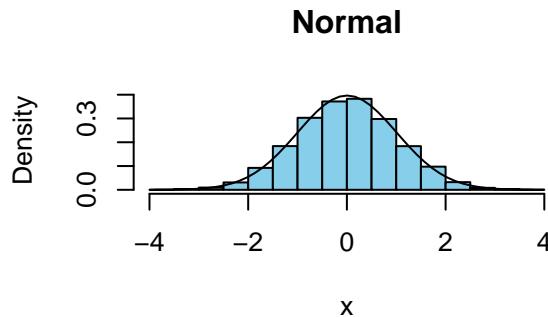
```
library(TeachingDemos)
```

This package has four distributions, the normal, the gamma, the uniform, and the beta. They each have different degrees of symmetry/skewness.

As a baseline, here are the four distributions,

```
clt.examp(1)
```

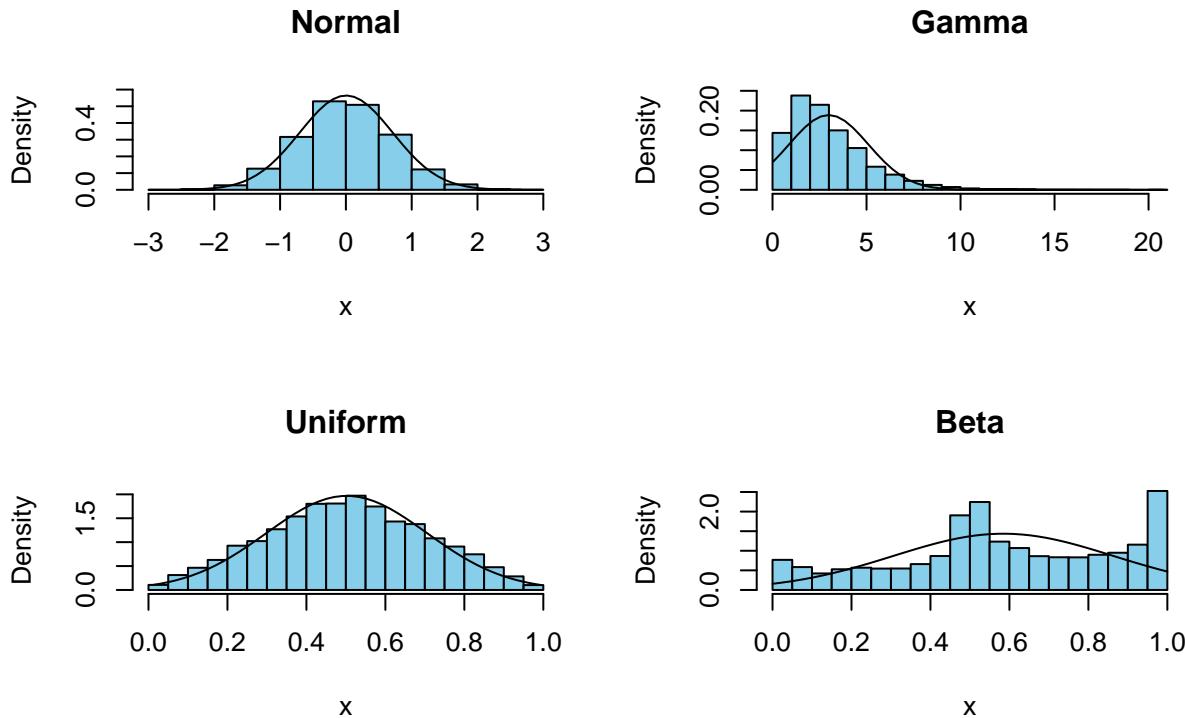
sample size = 1



Now let's plot the distribution of the sample mean from each of these where the sample size is 2.

```
clt.examp(2)
```

sample size = 2

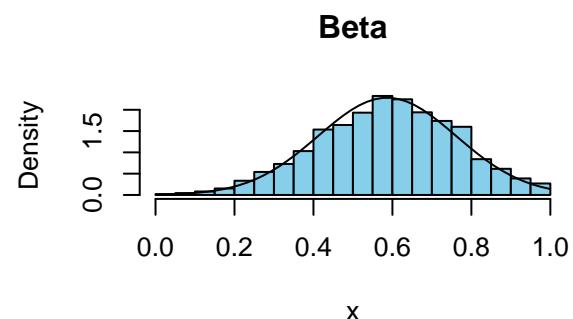
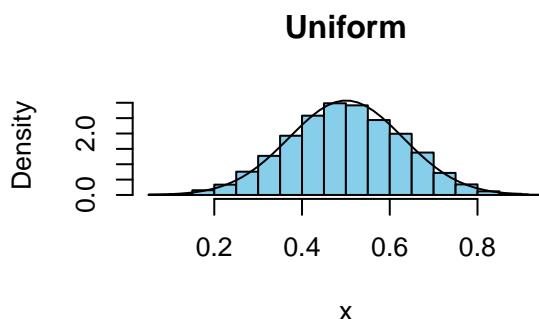
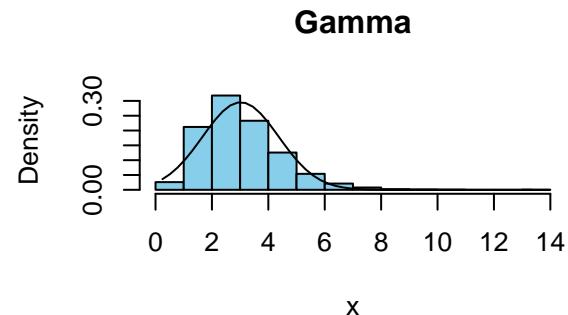
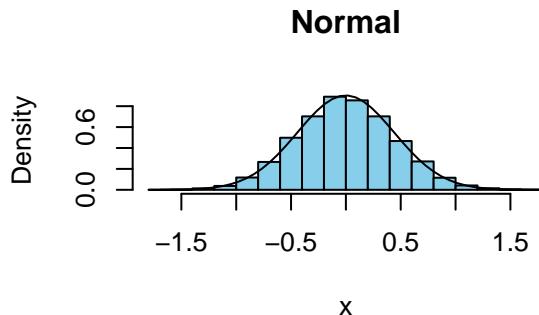


Of course, the sample mean from a normal is already normal. The uniform is already looking like a normal but it was symmetric to begin with.

Now let's take the sample size to 5.

```
clt.examp(5)
```

sample size = 5

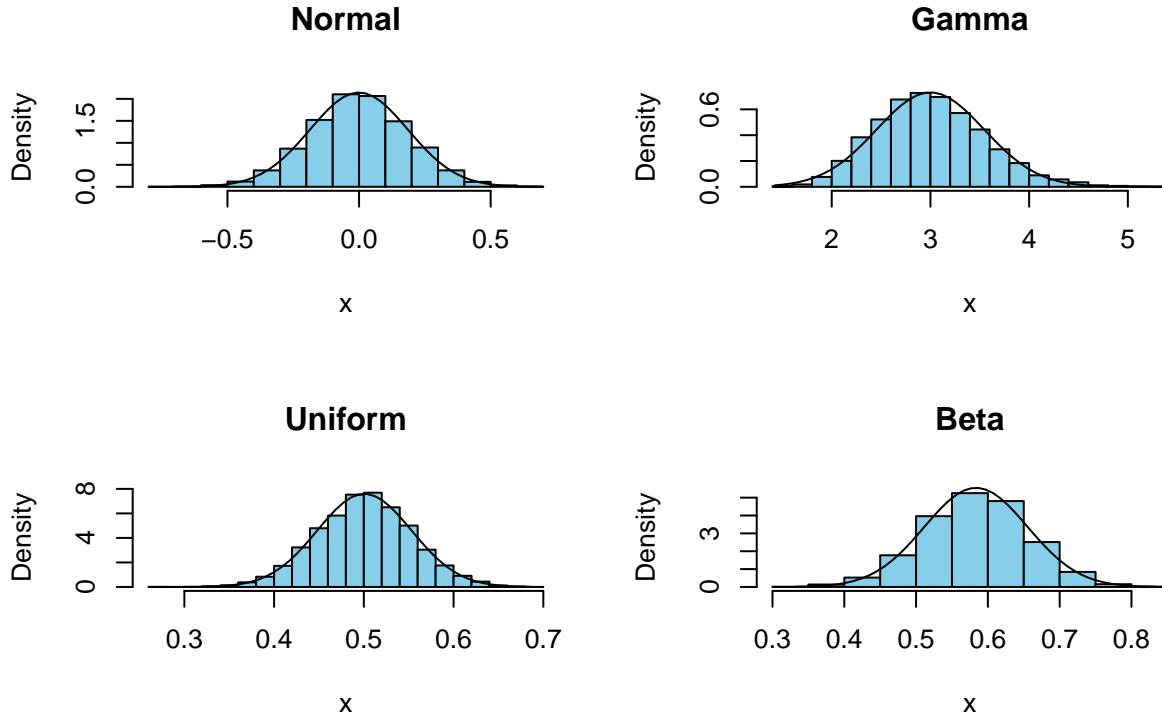


The results are even better.

Finally let's try 30.

```
clt.examp(30)
```

sample size = 30



A better plot would be the q-q plot. But you should get the idea.

In practice, people make the claim that a sample size of 30 is enough to use a normal approximation for the mean.

4.3.6 Continuity Correction

Since the binomial is discrete and the normal is continuous, we can do a better job approximating the binomial with a normal by expanding the limits of integration by 0.50.

```
pbinom(80,100,.75)-pbinom(69,100,.75)

## [1] 0.7966824

pnorm(80,75,sqrt(100*.75*.25))-pnorm(70,75,sqrt(100*.75*.25))

## [1] 0.7517869

pnorm(80.5,75,sqrt(100*.75*.25))-pnorm(69.5,75,sqrt(100*.75*.25))

## [1] 0.7959761
```

4.3.7 Practice

Homework 4.20, 4.21

4.4 Inference for Mean (Variance Known)

4.4.1 Objectives

- 1) Conduct and interpret a hypothesis test for the mean with variance known using correct terminology
- 2) Calculate and interpret a confidence interval for the mean
- 3) Use the link between confidence intervals and hypothesis testing to use confidence intervals for hypothesis testing

4.4.2 Background

The author of textbook does a nice job re-introducing us to the idea of hypothesis testing on page 200. Read the 5 points of the general framework again. The basic idea is that we want to make a decision about a population from a sample since we can't access the entire population due to time, money, or other practical constraints. We use statistics from the sample to make inference about the population.

4.4.3 Problem

We will look at statistical inference, that is obtaining information about a population parameter from a sample, by using both a hypothesis test and a confidence interval. These two ideas are linked and we will explore that relationship as well.

In 2016 there is a proposition, 106 on the Colorado ballot. Briefly, a “yes” vote supports making assisted death legal among patients with a terminal illness who receive a prognosis of death within six months. To estimate if the measure will pass, a poll of 504 voters was taken and 282 stated they would vote yes. Will proposition 106 pass?

To make things simple we will be performing statistical hypothesis testing for the population mean. The population are the voters and we want to estimate the proportion that will vote yes. For simplicity we will ignore not sure and assume that the outcome is either yes or no. Each vote is a binomial random variable $Y \sim \text{Binom}(1, \pi)$ where π is the probability of voting yes on proposition 106. From the method of moments, an estimate of π is \bar{Y} the mean of the number of yes votes from a sample of size n , see homework problem 4.1.

To setup as a hypothesis test, we have

$$H_0 : \pi = 0.50$$

$$H_A : \pi > 0.50$$

where π is the population proportion of yes votes. In Chapter 2, we solved this with the binomial test.

```
binom.test(282,504,.5,alt="greater")
```

```
## 
## 
## 
## data: 282 out of 504
## number of successes = 282, number of trials = 504, p-value =
## 0.004261
## alternative hypothesis: true probability of success is greater than 0.5
## 95 percent confidence interval:
```

```
##  0.5219685 1.0000000
## sample estimates:
## probability of success
##                 0.5595238
```

Now, let's use the Central Limit Theorem. From what we now know about the Central Limit Theorem, we can use a normal because the sample mean, treated as a random variable is

$$\bar{Y} \sim \text{Norm} \left(\pi, \sqrt{\frac{\pi(1-\pi)}{n}} \right)$$

The question is what to use for π in the standard deviation. Most people use the hypothesized value but you could also use the estimated value. Thus the p-value is

```
1-pnorm(282/504,0.50,sqrt(.5*(1-.5)/504))
```

```
## [1] 0.003763158
```

There is a built-in function

```
prop.test(282,504,p=.5,alt="greater",correct=FALSE)
```

```
##
##  1-sample proportions test without continuity correction
##
## data:  282 out of 504
## X-squared = 7.1429, df = 1, p-value = 0.003763
## alternative hypothesis: true p is greater than 0.5
## 95 percent confidence interval:
##  0.5229285 1.0000000
## sample estimates:
##               p
## 0.5595238
```

Since the binomial is discrete, we can do better using the continuity correction.

```
1-pnorm((282-.5)/504,0.50,sqrt(.5*(1-.5)/504))
```

```
## [1] 0.004293556
```

or using built-in function

```
prop.test(282,504,p=.5,alt="greater")
```

```
##
##  1-sample proportions test with continuity correction
##
## data:  282 out of 504
## X-squared = 6.9067, df = 1, p-value = 0.004294
## alternative hypothesis: true p is greater than 0.5
## 95 percent confidence interval:
##  0.5219332 1.0000000
## sample estimates:
##               p
## 0.5595238
```

Notice the output gives us a confidence interval. We will discuss this shortly.

4.4.4 Hypothesis Testing for the Mean

Below we give more insight to hypothesis testing. But example 4.5.1 gives a good example. If we assume that a sample size of 10 is sufficient to use the central limit theorem, a questionable assumption without more support, then to test

$$H_0 : \mu = 5$$

$$H_A : \mu < 5$$

By the Central Limit Theorem, the sample mean is

$$\bar{X} \sim \text{Norm} \left(\mu, \sqrt{\frac{\sigma^2}{n}} \right)$$

This is more difficult than the last example since we don't know σ . To simplify understanding, our author assumes we know σ . In practice this is often not the case but could be if we had historical data. Later in the chapter we will remove this assumption.

We can calculate the p-value as given the null is true. $\mu = 5$, then we want the probability of our data or more extreme.

```
pnorm(4.96,5,0.05/sqrt(10))
```

```
## [1] 0.005706018
```

We may want to know the power of this test. A tool to help us understand power comes from the `TeachingDemos` package. Use the command `run.power.examp(hscale=1.5, vscale=1.5, wait=FALSE)` to experiment.

4.4.4.1 Confidence Intervals

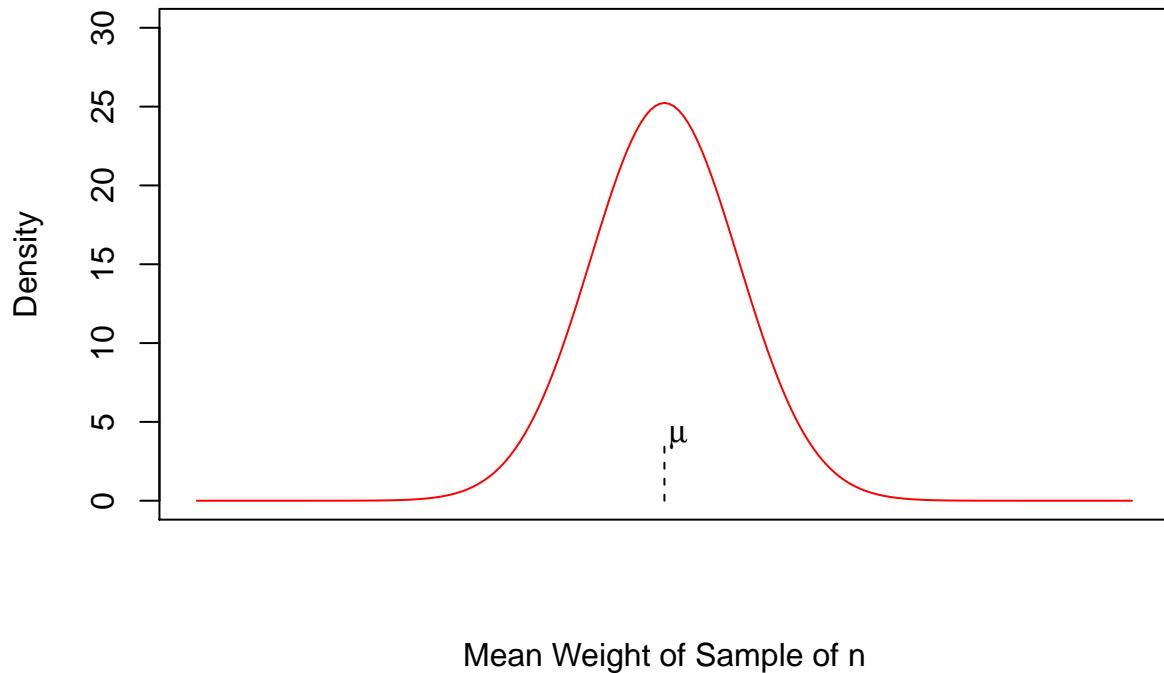
The idea of confidence intervals is to make use of the idea that if the variance is known then the distribution of \bar{X} will be, at least approximately:

$$\bar{X} \sim \text{Norm} \left(\mu, \frac{\sigma}{\sqrt{n}} \right)$$

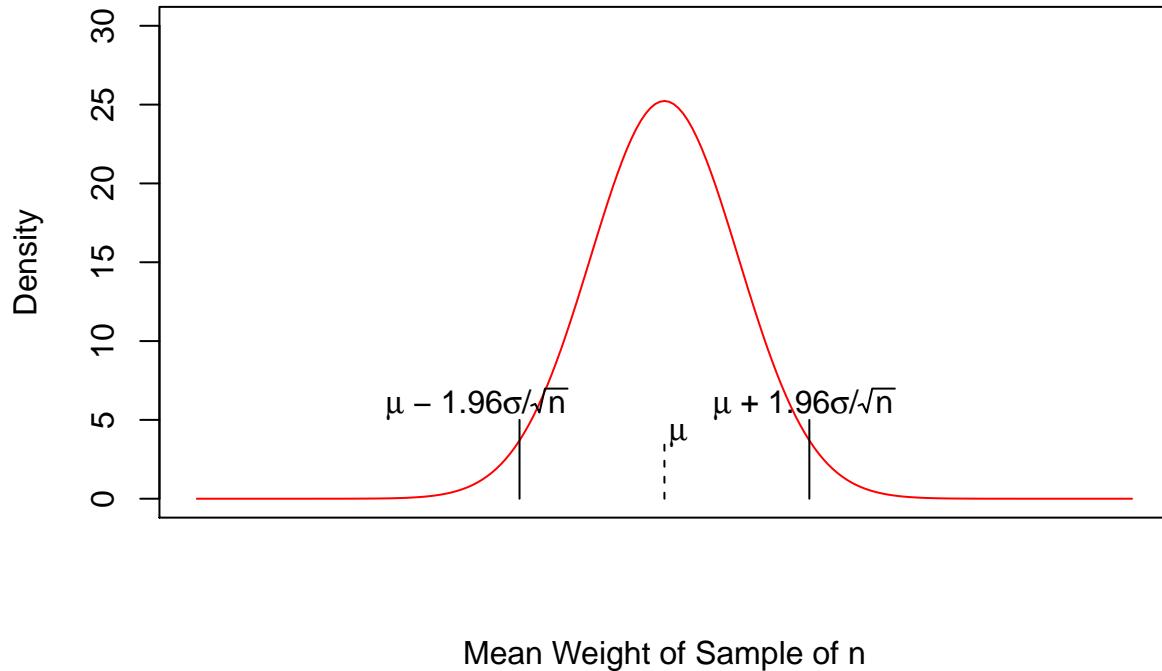
Going back to example 4.5.1, this means that

$$\bar{X} \sim \text{Norm} \left(\mu, \frac{0.05}{\sqrt{10}} \right)$$

A plot of this distribution is

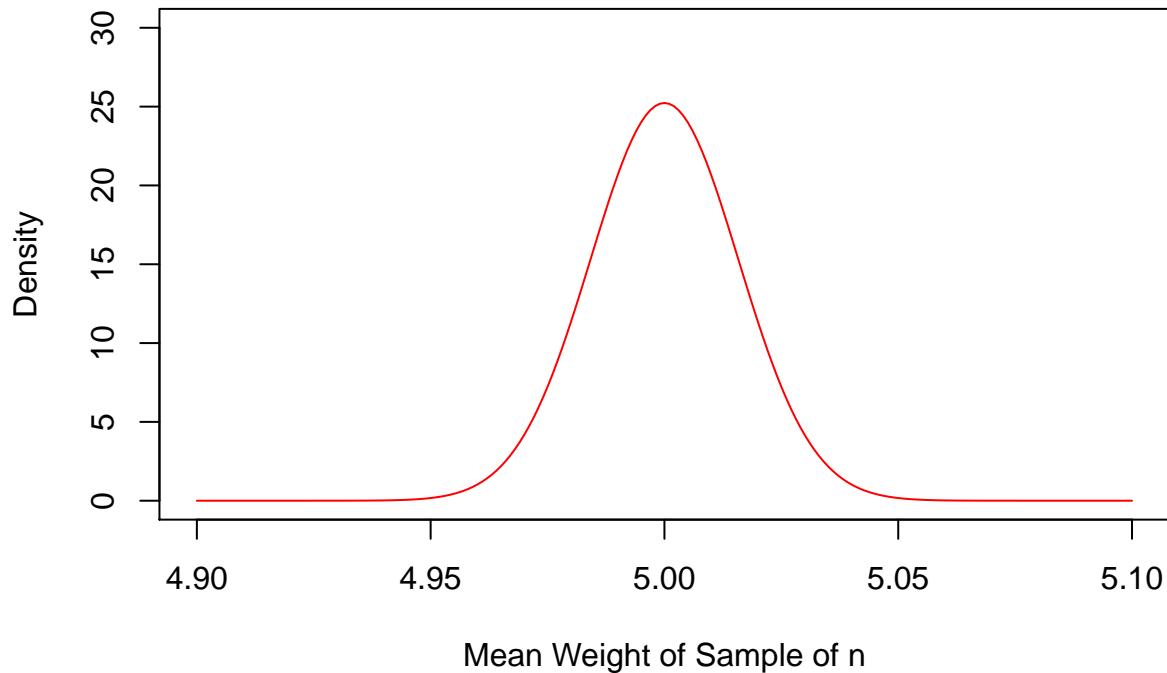


For a normal we know that 95% of the possible value will fall within ± 1.96 standard deviations.

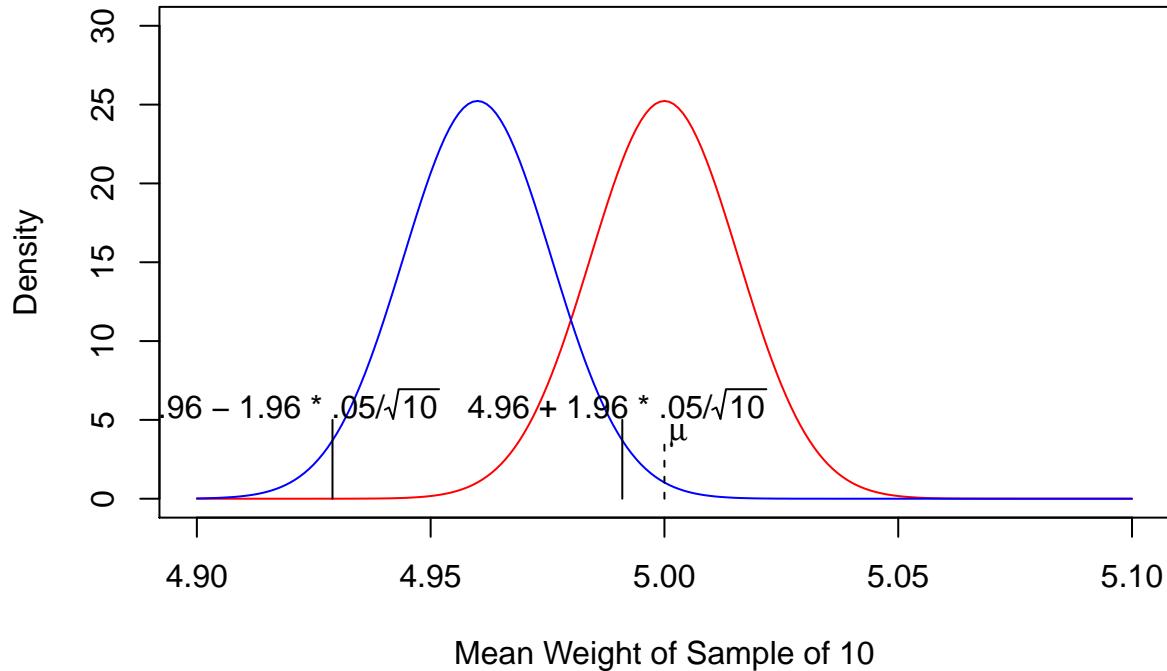


What a confidence interval does is invert this. It centers the distribution on the observed sample mean with the hope that the true mean is captured in an interval.

For our example, the standard deviation was 0.05 and the sample size was 10. Let's pretend that the true mean, unknown to us, is 5. Thus the sampling distribution of the mean would be



Our observed sample mean was 4.96. If we center the distribution on this value we hope that the true unknown population mean is capture in an interval around the value of 4.96.



Our 95% confidence interval in this case is

```
qnorm(.025,4.96,.05/sqrt(10))
```

```
## [1] 4.92901
```

```
qnorm(.975,4.96,.05/sqrt(10))
```

```
## [1] 4.99099
```

or equivalently

```
4.96-qnorm(.975)*.05/sqrt(10)
```

```
## [1] 4.92901
```

```
4.96+qnorm(.975)*.05/sqrt(10)
```

```
## [1] 4.99099
```

The discussion at the bottom of page 202 and top of 203 is important. Once data is used a confidence interval has no random value and thus we cannot use the word probability. Instead we use the word confidence to describe the coverage of the process. That is in our example, if we were to repeat the experiment many times, get 10 weights and calculate the 95% confidence interval, 95% of these intervals will capture the true unknown mean. We know nothing about our one particular interval.

Note that we can also change the coverage of the interval. In the extreme a 100% confidence interval will be over the entire domain and a 0% confidence interval will be the point estimate.

Figure 4.13 in the book illustrates the idea of coverage.

4.4.4.2 Link Between Confidence Intervals and Hypothesis Testing

If my confidence interval does not include the value of the mean under the null hypothesis, then I reject the null hypothesis. It is that simple. One-sided confidence intervals and their relationship to hypothesis testing is a little tricky. Think about it.

4.4.5 Hypothesis Testing Explained in Depth

Let's first start with hypothesis testing. To make things even easier I will use only simple hypothesis of the form:

$$H_0 : \mu = \mu_0$$

$$H_A : \mu = \mu_A$$

This is often not done in practice but it aids in understanding hypothesis testing. To make this concrete lets use example 4.5.1 from the book and modify it to have simple hypotheses.

4.4.5.1 Example 4.5.1 Modified

A manufacturer claims that its 5-pound free weights have a mean weight of 5 pounds with a standard deviation of 0.05 pounds. You believe they have a mean weight of 4.94 pounds. You decided to purchase 10 of these weights and measure them.

Before we continue with this let's setup the hypothesis test

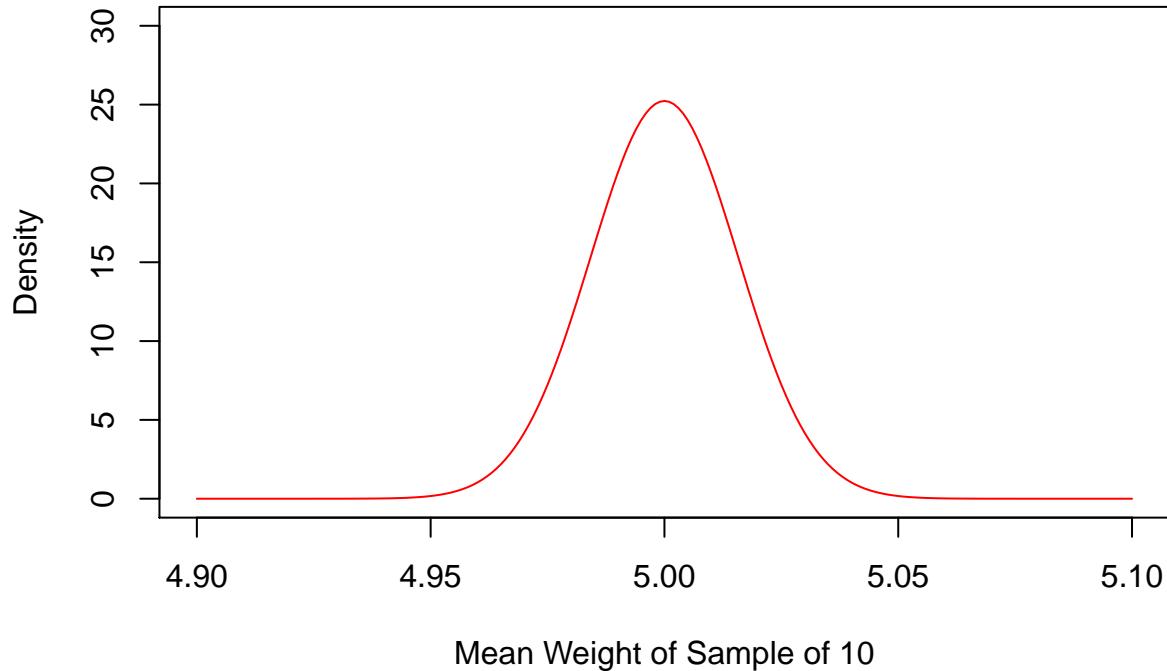
$$H_0 : \mu = 5.0$$

$$H_A : \mu = 4.94$$

We will use \bar{X} as the test statistic to test this hypothesis. If H_0 is true, then

$$\bar{X} \sim \text{Norm} \left(5.0, \frac{0.05}{\sqrt{10}} \right)$$

A plot of this will look like

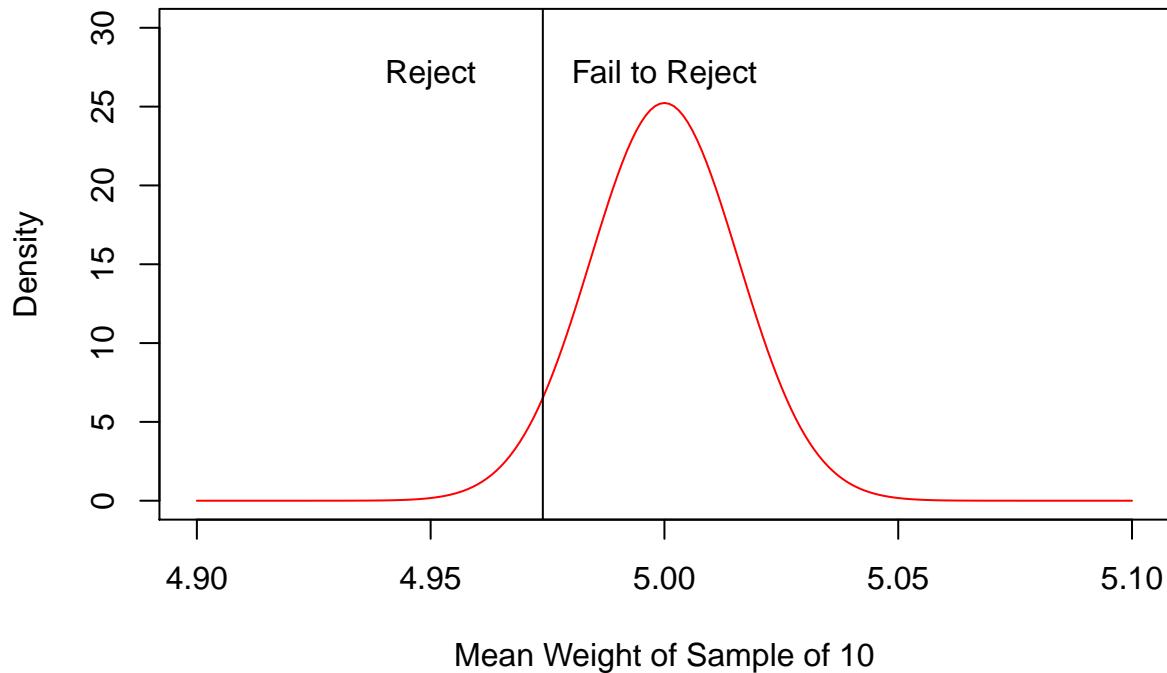


If we use α the level of significance or probability of a Type I error to be 0.05, we can setup a rejection region. Remember that a Type I error occurs when we reject given that the null hypothesis is true. We calculate this rejection region as follows:

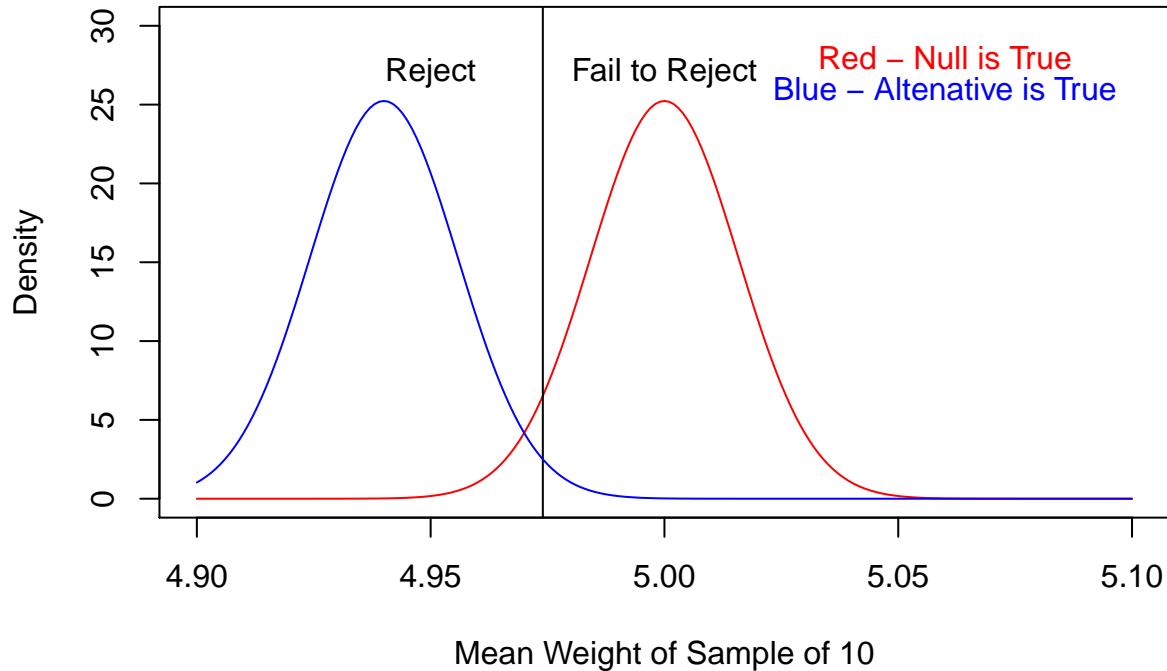
```
qnorm(.05,5,.05/sqrt(10))
```

```
## [1] 4.973993
```

Thus our plot



Now since we know the value of μ under the alternative hypothesis, we can calculate β the probability of a Type II error or its complement power. In the plot, if H_A were true we would have the following



The probability of a Type II error is the probability we fail to reject, given the alternative is true. In R we calculate this as

```
1-pnorm(4.973993, 4.94, .05/sqrt(10))
```

```
## [1] 0.01578132
```

So the power, the probability we reject given the alternative is true is

```
pnorm(4.973993, 4.94, .05/sqrt(10))
```

```
## [1] 0.9842187
```

Now that we have setup our test, we collect data. Here is the data for the weights of the 10 free weights

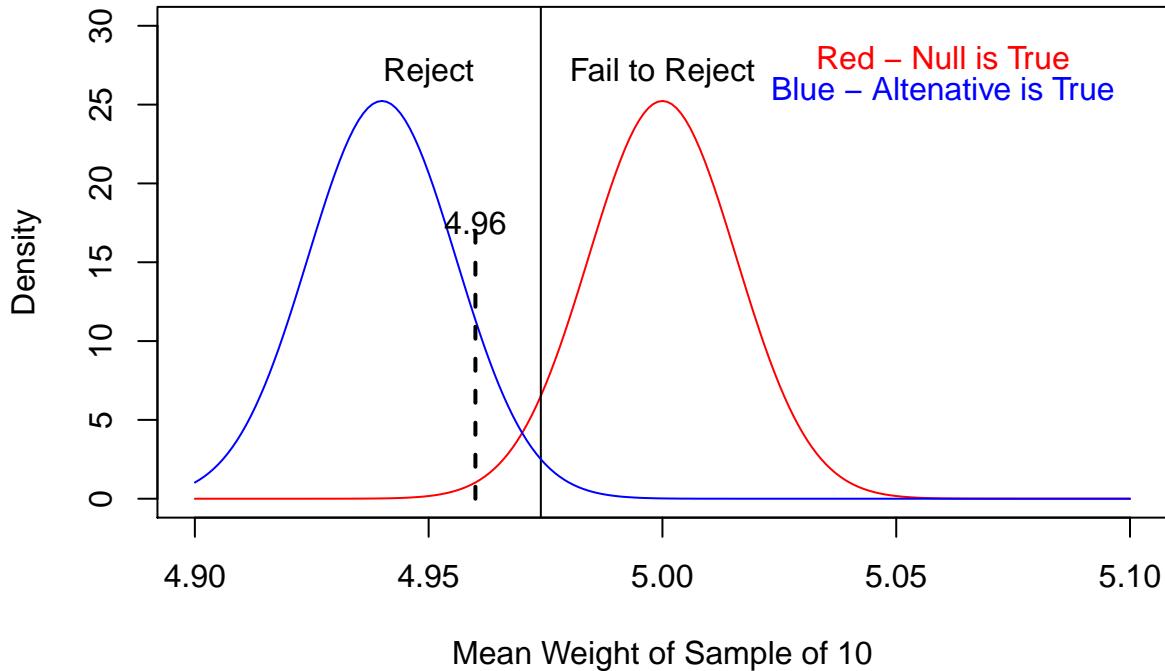
```
Less25Data
```

```
## [1] 4.9 5.0 5.0 5.0 4.8 4.9 4.9 4.9 5.0 5.2
```

```
mean(Less25Data)
```

```
## [1] 4.96
```

Our observed sample mean, \bar{x} is 4.96. In the plot, we have



Thus we reject. We could also calculate the p-value, the probability of the data or more extreme given that the null hypothesis is true.

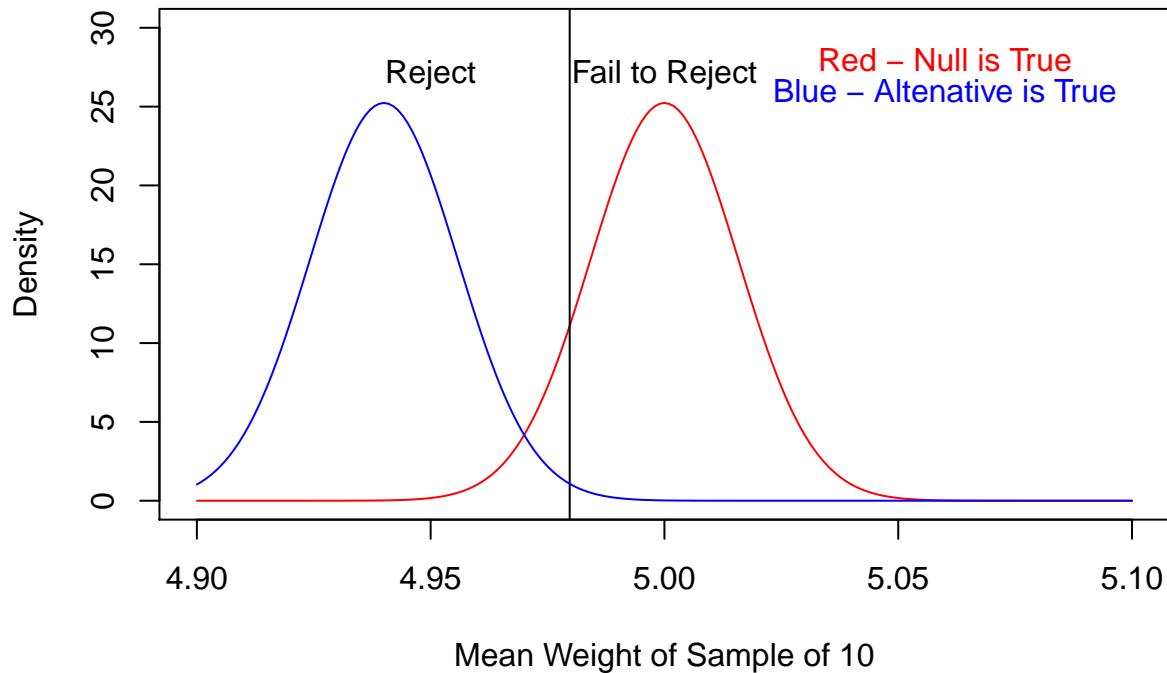
```
pnorm(4.96,5,.05/sqrt(10))
```

```
## [1] 0.005706018
```

Since the p-value is less than α we reject the null in favor of the alternative. That is based on our data, a sample of ten weights, if the true mean weight were 5 pounds, the probability of observing the sample mean of 4.96 or less is .006, thus we reject that the mean weight is 5 pounds in favor of the hypothesis that the mean weight is 4.94 pounds.

Now let's see what happens when we change some of the conditions of the problem.

1. First we will change α to 0.10. Here is the plot



The power of this test is

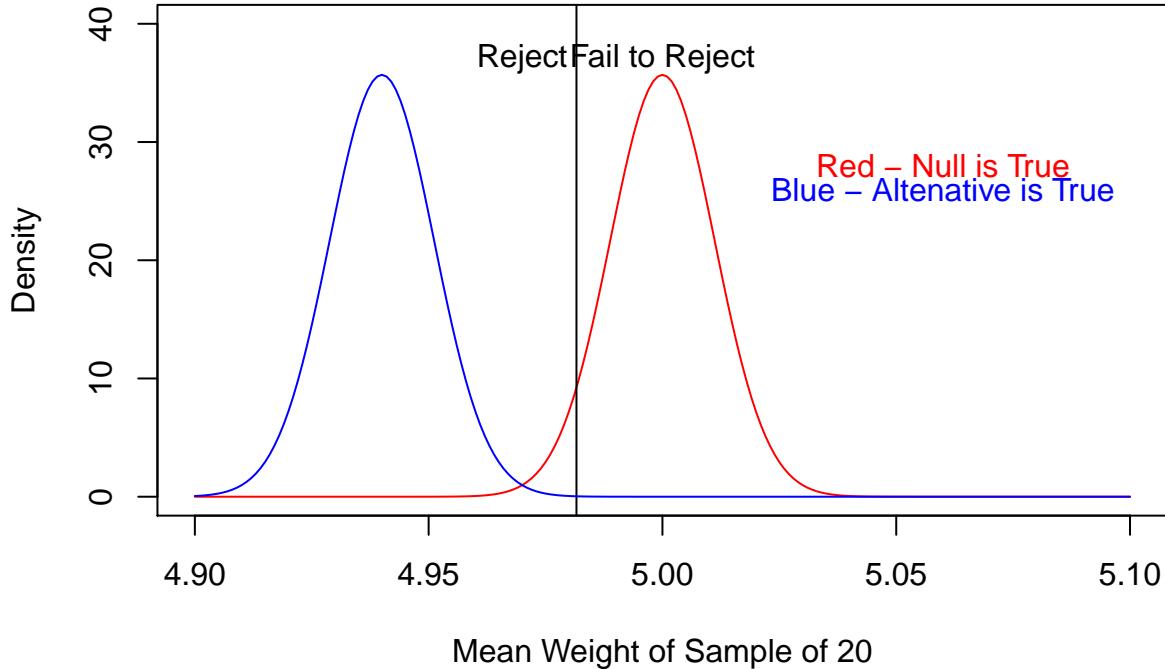
```
qnorm(.1,5,.05/sqrt(10))
```

```
## [1] 4.979737
pnorm(4.979737,4.94,.05/sqrt(10))
```

```
## [1] 0.9940177
```

Keeping everything the same, increasing α decreases β or equivalently increases power.

2. Change sample size, but leave α at 0.05. Here is the plot for a sample size of 20.



Here the power changed to

```
qnorm(.1,5,.05/sqrt(20))
## [1] 4.985672
pnorm(4.985672,4.94,.05/sqrt(20))
## [1] 0.999978
```

And the p-value, assuming that the sample mean still stayed at 4.96, is

```
pnorm(4.96,5,.05/sqrt(20))
```

```
## [1] 0.0001733097
```

3. It should be obvious what happens if we change the value of the alternative hypothesis keeping everything else the same.

In practice we use a complex alternative hypothesis such as

$$H_A : \mu \neq \mu_0$$

or

$$H_A : \mu < \mu_0$$

All the ideas are the same except that we don't know the value of μ under the alternative hypothesis and thus can't calculate power. What is done in practice is to specify a practical difference in means between the null and alternative hypothesis. That is, you need a subject matter expert to answer the question "How much would the mean have to differ from the null value for it to matter?" Then what is done is that power is specified, typically 0.8 or greater, and a sample size calculated.

The example 4.5.1 in the book show how to calculate the p-value for a two-sided test of means with a known variance. It also gives a nice summary of the possible interpretations of the results.

4.5 Estimating Variance

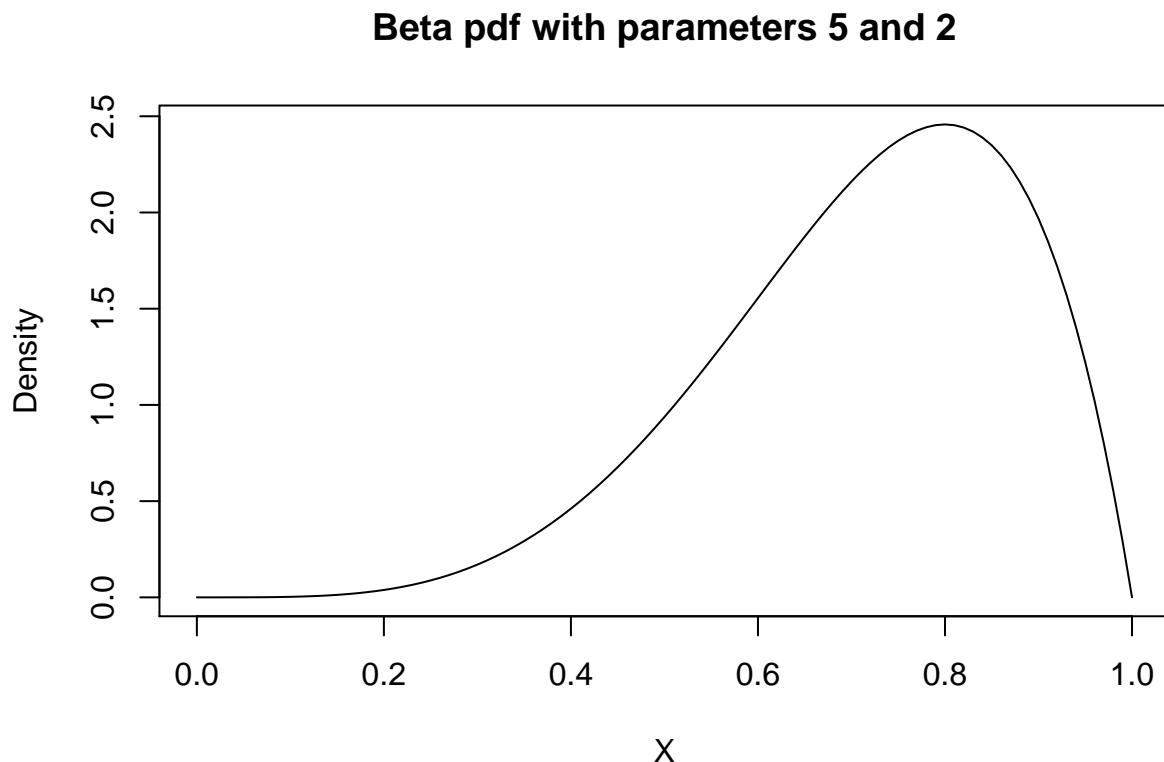
4.5.1 Objectives

1. Know the assumptions for hypotheses tests of the mean and associated confidence intervals for both known and unknown variance and interpret the results of these tests or confidence intervals
2. Know the link between and the important properties of the Chi-square, t, z, and F distributions.
Know how these distributions relate to the sample variance
3. Know and apply the rules of thumb for inferences about the mean

4.5.2 Sample Variance

The first idea of this lesson is that the sample variance is an unbiased estimator of population variance. The book shows this from a theoretical approach. We will do it using simulation in R.

I will pick a Beta distribution with parameters $\alpha=5$ and $\beta=2$, but you can select any other distribution. Here is a plot



From theory we know the variance of a Beta is

$$\frac{\alpha\beta}{(\alpha + \beta)^2(\alpha + \beta + 1)}$$

or for our specific problem

```
(5*2)/((5+2)^2*(5+2+1))
```

```
## [1] 0.0255102
```

Let's take a sample of size 10 from this distribution and find the sample variance (set the seed for reproducibility)

```
var(rbeta(10,5,2))
```

```
## [1] 0.02815764
```

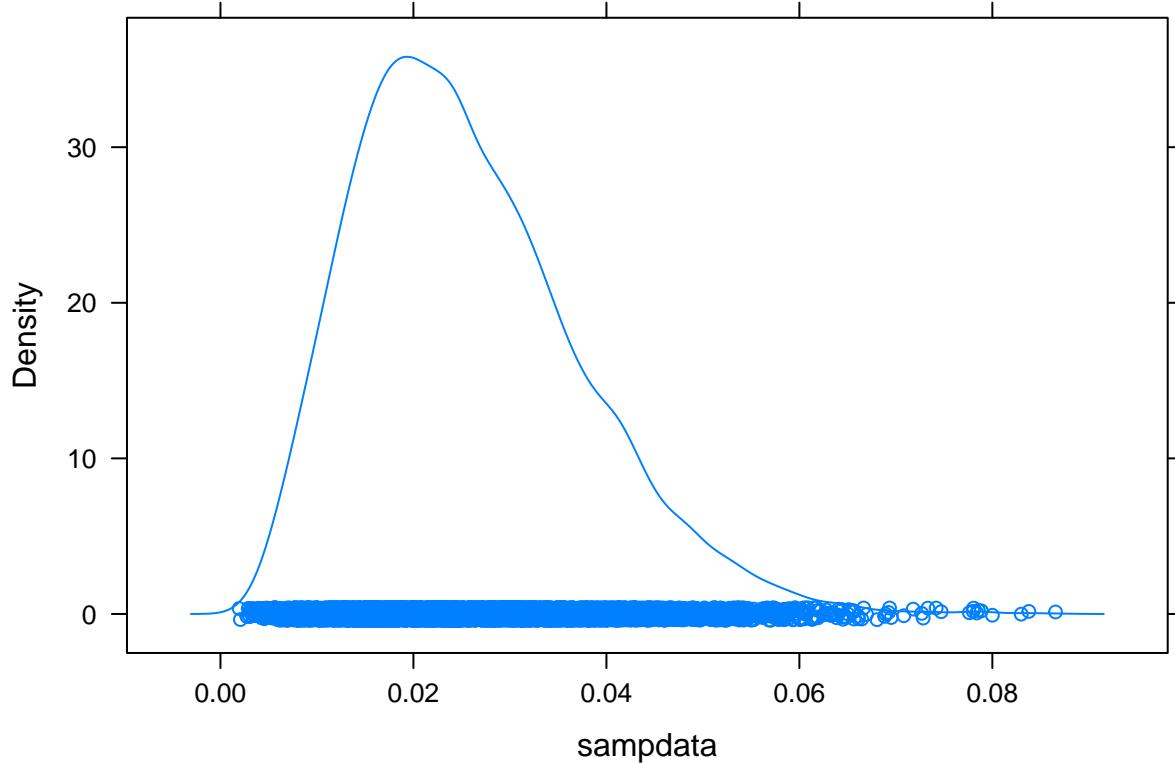
Now let's get the sampling distribution of the sample variance for this distribution using simulation

```
sampdata<-replicate(10000,var(rbeta(10,5,2)))
```

A plot of the data

```
library(fastR)
```

```
densityplot(sampdata)
```



The mean of this is

```
mean(sampdata)
```

```
## [1] 0.02558336
```

Which is close to the true population variance. Thus it seems reasonable that the sample variance is an unbiased estimator.

Note that dividing by n instead of $n - 1$ leads to a biased estimator.

```
sampdata2<-replicate(10000,var(rbeta(10,5,2))*(.9))
mean(sampdata2)
```

```
## [1] 0.02302502
```

You can change the sample size to convince yourself that it is a consistent estimator. Also note that sample standard deviation is a biased estimator of population standard deviation.

4.5.3 Inference for Variance

Remember to perform statistical inference we need an estimator of the population parameter and its distribution.

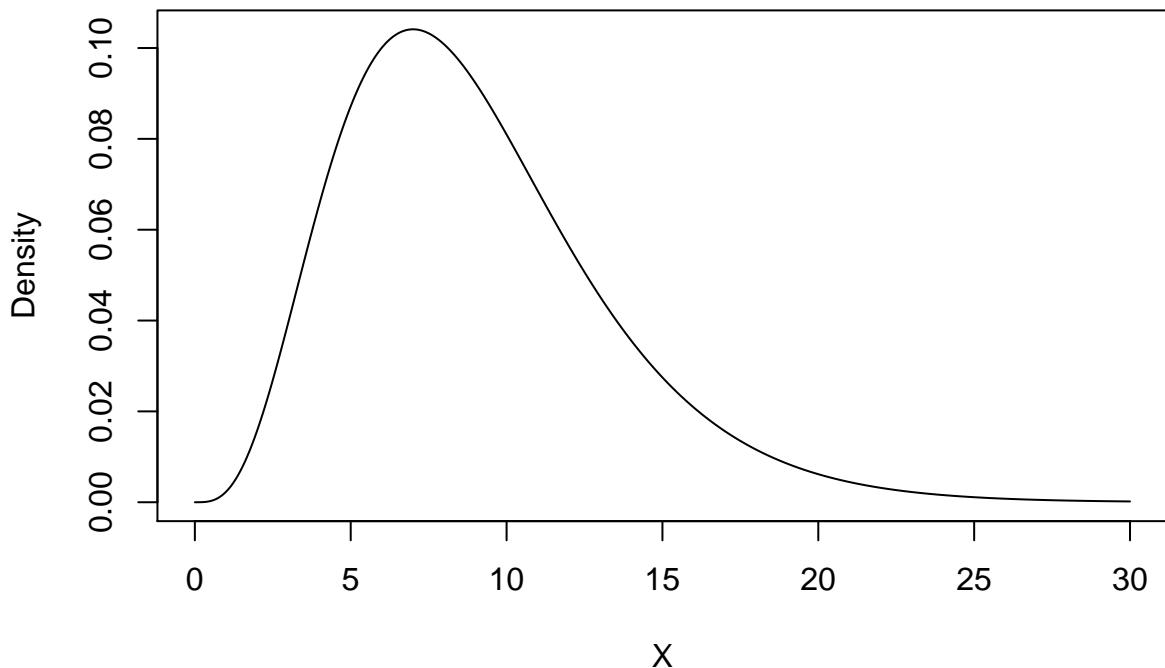
If the parent population is Normal, $X_i \stackrel{iid}{\sim} \text{Norm}(\mu, \sigma)$ then sample variance has a chi-squared distribution. This allows us to make inference about variance. Formally

$$\frac{(n-1)S^2}{\sigma^2} \sim \text{Chisq}(n-1) \text{ or } \chi^2(n-1)$$

To see what a chi-squared distribution looks like, plot it

```
plot(seq(0,30,.01),dchisq(seq(0,30,.01),9),type="l",
     xlab="X",ylab="Density",main="Chi-square with 9 degrees of freedom")
```

Chi-square with 9 degrees of freedom



Using the example from last class

Less25Data

```
## [1] 4.9 5.0 5.0 5.0 4.8 4.9 4.9 4.9 5.0 5.2
```

If we believe the parent population is Normal, then we could calculate a 95% confidence interval for the variance as follows

$$qchisq(.025, 9) \leq \frac{(n - 1)S^2}{\sigma^2} \leq qchisq(.975, 9)$$

or

$$\frac{(n - 1)S^2}{qchisq(.975, 9)} \leq \sigma^2 \leq \frac{(n - 1)S^2}{qchisq(.025, 9)}$$

For our problem, the limits are

```
9*var(Less25Data)/qchisq(.975,9)
```

```
## [1] 0.005467133
```

```
9*var(Less25Data)/qchisq(.025,9)
```

```
## [1] 0.03851296
```

4.5.4 Inference for Mean when Population Variance is Unknown

Next, let's look at inference of the mean where the variance is unknown. In this case, the test statistic is

$$T = \frac{\bar{X} - \mu}{\frac{S}{\sqrt{n}}}$$

This sampling distribution is called a t-distribution and is a ratio of a standard normal and chi-squared. It has one parameter, the degrees of freedom which is $n - 1$.

The assumptions of this test are that the sample is iid from a normal distribution.

The t-distribution is similar to the normal except that it has more density in the tails and center.

We could test the hypothesis from last lesson assuming we don't know the variance. Let the test be

$$H_0 : \mu = 5.0$$

$$H_A : \mu \neq 5.0$$

and again the data is

Less25Data

```
## [1] 4.9 5.0 5.0 5.0 4.8 4.9 4.9 4.9 5.0 5.2
```

```
mean(Less25Data)
```

```
## [1] 4.96
```

```
var(Less25Data)
```

```
## [1] 0.01155556
```

The test statistic is

```
(Less25teststat<-(mean(Less25Data)-5)/sqrt(var(Less25Data)/10))
```

```
## [1] -1.176697
```

The p-value is

```
2*pt(Less25teststat,9)
```

```
## [1] 0.2694995
```

We could generate a 95% confidence interval as well. Since we know that

$$T = \frac{\bar{X} - \mu}{\frac{s}{\sqrt{n}}} \sim t(n - 1)$$

we get

$$\bar{x} \pm t_{(.025,9)} \frac{s}{\sqrt{n}}$$

In R

```
mean(Less25Data)+c(1,-1)*qt(.025,9)*sqrt(var(Less25Data)/length(Less25Data))
```

```
## [1] 4.883101 5.036899
```

Of course there is a function in R that does this all for us

```
t.test(Less25Data, mu=5)
```

```
##
##  One Sample t-test
##
## data: Less25Data
## t = -1.1767, df = 9, p-value = 0.2695
## alternative hypothesis: true mean is not equal to 5
## 95 percent confidence interval:
##  4.883101 5.036899
## sample estimates:
## mean of x
##      4.96
```

The most important section of the lesson is the ideas of robustness and rules of thumb. Read these.

4.5.4.1 Practice

Try 4.29, 4.39

4.6 Two Additional Tests

4.6.1 Objectives

1. Construct and interpret Wald, Score, Wilson, and Clopper-Pearson confidence intervals for a proportion
2. Conduct and interpret a paired hypothesis test using t-test, sign test, and confidence intervals
3. Know the assumptions of the paired t-test

4.6.1.1 Confidence Intervals for Proportions

In Chapter 2 we made hypothesis tests about π the proportions of successes in a binomial trial. In this lesson we will generate confidence intervals.

To put things in context we will use an example. In game 7 of the 2014 World Series, the National League champion San Francisco Giants' pitcher Madison Bumgarner threw 50 strikes in 68 pitches. Let's use this data to estimate his true unknown proportion of strikes.

The first interval uses the normal approximation to the binomial. The confidence interval then is

$$\hat{\pi} \pm z_{\alpha/2} \sqrt{\frac{\hat{\pi}(1 - \hat{\pi})}{n}}$$

In R, the limits of the confidence interval are:

```
(phat<-50/68)
```

```
## [1] 0.7352941
phat+c(1,-1)*qnorm(.025)*sqrt(phat*(1-phat)/68)
```

```
## [1] 0.6304351 0.8401532
```

If I wanted to get fancy, I could write my own function in r;

```
wald.ci=function(x,n,conf.level=.95,alternative = c("two.sided", "less", "greater")){
  DNAME <- deparse(substitute(x))
  DNAME <- paste(DNAME, "successes and", deparse(substitute(n)), "trials")
  alternative <- match.arg(alternative)
  CONFINT <- switch(alternative,
    two.sided = x/n +
      c(-1,1)*qnorm(1-(1-conf.level)/2)*sqrt(x/n*(1-x/n)/n),
    less = c(-Inf, x/n+qnorm(conf.level)*sqrt(x/n*(1-x/n)/n)),
    greater = c(x/n-qnorm(conf.level)*sqrt(x/n*(1-x/n)/n), Inf)
  )
  attr(CONFINT,"conf.level")<-conf.level
  structure(list(conf.int=CONFINT,data.name=DNAME),class="htest")
}
```

```
wald.ci(50,68)
```

```
##
##
##
## data: 50 successes and 68 trials
##
## 95 percent confidence interval:
##  0.6304351 0.8401532
```

The score interval works by inverting the hypothesis test

```
(phat+qnorm(.025)^2/(2*68)+c(1,-1)*qnorm(.025)*sqrt(phat*(1-phat)/68+qnorm(.025)^2/(4*68^2)))/(1+qnorm(
```

```
## [1] 0.6199227 0.8255026
```

This is also what we get from

```
prop.test(50,68,correct=FALSE)
```

```
##
## 1-sample proportions test without continuity correction
##
## data: 50 out of 68
## X-squared = 15.059, df = 1, p-value = 0.0001042
## alternative hypothesis: true p is not equal to 0.5
## 95 percent confidence interval:
## 0.6199227 0.8255026
## sample estimates:
##          p
## 0.7352941
```

The Wilson is a plus 4 and we get as follows

```
(phat<-52/72)
```

```
## [1] 0.7222222
phat+c(1,-1)*qnorm(.025)*sqrt(phat*(1-phat)/72)
## [1] 0.6187638 0.8256807
```

The Clopper-Pearson comes from looking at a beta distribution. Here is some code

```
CPCI<-function(x, n, alternative = c("two.sided", "upper", "lower"), conf.level = 0.95, ... ){
  alternative <- match.arg(alternative)
  phat <- (x)/(n)
  out <- list(method="Clopper-Pearson Confidence Interval")
  class(out) <- 'htest'
  out$parameter <- c("Sample size"=n, "Number of Successes" = x)
  out$conf.int <- switch(alternative,
    two.sided = c(qbeta((1-conf.level)/2,x,n-x+1),qbeta(1-(1-conf.level)/2,x+1,n-x)),
    upper = c(0, qbeta(conf.level,x+1,n-x)),
    lower = c(qbeta(1-conf.level,x,n-x+1), 1)
  )
  attr(out$conf.int, "conf.level") <- conf.level
  out$statistic <- phat
  out$data.name <- "Data entered as summary numbers"
  names(out$statistic) <- "Estimated probability of success"

  return(out)
}
```

```
CPCI(50,68)
```

```
##
## Clopper-Pearson Confidence Interval
##
## data: Data entered as summary numbers
## Estimated probability of success = 0.73529, Sample size = 68,
## Number of Successes = 50
## 95 percent confidence interval:
## 0.6142896 0.8349615
```

But this is what `binom.test` returns

```
binom.test(50,68)
```

```
##
```

```
##
## data: 50 out of 68
## number of successes = 50, number of trials = 68, p-value =
## 0.0001308
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
## 0.6142896 0.8349615
## sample estimates:
## probability of success
## 0.7352941
```

The book mentions that the best comprise in terms of coverage is the score interval.

4.6.1.2 Paired Tests

```
library(fastr)
library(MASS)
```

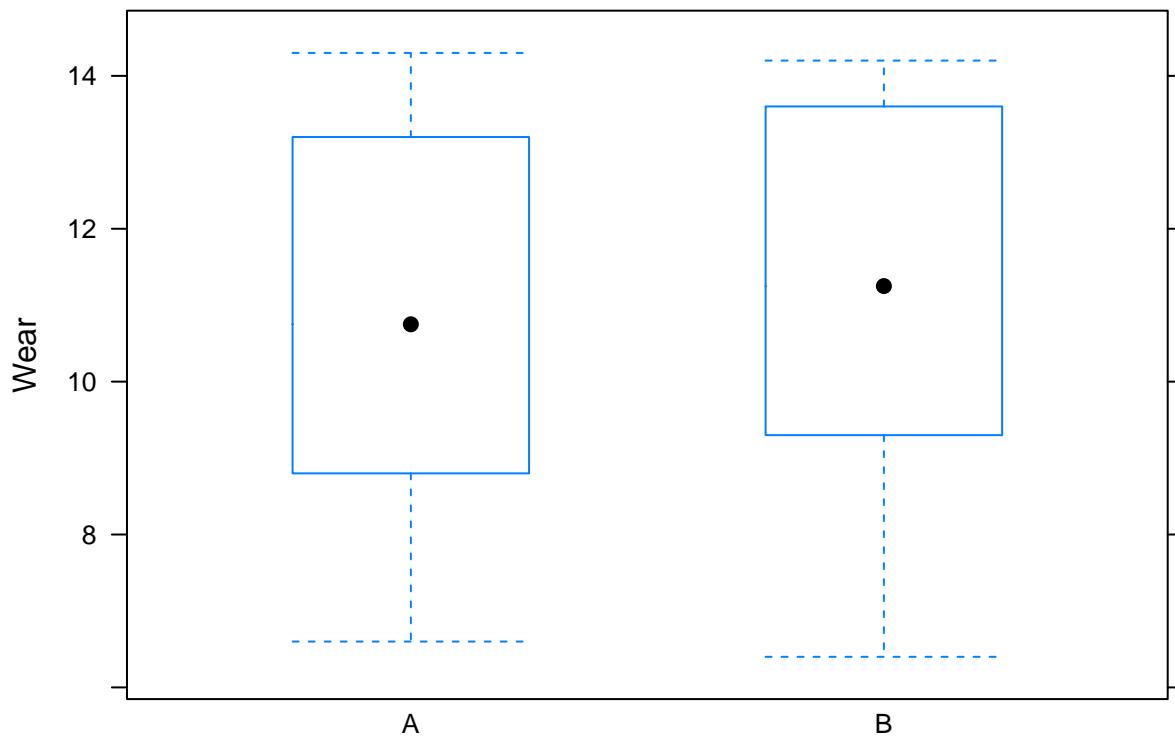
Suppose I want to test the wear of a material on the sole of a shoe. I put the shoes on 20 boys. Here is the data

Shoe

```
##   Boy Wear Material
## 1  1 13.2      A
## 2  2  8.2      A
## 3  3 10.9      A
## 4  4 14.3      A
## 5  5 10.7      A
## 6  6  6.6      A
## 7  7  9.5      A
## 8  8 10.8      A
## 9  9  8.8      A
## 10 10 13.3     A
## 11  1 14.0     B
## 12  2  8.8     B
## 13  3 11.2     B
## 14  4 14.2     B
## 15  5 11.8     B
## 16  6  6.4     B
## 17  7  9.8     B
## 18  8 11.3     B
## 19  9  9.3     B
## 20 10 13.6     B
```

If I simply look at the two materials it does not appear there is much of a difference

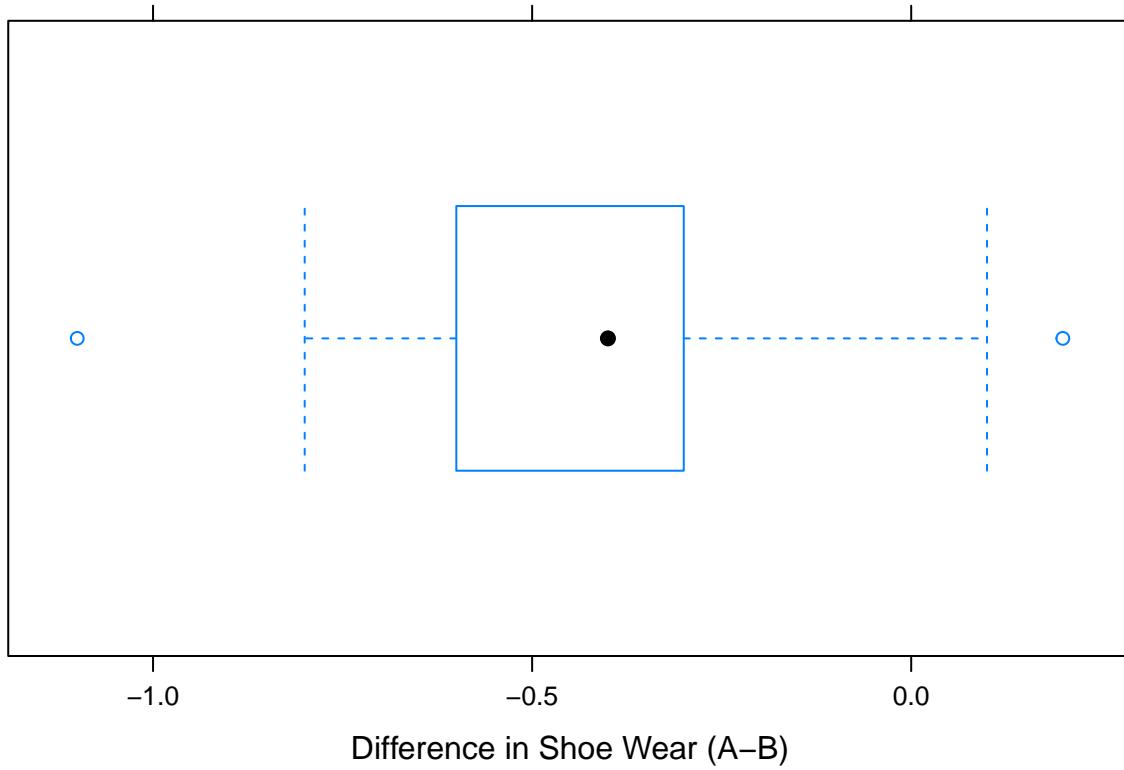
```
bwplot(Wear~Material,Shoe)
```



This is because there is so much variability in wear from boy to boy and this variance masks the difference in the materials. Thus the experiments put each type of material on each of the shoes for the boys. Thus one shoe had type A and the other type B. This is called a blocked design or paired design. Now I look at the difference in wear within the boys. This data looks like

```
Shoe[1:10,2]-Shoe[11:20,2]
```

```
## [1] -0.8 -0.6 -0.3  0.1 -1.1  0.2 -0.3 -0.5 -0.5 -0.3
bwplot(~Shoe[1:10,2]-Shoe[11:20,2],xlab="Difference in Shoe Wear (A-B)")
```



The hypothesis test is

$$H_0 : D = 0$$

$$H_A : D \neq 0$$

where D is the difference. If the differences are iid and normal, then I can use a t-test on this data.

First we could get the data in wide format

```
Shoe2<-reshape(Shoe,v.names="Wear",direction="wide",idvar="Boy",timevar="Material")
t.test(Shoe[1:10,2]-Shoe[11:20,2])

##
##  One Sample t-test
##
## data: Shoe[1:10, 2] - Shoe[11:20, 2]
## t = -3.3489, df = 9, p-value = 0.008539
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## -0.6869539 -0.1330461
## sample estimates:
## mean of x
##      -0.41
t.test(Shoe2["Wear.A"]-Shoe2["Wear.B"])

##
```

```

## One Sample t-test
##
## data: Shoe2["Wear.A"] - Shoe2["Wear.B"]
## t = -3.3489, df = 9, p-value = 0.008539
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## -0.6869539 -0.1330461
## sample estimates:
## mean of x
##      -0.41

t.test(diff(Shoe[,2],lag=10))

##
## One Sample t-test
##
## data: diff(Shoe[, 2], lag = 10)
## t = 3.3489, df = 9, p-value = 0.008539
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## 0.1330461 0.6869539
## sample estimates:
## mean of x
##      0.41

or

t.test(Wear~Material,data=Shoe,paired=T)

##
## Paired t-test
##
## data: Wear by Material
## t = -3.3489, df = 9, p-value = 0.008539
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.6869539 -0.1330461
## sample estimates:
## mean of the differences
##      -0.41

```

We conclude that there is a difference in the mean differential wear on the materials.

4.6.1.3 Signed test

If the assumption that the differences are normal is not reasonable, we could use the sign test. This test makes no assumptions about the distribution other than it is continuous. The idea is that if the two materials came from the same distribution, then half the time one should be larger than the other. Thus the hypothesis is

$$H_0 : \pi = 0.5$$

$$H_A : \pi \neq 0.5$$

I can test this with the binomial `binom.test`.

```
Shoe[1:10,2]>Shoe[11:20,2]
```

```
## [1] FALSE FALSE FALSE TRUE FALSE TRUE FALSE FALSE FALSE
sum(Shoe[1:10,2]>Shoe[11:20,2])
```

```
## [1] 2
binom.test(sum(Shoe[1:10,2]>Shoe[11:20,2]),10)
```

```
##
##
##
## data: sum(Shoe[1:10, 2] > Shoe[11:20, 2]) out of 10
## number of successes = 2, number of trials = 10, p-value = 0.1094
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
## 0.02521073 0.55609546
## sample estimates:
## probability of success
## 0.2
```

So we fail to reject that there is a difference. Because of the small sample size, the fewer assumptions makes this test have less power.

In the case of ties, most people exclude that observation. Here is my function to do this.

```
sign.test=function(x, y = NULL, md = 0, alternative = c("two.sided", "less", "greater"), conf.level = 0.95) {
  if(is.null(y)) y=rep(md,length(x))
  if(sum(which(x==y))!=0){
    xx=x
    yy=y
    x=xx[-1*which(xx==yy)]
    y=yy[-1*which(xx==yy)]
  }
  ans=binom.test(sum(x>y),length(x),alternative=alternative,conf.level=conf.level)
  ans$method="Sign Test"
  return(ans)
}

sign.test(Shoe[1:10,2],Shoe[11:20,2])

##
## Sign Test
##
## data: sum(x > y) out of length(x)
## number of successes = 2, number of trials = 10, p-value = 0.1094
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
## 0.02521073 0.55609546
## sample estimates:
## probability of success
## 0.2
```

4.7 Permutations Tests

4.7.1 Objectives

1. Create a test statistic and calculate empirical p-values in R
2. Conduct permutation tests in R

4.7.2 Introduction

This is one of the most important sections of this course as it gives us an idea how the use of technology is altering the way statistical inference is done. In this section we will learn how to perform statistical inference using a computer thus removing the need to know exact sampling distributions.

This is our first departure from a traditional statistics course and an introduction to computer-intensive methods.

4.7.3 Review

Let's start with a review of the paired t-test. We have two methods that measure the strength of a material. Since the variation in strength may vary greatly from sample to sample, we test both methods on each sample. Here is the data

```
Less28.Strength.Data<-data.frame(Method1=c(38.25,31.68,26.24,41.29,44.81,46.37,35.42,38.41,42.68,46.71,29.20,30.76,38.27,31.71),Method2=c(38.27,31.71,26.22,41.33,44.80,46.39,35.42,38.41,42.68,46.71,29.20,30.76,38.27,31.71))
```

```
##   Method1 Method2
## 1    38.25   38.27
## 2    31.68   31.71
## 3    26.24   26.22
## 4    41.29   41.33
## 5    44.81   44.80
## 6    46.37   46.39
```

A longer form of this data is on the course web site in a file called Less.csv.

We can change the format of the data using reshape library of stack

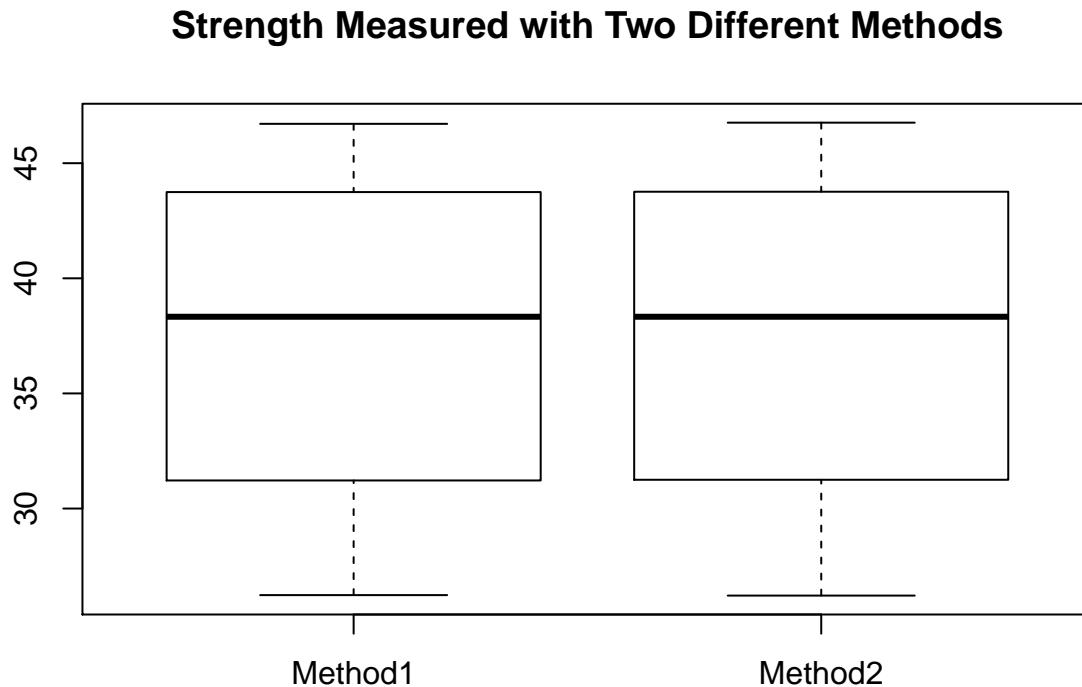
```
(Lesson28StrengthLongForm<-stack(Less28.Strength.Data))
```

```
##   values     ind
## 1  38.25 Method1
## 2  31.68 Method1
## 3  26.24 Method1
## 4  41.29 Method1
## 5  44.81 Method1
## 6  46.37 Method1
## 7  35.42 Method1
## 8  38.41 Method1
## 9  42.68 Method1
## 10 46.71 Method1
## 11 29.20 Method1
## 12 30.76 Method1
## 13 38.27 Method2
## 14 31.71 Method2
```

```
## 15 26.22 Method2
## 16 41.33 Method2
## 17 44.80 Method2
## 18 46.39 Method2
## 19 35.46 Method2
## 20 38.39 Method2
## 21 42.72 Method2
## 22 46.76 Method2
## 23 29.18 Method2
## 24 30.79 Method2
```

A plot of the data:

```
boxplot(values~ind,data=Lesson28StrengthLongForm,main="Strength Measured with Two Different Methods")
```

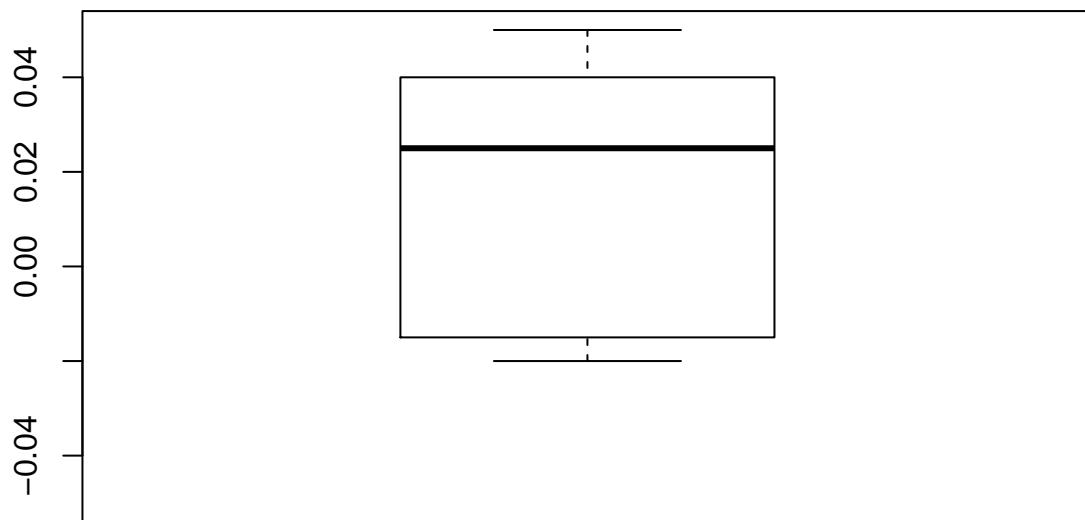


Again, the sample to sample variation is so large that it is hard to see a difference in means. If we look at the differences within sample we get:

```
(Lesson28Strength<-transform(Less28.Strength.Data,Diff=Method2-Method1))
```

```
##   Method1 Method2 Diff
## 1    38.25   38.27  0.02
## 2    31.68   31.71  0.03
## 3    26.24   26.22 -0.02
## 4    41.29   41.33  0.04
## 5    44.81   44.80 -0.01
## 6    46.37   46.39  0.02
## 7    35.42   35.46  0.04
```

```
## 8    38.41  38.39 -0.02
## 9    42.68  42.72  0.04
## 10   46.71  46.76  0.05
## 11   29.20  29.18 -0.02
## 12   30.76  30.79  0.03
boxplot(Lesson28Strength$Diff, ylim=c(-.05, .05))
```



Now the t-test. The following are all equivalent:

```
t.test(Lesson28Strength$Diff)

##
##  One Sample t-test
##
## data: Lesson28Strength$Diff
## t = 2.1589, df = 11, p-value = 0.0538
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
## -0.0003245909  0.0336579242
## sample estimates:
## mean of x
## 0.01666667

t.test(Lesson28Strength$Method2, Lesson28Strength$Method1, paired=T)

##
## Paired t-test
```

```
##
## data: Lesson28Strength$Method2 and Lesson28Strength$Method1
## t = 2.1589, df = 11, p-value = 0.0538
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.0003245909 0.0336579242
## sample estimates:
## mean of the differences
## 0.01666667
t.test(values~ind,data=Lesson28StrengthLongForm,paired=T)
```

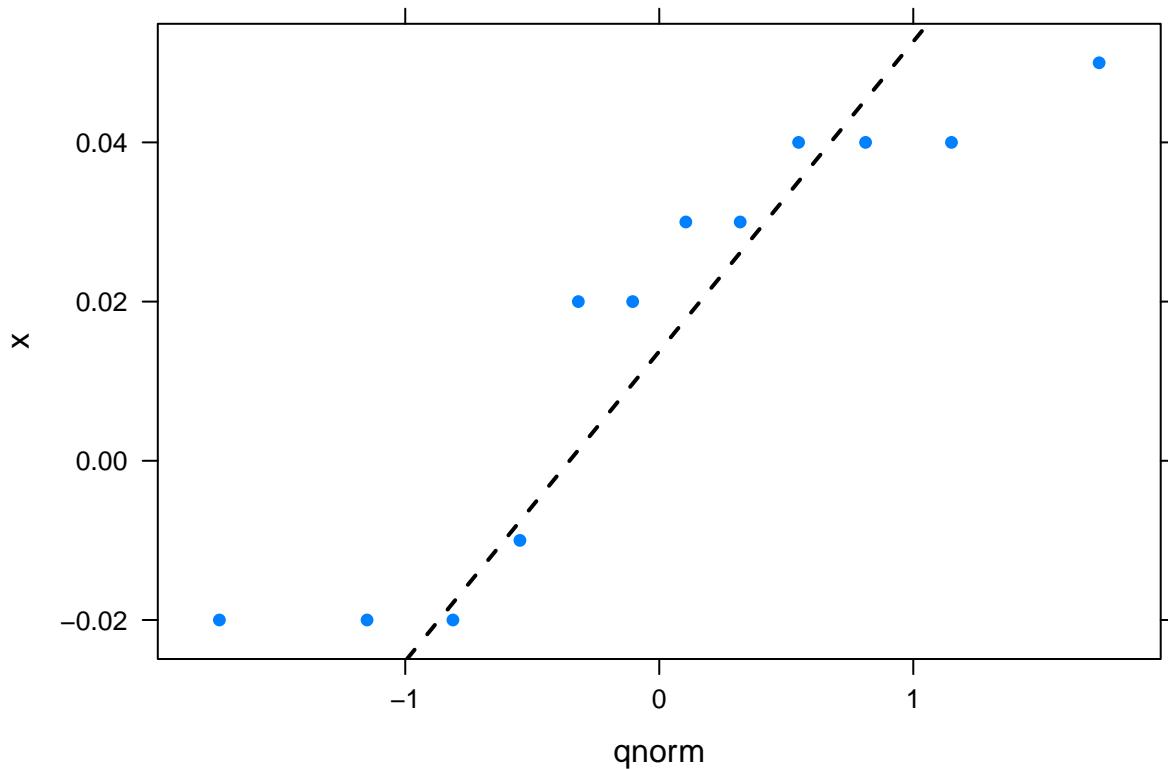
```
##
## Paired t-test
##
## data: values by ind
## t = -2.1589, df = 11, p-value = 0.0538
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.0336579242 0.0003245909
## sample estimates:
## mean of the differences
## -0.01666667
```

The p-value is on the margin of being significant. More data would be needed for this problem to detect a difference.

The sample is so small that it will be hard to check the normality assumption. As a reference here is the qq-plot:

```
library(fastR)
xqqmath(Lesson28Strength$Diff)
```

```
## Warning in qqmath.numeric(x, data = data, panel = panel, ...): explicit
## 'data' specification ignored
```



If we are not comfortable with the normality assumption, we could use the sign test we learned about from last lesson. If the null hypothesis were true, the number of positive difference would be equal to the number of negative differences. The result of the sign test is:

```
binom.test( sum(Lesson28Strength$Diff > 0) , length(Lesson28Strength$Diff) )
```

```
## 
## 
## 
## data: sum(Lesson28Strength$Diff > 0) out of length(Lesson28Strength$Diff)
## number of successes = 8, number of trials = 12, p-value = 0.3877
## alternative hypothesis: true probability of success is not equal to 0.5
## 95 percent confidence interval:
##  0.3488755 0.9007539
## sample estimates:
## probability of success
##                      0.6666667
```

Again, you can see this test does not have much power because we took a continuous variable and made it binary.

4.7.3.1 Permutation Test

The idea of the permutation test is that if we have the null hypothesis and a test statistics, we could simulate the sampling distribution. Even though the strength data is small, we will try the permutation method for this problem.

Under the null hypothesis, there is no difference between the measured strength of either method. Thus the test statistic is the sum of the difference. If there were no difference in the methods, then the difference could either be positive or negative. Thus our permutation test would be to randomly switch the sign on the differences.

First we will get the observed value of the test statistic.

```
(Les28teststat<-sum(Lesson28Strength$Diff))
```

```
## [1] 0.2
```

As an example of one permutation, we get another value of the test statistic

```
set.seed(1024)
sum(Lesson28Strength$Diff*sample(c(-1,1),12,replace=TRUE))
```

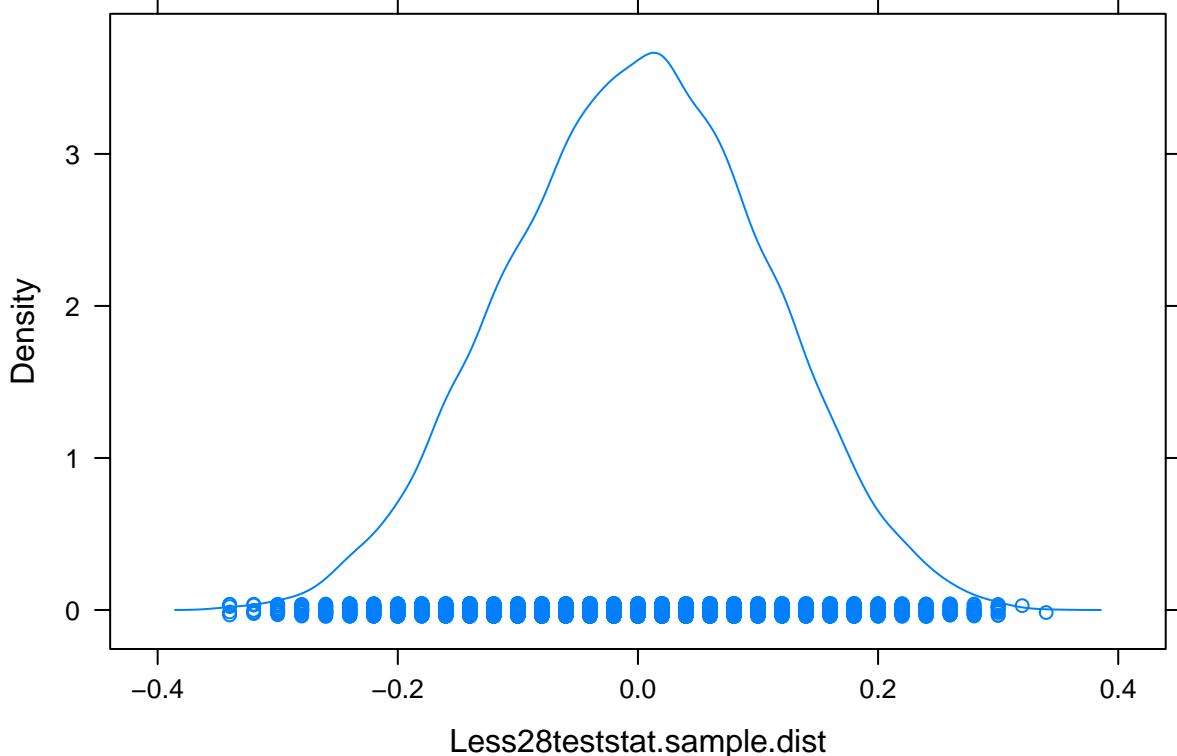
```
## [1] 0.14
```

Now we will repeat the process many times, say 10000.

```
Less28teststat.sample.dist<-replicate(10000,sum(Lesson28Strength$Diff*sample(c(-1,1),12,replace=TRUE)))
```

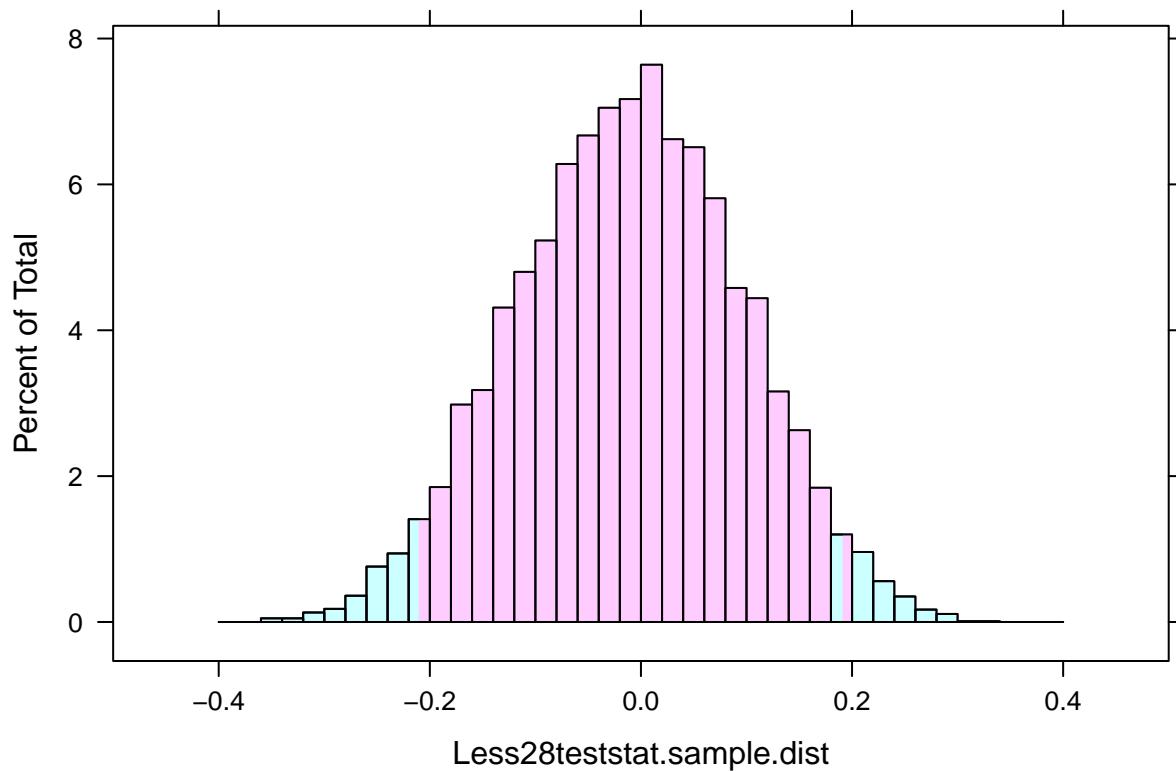
Here is a plot of the sampling distribution of the test statistic.

```
densityplot(Less28teststat.sample.dist)
```



Or using a “fancy” histogram

```
histogram(Less28teststat.sample.dist, breaks=seq(-.4,.4,.02), xlim=c(-.5, .5),
groups=(Les28teststat>Less28teststat.sample.dist)&(-Les28teststat<Less28teststat.sample.dist), pch=16,
```



Now we can calculate the simulated p-value.

```
sum(abs(Less28teststat.sample.dist)>=Les28teststat)/10000
```

```
## [1] 0.0609
```

The p-value is close to the paired t-test and much smaller than the sign test.

In class, we came up with a test statistic of the difference of means for the two methods. This is tricky to code but here was our attempt.

```
temp.data<-Less28.Strength.Data
results<-rep(0,10000)
for (j in 1:10000){
  for (i in 1:12){
    temp<-sample(t(Less28.Strength.Data[i,]),2)
    temp.data[i,1]<-temp[1]
    temp.data[i,2]<-temp[2]
  }
  results[j]<-diff(apply(temp.data,2,mean))
}
sum(abs(results)>diff(apply(Less28.Strength.Data,2,mean)))/10000
```

```
## [1] 0.0446
```

Notice that this p-value is a little smaller but still close to the others. Which is better? The best way to answer is the one that is the most powerful. Unfortunately, we do not have the tools to answer this question mathematically. We could do some simulations to gain insight.

4.7.4 Another Example

Let's try another problem. In the `fastR` package there is a data set called `batting`. This is baseball data from the years 2000 to 2005. If we assume that this data is representative of the future, a big leap, we can use it to conduct a hypothesis test. We want to answer the question of whether there is a difference in the home runs between the American League and National League. One way to answer this is to compare the average number of home runs. Thus the hypothesis test would be

$$H_0 : \mu_{AL} = \mu_{NL}$$

$$H_a : \mu_{AL} \neq \mu_{NL}$$

We could answer this with two-sample t-test even though we have not learned about this.

First we need to subset and clean the data.

```
mybatting<-batting[,c("HR","league")]
head(mybatting)

##      HR league
## 34289  3    AL
## 34290  0    AL
## 34291  4    AL
## 34292  4    AL
## 34293  6    AL
## 34294  0    AL

str(mybatting)

## 'data.frame': 8062 obs. of 2 variables:
##   $ HR    : int 3 0 4 4 6 0 2 19 7 0 ...
##   $ league: Factor w/ 3 levels "AA","AL","NL": 2 2 2 2 2 2 2 2 2 ...
mybatting$league<-as.character(mybatting$league)
```

If we learned about the two-sample t-test, we could perform the test as follows:

```
t.test(HR~league,data=mybatting)

##
##  Welch Two Sample t-test
##
## data: HR by league
## t = 0.83371, df = 7912.2, p-value = 0.4045
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.2024097 0.5019960
## sample estimates:
## mean in group AL mean in group NL
##           4.034776          3.884983
```

We can generate our own permutation test. The test statistic is the difference in means between the two leagues.

```
with(mybatting,tapply(HR,league,mean))
```

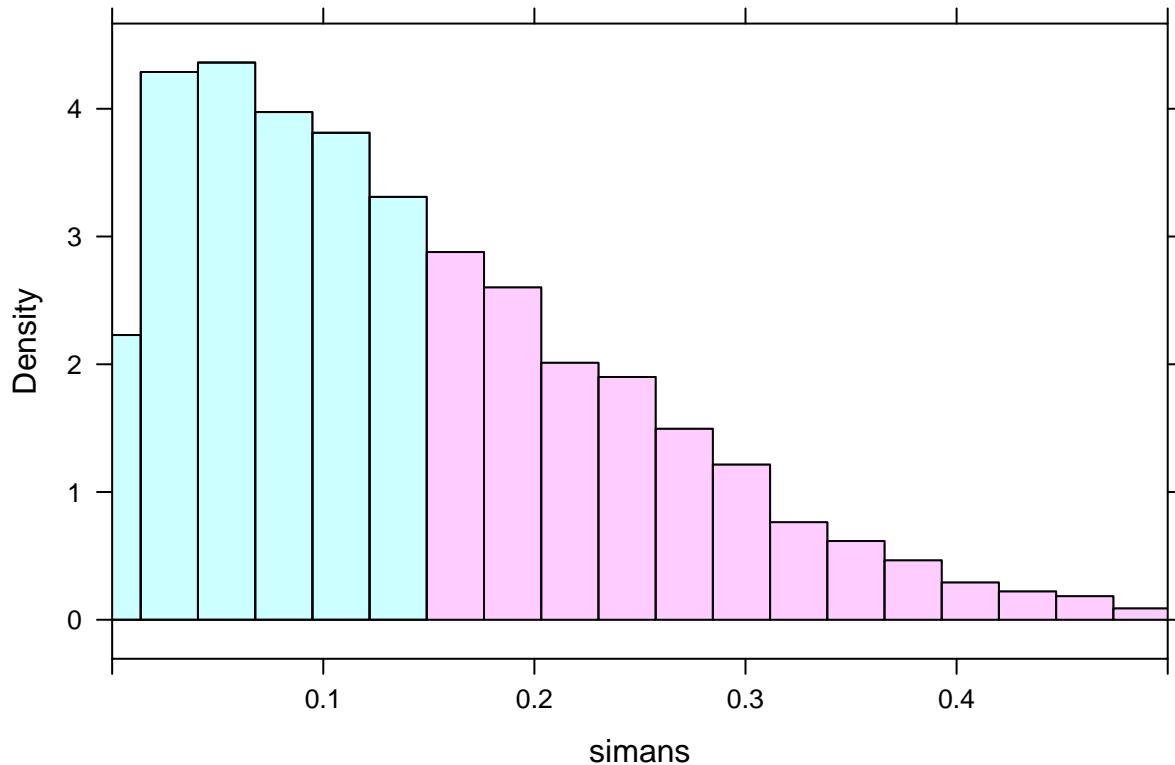
```
##      AL      NL
## 4.034776 3.884983
```

```
(teststat<-with(mybatting,abs(diff(tapply(HR,league,mean)))))
```

```
##          NL
## 0.1497931
```

Now we can simulate the distribution of the test statistic.

```
simans<-with(mybatting,replicate(10000,abs(diff(tapply(HR,sample(league),mean)))))  
sum(simans>=teststat)/10000  
  
## [1] 0.4028  
  
histogram(simans,n=25, xlim=c(0, .5),groups=simans >= teststat, pch=16, cex=.8)
```



This is close to the two-sample t-test.

Of course with the permutation test, we could use different test statistics. Suppose instead of mean we look at a difference of the 90th-percentile.

I will write a function to find the 90th-percentile.

```
myquantile<-function(x){quantile(x,probs=.9)}  
  
with(mybatting,tapply(HR,league,myquantile))  
  
## AL NL  
## 15 13  
  
(teststat2<-with(mybatting,abs(diff(tapply(HR,league,myquantile)))))  
  
## NL
```

```
## 2
```

Now we can simulate the distribution of the test statistic.

```
simans2<-with(mybatting,replicate(10000,abs(diff(tapply(HR,sample(league),myquantile)))))  
sum(simans2>=teststat2)/10000
```

```
## [1] 0.0601
```

This is marginally significant. Interesting result but probably not a good test as there are not many unique values.

```
unique(simans2)
```

```
## [1] 1.0 2.0 0.0 0.4 0.6 1.6 1.4 2.4 3.0
```

4.7.5 Test of the Median

Instead of testing a hypothesis about the mean, you may want to test a hypothesis about the median. This is easily done using the idea of a permutation test.

To keep things simple, suppose the null hypothesis is that the median strength measurement for method 1 is 40. This means that 50% of the data values should be above 40. We could use the binomial test. We first subtract 40 from each value and then determine the number that are positive.

```
sum((Less28.Strength.Data$Method1-40)>0)
```

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

```
binom.test(sum((Less28.Strength.Data$Method1-40)>0),length(Less28.Strength.Data$Method1))
```

```
##  
##  
##  
## data: sum((Less28.Strength.Data$Method1 - 40) > 0) out of length(Less28.Strength.Data$Method1)  
## number of successes = 5, number of trials = 12, p-value = 0.7744  
## alternative hypothesis: true probability of success is not equal to 0.5  
## 95 percent confidence interval:  
## 0.1516522 0.7233303  
## sample estimates:  
## probability of success  
## 0.4166667
```

Thus we fail to reject.

Chapter 5

Likelihood-Based Statistics

This is a difficult chapter for students. Even though it is only seven sections, they are difficult. We only teach from sections 5.1, 5.2, 5.4, and 5.5. This was done based on trying to introduce linear regression as well as students struggling with the other sections.

You could drop the material from Chapter 6 and spend more time on Chapter 5.

5.1 Maximum Likelihood Estimators

5.1.1 Objectives

1. Find maximum likelihood estimators and estimates both analytically and numerically
2. Know the assumptions and find probabilities from a multinomial distribution

There are a couple of videos that I made several years ago on maximum likelihood estimators that may help you. The links are:

Part 1

Part 2

5.1.2 Introduction

The second method we will use to estimate parameters is called maximum likelihood. The first method was called method of moments and the idea there was that sample moments should be close to population moments. We are matching moments from the population distribution and sample distribution. In maximum likelihood estimation the idea is what value of the parameter make the data most likely? We are finding parameters that make the data most likely. Again, just as in the method of moments, we need a model, that is a distribution. We will use the pmf or pdf for this type of estimation.

As a simple example of the maximum likelihood idea, let's consider a discrete case. Suppose the lab that performs urinalysis has 10 samples from Base X and found 3 positive results. They also have a second sample of 10 from Base Y and found 5 positive samples. Unfortunately, the technician has mixed up the samples and now does not know which came from Base X and which came from Base Y. The test is expensive so you decide to test two samples from one of the groups. You find one sample positive and one negative. Do you believe it is from Base X or Base Y?

Since this is a sampling without replacement scheme, you realize that a hypergeometric will help you. If the sample came from Base X, the probability of getting one positive result and one negative result is:

$$\frac{\binom{3}{1} \binom{7}{1}}{\binom{10}{2}}$$

This is because we have three positives and want to select one, seven negatives and want to select one all divided by the number of ways to select two from ten. This value is

$(3*7)/45$

```
## [1] 0.4666667
```

```
dhyper(1,3,7,2)
```

```
## [1] 0.4666667
```

If the two tested samples came from Base Y then we would have

$$\frac{\binom{5}{1} \binom{5}{1}}{\binom{10}{2}}$$

$(5*5)/45$

```
## [1] 0.5555556
```

```
dhyper(1,5,5,2)
```

```
## [1] 0.5555556
```

Thus we would conclude that the samples came from Base Y because this choice maximizes the probability. This is the idea of maximum likelihood.

In more detail:

If

$$X_1, X_2, X_3, \dots, X_n \stackrel{iid}{\sim} f(X|\theta)$$

where $f(X|\theta)$ is the pdf or pmf with θ the parameter(s), then, since the random variables are independent, the joint pdf or pmf is

$$f(X_1, X_2, X_3, \dots, X_n | \theta) = f(X_1 | \theta) f(X_2 | \theta) f(X_3 | \theta) \dots f(X_n | \theta) = \prod_{i=1}^n f(X_i | \theta)$$

If we change our view of this formula, we get the likelihood function. We consider the data known and the parameter unknown. Thus the likelihood function is:

$$L(\theta | X_i) = \prod_{i=1}^n f(X_i | \theta)$$

The idea of maximum likelihood estimation is to find the value of θ that maximizes $L(\theta)$ for the given data. The difficulty is that finding a global maximum is not always easy. If the function is continuous in the parameter, we may try using calculus but we still need to check boundary conditions. The question of optimization is important and a field of study in itself.

Note: Since the likelihood function often involves products and exponents it is often easier to maximize the log of the likelihood. This is because the log function is a monotonic increasing function. That is, if $x_1 > x_2$ then $\log(x_1) > \log(x_2)$. Thus

$$\log(L(\theta)) = l(\theta) = \log(\prod_{i=1}^n f(X_i|\theta)) = \sum_{i=1}^n \log(f(X_i|\theta))$$

5.1.3 Example:

Suppose we have a discrete random variable with the following probability mass function:

x	0	1	2	3
$f(x \theta)$	$\frac{2\theta}{3}$	$\frac{\theta}{3}$	$\frac{2(1-\theta)}{3}$	$\frac{(1-\theta)}{3}$

for $0 \leq \theta \leq 1$.

Find the method of moments estimator for this problem.

$$E(X) = 0 * \left(\frac{2\theta}{3}\right) + 1 * \left(\frac{\theta}{3}\right) + 2 * \left(\frac{2(1-\theta)}{3}\right) + 3 * \left(\frac{(1-\theta)}{3}\right) = \bar{X}$$

simplifying

$$\begin{aligned} \hat{\theta} + 4(1 - \hat{\theta}) + 3(1 - \hat{\theta}) &= 3\bar{X} \\ -6\hat{\theta} &= 3\bar{X} - 7 \\ \hat{\theta} &= \frac{(7 - 3\bar{X})}{6} \end{aligned}$$

The maximum likelihood estimate is derived by finding the likelihood function and then maximizing with respect to θ . The likelihood function is

$$L(\theta) = \left(\frac{(X_0 + X_1 + X_2 + X_3)!}{X_0! X_1! X_2! X_3!} \right) \left(\frac{2\theta}{3} \right)^{X_0} \left(\frac{\theta}{3} \right)^{X_1} \left(\frac{2(1-\theta)}{3} \right)^{X_2} \left(\frac{(1-\theta)}{3} \right)^{X_3}$$

where X_0 is the number of zero values in the data.

This is a multinomial because

1. The random process is repeated n times,
2. Each trial has 4 possible outcomes,
3. The probability of each outcome stays constant from trial to trial, and
4. The outcome of each trial is independent of the others.

The binomial is a special case of the multinomial.

It will be easier to maximize the log-likelihood, notice we drop the first term since it does not involve θ .

$$l(\theta) = X_0 \log(2/3) + X_0 \log(\theta) + X_1 \log(1/3) + X_1 \log(\theta) + X_2 \log(2/3) + X_2 \log(1-\theta) + X_3 \log(1/3) + X_3 \log(1-\theta)$$

Since the likelihood is a continuous function of θ , we will use calculus to find the maximum.

$$\frac{\partial l}{\partial \theta} = \frac{X_0}{\theta} + \frac{X_1}{\theta} - \frac{X_2}{(1-\theta)} - \frac{X_3}{(1-\theta)} = 0$$

$$(X_0 + X_1)(1 - \theta) = (X_2 + X_3)(\theta)$$

$$\hat{\theta} = \frac{(X_0 + X_1)}{(X_0 + X_1 + X_2 + X_3)}$$

At the endpoints, the likelihood function is zero and the likelihood function is non-negative, so we found a maximum.

5.1.4 Data

Now suppose we observe the following data:

```
(3,0,2,1,3,2,1,0,2,1)
```

The summary of the data is:

```
(Less31Data<-c(3,0,2,1,3,2,1,0,2,1))

## [1] 3 0 2 1 3 2 1 0 2 1

(TabLess31Data<-table(Less31Data))

## Less31Data
## 0 1 2 3
## 2 3 3 2

(Thetahat<-(TabLess31Data[1]+TabLess31Data[2])/sum(TabLess31Data))

## 0
## 0.5
```

Thus our maximum likelihood estimate of θ is 0.5 from this data.

We could have used R and done everything numerically.

```
library(fastR)

loglik<-function(theta,x){
  (x[1]+x[2])*log(theta)+(x[3]+x[4])*log(1-theta)
}
nlmax(loglik,p=.25,x=TabLess31Data)

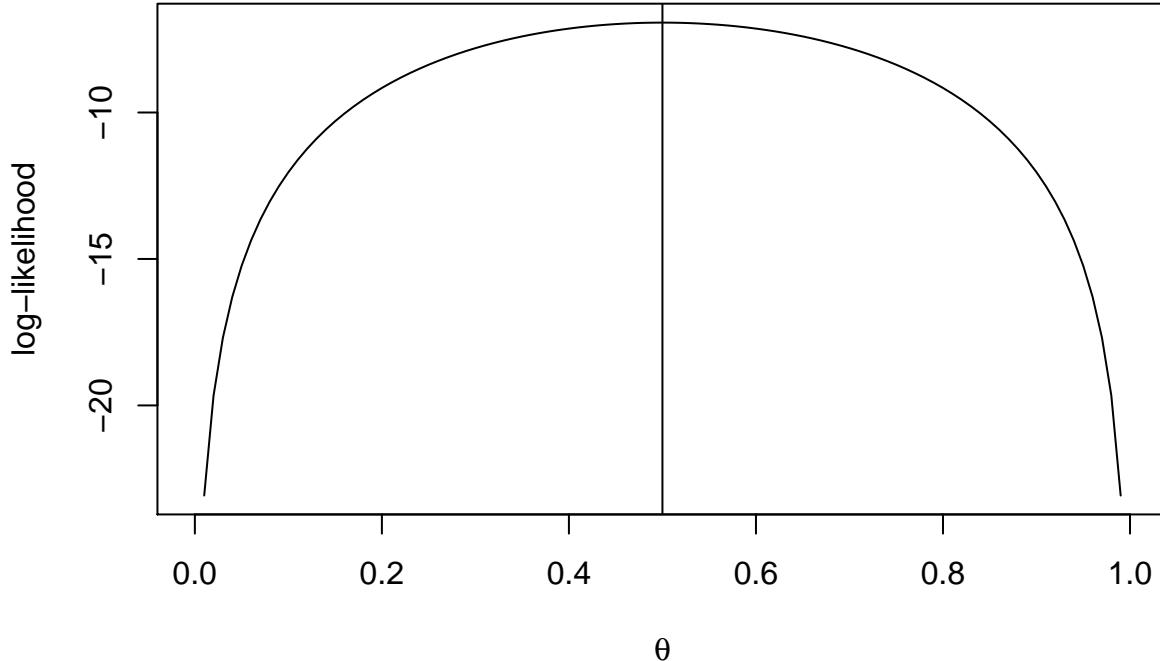
## Warning in log(1 - theta): NaNs produced
## Warning in nlm(g, ...): NA/Inf replaced by maximum positive value
## Warning in log(1 - theta): NaNs produced
## Warning in nlm(g, ...): NA/Inf replaced by maximum positive value

## $maximum
## [1] -6.931472
##
## $estimate
## [1] 0.4999995
##
## $gradient
## [1] -1.953993e-08
##
## $code
## [1] 1
##
## $iterations
```

```
## [1] 5
##
## attr(),"class")
## [1] "nlmax" "list"
```

A plot of the log-likelihood reveals that the function is flat for a wide range of θ values.

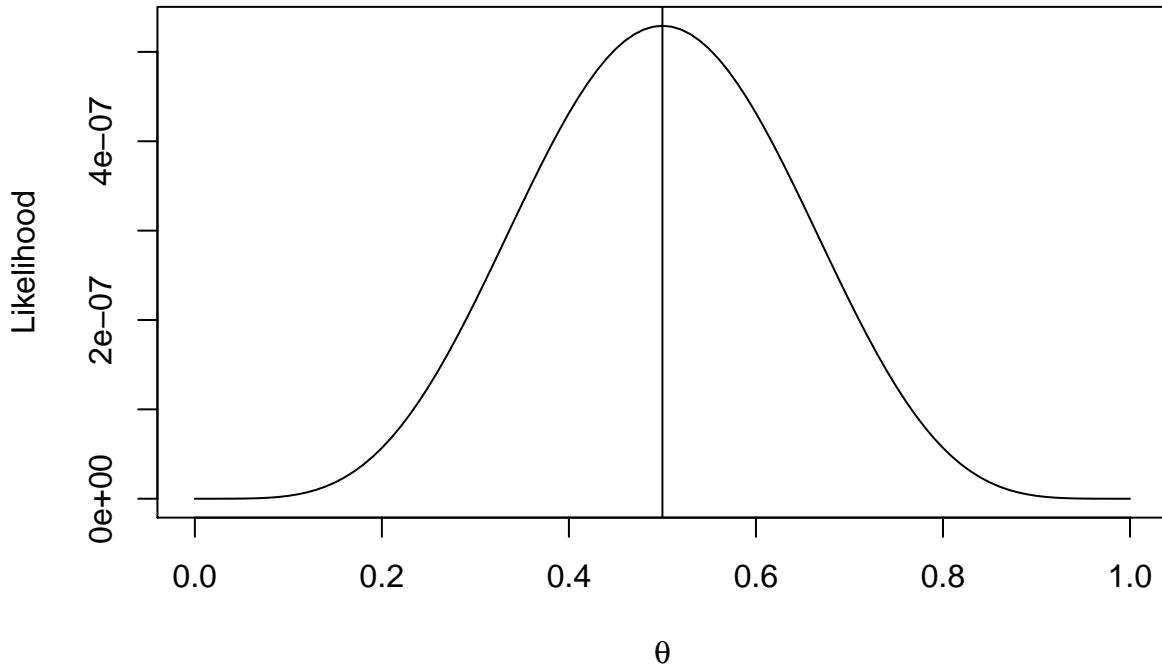
```
plot(seq(0,1,.01),loglik(seq(0,1,.01),TabLess31Data),
     type="l",xlab=expression(theta),ylab="log-likelihood")
abline(v=.5)
```



Just for interest, let's plot the likelihood. We will drop the terms that don't have θ in them as there are only constants.

```
lik<-function(theta,x){
  (2*theta/3)^x[1]*(theta/3)^x[2]*((2/3)*(1-theta))^x[3]*((1/3)*(1-theta))^x[4]
}

plot(seq(0,1,.01),lik(seq(0,1,.01),TabLess31Data),
     type="l",xlab=expression(theta),ylab="Likelihood")
abline(v=.5)
```



As a comparison, our method of moments estimate is

$$-\frac{(3 * \text{mean}(\text{Less31Data}) - 7)}{6}$$

```
## [1] 0.4166667
```

5.1.5 Practice

The angle θ at which electrons are emitted in muon decay has the distribution

$$f(x|\alpha) = \frac{(1 + \alpha x)}{2}$$

with $-1 \leq x \leq 1$ and $-1 \leq \alpha \leq 1$ with $x = \cos\theta$ and α related to polarization.

1. Find the method of moments estimator for α .
2. Find the maximum likelihood estimator for α .

5.2 Likelihood Ratio Tests

5.2.1 Objective

Find and evaluate likelihood ratio tests, both analytically and numerically.

5.2.2 Introduction

In the last chapter we found computational methods to conduct hypothesis testing. We used empirical p-values if we had a distribution and permutation methods if our null hypothesis was equality of two methods. Prior to the modern advance of computers, we needed analytic methods to conduct general hypothesis testing. The method developed is introduced in this section and is called the likelihood ratio test. Note that computational methods also aid likelihood ratio tests as we often have to perform non-linear optimization. The likelihood ratio test gives us a test statistic that we can use in our empirical p-value methods. As you may remember, we just came up with test statistics last chapter without any formal reasoning. The likelihood ratio test statistic tends to be more powerful than other test statistics and in this sense is best.

Warning: The later portion of this section of the book gets involved and detailed. There is also substantial code. The important idea here is to show the power of the likelihood ratio test. It can be used to test fairly complicated hypothesis tests. It is worth the time to at least try to follow the main idea in the author's example of the Yellowstone eruption data.

5.2.3 Review

From last class we had the problem

x	0	1	2	3
$f(x \theta)$	$\frac{2\theta}{3}$	$\frac{\theta}{3}$	$\frac{2(1-\theta)}{3}$	$\frac{(1-\theta)}{3}$

for $0 \leq \theta \leq 1$.

We found the maximum likelihood estimator to be

$$\hat{\theta} = \frac{(X_0 + X_1)}{(X_0 + X_1 + X_2 + X_3)}$$

The reason that maximum likelihood estimators are so popular is that asymptotically the maximum likelihood estimator will be unbiased and consistent. In addition, it will be approximately normal. Finally, the maximum likelihood estimator is invariant. That is, if $\hat{\theta}$ is a maximum likelihood estimator of θ , then for any function $\tau(\theta)$, the maximum likelihood estimator of $\tau(\theta)$, denoted $\widehat{\tau(\theta)}$, is $\tau(\hat{\theta})$. That is convenient.

Back to our problem, the maximum likelihood estimator of $\frac{2\theta}{3}$ is $\frac{2\hat{\theta}}{3}$.

5.2.4 Hypothesis Testing

```
library(fastrR)
```

Suppose we collected a sample of size 20 and we think the model above is appropriate, in fact we believe that θ is 0.5. Thus we want to perform a hypothesis test of the following:

$$H_0 : \theta = 0.5$$

$$H_a : \theta \neq 0.5$$

Next we need to develop a test statistic. In the next section, we will use a likelihood ratio test, but for this section let's use an empirical p-value from the last chapter.

We know that the maximum likelihood estimator is

$$\hat{\theta} = \frac{(X_0 + X_1)}{(X_0 + X_1 + X_2 + X_3)}$$

so I will use a test statistic of

$$\theta_0 - \hat{\theta} = 0.5 - \hat{\theta}$$

I just made this one up, but it seems reasonable that if the null hypothesis is true, then maximum likelihood estimator should be close to 0.5.

Now we collect data, here it is

```
Less32Data
```

```
## [1] 3 0 1 0 0 2 0 0 2 2 0 0 3 2 3 2 2 0 3 2
```

In table form, it is

```
table(Less32Data)
```

```
## Less32Data
## 0 1 2 3
## 8 1 7 4
```

The maximum likelihood estimate is:

```
Less32tab<-table(Less32Data)
(Less32tab[1]+Less32tab[2])/sum(Less32tab)
```

```
##      0
## 0.45
```

The test statistic is

```
(Less32teststat<-.5-(Less32tab[1]+Less32tab[2])/sum(Less32tab))
```

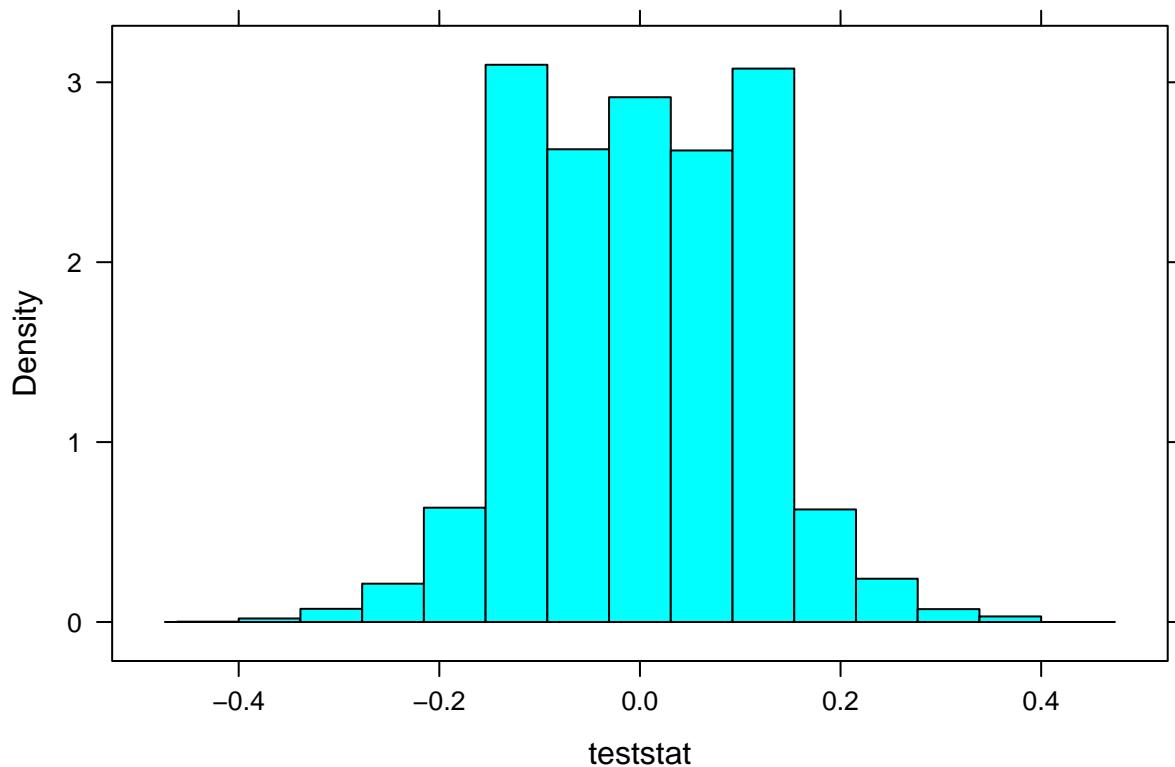
```
##      0
## 0.05
```

If the null is true, then we would have a multinomial distribution with probabilities of 1/3, 1/6, 1/3, 1/6. We will sample from this distribution and calculate the test statistic.

```
teststat<-apply(rmultinom(10000,20,c(1/3,1/6,1/3,1/6)),2,function(x)(.5-(x[1]+x[2])/sum(x)))
```

A plot of the values

```
histogram(teststat)
```



It looks normal. The empirical p-value is

```
sum(abs(teststat)>=Less32teststat)/10000
```

```
## [1] 0.8205
```

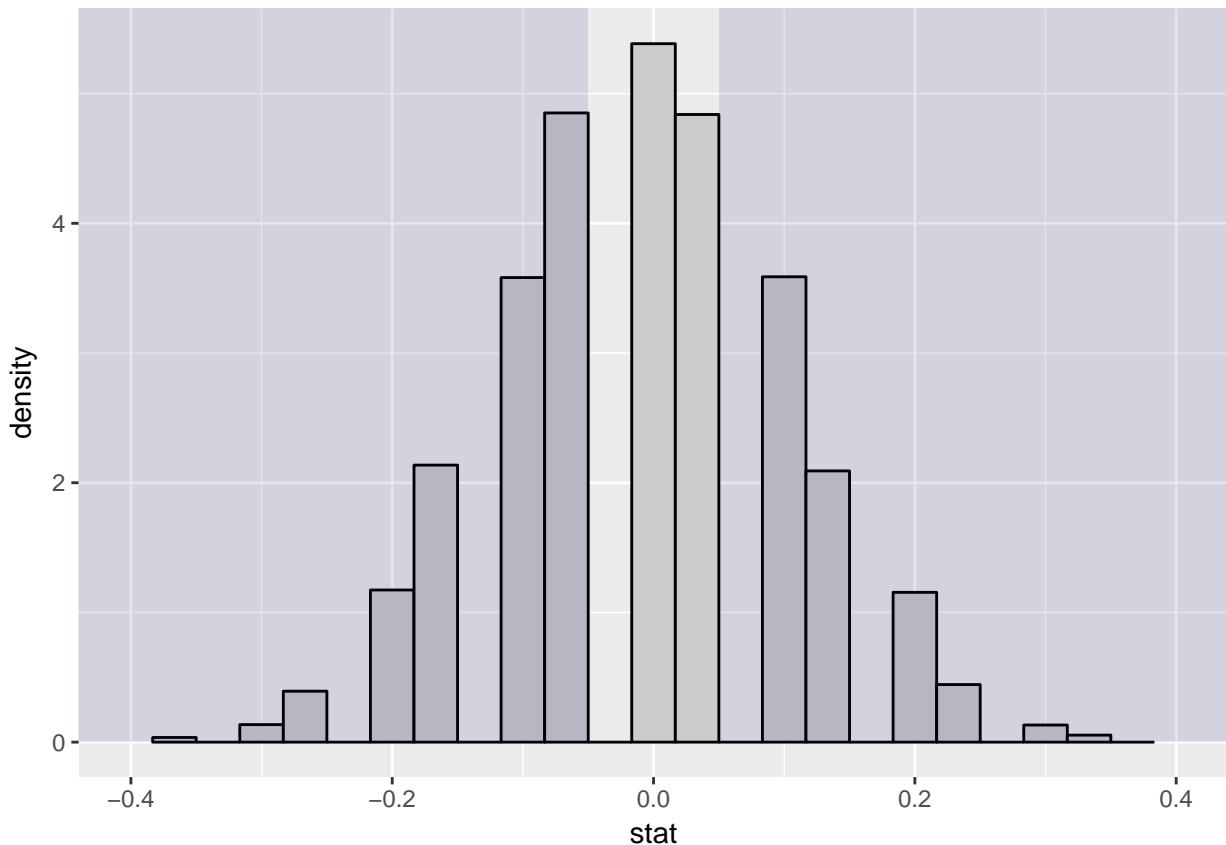
The fastR package has a function, `statTally` that makes this process a little easier.

```
rdata<-rmultinom(10000,20,c(1/3,1/6,1/3,1/6))
mystat<-function(x){
  .5-(x[1]+x[2])/sum(x)
}
mystat(Less32tab)

##      0
## 0.05
statTally(Less32tab,rdata,mystat,q = c(.01,.05,.1,.5, .9, .95),alt="two.sided")

##
## Test statistic applied to sample data =  0.05
##
## Quantiles of test statistic applied to random data:
##
##      1%      5%     10%     50%     90%    95%
## -0.25 -0.20 -0.15  0.00   0.15   0.20
```

```
## Of the 10001 samples (1 original + 10000 random),
##
## 1614 ( 16.14 % ) had test stats = 0.05
##
## 4103 ( 41.03 % ) had test stats <= -0.05
##
## 4103 ( 41.03 % ) had test stats >= 0.05
```



5.2.5 Likelihood Ratio Test

The idea behind the likelihood ratio test is that for a test statistic we use a ratio of the likelihood under the null hypothesis to the likelihood using the maximum likelihood estimate. The idea is that if the null hypothesis is true, then the ratio of these two likelihoods should be close to one. This test statistic is advantageous because the asymptotic distribution is known and the test tends to be more powerful than other test statistics.

Continuing with our problem from above. The hypothesis test is

$$H_0 : \theta = 0.5$$

$$H_a : \theta \neq 0.5$$

The likelihood ratio, our test statistic, is

$$\lambda = \frac{L(\theta_0)}{L(\hat{\theta})}$$

where $\theta_0 = 0.5$ and $\hat{\theta} = 0.45$

The likelihood function is

$$L(\theta) = \left(\frac{(X_0 + X_1 + X_2 + X_3)!}{X_0! X_1! X_2! X_3!} \right) \left(\frac{2\theta}{3} \right)^{X_0} \left(\frac{\theta}{3} \right)^{X_1} \left(\frac{2(1-\theta)}{3} \right)^{X_2} \left(\frac{(1-\theta)}{3} \right)^{X_3}$$

We will write a function in R to calculate the likelihood, note we made use of equation 5.3 of the text:

```
like<-function(x,theta){
  choose(sum(x),x[1])*choose(sum(x)-x[1],x[2])*choose(sum(x)-x[1]-x[2],x[3])*(2*theta/3)^(x[1])*(theta/3)^x[3]
}
```

We know that $-2\ln(\lambda) \sim \chi^2(1)$

The degrees of freedom comes from that under the unrestricted model there is one parameter that needs to be estimated, θ , and under the null no parameters.

Our p-value is

```
1-pchisq(-2*log(like(Less32tab,.5)/like(Less32tab,.45)),1)
```

```
##          0
## 0.6544508
```

That is we fail to reject the null hypothesis.

5.2.6 Practice

Let X be the time to failure of a computer in years, an exponential model.

1. Find the maximum likelihood estimator of λ .
2. Using a likelihood ratio test, test the hypothesis

$$H_0 : \lambda = 10$$

$$H_a : \lambda \neq 10$$

for the data

```
lesson32a
```

```
## [1] 0.09174087 0.15185291 0.29387550 0.23516074 0.01433223 0.02978746
## [7] 0.11316773
```

5.3 Goodness of Fit Testing

5.3.1 Objectives

1. Setup and conduct a goodness of fit test using both the Pearson chi-squared statistic and the likelihood ratio test. This includes binning and collapsing cells in an appropriate manner
2. Give a bound on the p-value from a Pearson chi-squared or likelihood ratio statistics
3. Generate empirical p-values for the Pearson chi-squared or likelihood ratio statistics

5.3.2 Introduction

In the estimation problem, either method of moments or maximum likelihood, we needed a model, a parent population distribution, to derive our results. Earlier we had talked about using q-q plots and density estimation to help with the problem of model selection but now we will do it as a hypothesis test. The problem we are trying to solve is to verify that the assumed model is correct. We will do this as a hypothesis test, but in advance be warned that this method has many potential problems.

In this section, we are testing the idea that the data comes a specified probability model. To do this, we bin the data. We make it discrete. In the case of a multinomial problem, this is already done for us. For continuous data, we have to make it discrete by selecting bins. The choice of number of bins and bin size, similar to histograms, is subjective and does have an impact on the results. There are some heuristics to guide but these are often just best guesses.

5.3.3 Review

```
library(lattice)
```

Continuing with the previous problem where we had in 5.2

x	0	1	2	3
$f(x \theta)$	$\frac{2\theta}{3}$	$\frac{\theta}{3}$	$\frac{2(1-\theta)}{3}$	$\frac{(1-\theta)}{3}$

for $0 \leq \theta \leq 1$.

We found the maximum likelihood estimator to be

$$\hat{\theta} = \frac{(X_0 + X_1)}{(X_0 + X_1 + X_2 + X_3)}$$

Next we performed a likelihood ratio test of the hypothesis

$$H_0 : \theta = 0.5$$

$$H_a : \theta \neq 0.5$$

The likelihood ratio, our test statistic, is

$$\lambda = \frac{L(\theta_0)}{L(\hat{\theta})}$$

where $\theta_0 = 0.5$ and $\hat{\theta} = 0.45$. This is because for our data

```
table(Less32Data)
```

```
## Less32Data
## 0 1 2 3
## 8 1 7 4
```

the maximum likelihood estimate is 0.45.

The likelihood function is

$$L(\theta) = \left(\frac{(X_0 + X_1 + X_2 + X_3)!}{X_0! X_1! X_2! X_3!} \right) \left(\frac{2\theta}{3} \right)^{X_0} \left(\frac{\theta}{3} \right)^{X_1} \left(\frac{2(1-\theta)}{3} \right)^{X_2} \left(\frac{(1-\theta)}{3} \right)^{X_3}$$

We know that $-2\ln(\lambda) \sim \chi^2(1)$

The degrees of freedom are determined by counting the free parameters under the unrestricted model, in this case one θ , and the number of free parameters under the null, no free parameters.

Our p-value was 0.6545

The obvious question at this point is whether the probability mass function specified above is the correct model.

5.3.4 Goodness of Fit Test

5.3.4.1 Hueristic Test

We want to test the idea that our data comes from the distribution

x	0	1	2	3
$f(x \theta)$	$\frac{2\theta}{3}$	$\frac{\theta}{3}$	$\frac{2(1-\theta)}{3}$	$\frac{(1-\theta)}{3}$

for $0 \leq \theta \leq 1$.

To proceed we need to know if we also have a hypothesized value for θ as this will impact our test statistic. We will attack the problem in both cases so to start let's assume that we also believe that $\theta = 0.5$. Thus we want to test if our data comes from the distribution

x	0	1	2	3
$f(x \theta)$	$\frac{1}{3}$	$\frac{1}{6}$	$\frac{1}{3}$	$\frac{1}{6}$

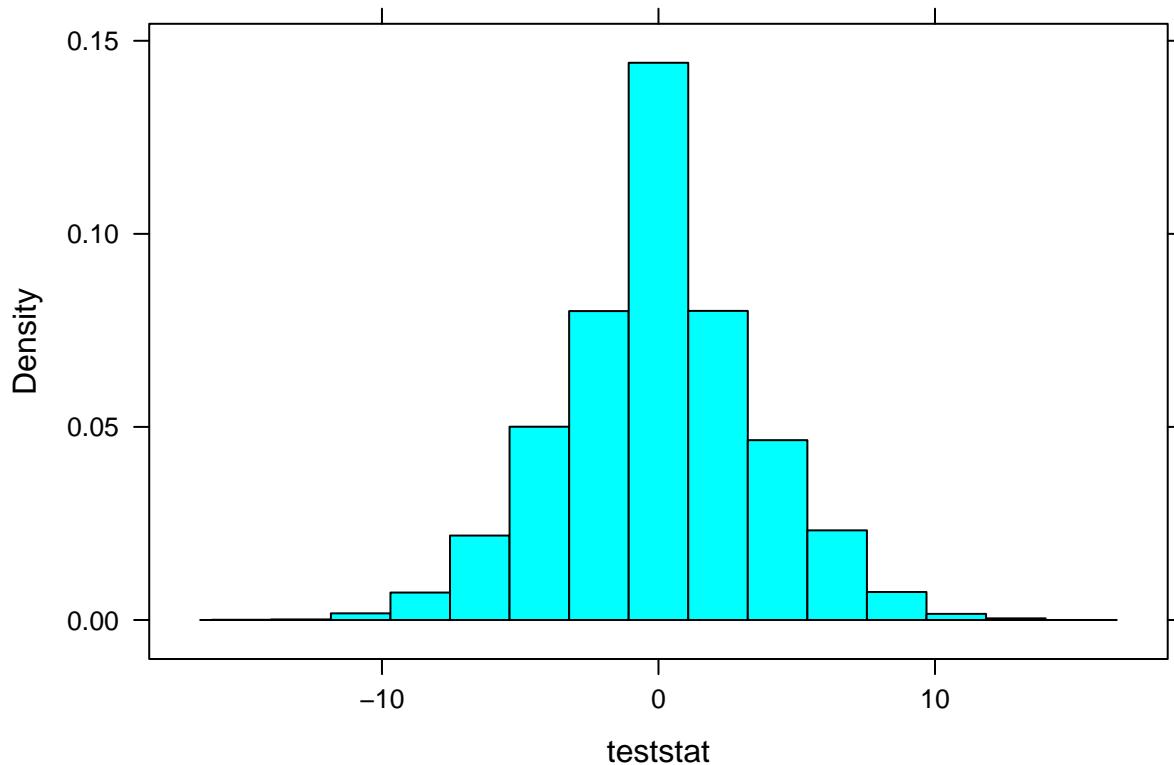
Next we need a test statistic. Again, just making one up, if the null hypothesis were true and the data came from the distribution above, the number of 0's should equal the number of 2's. My test statistic is the difference between the number of 0's and 2's.

Since I don't know the distribution of this test statistic, I will use an empirical p-value. We will generate random samples from a multinomial and calculate the test statistic.

```
teststat<-apply(rmultinom(10000,20,c(1/3,1/6,1/3,1/6)),2,function(x)(x[1]-x[3]))
```

A plot of the values

```
histogram(teststat)
```



This is our data

```
Less32Data
```

```
## [1] 3 0 1 0 0 2 0 0 2 2 0 0 3 2 3 2 2 0 3 2





```

```
## Less32Data
## 0 1 2 3
## 8 1 7 4
```

The observed value of the test statistic is

```
table(Less32Data)[1]-table(Less32Data)[3]
```

```
## 0
## 1
```

And our empirical p-value is

```
sum(abs(teststat)>=1)/10000
```

```
## [1] 0.8913
```

Thus we have no reason to reject the hypothesis that our data comes from the distribution above. We do have to worry about the Type II error which could be extremely high for this test.

5.3.5 Improved Test

The test we developed above does not use all the information in the cells. An improved test statistic would use all four cells. To do this consider what the expected cell count would be in each cell if the null hypothesis were true. In other words, if the distribution were really

x	0	1	2	3
$f(x \theta)$	$\frac{1}{3}$	$\frac{1}{6}$	$\frac{1}{3}$	$\frac{1}{6}$

We would expect $20 * (\frac{1}{3})$ or $\frac{20}{3}$ zeros in the first cell. Similar calculations can be done for the other cells. We call these values the expected cell counts. We could come up with several test statistics that use all the cells, such as

$$\begin{aligned} & \sum_{i=1}^n |o_i - e_i| \\ & \sum_{i=1}^n (o_i - e_i)^2 \\ & \sum_{i=1}^n \frac{(o_i - e_i)^2}{e_i} \end{aligned}$$

where o_i is the observed cell count and e_i is the expected cell count under the null hypothesis.

The problem again is knowing the distribution of these test statistics. We could use empirical p-values such as we did above. However, the last test statistic is called the Pearson chi-squared statistic and asymptotically has a chi-squared distribution with $c - 1$ degrees of freedom, where c is the number of cells.

First let's calculate an empirical p-value using the Pearson chi-squared statistic and then compare it with the calculated value from the asymptotic distribution.

```
(e<-20*c(1/3,1/6,1/3,1/6))
```

```
## [1] 6.666667 3.333333 6.666667 3.333333
set.seed(8913)
teststat<-apply(rmultinom(10000,20,c(1/3,1/6,1/3,1/6)),2,function(x)(sum((x-e)^2/e)))
obsstat<-sum((table(Less32Data)-e)^2/e)
sum(teststat>=obsstat)/10000
```

```
## [1] 0.57
```

The calculated value is

```
1-pchisq(obsstat,3)
```

```
## [1] 0.5620941
```

Both of these are close to each other. The power of this test is higher than the previous heuristic test statistic we used.

5.3.5.1 Likelihood Ratio Goodness of Fit Test

We could also test the hypothesis using a likelihood ratio test. The hypothesis would be

$$H_0 : (\pi = (1/3, 1/6, 1/3, 1/6))$$

$$H_a : \pi_i \geq 0 \text{ and } \sum_i \pi_i = 1$$

Where π_i are the cell probabilities. The likelihood ratio test is

$$\lambda = \frac{L(H_0)}{L(H_a)}$$

Under the alternative, we would maximize the likelihood by estimating each of the cell probabilities of a multinomial. This is a constrained optimization problem as the cell probabilities must add up to one. The maximum likelihood estimators of the cell probabilities are

$$\frac{o_i}{n}$$

Here o_i is what we have been calling n_i in previous sections.

Thus the likelihood ratio is

$$\lambda = \left(\frac{\left(\frac{1}{3}\right)}{\left(\frac{o_0}{n}\right)} \right)^{o_0} \left(\frac{\left(\frac{1}{6}\right)}{\left(\frac{o_1}{n}\right)} \right)^{o_1} \left(\frac{\left(\frac{1}{3}\right)}{\left(\frac{o_2}{n}\right)} \right)^{o_2} \left(\frac{\left(\frac{1}{6}\right)}{\left(\frac{o_3}{n}\right)} \right)^{o_3}$$

The notation is a little different in that most books would use o_1 for the first cell but we are using o_0 since the first cell is the number of zeros.

Note that $e_i = n * \pi_i$ so the likelihood statistic could be written

$$\lambda = \left(\frac{e_0}{o_0} \right)^{o_0} \left(\frac{e_1}{o_1} \right)^{o_1} \left(\frac{e_2}{o_2} \right)^{o_2} \left(\frac{e_3}{o_3} \right)^{o_3}$$

The distribution of $-2\log\lambda$ is known to be a chi-squared with 3 degrees of freedom.

$$-2\log(\lambda) = 2 \sum_i o_i \log \left(\frac{o_i}{e_i} \right)$$

```
2*sum(table(Less32Data)*log(table(Less32Data)/e))
## [1] 2.650834
1-pchisq(2*sum(table(Less32Data)*log(table(Less32Data)/e)),3)
## [1] 0.4486473
```

This is similar to the Pearson chi-squared test.

5.3.6 θ Unknown

In this case we have to estimate θ using maximum likelihood. Thus under the null hypothesis, the estimated cell probabilities are

```
c(2*.45/3,.45/3,2*(1-.45)/3,(1-.45)/3)
```

```
## [1] 0.3000000 0.1500000 0.3666667 0.1833333
```

The likelihood ratio test is

```
(e2<-20*c(2*.45/3, .45/3, 2*(1-.45)/3, (1-.45)/3))
## [1] 6.000000 3.000000 7.333333 3.666667
2*sum(table(Less32Data)*log(table(Less32Data)/e2))

## [1] 2.450499
1-pchisq(2*sum(table(Less32Data)*log(table(Less32Data)/e2)), 2)

## [1] 0.2936844
```

There are 2 degrees of freedom because we have three free parameters in the alternative hypothesis and one free parameter in the null hypothesis.

Using a Pearson chi-squared statistic, we get

```
(teststat2<-sum((table(Less32Data)-e2)^2/e2))

## [1] 2.045455
1-pchisq(teststat2, 2)

## [1] 0.3596128
```

This p-value tends to be anti-conservative and thus too small. Some people like to be conservative and use 3 degrees of freedom.

```
1-pchisq(teststat2, 3)

## [1] 0.5630262
```

In this case it does not change our conclusion.

5.3.7 Practice

Try testing a complex hypothesis such as for the problem we have been working, test:

$$\begin{aligned} H_0 : \pi_0 &= \pi_2 \text{ and } \pi_1 = \pi_3 \\ H_0 : \pi_0 &\neq \pi_2 \text{ or } \pi_1 \neq \pi_3 \end{aligned}$$

Try testing a goodness of fit for a continuous distribution. Test that the following data comes from an exponential distribution.

```
lesson32a

## [1] 0.09174087 0.15185291 0.29387550 0.23516074 0.01433223 0.02978746
## [7] 0.11316773
```

5.3.8 Solution

First, seven data points is small and thus we are off to a weak start. We don't want empty cells and would like at least 4 or 5 values per cell. This data does not support it so we will make our best attempt but we should already suspect that this test will not have much power.

Our null hypothesis is that the data comes from an exponential distribution. The alternative is that it does not. This is a large set of alternatives and thus another reason to believe we will not have much power.

Let's bin the data. Since we only have 7 data points, I will pick three bins.

```
cutpoints<-c(0, .1, .2, Inf)
bin.data<-cut(lesson32a, cutpoints)
```

Notice that since the domain of an exponential is all non-negative real numbers, we used infinite in our bins.

Our estimate of θ is $\frac{1}{\bar{x}}$

```
mle<-1/mean(lesson32a)
```

Now to find the expected number of values in each cell, we need the probability of being in the cell from an exponential.

```
e<-rep(0,3)
e[1]<-pexp(cutpoints[2],mle)*7
e[2]<-(pexp(cutpoints[3],mle)-pexp(cutpoints[2],mle))*7
e[3]<-(1-pexp(cutpoints[3],mle))*7
```

Now the table of values

```
o<-table(bin.data)
cbind(o=o,e=e)
```

```
##          o          e
## (0,0.1]   3 3.702531
## (0.1,0.2] 2 1.744140
## (0.2,Inf] 2 1.553329
```

The likelihood ratio test is

```
(lrt<-2*sum(o*log(o/e)))
```

```
## [1] 0.2961037
```

The degrees of freedom are tricky. Under the unrestricted model, we have estimated 2 two parameters. Under the null we have estimated 1. This is anti-conservative to use 2-1 or 1 degree of freedom. It makes the p-value too small. So some people just use 2 degrees of freedom. We will check both.

```
1-pchisq(lrt,2)
```

```
## [1] 0.8623864
```

```
1-pchisq(lrt,1)
```

```
## [1] 0.5863354
```

In both cases we fail to reject but the test does not have much power.

If we used Pearson's test statistic we get:

```
pearson<-sum((o-e)^2/e)
1-pchisq(pearson,2)
```

```
## [1] 0.8610186
```

```
1-pchisq(pearson,1)
```

```
## [1] 0.5843353
```

5.3.9 Practice

Problem 5.21 in the book.

5.4 Two-way Tables

5.4.1 Objective

Conduct and interpret hypothesis test for two-way tables

5.4.2 Background

We are going to move towards looking at two random variables. The tools we have developed for parameter estimation and hypothesis testing will apply in this scenario as well.

```
library(fastR)
```

5.4.3 Review

To review, let's make a more complicated hypothesis test for a univariate case and review the key ideas.

We want to test the following complex hypothesis:

$$\begin{aligned} H_0 : \pi_0 &= \pi_2 \text{ and } \pi_1 = \pi_3 \\ H_0 : \pi_0 &\neq \pi_2 \text{ or } \pi_1 \neq \pi_3 \end{aligned}$$

Again, for this problem the data is:

```
(Less32tab<-table(Less32Data))
```

```
## Less32Data
## 0 1 2 3
## 8 1 7 4
```

The model for the distribution is

x	0	1	2	3
$f(x \theta)$	π_0	π_1	π_2	π_3

for $0 \leq \theta \leq 1$.

Now that the hypotheses are specified, we need to calculate the expected cell counts. Under the null we need to calculate the maximum likelihood estimate. Remember that the likelihood function is

$$L(H_0) = \left(\frac{(X_0 + X_1 + X_2 + X_3)!}{X_0!X_1!X_2!X_3!} \right) (\pi_0)^{X_0} (\pi_1)^{X_1} (\pi_2)^{X_2} (\pi_3)^{X_3}$$

Under the null hypothesis and also to keep the notation simple, use α to denote π_0 and π_2 and β to denote π_1 and π_3 so the likelihood function is

$$L(H_0) = \left(\frac{(X_0 + X_1 + X_2 + X_3)!}{X_0!X_1!X_2!X_3!} \right) (\alpha)^{X_0} (\beta)^{X_1} (\alpha)^{X_2} (\beta)^{X_3}$$

For our data this becomes

$$L(H_0) = K (\alpha)^8 (\beta)^1 (\alpha)^7 (\beta)^4$$

Where K is the factorial which is simply a constant with respect to α and β .

We know that $2\alpha + 2\beta = 1$ so the likelihood becomes

$$L(H_0) = K (\alpha)^{15} (1/2 - \alpha)^5$$

and then

$$l(H_0) = \log(L(H_0)) = \log(K) + 15\log(\alpha) + 5\log(1/2 - \alpha)$$

We used a Lagrange multiplier indirectly by replacing β with $1/2 - \alpha$.

Maximizing by taking the derivative, setting equal to zero, and solving yields

$$\hat{\alpha} = \frac{15}{40}$$

$$\hat{\beta} = \frac{5}{40}$$

The expected cell counts are

```
e<-20*rep(c(15/40,5/40),2)
```

Next we can use either a Pearson chi-squared statistic or likelihood ratio statistic to calculate the p-value. Using the Pearson chi-squared, we get:

```
1-pchisq(sum(((Less32tab-e)^2)/e),2)
```

```
## [1] 0.3932407
```

and using the likelihood ration test statistic, we get:

```
1-pchisq(2*sum(Less32tab*log(Less32tab/e)),2)
```

```
## [1] 0.3689545
```

There are two degrees of freedom because there are 3 free parameters under the alternative, remember the probabilities sum to one, and only one free parameter in the null hypothesis, again because $2\alpha + 2\beta = 1$.

These p-values are anti-conservative but since we fail to reject there is no need to find the conservative p-value.

The conservative p-values would be

```
1-pchisq(sum(((Less32tab-e)^2)/e),3)
```

```
## [1] 0.6005361
```

```
1-pchisq(2*sum(Less32tab*log(Less32tab/e)),3)
```

```
## [1] 0.5736189
```

R also has a built-in function that does this for us but it is not that much of an advantage.

```
chisq.test(Less32tab,p=e,rescale.p=TRUE)
```

```
## Warning in chisq.test(Less32tab, p = e, rescale.p = TRUE): Chi-squared
## approximation may be incorrect
```

```
##
## Chi-squared test for given probabilities
##
## data: Less32tab
## X-squared = 1.8667, df = 3, p-value = 0.6005
```

5.4.4 Introduction to RxC Tables

For the final material in this area we will examine likelihood based statistics for use on R x C tables, we have two random variables with R rows and C columns. We typically have discrete random variables and we want to know if there is a relationship between them. Before looking into hypothesis testing, it is important to discuss the different methods to collect data.

Consider the scenario where the State of Massachusetts is interested in the relationship between seat-belt use (yes or no) and outcome of crash (fatality, non-fatality). They summarize the data in a 2x2 table with outcome of crash in the columns. Now let's look at different ways to collect the data.

1. The state police catalog all accidents on the turnpike for the next year classifying each by seat-belt use and result of crash. The total sample size is random and each cell represents a Poisson random variable. We will not analyze this type of data in this course.
2. The state police randomly sample 100 police reports of crashes on the turnpike and classify each. This is a cross-sectional study with the total sample size fixed but each row and column is random. Each cell is a random variable from a multinomial distribution and typically we would want to test if the two variables are independent.
3. Suppose police records for accidents involving fatalities were filed separately from the others. The researchers randomly sample 50 records from accidents with fatalities and 50 records from accidents without fatalities. This is a retrospective study where fatality is the dependent variable and has fixed size. Each column, the variable of seat-belt use, associated with fatality are independent binomials and we could test if they are equal. That is the probability of seat-belt use is equal for both fatalities and non-fatalities.
4. We could fix the row totals. Suppose non-use of seat belts is rare so we sample 20 records without seat belts and 20 with seat belts. This is a prospective study and we could test for independent binomials. Most prospective studies apply the treatment and then observe the outcome. Obviously in this scenario, we would not require drivers to drive without seat belts.

5.4.5 Example

Kennedy Assassination: 900 people were polled by Fox News in 2003 and asked their political affiliation and thoughts on whether the President Kennedy assassination was a conspiracy. This is a cross-sectional study. The data is as follows

```
Kennedy=rbind(Dem=c(42,309,31),Rep=c(64,246,46),Other=c(20,115,27))
colnames(Kennedy)=c("Know All Facts","Some Facts Withheld","Not Sure")
Kennedy
```

	Know All Facts	Some Facts Withheld	Not Sure
## Dem	42	309	31
## Rep	64	246	46
## Other	20	115	27

The hypothesis test is

H_0 : Party Affiliation is independent of Conspiracy Views

H_a : Not Independent

Some notation, let o_{ij} be the observed cell count in the cell in row i and column j ; $n_i = \sum_j o_{ij}$ is the row total of row i ; $n_j = \sum_i o_{ij}$ is the column total of column j ; the total observations $n = \sum_i \sum_j o_{ij}$; $\hat{\pi}_{ij} = o_{ij}/n$ is the estimated probability of cell ij or similarly the estimated joint probability $P(X = i, Y = j)$; and $\hat{\pi}_j = \sum_i n_{ij}/n = n_j/n$ is the estimated marginal probability $P(Y = j)$.

If the variables are independent, then $e_{ij} = n * \hat{\pi}_i * \hat{\pi}_j$. This comes from the null hypothesis that assumes independence and thus that joint probabilities are the product of marginal probabilities as well maximum likelihood estimation of marginal probabilities using the constraint that the sum of the column or row marginal probabilities are one.

We now can generate a Pearson chi-squared or likelihood ratio test. First we calculate the expected cell counts under the null hypothesis.

```
(row.sum<-apply(Kennedy, 1, sum))
```

```
##   Dem   Rep Other
## 382   356   162
```

```
(col.sum<-apply(Kennedy, 2, sum))
```

```
##      Know All Facts Some Facts Withheld      Not Sure
##           126          670                  104
sum(Kennedy)
```

```
## [1] 900
```

```
(e<-outer(row.sum,col.sum)/900)
```

```
##      Know All Facts Some Facts Withheld Not Sure
## Dem      53.48     284.3778 44.14222
## Rep      49.84     265.0222 41.13778
## Other    22.68     120.6000 18.72000
```

The Pearson chi-squared test is

```
1-pchisq(sum((Kennedy-e)^2/e),4)
```

```
## [1] 0.0008956518
```

And the likelihood ratio test is

```
1-pchisq(2*sum(Kennedy*log(Kennedy/e)),4)
```

```
## [1] 0.0009591528
```

There are four degrees of freedom because under the null hypothesis we are estimating the marginal probabilities. There are three marginal probabilities for the rows but there are only two that are free since the sum of the probabilities must be one. The same for the columns. Thus we are estimating 4 parameters under the null. Under the alternative there are nine cell probabilities but again only eight are free. The difference between 8 and 4 is 4. In general for a table of size $I \times J$, under the null there are $(I-1)+(J-1)$ free parameters and under the alternative there are $IJ-1$ free parameters. Thus $(IJ - 1) - (I-1) - (J-1) = (I-1)(J-1)$ degrees of freedom.

Of course R has a command to automatic this for us.

```
chisq.test(Kennedy)
```

```
##
##  Pearson's Chi-squared test
##
```

```
## data: Kennedy
## X-squared = 18.711, df = 4, p-value = 0.0008957
```

We can also examine the expected and observed counts using the `xchisq` function in the `fastR` package.

```
xchisq.test(Kennedy)
```

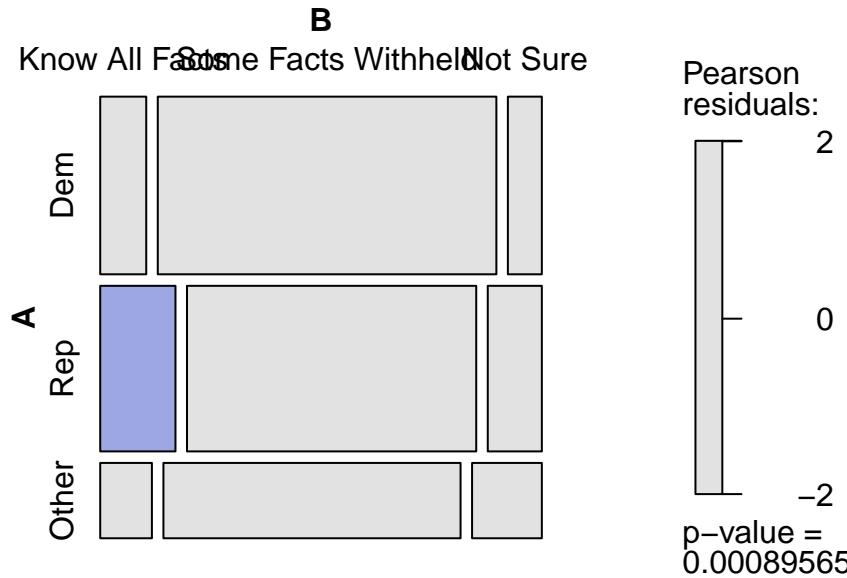
```
##
## Pearson's Chi-squared test
##
## data: x
## X-squared = 18.711, df = 4, p-value = 0.0008957
##
##    42.00   309.00   31.00
## ( 53.48) (284.38) ( 44.14)
## [2.46]   [2.13]   [3.91]
## <-1.57>  < 1.46>  <-1.98>
##
##    64.00   246.00   46.00
## ( 49.84) (265.02) ( 41.14)
## [4.02]   [1.37]   [0.57]
## < 2.01>  <-1.17>  < 0.76>
##
##    20.00   115.00   27.00
## ( 22.68) (120.60) ( 18.72)
## [0.32]   [0.26]   [3.66]
## <-0.56>  <-0.51>  < 1.91>
##
## key:
## observed
## (expected)
## [contribution to X-squared]
## <Pearson residual>
```

Notice that fewer democrats are not sure and more republicans are sure we know all the facts than expected under independence. These are the primary reasons for the rejection of the null hypothesis.

Using the package `vcg` we can visualize the results.

```
library(vcd)
```

```
mosaic(Kennedy, shade=T)
```



From this visual analysis, the republicans that claim we know all the facts are the significant reason for rejection of the null hypothesis.

5.4.6 Second Example

Consider a study where a researcher is interested in how different wards vote for an issue. The researcher selects 200 people at random from each ward and asks if they will vote for or against the ballot measure. The data are:

```
Bill1A=rbind(Ward1=c(76,124),Ward2=c(53,147),Ward3=c(59,141),Ward4=c(48,152))
colnames(Bill1A)=c("In Favor","Not in Favor")
Bill1A
```

```
##           In Favor Not in Favor
## Ward1      76        124
## Ward2      53        147
## Ward3      59        141
## Ward4      48        152
```

The hypotheses are:

$$H_0 : \pi_1 = \pi_2 = \pi_3 = \pi_4$$

$$H_a : \text{At least one different}$$

where π_i is the proportion in Ward i in favor of the measure.

Next we need to calculate the expected cell counts. If the probabilities are equal, then the estimate of proportion in favor is $\sum_i \frac{o_{ii}}{n}$ or $\frac{236}{800}$. Thus the expected cell counts in favor are $200 * \frac{236}{800}$ or 59.

The Pearson chi-squared test is

```
(e2<-cbind(rep(59,4),rep(141,4)))

##      [,1] [,2]
## [1,]    59   141
## [2,]    59   141
## [3,]    59   141
## [4,]    59   141

(sum((BillA-e2)^2/e2))

## [1] 10.72244

1-pchisq((sum((BillA-e2)^2/e2)),3)

## [1] 0.01332543
```

There are three degrees of freedom because under the alternative there are 4 free parameters and under the null only one.

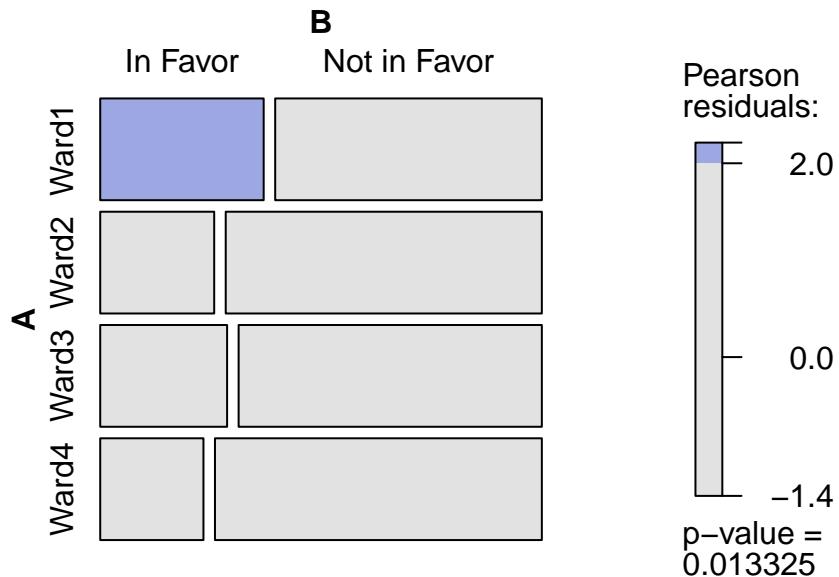
Or using R

```
chisq.test(BillA)

##
##  Pearson's Chi-squared test
##
## data: BillA
## X-squared = 10.722, df = 3, p-value = 0.01333
xchisq.test(BillA)

##
##  Pearson's Chi-squared test
##
## data: x
## X-squared = 10.722, df = 3, p-value = 0.01333
##
##    76.00    124.00
## ( 59.00) (141.00)
## [4.90]    [2.05]
## < 2.21>  <-1.43>
##
##    53.00    147.00
## ( 59.00) (141.00)
## [0.61]    [0.26]
## <-0.78>  < 0.51>
##
##    59.00    141.00
## ( 59.00) (141.00)
## [0.00]    [0.00]
## < 0.00>  < 0.00>
##
##    48.00    152.00
## ( 59.00) (141.00)
## [2.05]    [0.86]
## <-1.43>  < 0.93>
##
```

```
## key:
##   observed
##   (expected)
##   [contribution to X-squared]
##   <Pearson residual>
mosaic(BillA, shade=T)
```



```
prop.test(BillA[, 1], rep(200, 4))

##
## 4-sample test for equality of proportions without continuity
## correction
##
## data: BillA[, 1] out of rep(200, 4)
## X-squared = 10.722, df = 3, p-value = 0.01333
## alternative hypothesis: two.sided
## sample estimates:
## prop 1 prop 2 prop 3 prop 4
## 0.380 0.265 0.295 0.240
pairwise.prop.test(BillA[, 1], rep(200, 4), p.adj="fdr")

##
## Pairwise comparisons using Pairwise comparison of proportions
##
## data: BillA[, 1] out of rep(200, 4)
##
```

```
##      Ward1 Ward2 Ward3
## Ward2 0.056 -    -
## Ward3 0.181 0.645 -
## Ward4 0.021 0.645 0.388
##
## P value adjustment method: fdr
```

It appears that Ward 1 has a higher proportion in favor of the measure. The last command does a two-sample proportion test to determine which ward is different. There is also a correction since we are doing 6 tests. Again, the results support that Ward 1 is different from Ward 2 and Ward 4.

Note that if did not pay attention to the data collection and ran the problem as if both the row and column total were random, we would get the same result.

```
(row.sum<-apply(BillA,1,sum))

## Ward1 Ward2 Ward3 Ward4
##   200   200   200   200

(col.sum<-apply(BillA,2,sum))

##      In Favor Not in Favor
##           236          564

sum(BillA)

## [1] 800

(e3<-outer(row.sum,col.sum)/800)
```

```
##      In Favor Not in Favor
## Ward1      59       141
## Ward2      59       141
## Ward3      59       141
## Ward4      59       141
```

with the p-value

```
1-pchisq(sum((BillA-e3)^2/e3),3)

## [1] 0.01332543
```

The answer is the same. A nice coincidence.

Chapter 6

Introduction to Linear Models

This is just a brief, 4 lesson, introduction to linear models and in particular linear regression. This chapter is an excellent chapter and it is unfortunate these is not enough time to cover the entire chapter. The linear algebra approach does take some time to introduce to the students and thus I spend an entire lesson on section 6.1.

6.1 Introduction to Linear Models

6.1.1 Objectives

1. Know and use all new terms for the linear model framework
2. Use R or linear algebra to find various vectors or matrices needed in simple linear regression
3. Create model using R formulas

6.1.2 Linear Regression

A more powerful way to conduct analysis is to consider a response variable, typically called Y , output, or dependent, and one or more predictor variables, typically called X or input, independent, explanatory. Then from a model perspective, the following relationship is explored

$$Y = f(X_1, X_2, X_3, \dots, X_p) + \epsilon$$

where ϵ is the error and $E[\epsilon] = 0$.

The goal is to determine f and many techniques have been developed. One of the oldest and most successful is to assume that f is linear. That is

$$f(X_1, X_2, X_3, \dots, X_p) = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_p X_p$$

This model has $p + 1$ parameters denoted by β_i . Note that it is linear in the parameters and not in the dependent variables. The following is a linear model:

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2^2 + \epsilon$$

Finding the parameters β is a linear algebra problem. Before explaining the linear algebra, let's look at a couple of examples to demonstrate the power of this model.

6.1.3 Examples

From the `fastR` package, consider the `gpa` data set.

```
library(fastR)

summary(gpa)

##      satm          satv          act          gpa 
##  Min.   :370   Min.   :280.0   Min.   :15.0   Min.   :1.704 
##  1st Qu.:560   1st Qu.:560.0   1st Qu.:25.0   1st Qu.:3.034 
##  Median :630   Median :630.0   Median :28.0   Median :3.475 
##  Mean    :623   Mean    :614.6   Mean    :27.7   Mean    :3.352 
##  3rd Qu.:690   3rd Qu.:680.0   3rd Qu.:31.0   3rd Qu.:3.764 
##  Max.    :800   Max.    :800.0   Max.    :35.0   Max.    :4.000 

head(gpa)

##   satm satv act  gpa
## 1  430  470 15 2.239
## 2  560  350 16 2.488
## 3  400  330 17 2.982
## 4  410  450 17 2.155
## 5  430  460 17 2.712
## 6  430  370 18 1.913
```

Using R and its model notation, consider the model

```
lm(act~1,data=gpa)

##
## Call:
## lm(formula = act ~ 1, data = gpa)
##
## Coefficients:
## (Intercept)
##              27.7
```

Notice that this gave us a model where the function is a constant, in this case the mean.

The model matrix will be a column vector of one's.

```
head(model.matrix(lm(act~1,data=gpa)),n=20)

##      (Intercept)
## 1            1
## 2            1
## 3            1
## 4            1
## 5            1
## 6            1
## 7            1
## 8            1
## 9            1
## 10           1
## 11           1
## 12           1
## 13           1
```

```
## 14      1
## 15      1
## 16      1
## 17      1
## 18      1
## 19      1
## 20      1
```

Likewise we could explore a relationship between two continuous variables

```
lm(gpa~act,data=gpa)
```

```
##
## Call:
## lm(formula = gpa ~ act, data = gpa)
##
## Coefficients:
## (Intercept)      act
##       1.5024      0.0668
```

This model suggests that

$$GPA = 1.5 + .07 * ACT + \epsilon$$

The model matrix is

```
head(model.matrix(lm(gpa~act,data=gpa)),n=20)
```

```
##   (Intercept) act
## 1      1      15
## 2      1      16
## 3      1      17
## 4      1      17
## 5      1      17
## 6      1      18
## 7      1      18
## 8      1      18
## 9      1      18
## 10     1      19
## 11     1      19
## 12     1      19
## 13     1      19
## 14     1      20
## 15     1      20
## 16     1      20
## 17     1      20
## 18     1      20
## 19     1      21
## 20     1      21
```

The predicted values are

```
head(lm(gpa~act,data=gpa)$fitted,n=20)
```

```
##      1      2      3      4      5      6      7      8
## 2.504329 2.571125 2.637921 2.637921 2.637921 2.704718 2.704718 2.704718
##      9     10     11     12     13     14     15     16
## 2.704718 2.771514 2.771514 2.771514 2.771514 2.838310 2.838310 2.838310
##     17     18     19     20
```

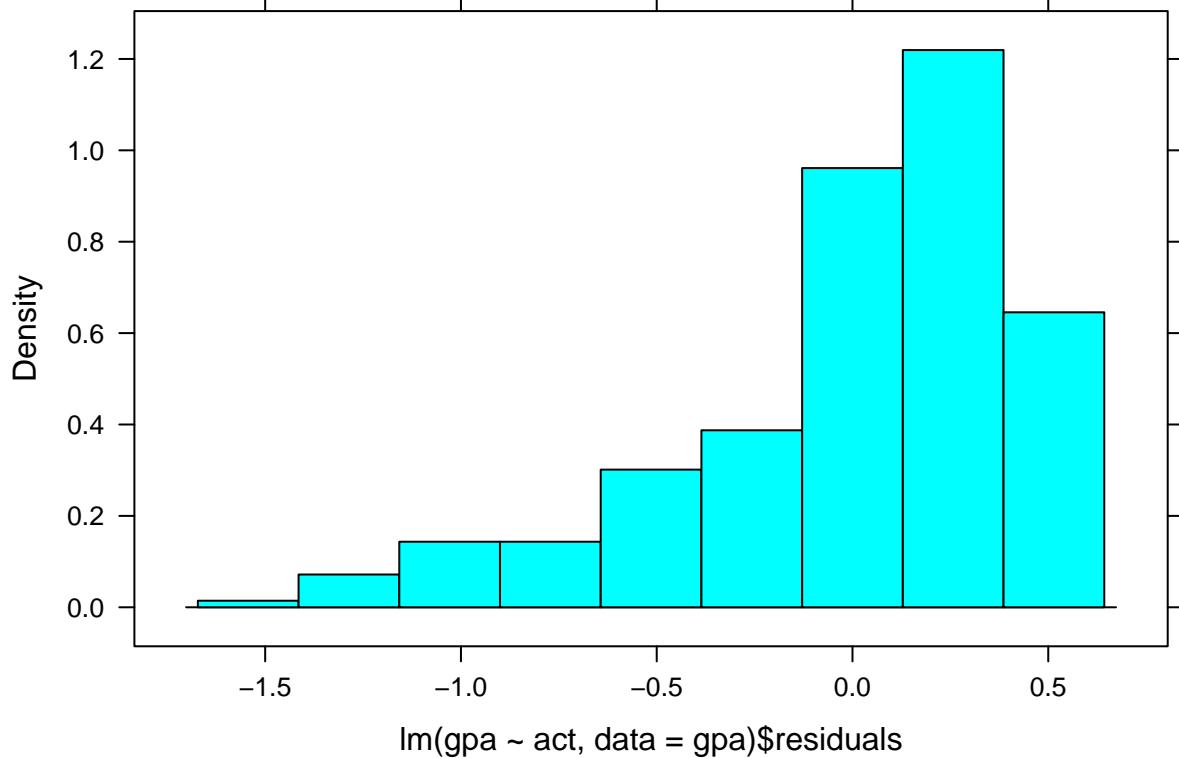
```
## 2.838310 2.838310 2.905106 2.905106
```

And the residuals, the difference between observed and predicted are

```
head(lm(gpa~act,data=gpa)$residuals,n=20)
```

```
##          1          2          3          4          5          6 
## -0.26532883 -0.08312508  0.34407867 -0.48292133  0.07407867 -0.79171757 
##          7          8          9         10         11         12 
##  0.24828243 -0.04071757  0.22728243 -0.10151382 -0.69151382  0.02648618 
##         13         14         15         16         17         18 
##  0.02448618  0.52668993  0.07468993  0.20568993 -0.23031007 -1.04931007 
##         19         20        
##  0.29689368  0.33889368
```

```
histogram(lm(gpa~act,data=gpa)$residuals)
```



As another example, consider the baseball batting data set

```
summary(batting)
```

```
##      player      year      stint      team      league 
##  chenbr01 : 11  Min.   :2000  Min.   :1.000  SDN    : 307  AA:   0 
##  micelda01: 10  1st Qu.:2001  1st Qu.:1.000  CLE    : 302  AL:3767 
##  chrisja01:  9  Median :2002  Median :1.000  TEX    : 300  NL:4295 
##  dejjeami01:  9  Mean    :2002  Mean   :1.089  KCA    : 297 
##  embreal01:  9  3rd Qu.:2004  3rd Qu.:1.000  COL    : 296 
##  garcika01:  9  Max.    :2005  Max.   :4.000  BOS    : 288 
##  (Other)   :8005                               (Other):6272
```

```

##      G          AB          R          H
##  Min.   : 1.00   Min.   : 0   Min.   : 0.00   Min.   : 0.00
##  1st Qu.: 7.00   1st Qu.: 1   1st Qu.: 0.00   1st Qu.: 0.00
##  Median : 29.00   Median : 20   Median : 1.00   Median : 3.00
##  Mean   : 46.96   Mean   :124   Mean   : 17.27   Mean   : 32.87
##  3rd Qu.: 74.00   3rd Qu.:186   3rd Qu.: 23.00   3rd Qu.: 47.00
##  Max.   :163.00   Max.   :704   Max.   :152.00   Max.   :262.00
##
##      H2B         H3B         HR         RBI
##  Min.   : 0.000   Min.   : 0.0000   Min.   : 0.000   Min.   : 0.00
##  1st Qu.: 0.000   1st Qu.: 0.0000   1st Qu.: 0.000   1st Qu.: 0.00
##  Median : 0.000   Median : 0.0000   Median : 0.000   Median : 1.00
##  Mean   : 6.577   Mean   : 0.6848   Mean   : 3.955   Mean   : 16.44
##  3rd Qu.: 9.000   3rd Qu.: 1.0000   3rd Qu.: 4.000   3rd Qu.: 22.00
##  Max.   :59.000   Max.   :20.0000   Max.   :73.000   Max.   :160.00
##
##      SB          CS          BB          SO
##  Min.   : 0.000   Min.   : 0.0000   Min.   : 0.00   Min.   : 0.00
##  1st Qu.: 0.000   1st Qu.: 0.0000   1st Qu.: 0.00   1st Qu.: 0.00
##  Median : 0.000   Median : 0.0000   Median : 1.00   Median : 6.00
##  Mean   : 2.047   Mean   : 0.9072   Mean   : 12.11  Mean   : 23.37
##  3rd Qu.: 1.000   3rd Qu.: 1.0000   3rd Qu.: 16.00  3rd Qu.: 35.00
##  Max.   :70.000   Max.   :24.0000   Max.   :232.00  Max.   :195.00
##
##      IBB         HBP         SH         SF
##  Min.   : 0.0000   Min.   : 0.000   Min.   : 0.000   Min.   : 0.000
##  1st Qu.: 0.0000   1st Qu.: 0.000   1st Qu.: 0.000   1st Qu.: 0.000
##  Median : 0.0000   Median : 0.000   Median : 0.000   Median : 0.000
##  Mean   : 0.9871   Mean   : 1.329   Mean   : 1.221  Mean   : 1.036
##  3rd Qu.: 1.0000   3rd Qu.: 1.000   3rd Qu.: 1.000   3rd Qu.: 1.000
##  Max.   :120.0000  Max.   :30.000   Max.   :24.000  Max.   :16.000
##  NA's   :1           NA's   :10                NA's   :1
##
##      GIDP
##  Min.   : 0.000
##  1st Qu.: 0.000
##  Median : 0.000
##  Mean   : 2.846
##  3rd Qu.: 4.000
##  Max.   :32.000
##

```

This model will give us the average hits for each league

```
lm(H~league,data=batting)
```

```

##
## Call:
## lm(formula = H ~ league, data = batting)
##
## Coefficients:
## (Intercept)    leagueNL
##            33.485     -1.162
33.485-1.162

```

```
## [1] 32.323
```

```
tapply(batting$H,batting$league,mean)

##      AA      AL      NL
##    NA 33.4850 32.3234
```

6.1.4 Least Squares

The parameters are found by minimizing the sum of the residuals squared. That is we want to find the difference between the observed and predicted, square the values to make sure all values are positive, and sum the values. This is our objective function and we want to find the values β that minimize this metric. This metric was developed because it has nice mathematical properties. In particular it is quadratic and thus has a nice closed form solution for the minimum. We will explore this in the next lesson.

Section 6-1 Additional Problems:

1. Verify the relationship in equation 6.5 of your text. Note: you will have to use properties of the inner product, see C.2.
2. Suppose that SATM and SATV, these variables are explained in the reading, are used to predict gpa. Write the model formula that correspond to the following R commands:
 - a) `lm(gpa~I(SATV+SATM))`
 - b) `lm(gpa~SATV+SATM)`
3. Let $y = 1,2,0$ be the response and $(x_1) = 1,2,3$ the predictor. These are used to create a linear model with an intercept. Answer the following questions using matrices and vectors:
 - a) Write the design matrix
 - b) Find the vector of fitted values. Using the following commands in R will give you the intercept and slope. Make these values a vector and use linear algebra to find the solution. (`Prob6.1<-data.frame(y=c(1,2,0),x=c(1,2,3)) lm(y~x,Prob6.1)`)
 - c) Find the vector of residuals
 - d) Find the vector of effects
 - e) Find the vector of variance
 - f) Show that the vectors in parts c and d are orthogonal
 - c) Show that the vector in part e is the sum of the vectors in parts c and d.

Here is a vector view of the third problem on the handout.

Here is a different view of the data

```
x<-c(1,2,3)
y<-c(1,2,0)
plot(x,y)
lm(y~x)

##
## Call:
## lm(formula = y ~ x)
##
## Coefficients:
## (Intercept)           x
##           2.0            -0.5
abline(a=2,b=-.5)
points(x,lm(y~x)$fitted,col="red")
```

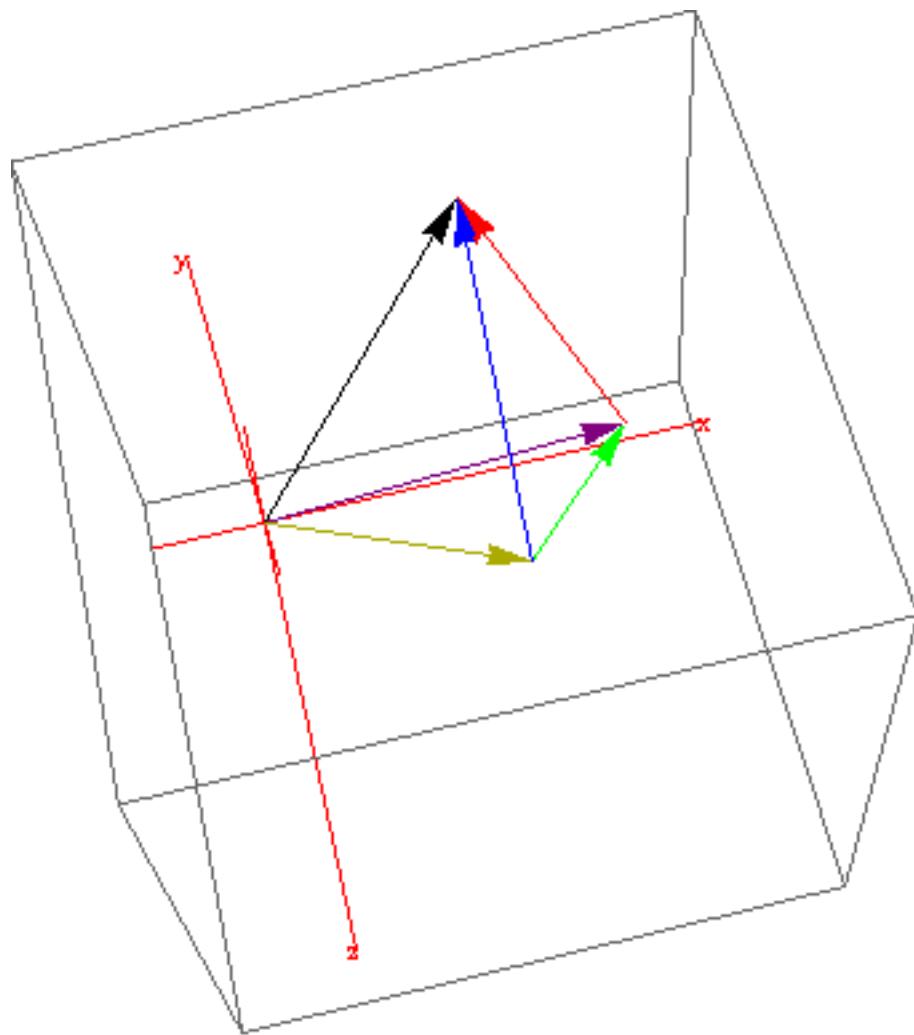
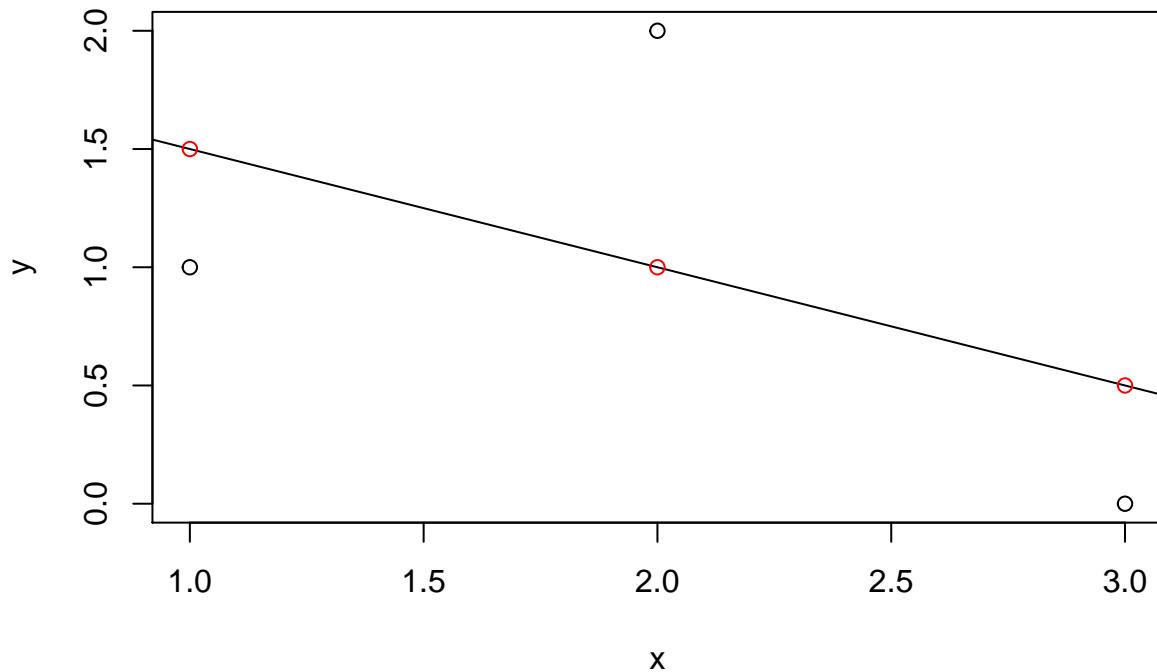


Figure 6.1: Least Squares



Or using a data frame

```
(Prob6.1<-data.frame(y=c(1,2,0),x=c(1,2,3)))
```

```
##   y x
## 1 1 1
## 2 2 2
## 3 0 3
lm(y~x,Prob6.1)
```

```
##
## Call:
## lm(formula = y ~ x, data = Prob6.1)
##
## Coefficients:
## (Intercept)          x
##           2.0         -0.5
lm(y~x,Prob6.1)$fitted
```

```
##   1   2   3
## 1.5 1.0 0.5
lm(y~x,Prob6.1)$residual
```

```
##   1   2   3
## -0.5 1.0 -0.5
```

6.2 Simple Linear Regression

6.2.1 Objectives

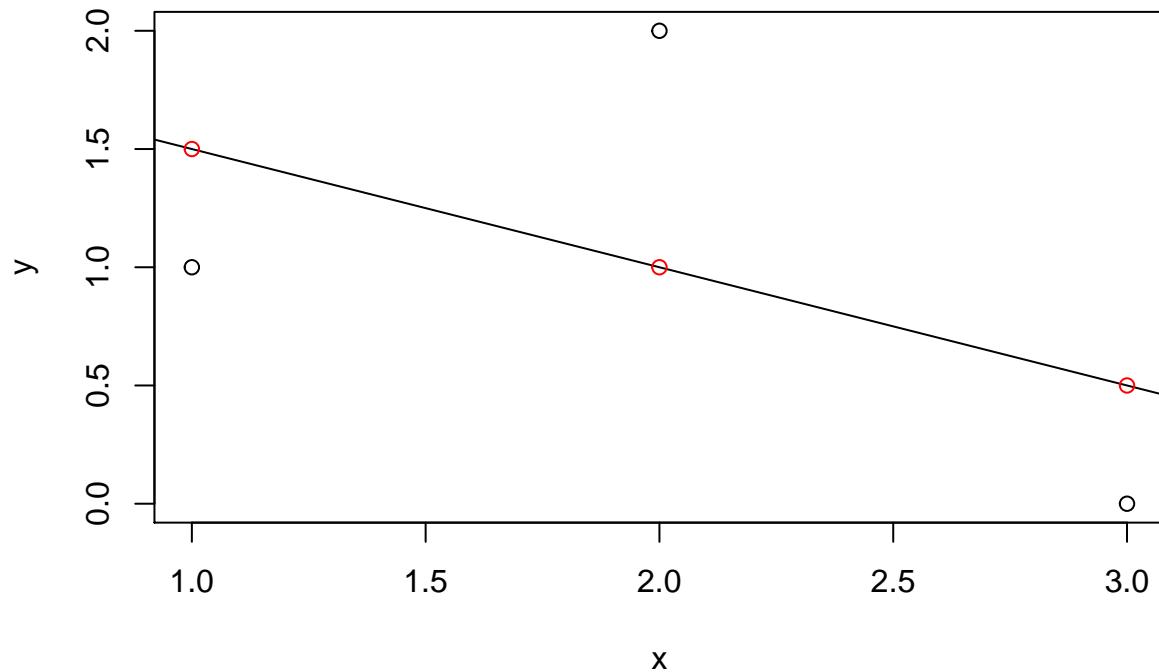
1. Find simple linear regression coefficients using least square, maximum likelihood, and linear algebra
2. Fit a simple linear regression model in R; find coefficients, fitted values, and plot results
3. Interpret the regression coefficients in the context of the problem

6.2.2 Review

Using the data from last lesson, let's look at the regression problem from three different perspectives. First if we plot the data

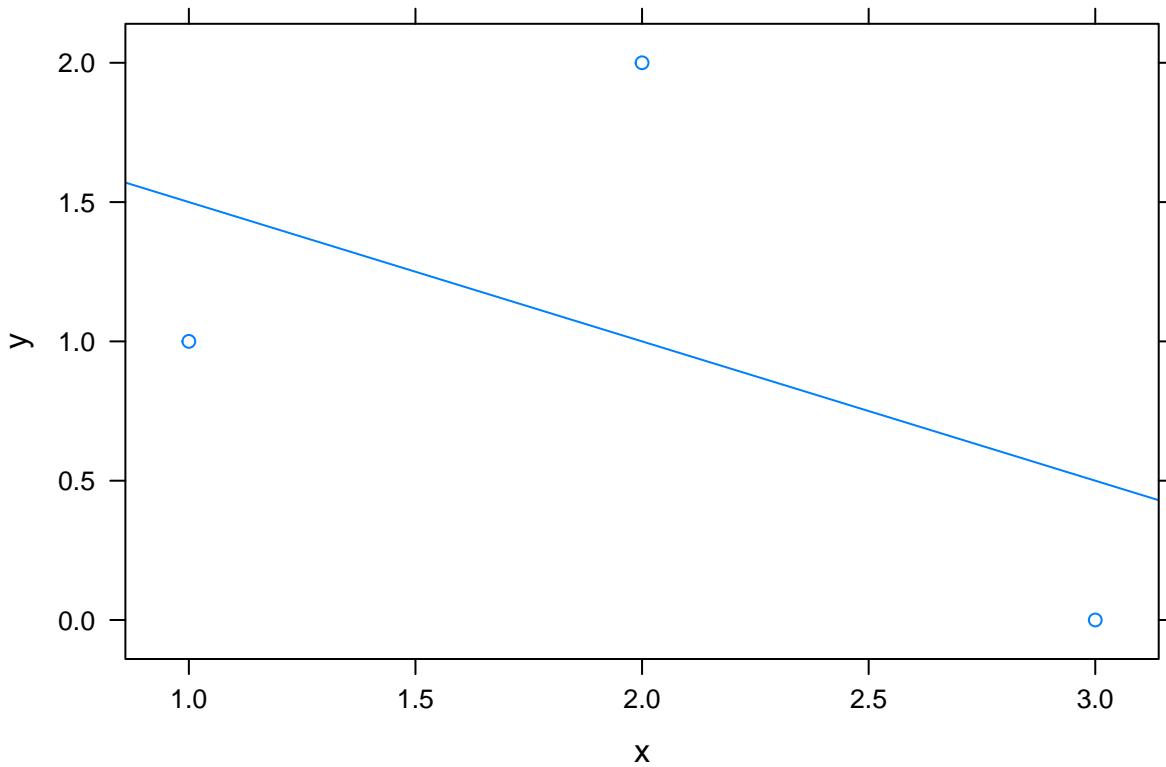
```
x<-c(1,2,3)
y<-c(1,2,0)
plot(x,y)
lm(y~x)
```

```
##
## Call:
## lm(formula = y ~ x)
##
## Coefficients:
## (Intercept)          x
##           2.0         -0.5
abline(a=2,b=-.5)
# abline(lm(y~x)) also works
points(x,lm(y~x)$fitted,col="red")
```



or using the lattice package

```
library(lattice)  
xyplot(y~x,type=c("p","r"))
```



In this situation we want the best line, the line that minimizes the sum of the squared errors, of the form $y = \beta_0 + \beta_1 x$.

Another perspective is to solve an over-determined set of linear equations

$$1 = \beta_0 + 1\beta_1$$

$$2 = \beta_0 + 2\beta_1$$

$$0 = \beta_0 + 3\beta_1$$

And finally, similar but using matrices and vectors, solving

$$\begin{pmatrix} 1 \\ 2 \\ 0 \end{pmatrix} = \begin{pmatrix} 1 & 1 \\ 1 & 2 \\ 1 & 3 \end{pmatrix} \begin{pmatrix} \beta_0 \\ \beta_1 \end{pmatrix}$$

6.2.3 Estimating parameters

We find estimates for β_0 and β_1 by minimizing the sum of squared errors. This metric was selected because it is a quadratic and has nice properties when you minimize it.

The sum of square errors is

$$\sum_i (y_i - \hat{y}_i)^2 = \sum_i (y_i - \beta_0 - \beta_1 x_i)^2$$

Taking the derivative and setting equal to zero yields

$$\hat{\beta}_1 = \frac{\sum_i (y_i - \bar{y}) x_i}{\sum_i (x_i - \bar{x}) x_i}$$

$$\hat{\beta}_0 = \bar{y} - \hat{\beta}_1 \bar{x}$$

for our problem

```
(beta1<-sum((y-mean(y))*x)/sum((x-mean(x))*x))

## [1] -0.5

(beta0<-mean(y)-beta1*mean(x))

## [1] 2
```

Using linear algebra

$$\begin{aligned}\vec{Y} &= X\vec{\beta} \\ X^T\vec{Y} &= X^TX\vec{\beta} \\ \vec{\beta} &= (X^TX)^{-1}X^T\vec{Y}\end{aligned}$$

Note that the columns of the model matrix must be linearly independent for the inverse to exist. The estimates of \vec{Y} are

$$\vec{Y} = X(X^TX)^{-1}X^T\vec{Y}$$

where $X(X^TX)^{-1}X^T$ is called the hat matrix.

```
(X<-as.matrix(cbind(1,x)))
```

```
##      x
## [1,] 1 1
## [2,] 1 2
## [3,] 1 3

solve(t(X)%%X)%%t(X)%%y

## [,1]
##    2.0
## x -0.5

X%%solve(t(X)%%X)%%t(X)%%y

## [,1]
## [1,] 1.5
## [2,] 1.0
## [3,] 0.5
```

Note that the interpretation of the slope coefficient is the change in the average value of y for one unit of change in x .

For maximum likelihood, we need a distribution for the error term. This is not needed for the methods above. If we assume the errors are independent and identically distributed from a normal with mean 0 and standard deviation σ , then the maximum likelihood estimates are

$$\hat{\beta}_1 = \frac{\sum_i (y_i - \bar{y})x_i}{\sum_i (x_i - \bar{x})x_i}$$

$$\hat{\beta}_0 = \bar{y} - \hat{\beta}_1 \bar{x}$$

$$\hat{\sigma}^2 = \frac{\sum_i e_i^2}{n}$$

The variance estimate is biased. An unbiased estimate divides by $n - 2$.

6.2.4 In R

We can compute all this information in R.

```
lm(y~x)
```

```
##  
## Call:  
## lm(formula = y ~ x)  
##  
## Coefficients:  
## (Intercept)          x  
##           2.0          -0.5  
summary(lm(y~x))
```

```
##  
## Call:  
## lm(formula = y ~ x)  
##  
## Residuals:  
##      1      2      3  
## -0.5  1.0 -0.5  
##  
## Coefficients:  
##             Estimate Std. Error t value Pr(>|t|)  
## (Intercept)  2.000     1.871   1.069   0.479  
## x          -0.500     0.866  -0.577   0.667  
##  
## Residual standard error: 1.225 on 1 degrees of freedom  
## Multiple R-squared:  0.25, Adjusted R-squared: -0.5  
## F-statistic: 0.3333 on 1 and 1 DF, p-value: 0.6667
```

```
names(lm(y~x))
```

```
## [1] "coefficients"  "residuals"       "effects"        "rank"  
## [5] "fitted.values" "assign"         "qr"            "df.residual"  
## [9] "xlevels"        "call"          "terms"         "model"
```

```
names(summary(lm(y~x)))
```

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

```
fitted(lm(y~x))
```

```
## 1 2 3  
## 1.5 1.0 0.5
```

```
residuals(lm(y~x))
```

```
## 1 2 3  
## -0.5 1.0 -0.5
```

Thus the maximum likelihood estimate of σ is

```
sqrt(sum(residuals(lm(y~x))^2)/3)
```

```
## [1] 0.7071068
(summary(lm(y~x))$sigma)*sqrt(1/3)
```

```
## [1] 0.7071068
```

Try Prob 6.4 and 6.5

6.3 Inference for Simple Linear Regression

6.3.1 Objectives

1. Conduct and interpret a hypothesis test and confidence interval for the slope of a simple linear regression
2. Find and interpret a confidence interval and prediction interval for the estimated response
3. Construct and interpret an ANOVA, analysis of variance, table to also include the coefficient of determinism

6.3.2 Inference for Regression Model Slope

In regression we are typically interested in inference for the slope coefficient and the predicted values. Inference could be in the form of a hypothesis test or confidence interval. We could also perform inference for the intercept but this is not common because the intercept is typically not relevant to the context of the problem. For example, if we have weight and height data on males and want to build a model with weight as the response and height as the predictor. The intercept has the interpretation of being the weight of a male who has no height. It is not relevant to the problem.

To perform inference for the predicted/fitted values and the slope we need their probability distributions. Since the model has the form

$$Y = \beta_0 + \beta_1 X + \epsilon$$

we really need the distribution of ϵ , the errors. If the errors are normally distributed, then the slope and intercept estimators from least squared regression are normally distributed and in fact are unbiased. The inference problems for the slope then become similar to inference for a mean. Thus if the variance is not known, as is often the case, we will use a t distribution. The big difference from testing a mean is that the degrees of freedom is $n - 2$ for simple linear regression.

As an example, let's consider the problem we have been working

```
x<-c(1,2,3)
y<-c(1,2,0)
```

The standard error of the slope is

$$\frac{s}{\sqrt{\sum (x_i - \bar{x})^2}}$$

where s is an estimate of the standard deviation. It is important to note the standard error depends on the distribution of the x values. In a designed experiment, we typically pick x values at the endpoints of the region of interest. This will make the denominator large and thus the standard error small.

For this problem the estimate of the slope is -0.5 and the estimate of the intercept is 2.0. The predicted values are

```
X<-cbind(1,x)
beta<-c(2.0,-.5)
(yhat<-as.vector(X%*%beta))

## [1] 1.5 1.0 0.5
s<-sqrt(sum((yhat-y)^2)/(3-2))
(slopes<-s/sqrt(sum((x-mean(x))^2)))

## [1] 0.8660254
```

To test the hypothesis that the slope is zero, that is that x is not correlated with y

$$H_0 : \beta_1 = 0$$

$$H_1 : \beta_1 \neq 0$$

The test statistic is

$$t = \frac{\hat{\beta}_1 - \beta_{H_0}}{SE(\hat{\beta}_1)}$$

or

```
(tstat<=(-.5 - 0)/slopes)
```

```
## [1] -0.5773503
```

and the p-value is

```
2*pt(tstat,1)
```

```
## [1] 0.6666667
```

Thus we fail to reject the null hypothesis.

This is the same as the output from the `lm` function in R.

```
summary(lm(y~x))
```

```
##
## Call:
## lm(formula = y ~ x)
##
## Residuals:
##   1    2    3 
## -0.5  1.0 -0.5 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.000     1.871    1.069   0.479    
## x          -0.500     0.866   -0.577   0.667    
## 
## Residual standard error: 1.225 on 1 degrees of freedom
## Multiple R-squared:  0.25, Adjusted R-squared:  -0.5  
## F-statistic: 0.3333 on 1 and 1 DF,  p-value: 0.6667
```

However, if we want to test

$$H_0 : \beta_1 = -.75$$

$$H_1 : \beta_1 \neq -.75$$

then we would have to generate our own p-value but we could use the values from the output `lm`.

```
(tstat<-(-.5 - (-.75))/summary(lm(y~x))$coefficients[2,2])  
  
## [1] 0.2886751  
2*(1-pt(tstat,1))  
  
## [1] 0.8210876
```

Confidence intervals can be generated as follows

$$\hat{\beta}_1 \pm t_{(1-\frac{\alpha}{2}, n-2)} SE(\hat{\beta}_1)$$

```
-.5+c(-1,1)*qt(.975,1)*slopes  
  
## [1] -11.5039 10.5039
```

or

```
confint(lm(y~x))  
  
##                 2.5 %    97.5 %  
## (Intercept) -21.77113 25.77113  
## x           -11.50390 10.50390
```

Since zero is in the confidence interval, we fail to reject the hypothesis that the slope is zero.

6.3.3 Inference for Regression Model Predicted Values

Remember that the predicted values from the regression model are average values. We typically want to form prediction intervals for both the average value and an individual value for a given x value. These intervals again will be formed as above using the t distribution but the standard errors are more difficult to determine. We will use software to do this portion.

For our example, assume we want to form a 90% prediction interval for the average value of y when x equals 1.5. The interval is

```
(simple_model<-lm(y~x))  
  
##  
## Call:  
## lm(formula = y ~ x)  
##  
## Coefficients:  
## (Intercept)          x  
##           2.0         -0.5  
  
predict(simple_model,newdata=data.frame(x=1.5),interval="confidence",level=.9)  
  
##     fit      lwr      upr  
## 1 1.25 -3.985086 6.485086
```

Note that we need to send a `data.frame` to the function even though we only had one value. This is because the function allows us to send multiple values. The interpretation is that we are 90% confident that the average value of y is between -3.99 and 6.49 when x equals 1.5.

As an example of multiple values

```
predict(simple_model,newdata=data.frame(x=c(1,2,3)),interval="confidence",level=.9)

##    fit      lwr      upr
## 1 1.5 -5.558989 8.558989
## 2 1.0 -3.464497 5.464497
## 3 0.5 -6.558989 7.558989
```

If we want an interval for a single value of y , we would use

```
predict(simple_model,newdata=data.frame(x=1.5),interval="prediction",level=.9)

##    fit      lwr      upr
## 1 1.25 -8.088164 10.58816
```

Notice that this interval is wider than the interval for the average value of y as we would expect since it is for a single value. The interpretation is that we are 90% confident the next value of y will be between -8.09 and 10.59 when x is 1.5.

6.3.4 ANOVA

We saw the results from R using the linear model function, `lm`, was

```
summary(lm(y~x))

##
## Call:
## lm(formula = y ~ x)
##
## Residuals:
##   1   2   3
## -0.5  1.0 -0.5
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.000     1.871   1.069   0.479
## x          -0.500     0.866  -0.577   0.667
##
## Residual standard error: 1.225 on 1 degrees of freedom
## Multiple R-squared:  0.25, Adjusted R-squared:  -0.5
## F-statistic: 0.3333 on 1 and 1 DF, p-value: 0.6667
```

There is some additional information to cover in the output. The output in the coefficients section provides the estimates of the intercept and slope, their standard errors, and test statistics and p-values for testing that these estimates are zero. The bottom portion provides some additional information. The residual standard error is an estimate of the standard deviation of the errors. It is also called the square root of the mean squared errors. Thus MSE, mean squared errors, is

$$MSE = \frac{\sum_i (y_i - \hat{y}_i)^2}{n - 2}$$

The multiple R-squared is a ratio of the SSM, sum of squares model, over SST, sum of square total, where

$$SSM = \sum_i (\hat{y}_i - \bar{y})^2$$

$$SST = \sum_i (y_i - \bar{y})^2$$

The sum of squares total is the variance in y . The sum of squares model is the variance explained by the model. Thus R-squared is the proportion of total variance explained by the model. This is a useful metric. We will not discuss the adjusted R-squared but it is a penalized version of the R-squared.

```
(SST<-sum((y-mean(y))^2))
```

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

```
(SSM<-sum((yhat-mean(y))^2))
```

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

```
SSM/SST
```

```
## [1] 0.25
```

The F-statistic simultaneous tests all the slope coefficients being equal to zero, which is helpful if we have multiple predictors. Since we only have one predictor, the p-value associated with the F-statistic is the same as the p-value for testing that the slope is zero. The F-statistic is the ratio of the mean squares for the model over the mean squares for the errors. Note that the sum of squares for the model and error as well as their degrees of freedom must add to the sum of squares total. The degrees of freedom for the mean squares total is $n-1$, this is because we are calculating a variance for y .

```
(SSE<-sum((y-yhat)^2))
```

```
## [1] 1.5
```

```
SSE+SSM
```

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

```
SST
```

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

The F-statistic is

```
(SSM/1)/(SSE/(3-2))
```

```
## [1] 0.3333333
```

And the p-value

```
2*pf((SSM/1)/(SSE/(3-2)),1,1)
```

```
## [1] 0.6666667
```

Sometimes this same information is summarized in an ANOVA table.

```
anova(lm(y~x))
```

```
## Analysis of Variance Table
##
## Response: y
##             Df Sum Sq Mean Sq F value Pr(>F)
## x            1    0.5     0.5   0.3333 0.6667
## Residuals   1    1.5     1.5
```

To assess the fit of the model, people use the p-value(s) for the slope, the F-statistic, and the R-squared values.

6.3.5 Example

Using the `gpa` from `fastR`, we could see if there is a linear relationship between total SAT score and gpa.

```
library(fastR)

head(gpa)

##   satm satv act   gpa
## 1  430  470 15 2.239
## 2  560  350 16 2.488
## 3  400  330 17 2.982
## 4  410  450 17 2.155
## 5  430  460 17 2.712
## 6  430  370 18 1.913

summary(lm(gpa~I(satm+satv),data=gpa))

##
## Call:
## lm(formula = gpa ~ I(satm + satv), data = gpa)
##
## Residuals:
##       Min     1Q Median     3Q    Max 
## -1.5883 -0.2074  0.1093  0.3178  0.7916 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 1.2162611  0.1989227  6.114 3.4e-09 ***
## I(satm + satv) 0.0017261  0.0001594 10.831 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4271 on 269 degrees of freedom
## Multiple R-squared:  0.3037, Adjusted R-squared:  0.3011 
## F-statistic: 117.3 on 1 and 269 DF,  p-value: < 2.2e-16

confint(lm(gpa~I(satm+satv),data=gpa),level=.9)

##
##           5 %      95 %
## (Intercept) 0.887931668 1.544590630
## I(satm + satv) 0.001463102 0.001989174
```

For a given set of scores on the SAT, we can generate a confidence interval for the average gpa and a prediction interval for an individual with those scores.

```
predict(lm(gpa~I(satm+satv),data=gpa),newdata=data.frame(satm=600,satv=600),interval="confidence",level=.9)

##
##       fit      lwr      upr
## 1 3.287627 3.243675 3.331579

predict(lm(gpa~I(satm+satv),data=gpa),newdata=data.frame(satm=600,satv=600),interval="prediction",level=.9)

##
##       fit      lwr      upr
## 1 3.287627 2.581233 3.994021
```

Notice that the prediction interval is wider.

6.4 Regression Diagnostics

6.4.1 Objective

Generate diagnostic plots to check for

- i. Normality
- ii. Equal variance
- iii. Outliers
- iv. Quality of fit

6.4.2 Review

The linear regression model assumes that the errors are

1. Independent
2. Normally distributed
3. Constant variance (homoskedastic)

In this section we will test these assumptions.

We are also assuming that a linear fit is appropriate, so we need to check this assumption.

Finally we need to check for observations that may have a large influence on the model. These are sometimes called outliers.

6.4.3 Assumptions about the Errors

To understand the assumptions, let's simulate data and then explore tools to evaluate the assumptions.

We will first build a data set where

$$y = 2x + \epsilon$$

where

$$\epsilon \sim N(0, 1.5)$$

```
set.seed(1282015)
(x<-sort(runif(40,min=1,max=10)))

## [1] 1.222363 1.570792 1.880924 2.085131 2.265512 2.396055 2.608625
## [8] 2.700767 3.133305 4.169626 4.230697 4.266002 4.347764 4.449684
## [15] 4.487690 4.715550 4.789777 4.838021 5.241457 5.596986 5.899153
## [22] 6.347361 6.418660 6.794570 6.957827 6.963492 7.215243 7.252023
## [29] 7.340929 7.506853 7.809755 7.833709 7.903431 7.960009 8.400092
## [36] 8.515763 8.603725 8.833631 9.156319 9.884379

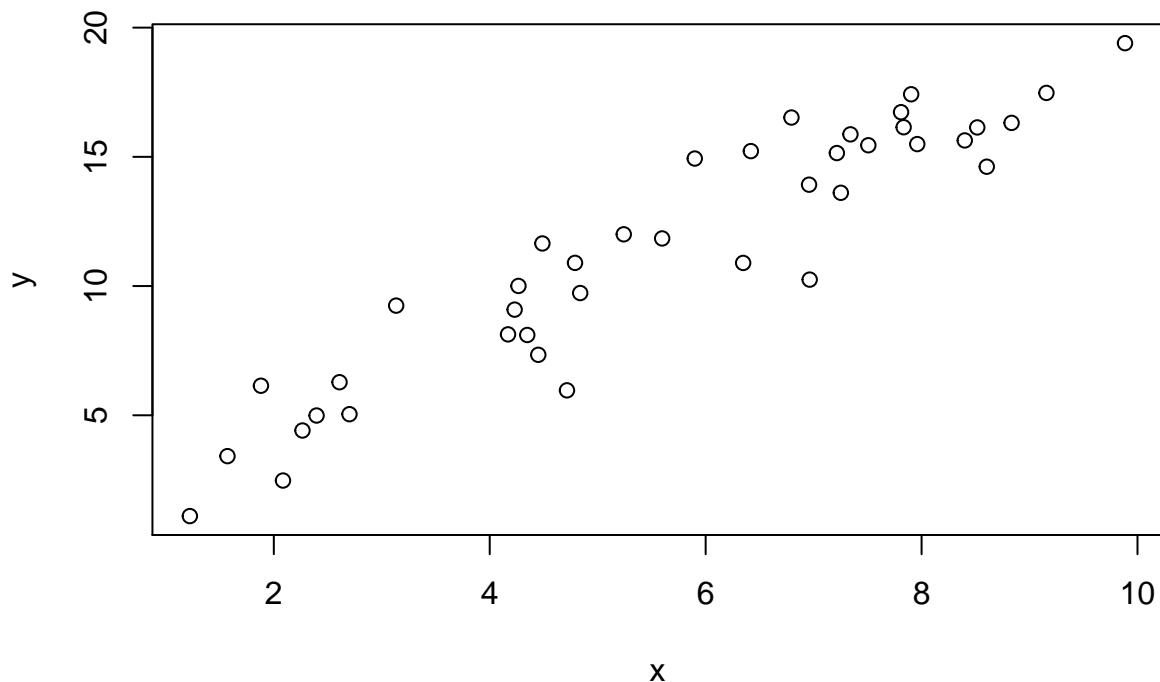
set.seed(2)
(error<-rnorm(40,0,1.5))

## [1] -1.345371820 0.277273777 2.381767997 -1.695563511 -0.120377635
## [6] 0.198630427 1.061932094 -0.359547036 2.976710905 -0.208180518
## [11] 0.626476126 1.472629166 -0.589043033 -1.559503465 2.673343440
## [16] -3.466603627 1.317906871 0.053710077 1.519243038 0.648397732
## [21] 3.136228808 -1.799888729 2.384457300 2.931977463 0.007406665
## [26] -3.677559582 0.715855954 -0.894837253 1.188304905 0.434455065
## [31] 1.108407906 0.478440602 1.614246531 -0.426236581 -1.165012911
## [36] -0.893490748 -2.588969669 -1.353876720 -0.838592872 -0.369768851
```

```
(y<-2*x+error)
```

```
## [1] 1.099355 3.418857 6.143617 2.474698 4.410647 4.990741 6.279181
## [8] 5.041987 9.243322 8.131071 9.087871 10.004633 8.106485 7.339865
## [15] 11.648724 5.964497 10.897461 9.729752 12.002157 11.842370 14.934534
## [22] 10.894832 15.221777 16.521117 13.923061 10.249425 15.146341 13.609209
## [29] 15.870163 15.448161 16.727917 16.145858 17.421108 15.493781 15.635171
## [36] 16.138036 14.618481 16.313386 17.474046 19.398989
```

```
plot(x,y)
```



Independence is difficult to evaluate and can typically only be done if the data is collected in an experiment and there is a time element. For example, if our data were collected so that the first value was 1.2223634 and the last value collected at a latter time was 9.8843788. Then we could check for independence by plotting the x-values, ordered by time, against the residuals. Again, in an observational study this is not possible but in an experiment it is. For our understanding, we will treat the simulated data as an experiment and check for independence.

First we build the model.

```
modles40<-lm(y~x)
summary(modles40)
```

```
##
## Call:
## lm(formula = y ~ x)
##
## Residuals:
```

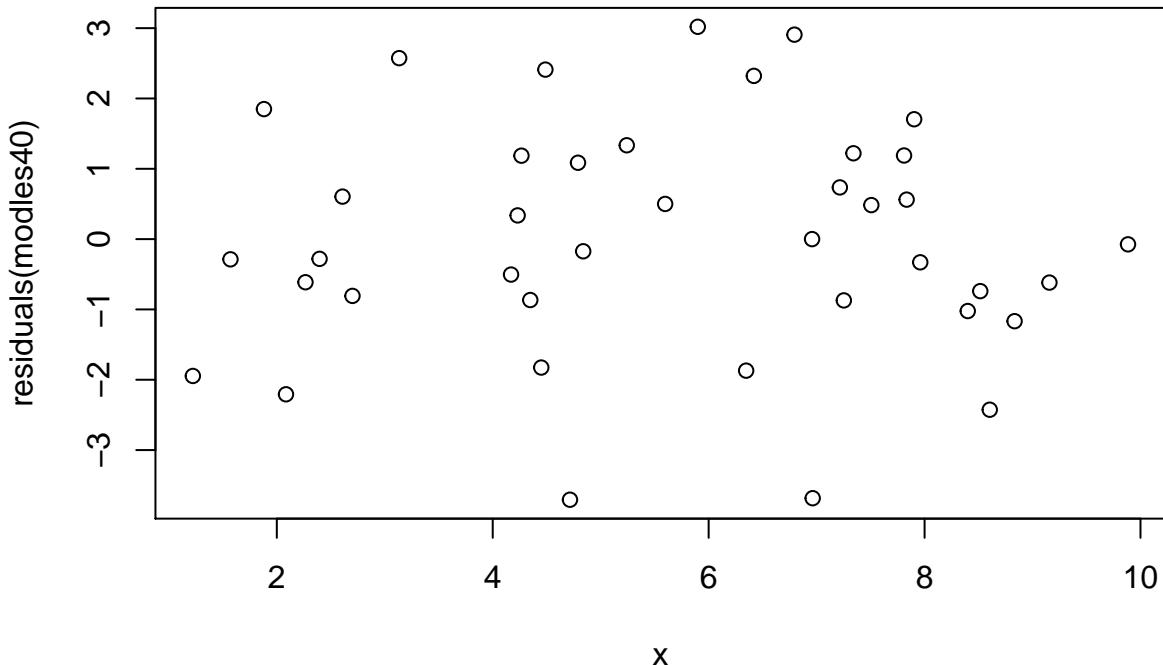
```

##      Min      1Q Median      3Q      Max
## -3.7060 -0.8679 -0.1237  1.1873  3.0193
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.7274    0.6792   1.071   0.291
## x           1.8965    0.1115  17.015 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.67 on 38 degrees of freedom
## Multiple R-squared:  0.884, Adjusted R-squared:  0.8809
## F-statistic: 289.5 on 1 and 38 DF, p-value: < 2.2e-16

```

Then plot the x-values versus the residuals.

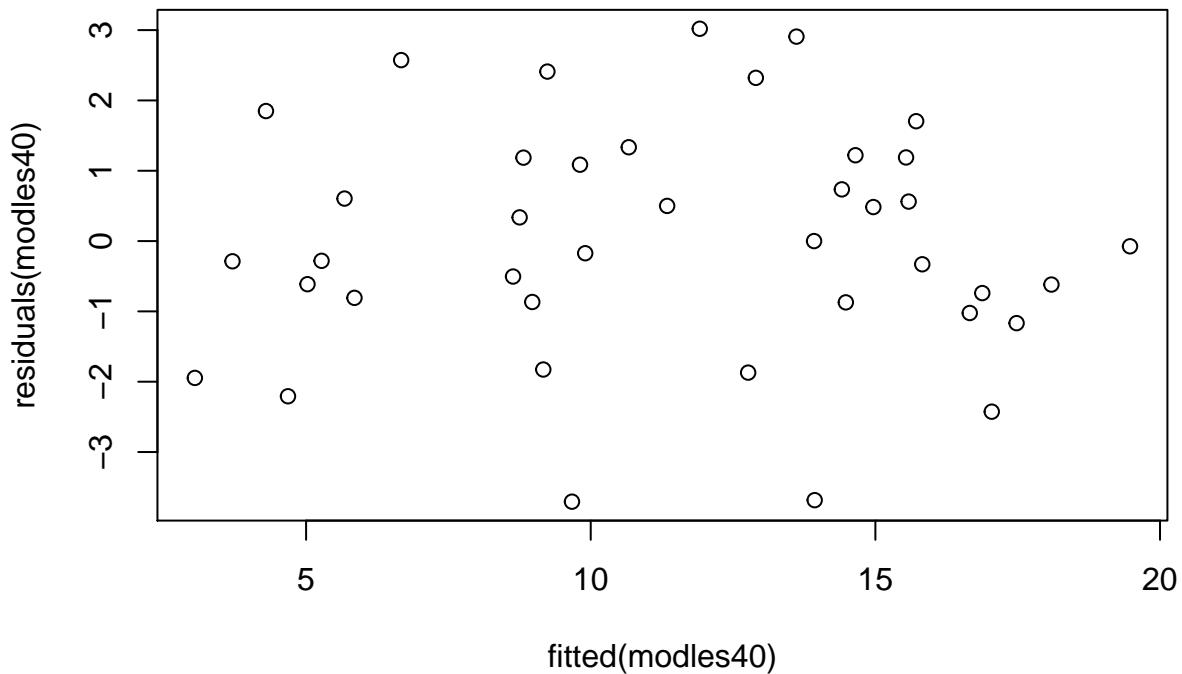
```
plot(residuals(modles40) ~ x)
```



If independence is not a valid assumption, then we would see a pattern in the plot. We do not see any pattern here. Some examples of patterns are a learning curve, where variance decreases or the slope changes, environmental effects such as heat or humidity which change during the day, or some change in the variable such as a different testing machine.

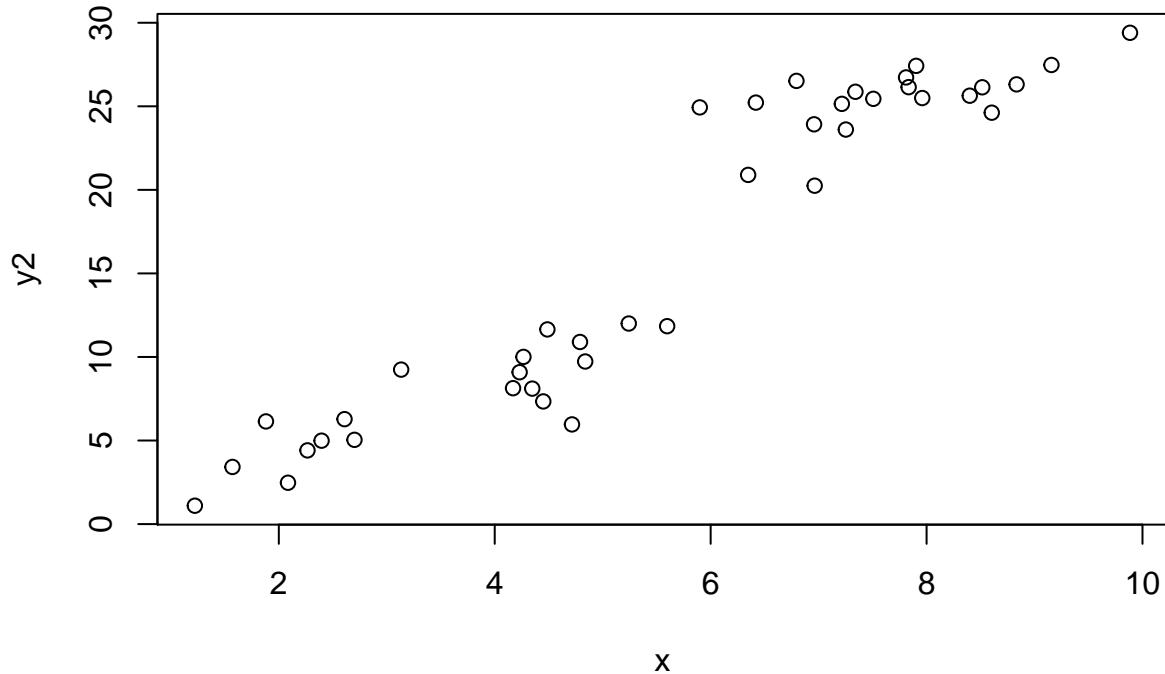
A similar plot which is more common, is to plot the fitted values against the residuals.

```
plot(residuals(modles40) ~ fitted(modles40))
```



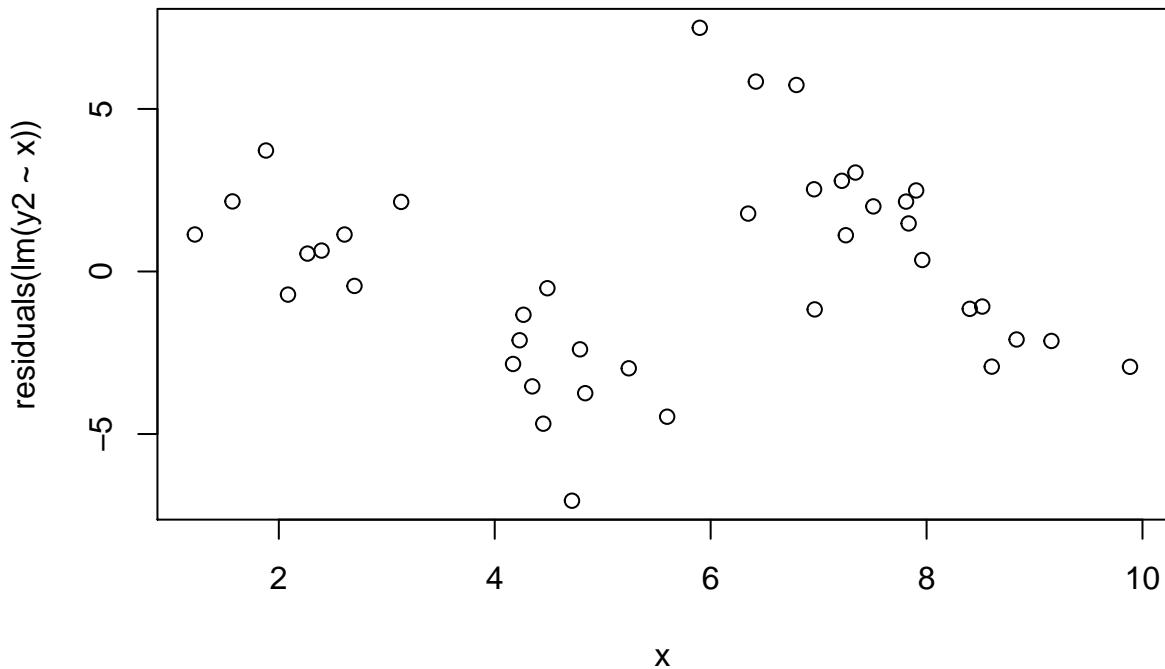
To help us understand a lack of independence, let's put a shift in the data after 20 data points have been observed.

```
y2<-y  
y2[21:40]<-y2[21:40]+10  
plot(x,y2)
```

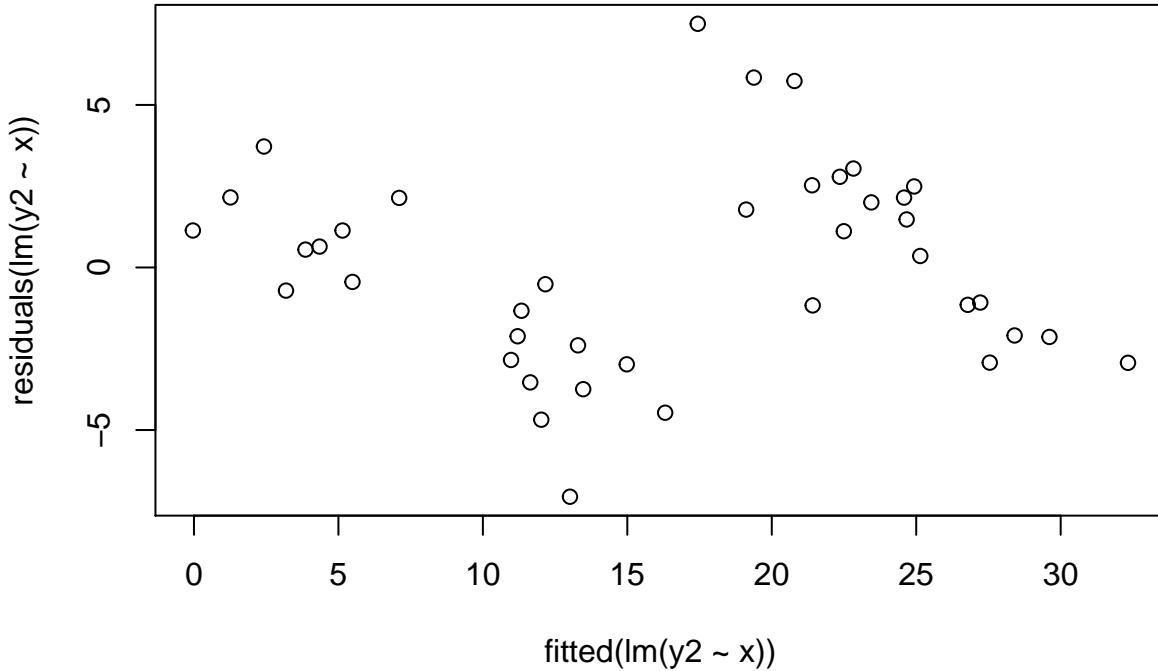


```
summary(lm(y2~x))

##
## Call:
## lm(formula = y2 ~ x)
##
## Residuals:
##    Min     1Q   Median     3Q    Max 
## -7.0509 -2.2012 -0.0452  2.1429  7.4960 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) -4.606     1.274  -3.616 0.000865 ***
## x            3.737     0.209  17.878 < 2e-16 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.131 on 38 degrees of freedom
## Multiple R-squared:  0.8937, Adjusted R-squared:  0.8909 
## F-statistic: 319.6 on 1 and 38 DF,  p-value: < 2.2e-16
plot(residuals(lm(y2~x))~x)
```



```
plot(residuals(lm(y2~x))~fitted(lm(y2~x)))
```



From the plot, it should be clear that the residuals are not in a random pattern, there is a dependency. You could in this simulation, introduce other types of dependencies.

The plot of residuals turns out to be one of the best diagnostic tools. We can also use it to check for constant variance as well as the quality of the linear fit.

Next, going back to our original data, let's let the variance decrease as the x-values increase.

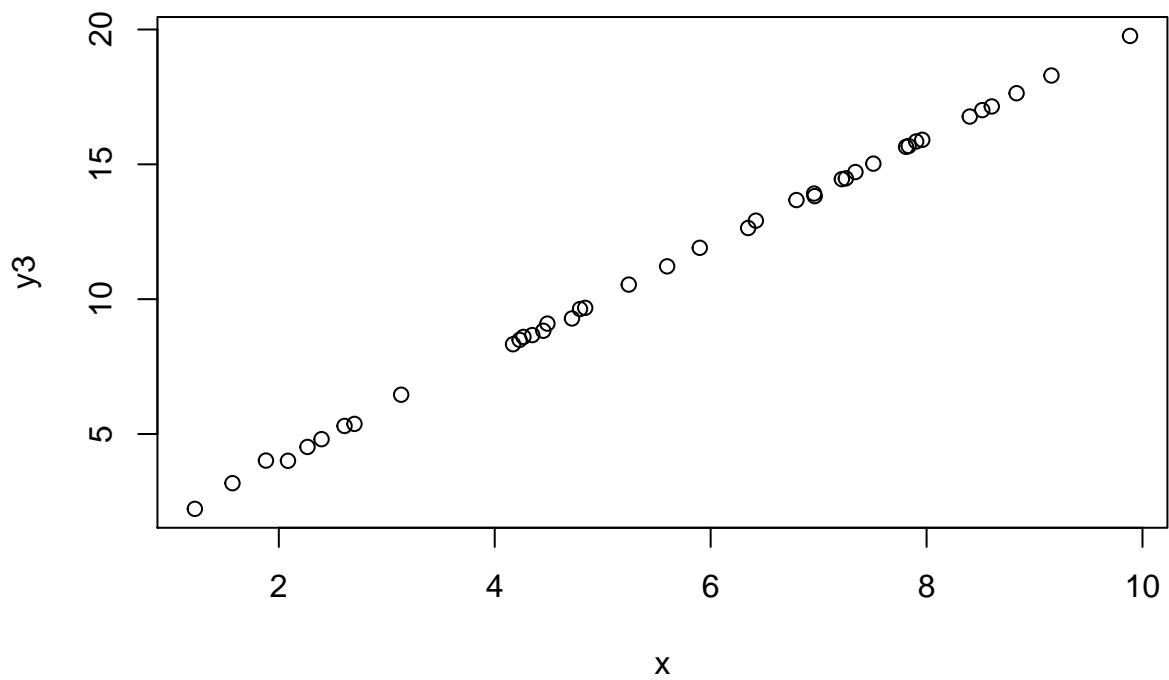
```
(error2<-error/(5*x))
```

```
## [1] -0.2201263333 0.0353037015 0.2532550356 -0.1626337812 -0.0106269674
## [6] 0.0165797866 0.0814170088 -0.0266255519 0.1900045228 -0.0099855730
## [11] 0.0296157372 0.0690402525 -0.0270963667 -0.0700950166 0.1191411784
## [16] -0.1470285982 0.0550299904 0.0022203326 0.0579702568 0.0231695320
## [21] 0.1063281089 -0.0567129823 0.0742976661 0.0863035495 0.0002129017
## [26] -0.1056240005 0.0198428798 -0.0246782792 0.0323747832 0.0115748922
## [31] 0.0283852169 0.0122149195 0.0408492614 -0.0107094497 -0.0277380991
## [36] -0.0209843961 -0.0601825269 -0.0306527790 -0.0183172482 -0.0074818835
```

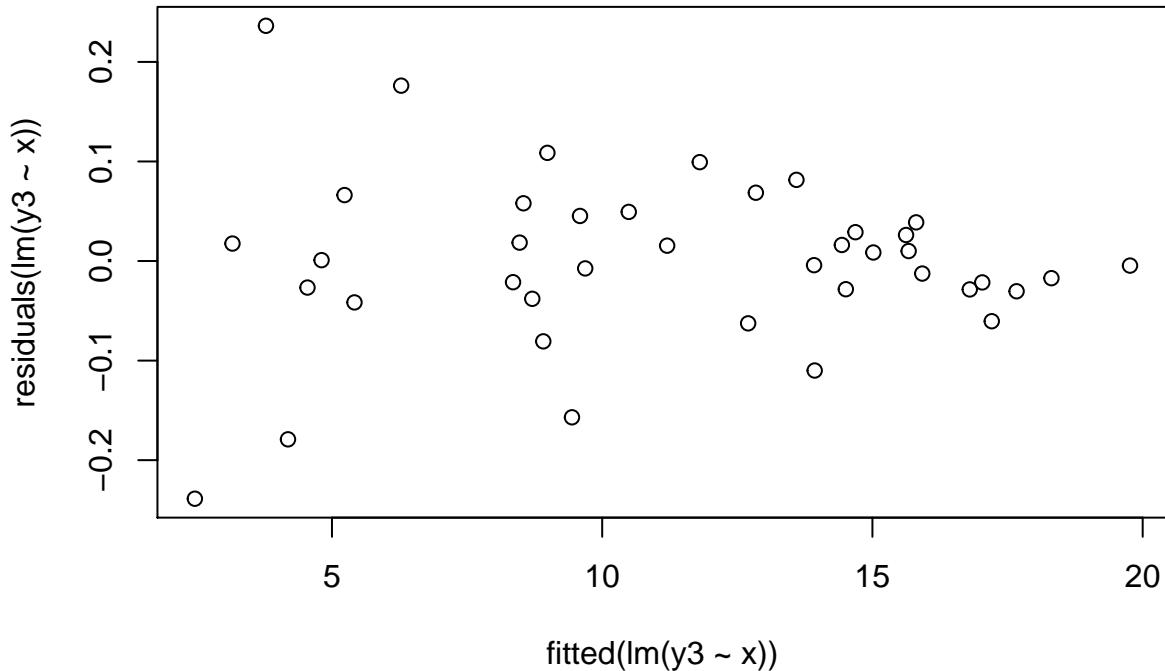
```
(y3<-2*x+error2)
```

```
## [1] 2.224600 3.176887 4.015104 4.007628 4.520398 4.808690 5.298666
## [8] 5.374908 6.456615 8.329266 8.491011 8.601044 8.668432 8.829274
## [15] 9.094521 9.284072 9.634584 9.678262 10.540884 11.217142 11.904634
## [22] 12.638008 12.911618 13.675443 13.915867 13.821361 14.450328 14.479368
## [29] 14.714233 15.025281 15.647895 15.679632 15.847711 15.909309 16.772446
## [36] 17.010542 17.147268 17.636610 18.294321 19.761276
```

```
plot(x,y3)
```



```
plot(residuals(lm(y3~x))-fitted(lm(y3~x)))
```



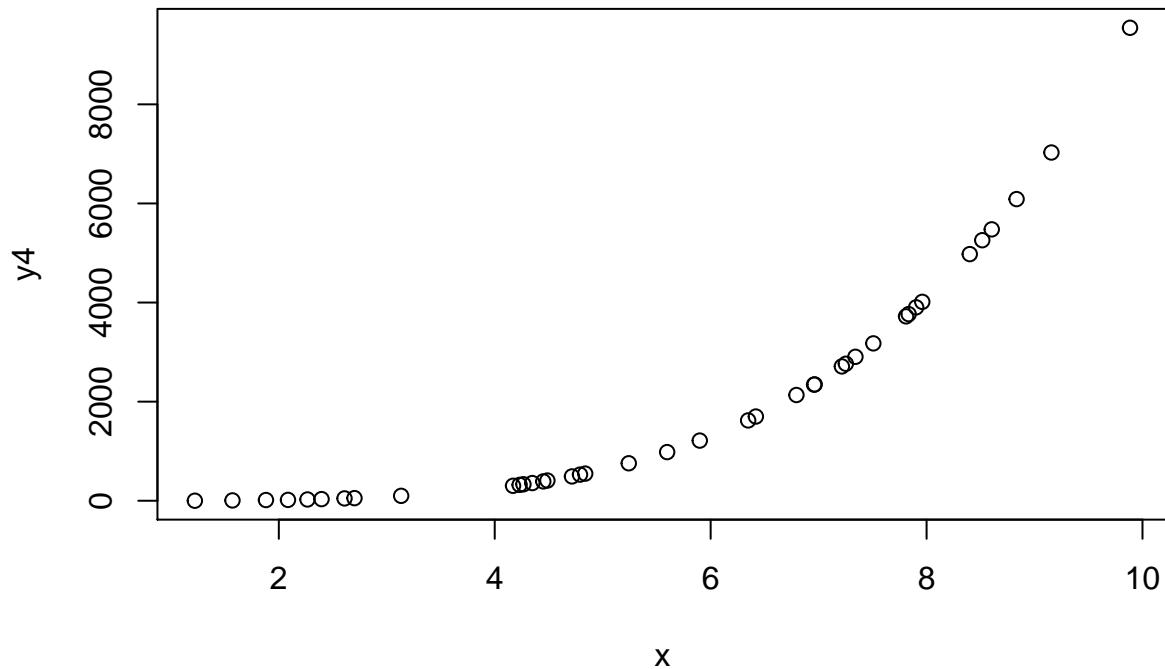
Notice how the spread of the residuals decreases as the fitted values get larger, this is an indication that variance is not constant.

Now let's change the underlying model to not be linear and look at the residual plot.

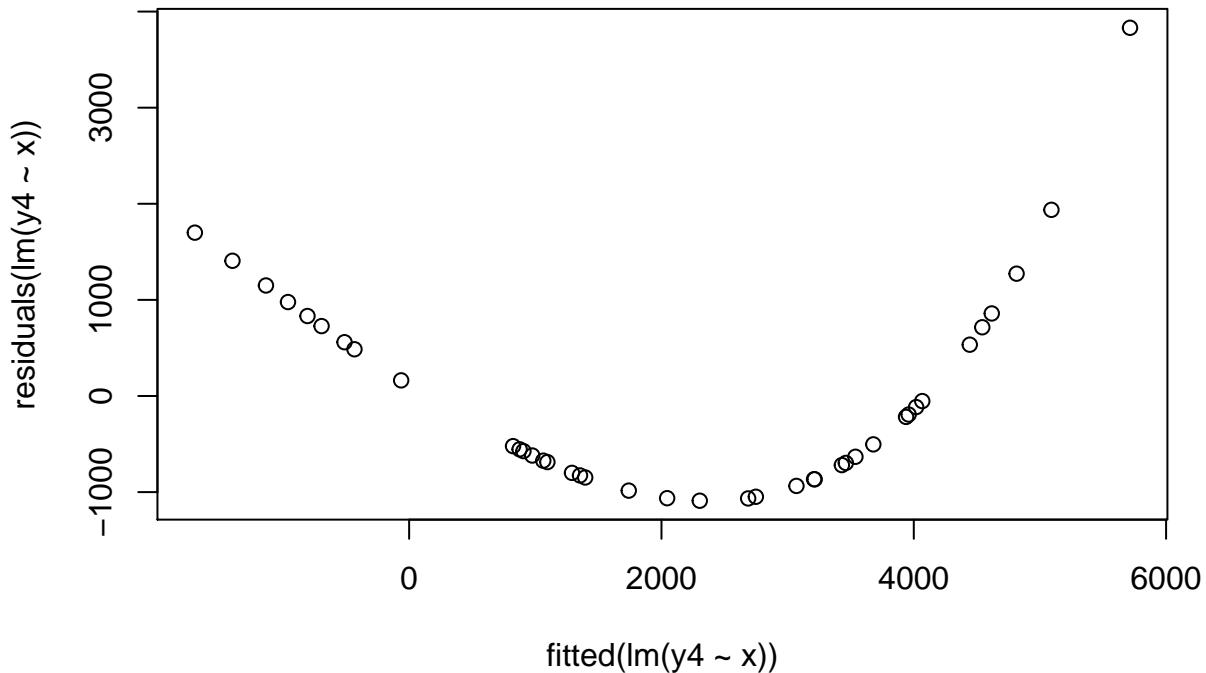
```
(y4<-x^4+error)
```

```
## [1] 0.8871787 6.3652676 14.8983413 17.2075435 26.2226581
## [6] 33.1586409 47.3689056 52.8449523 99.3620238 302.0571672
## [11] 320.9935650 332.6678704 356.7363122 390.4682270 408.2672661
## [16] 490.9914613 527.6515427 547.9154007 756.2779063 981.9824799
## [21] 1214.1764942 1621.4024905 1699.7582633 2134.2480641 2343.6669097
## [26] 2347.6243944 2710.9308302 2765.0066720 2905.2381582 3176.0770614
## [31] 3721.1652431 3766.3860278 3903.3926221 4014.2842430 4977.7665239
## [36] 5257.9993379 5476.9769666 6087.8014211 7028.0025738 9545.1046992
```

```
plot(x,y4)
```



```
plot(residuals(lm(y4~x))~fitted(lm(y4~x)))
```

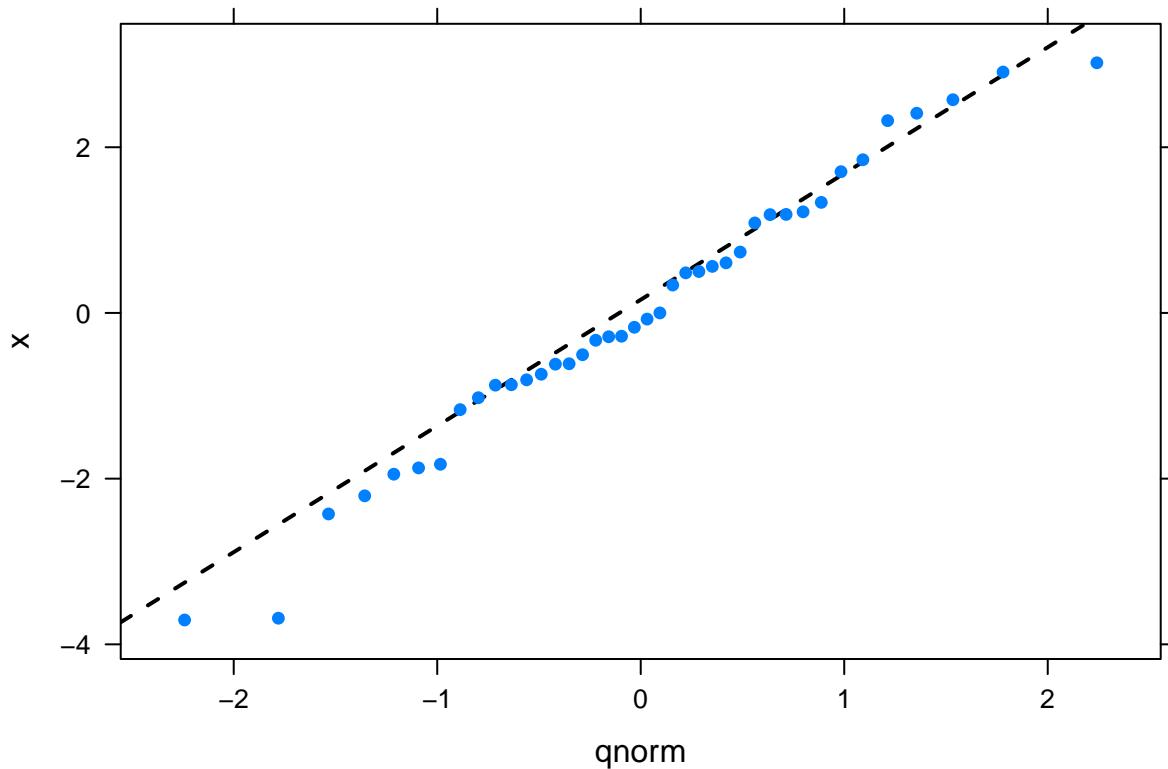


The plot indicates that there is a non-linear relationship between x and y.

Normality can be checked using a qq-plot.

```
xqqmath(residuals(modles40))
```

```
## Warning in qqmath.numeric(x, data = data, panel = panel, ...): explicit
## 'data' specification ignored
```



We have discussed this plot in detail in a previous lesson.

Often instead of using the residuals to check assumptions, standardized residuals are used. This is done to remove the bias that an interpreter of the plot may have just based on the size of the residuals. The easiest standardization is to divide the residuals by the estimate of standard error. The second method is called the studentized residual which accounts for the fact that the variance of the residual depends on the hat matrix. This second standardization is the most common.

6.4.4 Outliers, Leverage, and Influence

An outlier can be an observed value that is much different than the predicted value or a value of the predictor that is much different than the other predictor values. The second type is called a leverage point. The first simply an outlier. Outliers should be investigated to make sure there was not a data recording error or measurement error. Be careful about simply deleting them. There must be a reason to remove it other than it is an outlier.

Outliers in the response are again found from the residual plot.

Leverage can be measured by looking at the impact an observation has on the slope. This is done by calculating the slope without the observation and then with the observation and looking at the difference in slopes. This is called DFBETA, difference in the beta. We can also standardize it so that we can easily compare across data sets.

```
library(car)

dfbetaPlots(modles40, ylim=c(.15, -.15), xlab = "Observation Number", ylab = "DFBeta")
```

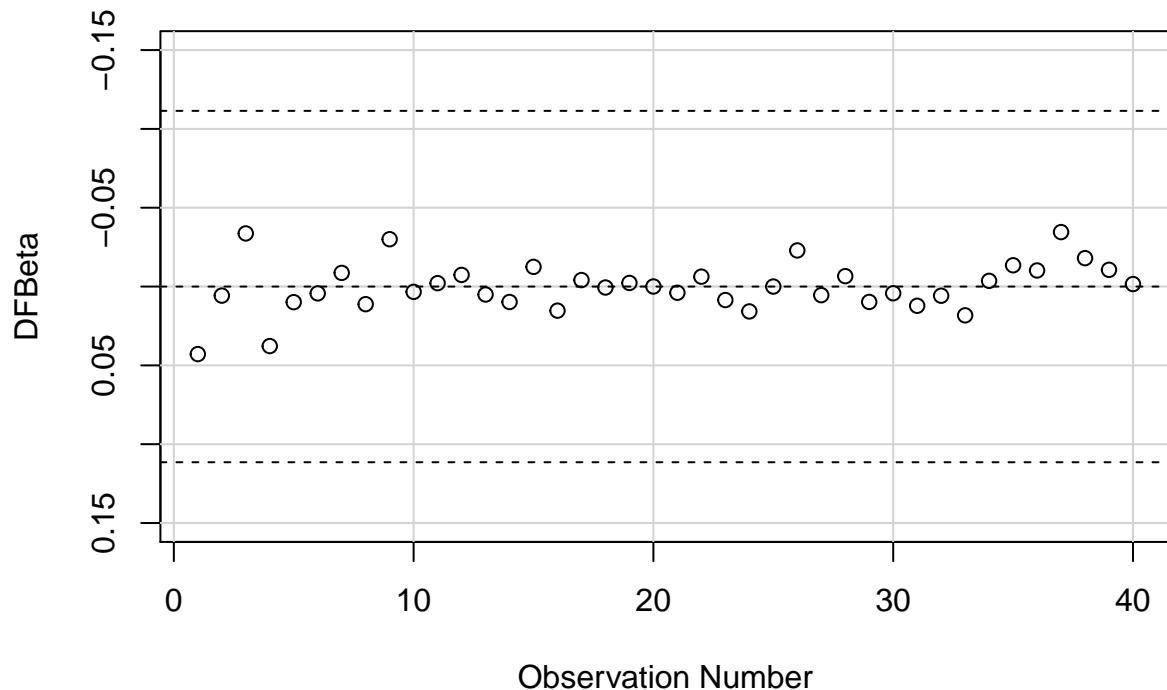


Figure 6.2: Impact of Each Observation on the Slope Using DFBETA

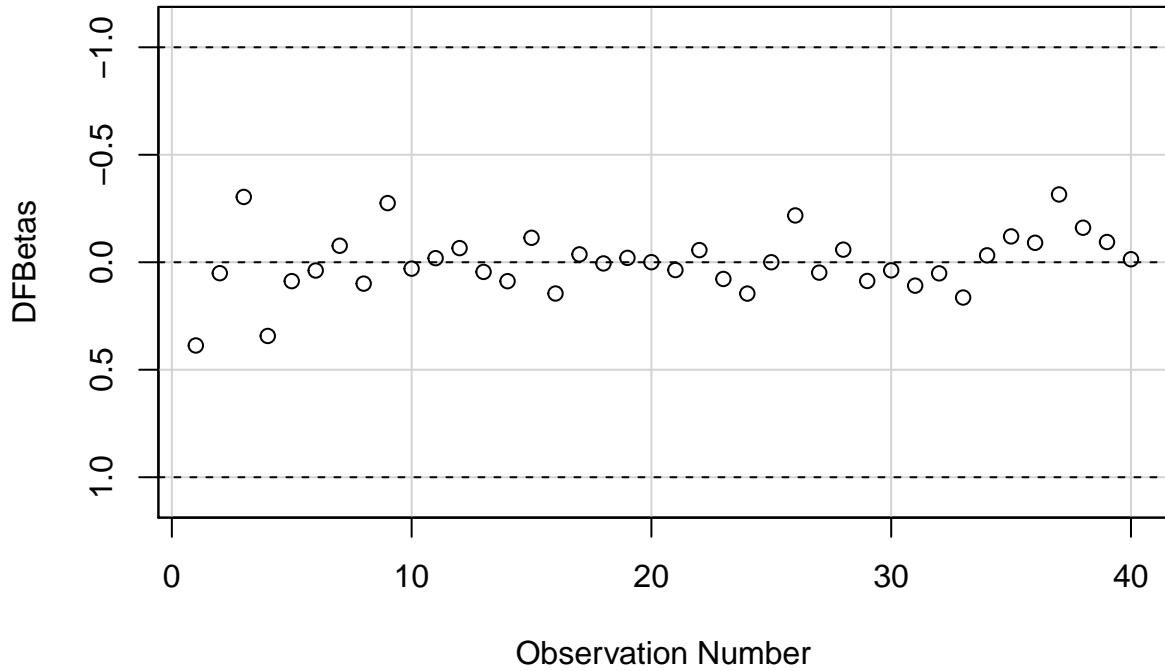


Figure 6.3: Impact of Each Observation on the Slope Using DFBETAs

Figure 6.2 illustrates how each observation impacts the slope. The dotted lines above and below the origin are one standard deviation. None of the values seem extreme. We could also standardize the output by using DFBETAS.

```
dfbetasPlots(modles40,ylim=c(1.1,-1.1),xlab = "Observation Number",ylab = "DFBetas")
```

Figure 6.3 is standardized and the dotted line is at positive and negative 1. Again, there are no points with high leverage.

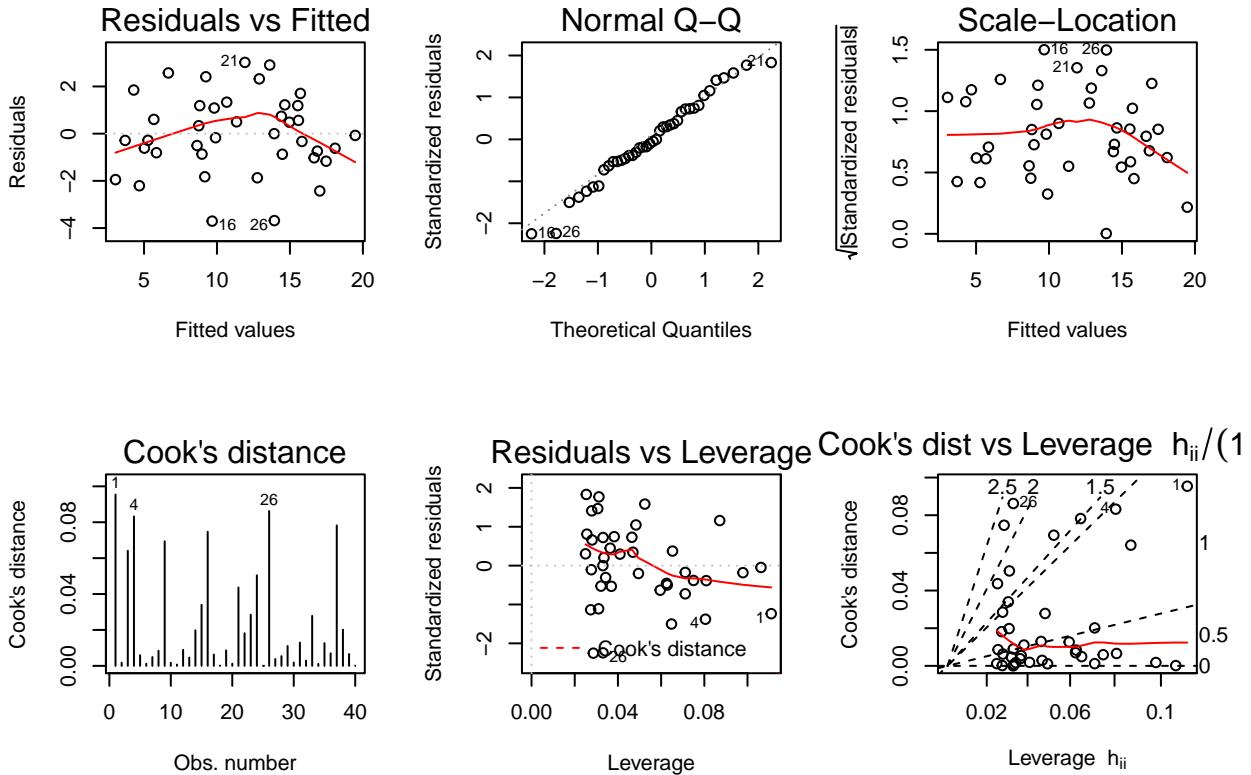
Another measure of leverage is to take the value from the hat matrix and compare it with $2p/n$ where p is the number of parameters. This is simply called leverage.

Influence is determined by how much the fitted values depend on an observation. We could calculate the difference between the fitted values with the observation in the model and without removed. This is called DFFIT. It can also be standardized.

The second measure of influence is called Cook's Distance. It measures the difference in all the observed and predicted values with the observation removed. It is a vector distance squared. It also gets standardized by the variance and number of parameters. A value in excess of 1 is a concern.

Luckily, R has plots and functions for all of these measures.

```
par(mfrow=c(2,3))
plot(modles40,w=1:6)
```



```
par(mfrow=c(1,1))
```

6.4.5 Example

In the library Stat2Data, there is a data set that has the price of a Porsche and its mileage. We will build a linear model and test the assumptions.

```
library(Stat2Data)
library(fastR)
library(DT)
```

```
data(PorschePrice)
head(PorschePrice)
```

```
##   Price Age Mileage
## 1  69.4   3    21.5
## 2  56.9   3    43.0
## 3  49.9   2    19.9
## 4  47.4   4    36.0
## 5  42.9   4    44.0
## 6  36.9   6    49.8
```

Instead of using `head` we can use a datatable which creates an html widget to examine the data.

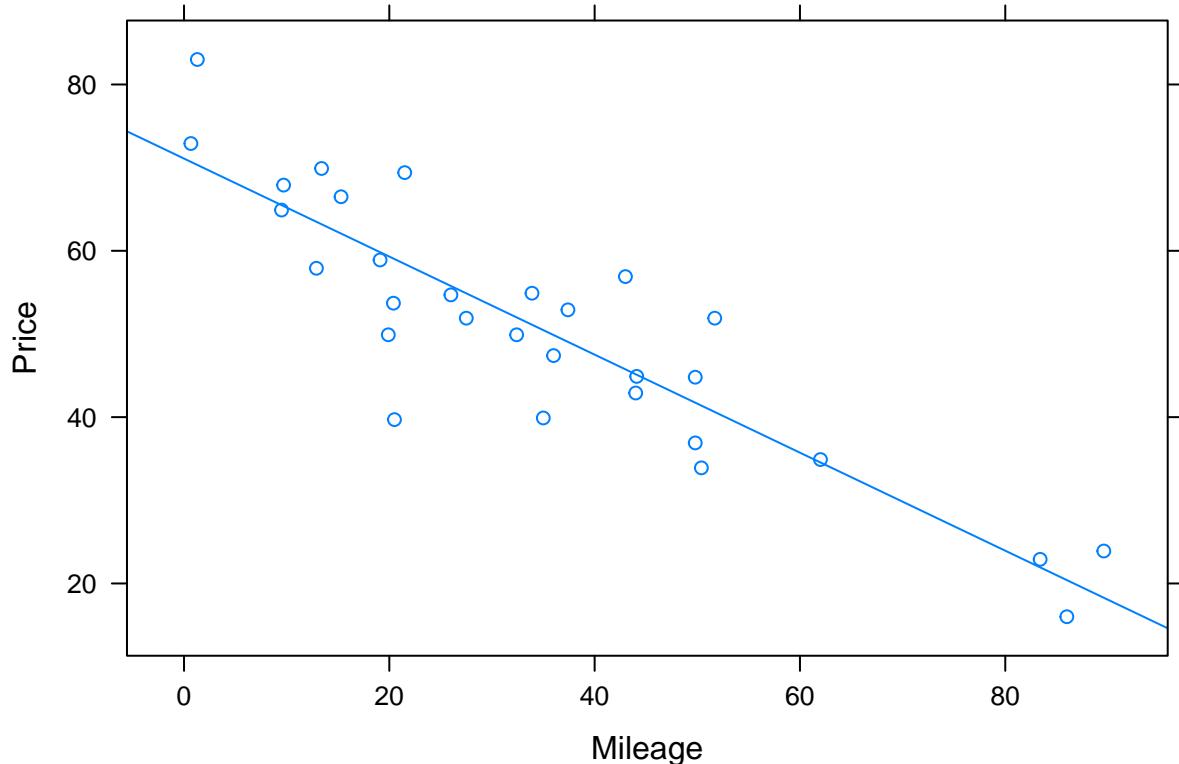
```
DT::datatable(PorschePrice)
```

	Price	Age	Mileage
1	69.4	3	21.5
2	56.9	3	43
3	49.9	2	19.9
4	47.4	4	36
5	42.9	4	44
6	36.9	6	49.8
7	83	0	1.3
8	72.9	0	0.67
9	69.9	2	13.4
10	67.9	0	9.7

Showing 1 to 10 of 30 entries

Previous 2 3 Next

```
xyplot(Price~Mileage,data=PorschePrice,type=c("p","r"))
```

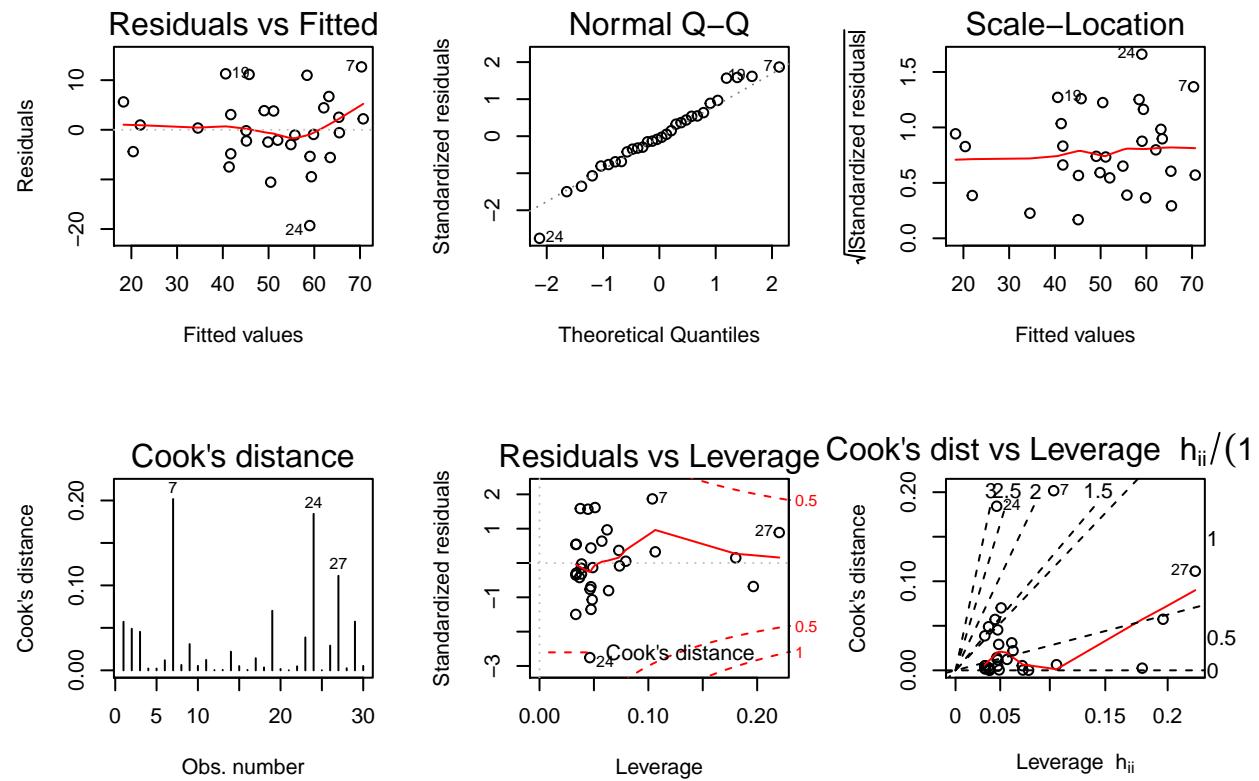


```
summary(lm(Price~Mileage, data=PorschePrice))

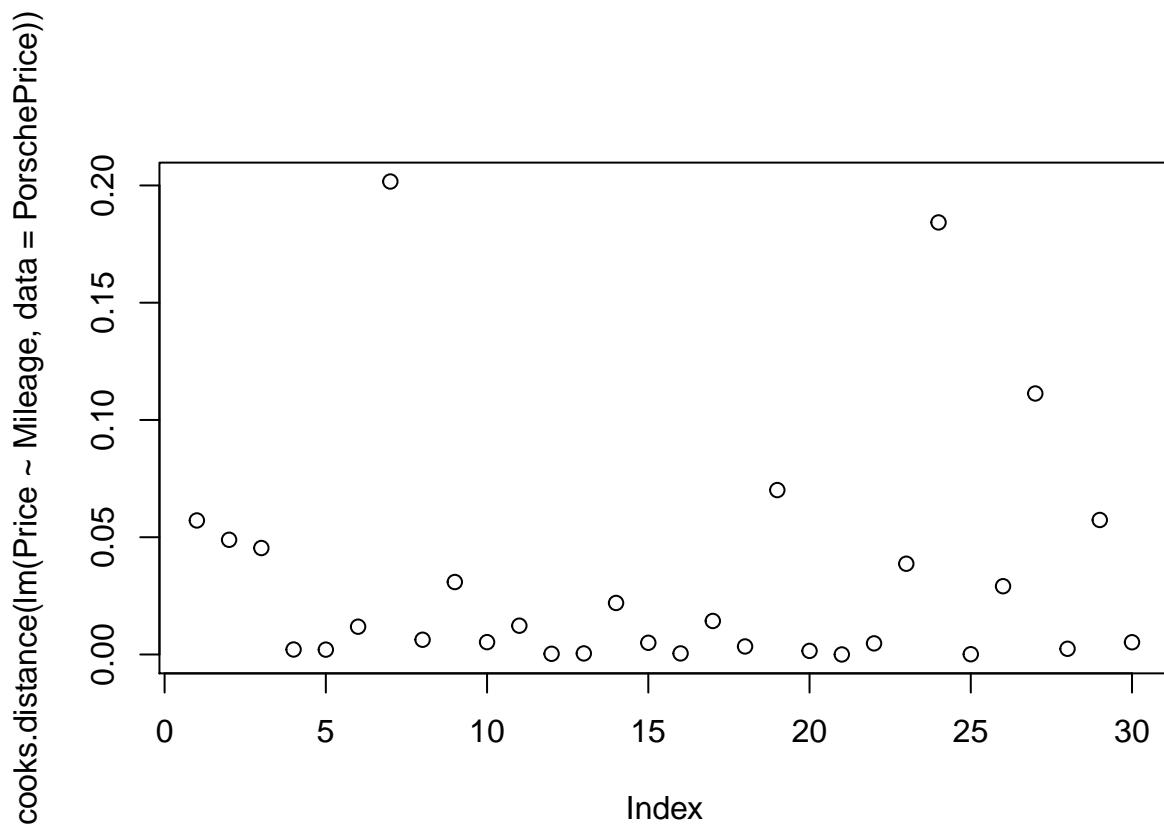
##
## Call:
## lm(formula = Price ~ Mileage, data = PorschePrice)
##
## Residuals:
##      Min        1Q    Median        3Q       Max
## -19.3077  -4.0470  -0.3945   3.8374  12.6758
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 71.09045   2.36986   30.0 < 2e-16 ***
## Mileage     -0.58940   0.05665  -10.4 3.98e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.17 on 28 degrees of freedom
## Multiple R-squared:  0.7945, Adjusted R-squared:  0.7872
## F-statistic: 108.3 on 1 and 28 DF,  p-value: 3.982e-11
```

Checking the assumptions.

```
par(mfrow=c(2,3))
plot(lm(Price~Mileage, data=PorschePrice), w=1:6)
```



```
par(mfrow=c(1,1))  
plot(cooks.distance(lm(Price~Mileage,data=PorschePrice)))
```



What are your conclusions from these plots?

Appendix A

Syllabus

Lesson Topic	Reading	Homework
Admin and Course Introduction	Page xv-xviii, A.1, A.2, A.4 up to A.4.1	
Summarizing Univariate Data	1.1 - 1.2	1.2, 1.4, 1.6, 1.8, 1.10, 1.13
Summarizing Multivariate Data	1.3 - 1.4	1.15, 1.16, 1.17, 1.19, 1.21, 1.25
Random Variables	2.1, B.1 - B.3	2.1, 2.2, B.1, B.2, B.3, B.4, B.6, B.19
Probability Rules	2.2-2.2.6	2.6, 2.7, 2.9, 2.10, 2.11, 2.29
Inclusion-Exclusion, Conditional Probability	2.2.7	2.14, 2.15, 2.18, 2.21, 2.24, 2.25
Discrete Distributions	2.3	2.30, 2.40, 2.43, 2.44, 2.45, 2.46
Intro to Hypothesis Testing	2.4	2.51, 2.52, 2.53, 2.55, 2.56
Mean and Variance of Discrete Random Variable	2.5	2.60, 2.61, 2.64, 2.65, 2.67
Discrete Joint Distributions	2.6	2.71, 2.76, 2.92, 2.95
Other Discrete Distributions	2.7 thru 2.7.3	2.80, 2.81, 2.85, 2.86, 2.88
Uniform and Exponential Distribution	3.1	3.1, 3.3 3.5, 3.7
Moments	3.2 thru 3.3 Stop at 3.3.1	3.8, 3.10, 3.12
Generating Functions	3.3.1 - 3.3.4	3.14, 3.19, 3.30a
Important Continuous Distributions	3.4	3.29, 3.31, 3.32, 3.33, 3.34
Plots of Distributions	3.5-3.6	3.38, 3.39, 3.40, 3.41
Continuous Joint Distributions	3.7	3.44, 3.45, 3.47, 3.50, 3.51
Method of Moments	4.1-4.2	4.1, 4.2, 4.3, 4.5, 4.7, 4.9
Estimates and Estimators	4.3	4.11, 4.13, 4.15, 4.16
Limit Theorems	4.4	4.14, 4.19, 4.20, 4.21
Inference for Mean (Variance Known)	4.5	4.22, 4.25, 4.26, 4.27, 4.28
Estimating Variance	4. 6 - 4.7	4.30, 4.39, 4.41, 4.42, 4.44
Two Additional Tests	4.8-4.9	4.50, 4.51, 4.52
Permutations Tests	4.10	4.53, 4.54, 4.56, 4.57
Maximum Likelihood Estimators	5.1	5.1, 5.2, 5.9, 5.12
Likelihood Ratio Tests	5.2	5.17, 5.18, 5.22
Goodness of fit	5.4	5.19, 5.20, 5.21

Lesson Topic	Reading	Homework
Two-Way Tables	5.5	5.23(not f), 5.27, 5.28
Introduction to Linear Models	6.1, C.2	Problem given in Notes
Simple Linear Regression	6.2	6.2, 6.4, 6.5, 6.6
Inference for Simple Linear Regression	6.3	6.7, 6.8, 6.25, 6.26
Diagnostics	6.4	6.27, 6.28, 6.29, 6.32 (not part b)

Appendix B

Project

B.0.1 Introduction

This project will guide you through a small research project. We will be building a simple probability based spell checker in R, this work is based on the blog of the same topic <https://www.r-bloggers.com/a-spell-checker-in-r/>. The objectives of this project are:

1. Read and summarize a research paper
2. Find and experiment with existing functions in R
3. Find existing code and pseudo code
4. Acquire appropriate materials
5. Implement in R
6. Test and validate

To complete this project you may need to run the 32-bit version of R in RStudio. That is because the `qdap` package has the capability to open interactive windows, widgets. This relies on `RJava` and this may mean you are running 32-bit java. We will not use the interactive windows in the package, which require `rjava`, but the package will not load if your version of java does not match your version of R.

Authorized Resources: Anyone and anything.

Points: 75

B.0.2 Deliverables

You must use reproducible research by creating an RMarkdown file where your compiled code and data is visible to the reader. There is an RMarkdown information sheet on the course website under reference materials to help get you started. You should add the following elements to your file to show at the top of the compiled document:

Title
Name
Section
Documentation

You will complete each of the sections below. You will turn in an html file with your section and name as the title on the course website. There are some suggested completion dates as well to help keep you on track.

B.0.3 Components

1. (5 pts) (September 8) Research the history of spell checkers using Wikipedia. Briefly, one paragraph, summarize your reading.
2. (10pts) (September 16) The package `qdap` in R has a spell checker. Load the package and use it in your RMarkdown file to get the spelling of the following using the function `check_spelling` and the default options.

```
c("Robots are evl creatures and derv exterimanitation.", "tes")
```

Notice that word `desv` is probably `deserve` but it did not appear in the list of suggestions. This is because `deserve` is too far away from `derv`. Run the following command:

```
adist("derv", "deserve")
```

Now change the appropriate option in `check_spelling` to get `deserve` as a suggestion.

3. (10pts) (October 15) Read Peter Norvig's article. Yes, the code is in Python but it gives us the ideas we need. Reading the article, we are going to use Bayes Theorem to find a probability for the suggestion given the typed word. You should spend some time thinking about Professor Norvig's claim that $P(c|w)$ is difficult to find empirically. Instead we need to find $P(c)$, the probability of correctly spelled word, and $P(w|c)$. To understand his code, we will work with a smaller data set. Go to the Gutenberg Project website and download the book the *Journal of a Soldier* as a text file. We need to read this data into R. It is a text file with line breaks so we need to use the `readLines` command. Here is my command for reading the first 10 lines from the file both from the website and my local hard drive.

```
readLines("http://www.gutenberg.org/files/49163/49163-0.txt", n=10)
```

```
## [1] "i>The Project Gutenberg EBook of Journal of a Soldier of the Seventy-First"
## [2] "or Glasgow Regiment Highland Light Infant, by Anonymous"
## [3] ""
## [4] "This eBook is for the use of anyone anywhere at no cost and with"
## [5] "almost no restrictions whatsoever. You may copy it, give it away or"
## [6] "re-use it under the terms of the Project Gutenberg License included"
## [7] "with this eBook or online at www.gutenberg.org/license"
## [8] ""
## [9] ""
## [10] "Title: Journal of a Soldier"
```

```
readLines("./data/Journal of a Soldier.txt", n=10)
```

```
## [1] "i>The Project Gutenberg EBook of Journal of a Soldier of the Seventy-First"
## [2] "or Glasgow Regiment Highland Light Infant, by Anonymous"
## [3] ""
## [4] "This eBook is for the use of anyone anywhere at no cost and with"
## [5] "almost no restrictions whatsoever. You may copy it, give it away or"
## [6] "re-use it under the terms of the Project Gutenberg License included"
## [7] "with this eBook or online at www.gutenberg.org/license"
## [8] ""
## [9] ""
## [10] "Title: Journal of a Soldier"
```

I am going to save the first 100 rows to an object and then see what I have to do to clean it up.

```
test_sample<-readLines("~/Classes/Math 377/Fall 2015/Project/Journal of a Soldier.txt", n=100)
str(test_sample)
```

```
## chr [1:100] "i>The Project Gutenberg EBook of Journal of the Seventy-First" ...
```

This is a vector of characters that I need to collapse to one vector using paste.

```
test_sample<-paste(test_sample,collapse=" ")
str(test_sample)
```

```
## chr "i»;The Project Gutenberg EBook of Journal of a Soldier of the Seventy-First or Glasgow Regiment High
```

Next, in Professor Norvig's paper, he converts everything to lower case.

```
test_sample<-tolower(test_sample)
str(test_sample)
```

```
## chr "i»;the project gutenberg ebook of journal of a soldier of the seventy-first or glasgow regiment high
```

The next part is a little tricky. Professor Norvig is using a regular expression to parse the character string. Luckily, R has a function called `strsplit` that will do this for us. It returns a list so we need to make it a vector.

```
test_sample<-strsplit(test_sample, "[^a-z]+")
test_sample<-unlist(test_sample)
str(test_sample)
```

```
## chr [1:363] "" "the" "project" "gutenberg" "ebook" "of" "journal" ...
```

Wow, that was powerful. Notice that there are several odd entries such as blank, www, or single letters. We could do more processing or simply hope that in a large corpus, these will be so rare as to not impact our answer. It appears that Professor Norvig assumes the later as he does no more data cleaning. Now let's table our data to get the frequencies and also the probabilities.

```
head(table(test_sample),n=30)
```

```
## test_sample
##                               a      account    accounts   accuracy
##      1                      8          2           1           1
##      adam      adventure advertisement almost alteration
##      1                      1          1           1           1
##      america   american        and anecdotes anonymous
##      1                      1          14          1           2
##      anyone   anywhere       archive army arrival
##      1                      1          1           1           4
##      ascertain at attack attempts author
##      1                      6          1           1           1
##      available away ayres b battle
##      1                      1          1           1           2
```

```
head(prop.table(table(test_sample)),n=30)
```

```
## test_sample
##                               a      account    accounts   accuracy
## 0.002754821 0.022038567 0.005509642 0.002754821 0.002754821
## adam      adventure advertisement almost alteration
## 0.002754821 0.002754821 0.002754821 0.002754821 0.002754821
## america   american        and anecdotes anonymous
## 0.002754821 0.002754821 0.038567493 0.002754821 0.005509642
## anyone   anywhere       archive army arrival
## 0.002754821 0.002754821 0.002754821 0.002754821 0.011019284
## ascertain at attack attempts author
## 0.002754821 0.016528926 0.002754821 0.002754821 0.002754821
## available away ayres b battle
```

```
## 0.002754821 0.002754821 0.002754821 0.002754821 0.005509642
```

I will save the data, sort it, and finally save the result as a character vector

```
probs_of_word<-sort(prop.table(table(test_sample)),decreasing=TRUE)
freq_word<-names(sort(prop.table(table(test_sample)), decreasing = TRUE))
head(freq_word)
```

```
## [1] "the" "of" "and" "a" "at" "for"
```

```
head(probs_of_word)
```

```
## test_sample
```

```
##      the          of          and          a          at          for
```

```
## 0.07713499 0.06887052 0.03856749 0.02203857 0.01652893 0.01652893
```

Based on this work, `the` is the most frequently used word and has a probability of occurring of .077. Thus we now have $P(c)$.

Your assignments is to now read in the entire document, Journal of a Soldier, and report the 10th most common word and its probability of occurrence.

4. (10pts) (October 30) Finding $P(w|c)$ is difficult. Professor Norvig made, what he called, the `trivial` model in the he looked at the distance from the given word to the closest words in the corpus and assumed that words with a distance of 1 were infinitely more likely than words with a distance of 2. Also, he wrote his own code to calculate the distance between two words but luckily for us, as we saw in part 2, R has a function called `adist` that does this for us. Thus Professor Norvig looked for words with a distance of zero and if it existed returned this as the correct spelling. If this was not the case, he found the words with distance one and returned the one that is most probable. If there was not a word or set of words with a distance of 1, he went to a distance of 2 and repeated. This stopped after 2 because he claimed that 98% of spelling errors were within a distance of 2. Let's implement this in R.

First we need to find the distance between our word and the words in the sorted list, this is what I called `freq_word` above. As an example, suppose my word is "tha". I would type:

```
adist("tha",freq_word)
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13]
## [1,]    1    3    3    2    3    3    5    6    3    7    6    4    6
##      [,14] [,15] [,16] [,17] [,18] [,19] [,20] [,21] [,22] [,23] [,24]
## [1,]    8    3    3    2    3    5    2    6    4    3    7
##      [,25] [,26] [,27] [,28] [,29] [,30] [,31] [,32] [,33] [,34] [,35]
## [1,]    8    7    3    7    9    5    4    4    9    8    7
##      [,36] [,37] [,38] [,39] [,40] [,41] [,42] [,43] [,44] [,45] [,46]
## [1,]    3    3    7    7    7    4    6    6    8    3    5
##      [,47] [,48] [,49] [,50] [,51] [,52] [,53] [,54] [,55] [,56] [,57]
## [1,]    4    6    4    1    2    3    5    3    5    3    3
##      [,58] [,59] [,60] [,61] [,62] [,63] [,64] [,65] [,66] [,67] [,68]
## [1,]    8    7    3    8    12   6    8    6    7    8    6
##      [,69] [,70] [,71] [,72] [,73] [,74] [,75] [,76] [,77] [,78] [,79]
## [1,]    7    6    4    8    4    7    4    8    3    5    3
##      [,80] [,81] [,82] [,83] [,84] [,85] [,86] [,87] [,88] [,89] [,90]
## [1,]    7    6    5    4    4    4    6    6    3    7    5
##      [,91] [,92] [,93] [,94] [,95] [,96] [,97] [,98] [,99] [,100] [,101]
## [1,]    4    3    3    9    7    11   4    9    4    5    4
##      [,102] [,103] [,104] [,105] [,106] [,107] [,108] [,109] [,110] [,111]
## [1,]    8    10   8    7    10   5    5    3    4    9
##      [,112] [,113] [,114] [,115] [,116] [,117] [,118] [,119] [,120] [,121]
## [1,]    3    6    8    10   4    4    5    7    4    3
```

```

##      [,122] [,123] [,124] [,125] [,126] [,127] [,128] [,129] [,130] [,131]
## [1,]      3      5     11      8      5      9      7      3      4      5
##      [,132] [,133] [,134] [,135] [,136] [,137] [,138] [,139] [,140] [,141]
## [1,]      5      4      2      8      6      6      5      3      5      4
##      [,142] [,143] [,144] [,145] [,146] [,147] [,148] [,149] [,150] [,151]
## [1,]      3      5     10      7      3      3      4      5      8      5
##      [,152] [,153] [,154] [,155] [,156] [,157] [,158] [,159] [,160] [,161]
## [1,]      6      4      4      6      6      8      9      6     11      9
##      [,162] [,163] [,164] [,165] [,166] [,167] [,168] [,169] [,170] [,171]
## [1,]      3      9      6      6     11      6      5      3      7      4
##      [,172] [,173] [,174] [,175] [,176] [,177] [,178] [,179] [,180] [,181]
## [1,]      4      9      5     11      3      2      4      1      1      2
##      [,182] [,183] [,184] [,185] [,186] [,187] [,188] [,189] [,190] [,191]
## [1,]      3      4      4      3      5      5      3      3      2      8
##      [,192] [,193] [,194] [,195] [,196]
## [1,]      8      7      4      6      3

```

Notice this gives us all the distances. Next we want to extract those words that meet a specified distance, Professor Norvig used 2.

```

freq_word[adist("tha", freq_word) <= 2]

## [1] "the"   "a"     "this"  "has"   "than"  "to"    "la"    "team"  "th"    "that"
## [11] "them"  "what"

```

Now the problem is that some of these words could have distance of 0, 1, or 2. Based on Professor Norvig's suggestion we should ignore higher distances. For example, if we have a distance of 1, we should ignore all distances of 2. We will now implement this idea:

```

freq_word[adist("tha", freq_word) <= min(adist("tha", freq_word), 2)]

## [1] "the"   "than"  "th"    "that"

```

Since the list is ordered by frequency, we would suggest the first element.

```

freq_word[adist("tha", freq_word) <= min(adist("tha", freq_word), 2)][1]

## [1] "the"

```

Write a function called, my_spell_checker that takes as input the character vector, the vector of sorted words, this is your dictionary, and an option for distance with a default of 2. In your code, you need to account for the issue that you might not find a word that is within the range. In that case, your code should return the original word. Read in the entire file Journal of a Soldier, I call it freq_word in my example below, and run your function on the following:

```

my_spell_checker("off", freq_word)
my_spell_checker("tha", freq_word)
my_spell_checker("drvvve", freq_word)
my_spell_checker("you're", freq_word)
my_spell_checker("hgkdjurhc", freq_word)
my_spell_checker("hgkdjurhc", freq_word, range=6)

```

5. (15pts) (November 17) I like that we have a list of suggestions but without knowing $P(w|c)$ we cannot calculate the probabilities. Let's modify Professor Norvig's code by instead of assuming an infinite probability let's assume that $P(w|c)$ for a distance of 1 has a probability of 3 times that of a distance of 2, and likewise a distance of 3 has 3 times the probability of 2. This could continue indefinitely but at some point we need to stop. Let's stop at 20 and call everything with a distance of 20 or higher the same probability. If the distance is 0, then we just return the word. For the rest, we have $P(w|c) = p$ for a distance of 1, $P(w|c) = p/3$ for a distance of 2, $P(w|c) = p/3^2$ for a distance of 3, and on. Find p and then use this to write a function

that returns the top three words, based on $P(c|w) = P(w|c)P(c)$, as a default with the option to change this value. Call the function, `my_suggestions`. For reference, the probability $P(w|c)$ for a distance of 2 is 0.22222.

Now I will run my function below as an example

```
my_suggestions("akk",probs_of_word2,p_of_w_given_c,2,3)
    and          a          at
0.006613722 0.004873876 0.001832024
my_suggestions("akk",probs_of_word2,p_of_w_given_c,2,5)
    and          a          at          as          all
0.006613722 0.004873876 0.001832024 0.001520926 0.001111889
my_suggestions("akk",probs_of_word2,p_of_w_given_c,3,5)
    and          the         a          of          to
0.006613722 0.004919964 0.004873876 0.002319796 0.002139282
my_suggestions("the",probs_of_word2,p_of_w_given_c,2,3)
    "the"
my_suggestions("thethethethethethethe",probs_of_word2,p_of_w_given_c,2,3)
    "thethethethethethethe"
my_suggestions("bradley",probs_of_word2,p_of_w_given_c,2,3)
    badly
1.152216e-05
```

The first option is the word, the second is the table of probabilities, the third is the conditional probabilities, the fourth the maximum distance, and the last the number of words to report.

Using your own code, perform the equivalent to the following statements:

```
my_suggestions("off",probs_of_word2,p_of_w_given_c,2,3)
my_suggestions("tha",probs_of_word2,p_of_w_given_c,2,3)
my_suggestions("drvvve",probs_of_word2,p_of_w_given_c,2,3)
my_suggestions("you're",probs_of_word2,p_of_w_given_c,2,3)
my_suggestions("hgkdjurhc",probs_of_word2,p_of_w_given_c,2,3)
my_suggestions("hgkdjurhc",probs_of_word2,p_of_w_given_c,6,3)
```

6. (December 4) The last thing we need to do is validate the spell checker. This is what Professor Norvig did in the final phase. We will only do an abbreviated evaluation.

a. (10 pts) First read into R Professor Norvig's big.txt document, on the course website, and process it as we did above for the Journal of a Soldier. We want to use this bigger document to improve the accuracy. Use the new word frequency table in your spell checker from part 4 on the following words:

```
off
tha
drvvve
you're
hgkdjurhc (with default settings)
hgkdjurhc (with range=6)
```

There are still some problems with the spell checker. But we will proceed any way.

b. (10pts) There is a file on the course website called test_data.txt that contains only up through the letter d of Professor Norvig's test data. The first few lines are below.

```
'access': 'acess'
'accessing': 'accesing'
'accommodation':'accomodation acommodation acomodation'
```

The correct spelling is before the colon and the incorrect is after. Read the data in and create a vector of the strings with the correct and all the incorrect spellings. This vector should be of length 48.

We next need to create a vector with the correct spelling and another with the incorrect spellings. This is not an easy matter since some words have multiple misspelled words. This is good practice because in analysis getting data into your computer in a clean and efficient manner is difficult. You may want to use functions such as gsub, strsplit, and unlist to split the data apart. You want to also remove leading and trailing blank spaces. You want two vectors, the first has the answers and the second has the common misspellings. Each of these vectors will be of length 78 because that is the total number of misspelled words in the text file. As an example, for the three lines above with the words access, accessing, and accommodation, your answer vector would be

```
access
accessing
accommodation
accommodation
accommodation
```

and your example vector would be

```
acess
accesing
accomodation
acommodation
acomodation
```

Print out the 53rd through the 70th value of each vector. Make sure you include your code to clean the data.

c. (5 pts) After cleaning your data, run the data through your function my_spell_checker and compare with the correct answer, this is easier if you use the sapply function. Report your error rate.

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