Introduction to Statistics for Researchers

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The problem with most introductory statistics courses is that they don't prepare the student for the use of advanced statistics. Rote hand calculation is easy to test, easy to grade, and easy for students to learn to do, but is useless for actually understanding how to apply statistics. Because students pursuing a Ph.D. will likely be using statistics for the rest of their professional careers, I feel that this sort of course should attempt to steer away from a "cookbook" undergraduate pedagogy, and give the student enough theoretical background to continue their statistical studies at a high level while staying away from the painful mathematical details that statisticians must work through.

Recent pedagogical changes have been made at the undergraduate level to introduce sampling distributions via permutation and bootstrap procedures. Because those are extremely useful tools in their own right and because of the ability to think about statistical inference from the very start of the course is invaluable, I've attempted to duplicate this approach. I am grateful to the ICOTS 9 organizers and presenters for their expertise, perspective, and motivation for making such a large shift in my teaching.

Statistical software has progressed by leaps and bounds over the last decades. Scientists need access to reliable software that is flexible enough to handle new problems, with minimal headaches. R has become a widely used, and extremely robust Open Source platform for statistical computing and most new methodologies will appear in R before being incorporated into commercial software. Second, data exploration is the first step of any analysis and a user friendly yet powerful mechanism for graphing is a critical component in a researchers toolbox. R succeeds in this area as R has the most flexible graphing library of any statistical software I know of and the basic plots can created quickly and easily. The only downside is that there is a substantial learning curve to learning a scripting language, particularly for students without any programming background.

Because the mathematical and statistical background of typical students varies widely, the course seems to have a split-personality disorder. We wish to talk about using calculus to maximize the likelihood function and define the expectation of a continuous random variable, but also must spend time defining how to calculate the a mean. I attempt to address both audiences, but recognize that it is not ideal.

As these notes are in a continual state of being re-written, I endeavor to keep the latest version available on the GitHub repository for this book at https://github.com/dereksonderegger/STA_570_Book/raw/master/Stat_570.pdf. In general, I recommend printing the chapter we are currently covering in class. If you wish to submit a bug report, or submit a patch, feel free to log an issue on the GitHub site or to fix it and submit a pull request. If you wish to use these notes for your own class, feel free to do so, but please acknowledge the source.

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Contents

The scientific method requires us to make observations about the world and then use those observations to make reasonable predictions. However the way we make those observations can have a profound effect on how well understand the phenomena or how well we predict some event.

During the 1936 US presidential election between Franklin Roosevelt (D) and Alfred Landon (R), the magazine *The Literary Digest* included a card that asked its readers who they were to vote for and to send it back to the magazine, which would tabulate and report the predicted winner. This scheme correctly predicted the 1920, 1924, 1928, and 1932 races and so many people respected the forecast. The supposed strength of the prediction was how many people responded (2.4 million!). However, the readers of *The Literary Digest* were typically more affluent and could afford a magazine subscription during the Great Depression. As a result, the magazine performed a highly biased survey and predicted that Landon would win. The actual outcome was that Roosevelt won 61% of the vote.

Another person also interested in predicting the 1936 election was the statistician George Gallup. He had a much smaller sample, (with 50,000 respondents) and correctly predicted the outcome. This was a clear demonstration of the power of a well selected random sample compared to a massive set of data collected in a biased fashion.

The goals of statistics can be

1. Collection of data

   (a) Sampling Design: Observational studies rely on the assumption that your sample is representative of the population of interest. Unfortunately, it is often difficult to randomly select individuals in a non-biased way and this branch of statistics focuses on how to leverage known population level data with sampled data to account for bias.

   (b) Experimental Design: The scientific gold standard is to perform an experiment where the factors of interest are manipulated, but how the manipulations are done to maximize the amount of information obtained from the experiment is a classic issue in statistics.

2. Process Modeling - Often we have some mathematical model that is a function of some population level parameters that we think represents some process of interest. We can use sample statistics calculated from our data to estimate those parameters of interest in the model.

   (a) Because our sample statistics will vary from sample to sample, we want to understand how much faith should we have in our estimate.

   (b) We often want confidence intervals for those parameters. For example, we might have a sample where 54% of the respondents support Bernie Sanders for president, but I don't expect that to be the population level percent. Instead we report that 52-56% of the population of likely voters supports Bernie Sanders.

   (c) We might ask if some particular value for a parameter is plausible. For example, could the association between person's income level and their probability of voting republican be zero?

3. Predictions - Once we have a process model (even if it is extremely complicated and not easily interpretable), we will often want to make predictions about future or unobserved observations.

   (a) We will want to consider how well we predict new observations, but, by definition, those are unavailable.

   (b) Quality of prediction can be used to update the process modeling steps.

The course covered by these notes will make some discuss some of the data collection step, but will focus primarily on the process modeling step.

Chapter 1

Summary Statistics and Graphing

When confronted with a large amount of data, we seek to summarize the data into statistics that somehow capture the essence of the data with as few numbers as possible. Graphing the data has a similar goal... to reduce the data to an image that represents all the key aspects of the raw data. In short, we seek to simplify the data in order to understand the trends while not obscuring important structure.

For this chapter, we will consider data from a the 2005 Cherry Blossom 10 mile run that occurs in Washington DC. This data set has 8636 observations that includes the runners `state` of residence, official `time` (gun to finish, in seconds), `net` time (start line to finish, in seconds), `age`, and `gender` of the runners.

```
library(mosaicData) # library of datasets we'll use
library(ggplot2)    # graphing functions
library(dplyr)      # data summary tools
head(TenMileRace)   # examine the first few rows of the data
```

```
##   state time  net age sex
## 1    VA 6060 5978  12   M
## 2    MD 4515 4457  13   M
## 3    VA 5026 4928  13   M
## 4    MD 4229 4229  14   M
## 5    MD 5293 5076  14   M
## 6    VA 6234 5968  14   M
```

In general, I often need to make a distinction between two types of data.

- Discrete (also called Categorical) data is data that can only take a small set of particular values. For example a college student's grade can be either A, B, C, D, or F. A person's sex can be only Male or Female.[1] Discrete data could also be numeric, for example a bird could lay 1, 2, 3, ... eggs in a breeding season.
- Continuous data is data that can take on an infinite number of numerical values. For example a person's height could be 68 inches, 68.2 inches, 68.23212 inches.

To decided if a data attribute is discrete or continuous, I often as "Does a fraction of a value make sense?" If so, then the data is continuous.

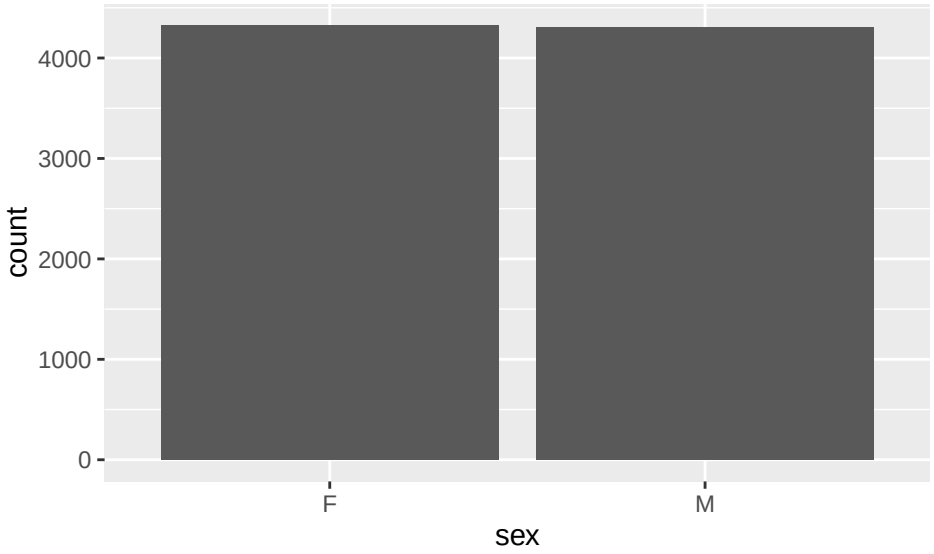
[1] Actually this isn't true as both gender and sex are far more complex. However from a statistical point of view it is often useful to simplify our model of the world. George Box famously said, "All models are wrong, but some are useful."

1.1 Graphical summaries of data

1.1.1 Univariate - Categorical

If we have univariate data about a number of groups, often the best way to display it is using barplots. They have the advantage over pie-charts that groups are easily compared. [2]

```
ggplot(TenMileRace, aes(x=sex)) + geom_bar()
```

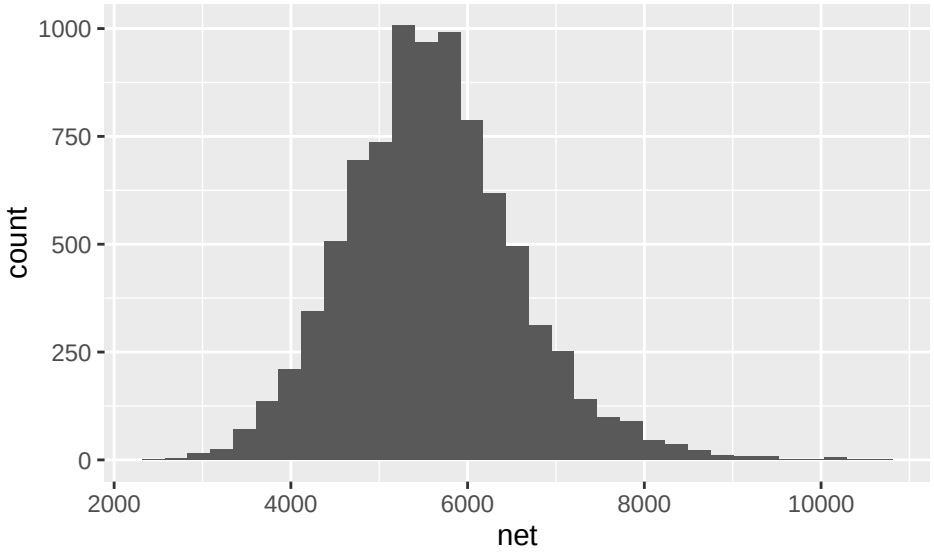


1.1.2 Univariate - Continuous

A histogram looks very similar to a bar plot, but is used to represent continuous data instead of categorical and therefore the bars will actually be touching.

[2] This is an example of a poorly labeled covariate, this really ought to be gender.

```
ggplot(TenMileRace, aes(x=net)) + geom_histogram()

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



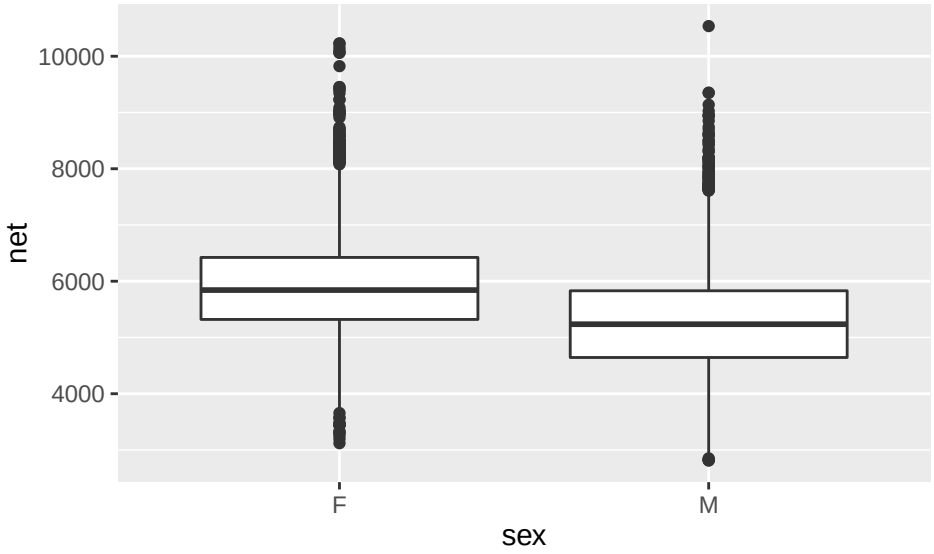
Often when a histogram is presented, the y-axis is labeled as "frequency" or "count" which is the number of observations that fall within a particular bin. However, it is often desirable to scale the y-axis so that if we were to sum up the area (height * width) then the total area would sum to 1. The rescaling that accomplishes this is

$$density = \frac{\#\ observations\ in\ bin}{total\ number\ observations} \cdot \frac{1}{bin\ width}$$

1.1.3 Bivariate - Categorical vs Continuous

We often wish to compare response levels from two or more groups of interest. To do this, we often use side-by-side boxplots. Notice that each observation is associated with a continuous response value and a categorical value.

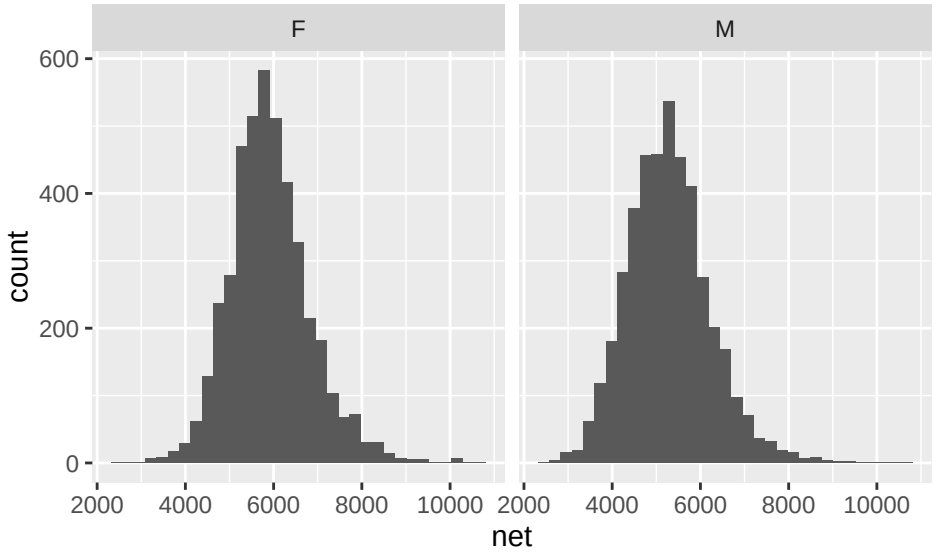
```
ggplot(TenMileRace, aes(x=sex, y=net)) + geom_boxplot()
```



In this graph, the edges of the box are defined by the 25% and 75% quantiles. That is to say, 25% of the data is to the below of the box, 50% of the data is in the box, and the final 25% of the data is to the above of the box. The dots are data points that traditionally considered outliers.[3]

Sometimes I think that box-and-whisker plot obscures too much of the details of the data and we should look at the side-by-side histograms instead.

```
ggplot(TenMileRace, aes(x=net)) +
  geom_histogram() +
  facet_grid( . ~ sex )  # side-by-side plots based on sex

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

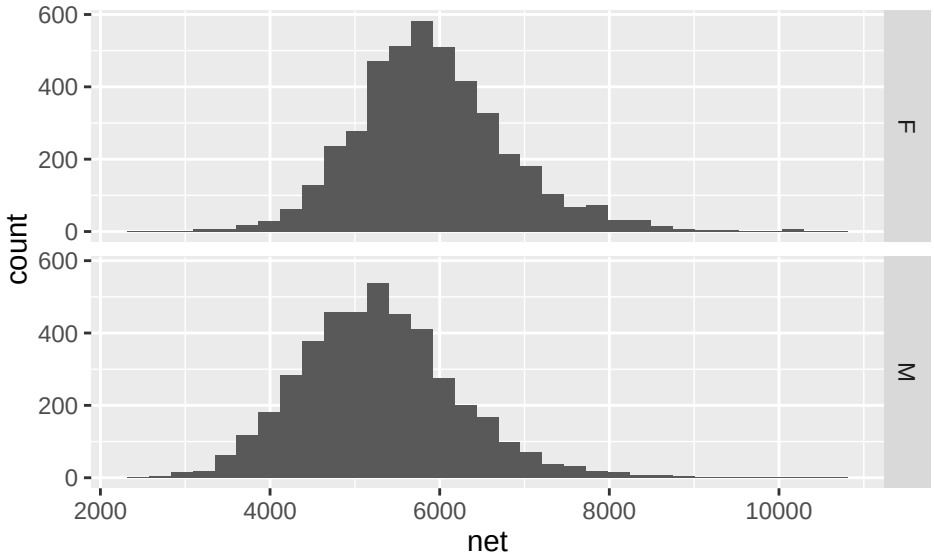


Orientation of graphs can certainly matter. In this case, it makes sense to *stack* the two graphs

[3]Define the Inter-Quartile Range (IQR) as the length of the box. Then any observation more than 1.5*IQR from the box is considered an outlier.

to facilitate comparisons.

```
ggplot(TenMileRace, aes(x=net)) +
  geom_histogram() +
  facet_grid( sex ~ . )  # side-by-side plots based on sex

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



1.1.4 Bivariate - Continuous vs Continuous

Finally we might want to examine the relationship between two continuous random variables.

```
ggplot(TenMileRace, aes(x=age, y=net, color=sex)) +
  geom_point()
```

1.2 Measures of Centrality

The most basic question to ask of any dataset is 'What is the typical value?' There are several ways to answer that question and they should be familiar to most students.

Mean

Often called the average, or arithmetic mean, we will denote this special statistic with a bar. We define

$$\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_i = \frac{1}{n}\left(x_1 + x_2 + \cdots + x_n\right)$$

If we want to find the mean of five numbers $\{3, 6, 4, 8, 2\}$ the calculation is

$$\begin{aligned} \bar{x} &= \frac{1}{5}\left(3 + 6 + 4 + 8 + 2\right) \\ &= \frac{1}{5}\left(23\right) \\ &= 23/5 \\ &= 4.6 \end{aligned}$$

This can easily be calculated in R by using the function `mean()`. We first extract the column we are interested in using the notation: `DataSet$ColumnName` where the `$` signifies grabbing the column.

```
mean( TenMileRace$net ) # Simplest way of doing this calculation

## [1] 5599.065

TenMileRace %>% summarise( mean(net) )  # using the dplyr package

##   mean(net)
## 1  5599.065
```

Median

If the data were to be ordered, the median would be the middle most observation (or, in the case that n is even, the mean of the two middle most values).

In our simple case of five observations $\{3, 6, 4, 8, 2\}$, we first sort the data into $\{2, 3, 4, 6, 8\}$ and then the middle observation is clearly 4.

In R the median is easily calculated by the function `median()`.

```
TenMileRace %>% summarise( median(net) )

##   median(net)
## 1        5555
```

Mode

This is the observation value with the most number of occurrences.

Examples

- If my father were to become bored with retirement and enroll in my STA 570 course, how would that affect the mean and median age of my 570 students?

  - The mean would move much more than the median. Suppose the class has 5 people right now, ages 21, 22, 23, 23, 24 and therefore the median is 23. When my father joins, the ages will be 21, 22, 23, 23, 24, 72 and the median will remain 23. However, the mean would move because we add in such a large outlier. Whenever we are dealing with skewed data, the mean is pulled toward the outlying observations.

- In 2010, the median NFL player salary was $770,000 while the mean salary was $1.9 million. Why the difference?

  - Because salary data is *skewed* superstar players that make huge salaries (in excess of 20 million) while the minimum salary for a rookie is $375,000. Financial data often reflects a highly skewed distribution and the median is often a better measure of centrality in these cases.

1.3 Measures of Variation

The second question to ask of a dataset is 'How much variability is there?' Again there are several ways to measure that.

Range

Range is the distance from the largest to the smallest value in the dataset.

```
max( TenMileRace$net ) - min( TenMileRace$net )

## [1] 7722

TenMileRace %>% summarise( range = max(net) - min(net) )

##   range
## 1  7722
```

Inter-Quartile Range

The **p-th** percentile is the observation (or observations) that has at most p percent of the observations below it and $(1 - p)$ above it, where p is between 0 and 100. The median is the 50th percentile. Often we are interested in splitting the data into four equal sections using the 25th, 50th, and 75th percentiles (which, because it splits the data into four sections, we often call these the 1st, 2nd, and 3rd quartiles).

In general I could be interested in dividing my data up into an arbitrary number of sections, and refer to those as *quantiles* of my data.

```
quantile( TenMileRace$net ) # this works

##    0%   25%   50%   75%  100%
##  2814  4950  5555  6169 10536

# I can't do the following because the quantile() function spits out 5 values, not 1
# TenMileRace %>% summarise( quantile(net) )
```

The inter-quartile range (IQR) is defined as the distance from the 3rd quartile to the 1st.

```
TenMileRace %>% summarise( IQR(net) )

##   IQR(net)
## 1     1219
```

Notice that we've defined IQR before when we looked at box-and-whisker plots and this is exactly the length of the box.

Variance

One way to measure the spread of a distribution is to ask "what is the average distance of an observation to the mean?" We could define the ith **deviate** as $e_i = x_i - \bar{x}$ and then ask what is the average deviate? The problem with this approach is that the sum (and thus the average) of all deviates is *always* 0.

$$\begin{aligned}\sum_{i=1}^{n}(x_i - \bar{x}) &= \sum_{i=1}^{n} x_i - \sum_{i=1}^{n} \bar{x} \\ &= n\frac{1}{n}\sum_{i=1}^{n} x_i - n\bar{x} \\ &= n\bar{x} - n\bar{x} \\ &= 0\end{aligned}$$

The big problem is that about half the deviates are negative and the others are positive. What we really care is the distance from the mean, not the sign. So we could either take the absolute value, or square it.

There are some really good theoretical reasons to chose the square option[4], so we square the deviates and then find the average deviate size (approximately) and call that the **sample variance**.

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

Why do we divide by $n-1$ instead of n?

1. If I divide by n, then on average, we would tend to underestimate the population variance σ^2.
2. The reason is because we are using the same set of data to estimate σ^2 as we did to estimate the population mean (μ). If I could use $\frac{1}{n}\sum_{i=1}^{n}(x_i - \mu)^2$ as my estimator, we would be fine. But since I have to replace μ with $\bar{x}$ we have to pay a price.
3. Because the estimation of σ^2 requires the estimation of one other quantity, and using using that quantity, you only need $n-1$ data points and can then figure out the last one, we have used one *degree of freedom* on estimating the mean and we need to adjust the formula accordingly.

In later chapters we'll give this quantity a different name, so we'll introduce the necessary vocabulary here. Let $e_i = x_i - \bar{x}$ be the *error* left after fitting the sample mean. This is the deviation from the observed value to the "expected value" $\bar{x}$. We can then define the Sum of Squared Error as

$$SSE = \sum_{i=1}^{n} e_i^2$$

[4]First, squared terms are easier to deal with compared to absolute values, but more importantly, the spread of the normal distribution is parameterized via squared distances from the mean. Because the normal distribution is so important, we've chosen to define the sample variance so it matches up with the natural spread parameter of the normal distribution.

and the Mean Squared Error as

$$MSE = \frac{SSE}{df} = \frac{SSE}{n-1} = s^2$$

where $df = n - 1$ is the appropriate degrees of freedom.

Calculating the variance of our small sample of five observations $\{3, 6, 4, 8, 2\}$, recall that the sample mean was $\bar{x} = 4.6$

x_i	$(x_i - \bar{x})$	$(x_i - \bar{x})^2$
3	-1.6	2.56
6	1.4	1.96
4	-0.6	0.36
8	3.4	11.56
2	-2.6	6.76
sum		23.2

and so the sample variance is $23.2/(n-1) = 23.2/4 = 5.8$

Clearly this calculation would get very tedious to do by hand and computers will be much more accurate in these calculations. In R, the sample variance is easily calculated by the function `var()`.

```
ToyData <- data.frame( x=c(3,6,4,8,2) )
ToyData %>% summarise( s2 = var(x) )

##    s2
## 1 5.8
```

For the larger `TenMileRace` data set, the variance is just as easily calculated.

```
TenMileRace %>% summarise( s2 = var(net) )

##         s2
## 1 940233.5
```

Standard Deviation

The biggest problem with the sample variance statistic is that the units are in the original units-*squared*. That means if you are looking at data about car fuel efficiency, then the values would be in mpg^2 which are units that I can't really understand. The solution is to take the positive square root, which we will call the sample standard deviation.

$$s = \sqrt{s^2}$$

But why do we take the jog through through variance? Mathematically the variance is more useful and most distributions (such as the normal) are defined by the variance term. Practically though, standard deviation is easier to think about.

The sample standard deviation is important enough for R to have function that will calculate it for you.

```
TenMileRace %>% summarise( s = sd(net) )

##          s
## 1 969.6564
```

Coefficient of Variation

Suppose we had a group of animals and the sample standard deviation of the animals lengths was 15 cm. If the animals were elephants, you would be amazed at their uniformity in size, but if they were insects, you would be astounded at the variability. To account for that, the **coefficient of variation** takes the sample standard deviation and divides by the absolute value of the sample mean (to keep everything positive)

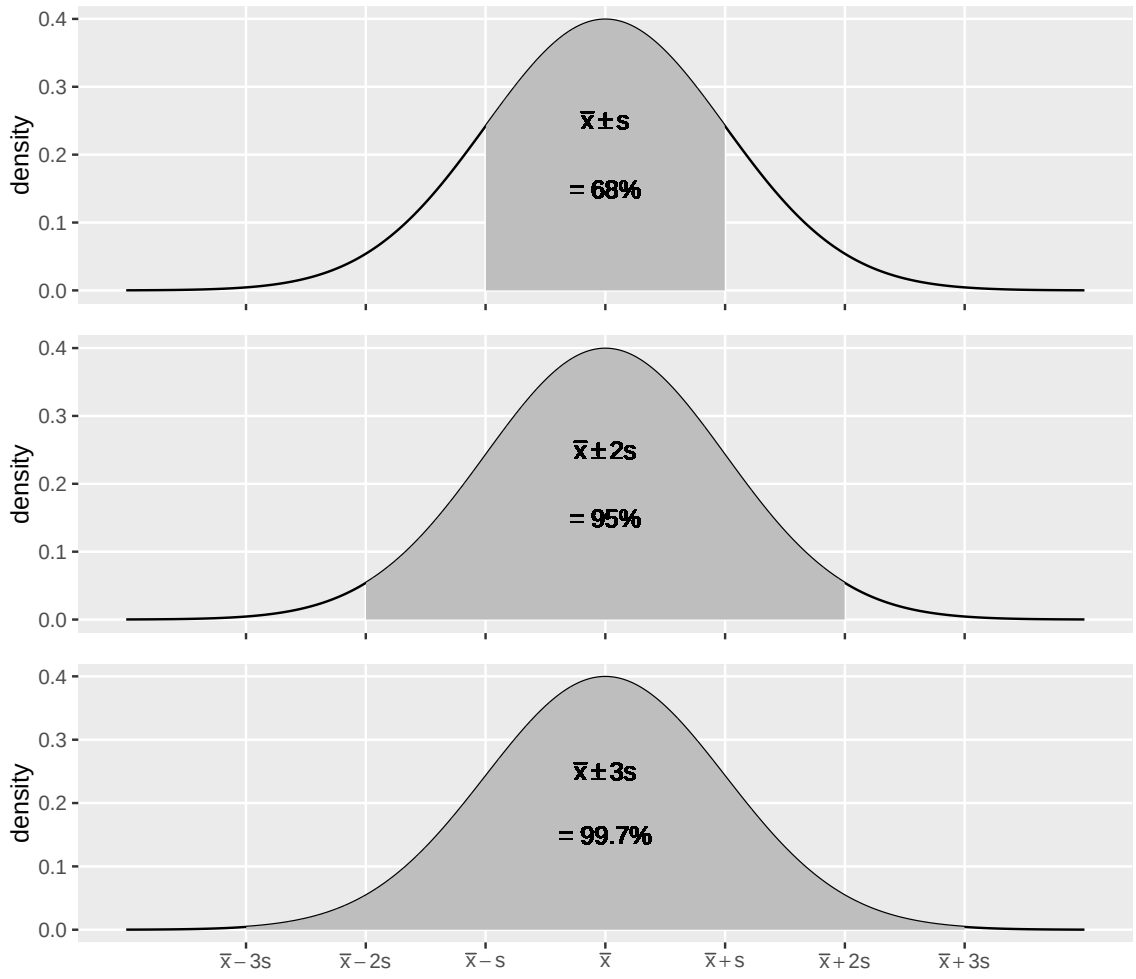
$$CV = \frac{s}{|\bar{x}|}$$

```
TenMileRace %>% summarise( s = sd(net),
                           xbar = mean(net),
                           cv = s / abs(xbar) )

##          s     xbar        cv
## 1 969.6564 5599.065 0.1731818

# For fun, lets calculate these same statistics but separated by sex...
TenMileRace %>%
  group_by(sex) %>%
  summarise( xbar = mean(net),
             s    = sd(net),
             cv   = s / abs(xbar) )

## Source: local data frame [2 x 4]
##
##      sex     xbar        s        cv
##   (fctr)    (dbl)    (dbl)     (dbl)
## 1      F 5916.398 902.1090 0.1524761
## 2      M 5280.702 929.9817 0.1761095
```

Empirical Rule of Thumb

For any mound-shaped sample of data the following is a reasonable rule of thumb:

Interval	Approximate percent of measurements
$\bar{x} \pm s$	68%
$\bar{x} \pm 2s$	95%
$\bar{x} \pm 3s$	99.7%



1.4 Exercises

1. O&L 3.21. The ratio of DDE (related to DDT) to PCB concentrations in bird eggs has been shown to have had a number of biological implications. The ratio is used as an indication of the movement of contamination through the food chain. The paper "The ratio of DDE to PCB concentrations in Great Lakes herring gull eggs and its us in interpreting contaminants data" reports the following ratios for eggs collected at 13 study sites from the five Great Lakes. The eggs were collected from both terrestrial and aquatic feeding birds.

	DDE to PCB Ratio										
Terrestrial	76.50	6.03	3.51	9.96	4.24	7.74	9.54	41.70	1.84	2.5	1.54
Aquatic	0.27	0.61	0.54	0.14	0.63	0.23	0.56	0.48	0.16	0.18	

   (a) By hand, compute the mean and median for the 21 ratios, ignoring the type of feeder.

   (b) By hand, compute the mean and median separately for each type of feeder.

   (c) Using your results from parts (a) and (b), comment on the relative sensitivity of the mean and median to extreme values in a data set.

   (d) Which measure, mean or median, would you recommend as the most appropriate measure of the DDE to PCB level for both types of feeders? Explain your answer.

2. O&L 3.31. *Consumer Reports* in its June 1998 issue reports on the typical daily room rate at six luxury and nine budget hotels. The room rates are give in the following table.

Luxury	$175	$180	$120	$150	$120	$125			
Budget	$50	$50	$49	$45	$36	$45	$50	$50	$40

   (a) By hand, compute the means and standard deviations of the room rates for each class of hotel.

   (b) Give a reason why luxury hotels might have higher variability than the budget hotels.

3. Use R to confirm your calculations in problem 1 (the pollution data). Show the code you used and the subsequent output. *It will often be convenient for me to give you code that generates a data frame instead of uploading an Excel file and having you read it in. The data can be generated using the following commands:*

```
PolutionRatios <- data.frame(
  Ratio = c(76.50, 6.03, 3.51, 9.96, 4.24, 7.74, 9.54, 41.70, 1.84, 2.5, 1.54,
            0.27, 0.61, 0.54, 0.14, 0.63, 0.23, 0.56,  0.48, 0.16, 0.18       ),
  Type  = c( rep('Terrestrial',11), rep('Aquatic',10) ) )

# Print out some of the data to confirm what the column names are
head( PolutionRatios )

##   Ratio        Type
## 1 76.50 Terrestrial
## 2  6.03 Terrestrial
## 3  3.51 Terrestrial
## 4  9.96 Terrestrial
## 5  4.24 Terrestrial
## 6  7.74 Terrestrial
```

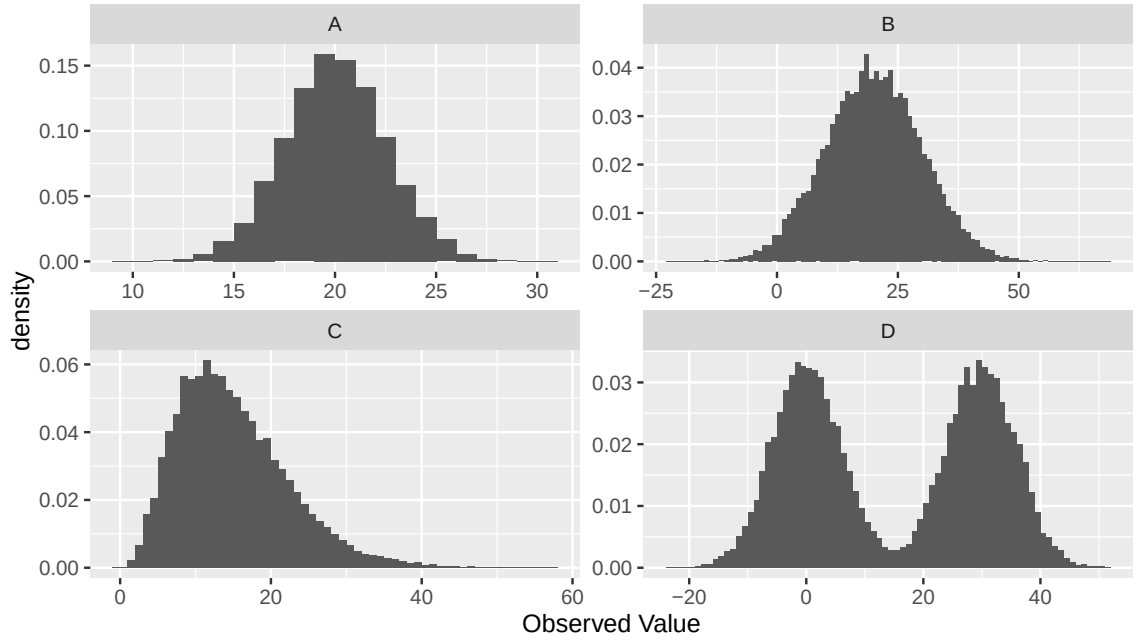
   Hint: for computing the means and medians for each type of feeder separately, there is a very convenient command

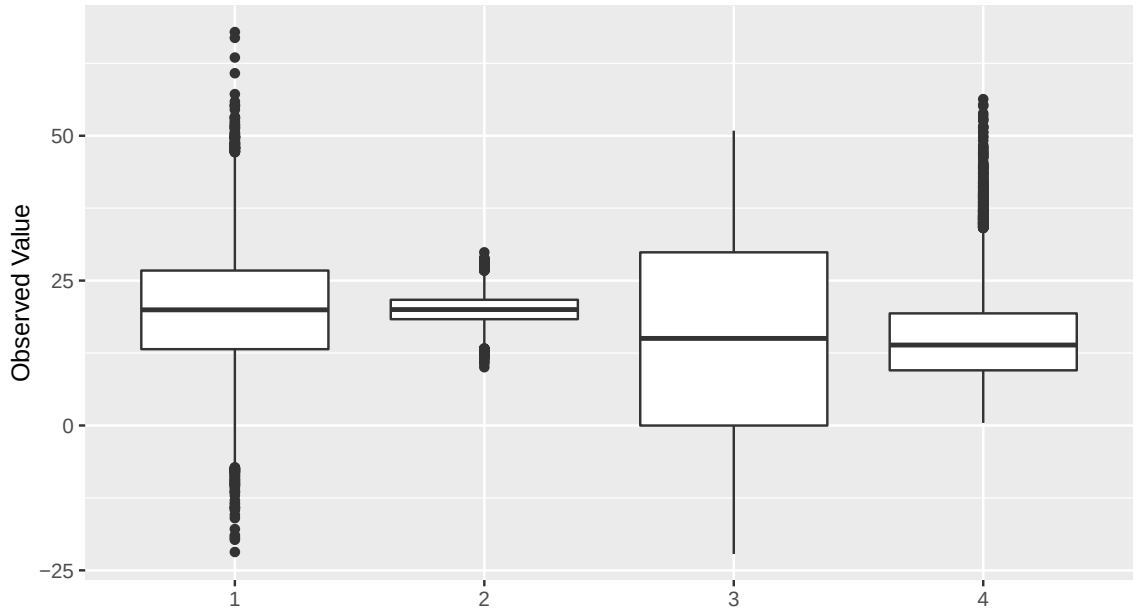
4. Use R to confirm your calculations in problem 2 (the hotel data). Show the code you used and the subsequent output. The data can be loaded into a data frame using the following commands Show the code you used and the subsequent output:

```
Hotels <- data.frame(
  Price = c(175, 180, 120, 150, 120, 125, 50, 50, 49, 45, 36, 45, 50, 50, 40),
  Type  = c( rep('Luxury',6),  rep('Budget', 9) ) )

# Print out some of the data to confirm what the column names are
head( Hotels )

##   Price   Type
## 1   175 Luxury
## 2   180 Luxury
## 3   120 Luxury
## 4   150 Luxury
## 5   120 Luxury
## 6   125 Luxury
```

5. For the hotel data, create side-by-side box-and-whisker plots to compare the prices.

6. Match the following histograms to the appropriate boxplot.





(a) Histogram A goes with boxplot _____

(b) Histogram B goes with boxplot _____

(c) Histogram C goes with boxplot _____

(d) Histogram D goes with boxplot _____

7. Twenty-five employees of a corporation have a mean salary of $62,000 and the sample standard deviation of those salaries is $15,000. If each employee receives a bonus of $1,000, does the standard deviation of the salaries change? Explain your reasoning.

Chapter 2

Probability

We need to work out the mathematics of what we mean by probability. To begin with we first define an *outcome*. An outcome is one observation from a random process or event. For example we might be interested in a single roll of a six-side die. Alternatively we might be interested in selecting one NAU student at random from the entire population of NAU students.

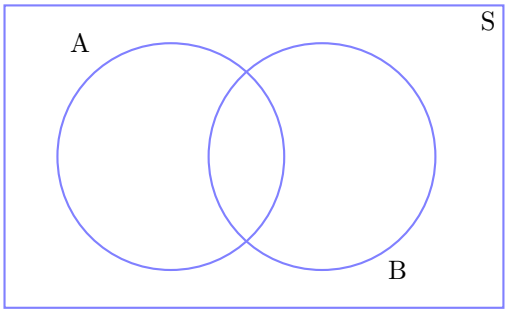
2.1 Introduction to Set Theory

Before we jump into probability, it is useful to review a little bit of set theory.

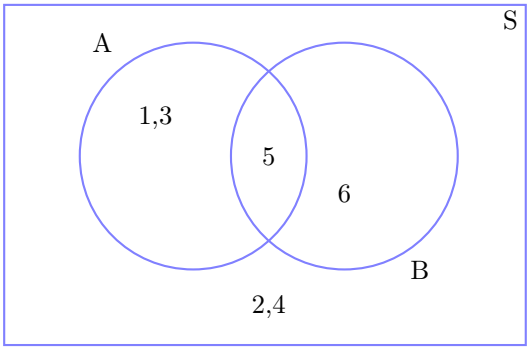
Events are properties of a particular outcome. For a coin flip, the event "Heads" would be the event that a heads was flipped. For the single roll of a six-sided die, a possible event might be that the result is even. For the NAU student, we might be interested in the event that the student is a biology student. A second event of interest might be if the student is an undergraduate.

2.1.1 Venn Diagrams

Let S be the set of all outcomes of my random trial. Suppose I am interested in two events A and B. The traditional way of representing these events is using a *Venn diagram.*



For example, suppose that my random experiment is rolling a fair 6-sided die once. The possible outcomes are $S = \{1, 2, 3, 4, 5, \text{ or } 6\}$. Suppose I then define events $A =$ *roll is odd* and $B =$ *roll is 5 or greater*. In this case our picture is:



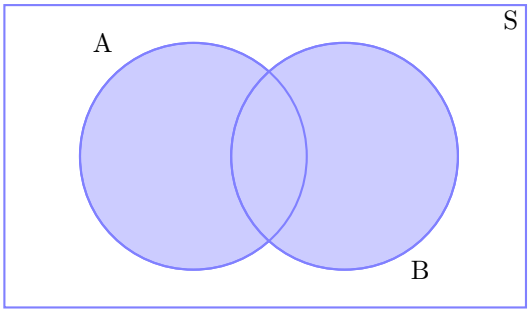
All of our possible events are present, and distributed amongst our possible events.

2.1.2 Composition of events

I am often interested in discussing the composition of two events and we give the common set operations below.

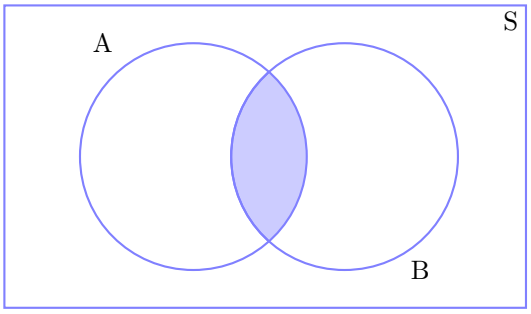
- Union: Denote the event that either A or B occurs as $A \cup B$.

$A \cup B$



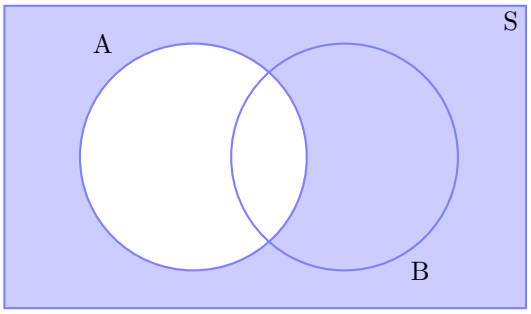
- Denote the event that both A and B occur as $A \cap B$

$A \cap B$



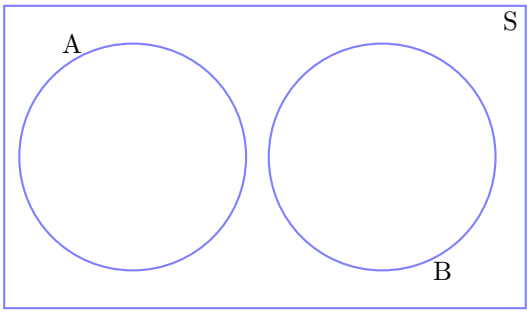
- Denote the event that A does not occur as $\bar{A}$ or A^C (different people use different notations)

$\bar{A}$ or A^C



Definition 1. Two events A and B are said to be mutually exclusive (or disjoint) if the occurrence of one event precludes the occurrence of the other. For example, on a single roll of a die, a two and a five cannot both come up. For a second example, define A to be the event that the die is even, and B to be the event that the die comes up as a 5.

A and B disjoint



2.2 Probability Rules

2.2.1 Simple Rules

We now take our Venn diagrams and use them to understand the rules of probability. The underlying idea that we will use is the the probability of an event is the *area* in the Venn diagram.

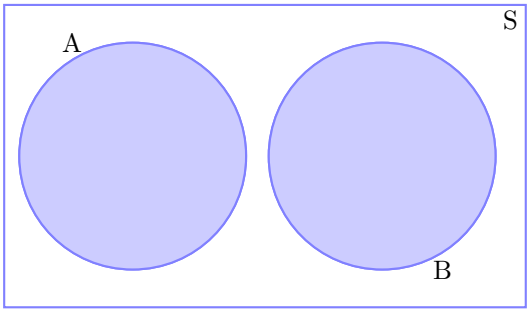
Definition 2. Probability is the proportion of times an event occurs in many repeated trials of a random phenomenon. In other words, probability is the long-term relative frequency.

Fact. *For any event A the probability of the event $P(A)$ satisfies $0 \leq P(A) \leq 1$ since proportions always lie in $[0, 1]$*

Because S is the set of all events that might occur, the area of our bounding rectangle will be 1 and the probability of event A occurring will be the area in the circle A.

Fact. *If two events are mutually exclusive, then $P(A \cup B) = P(A) + P(B)$*

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



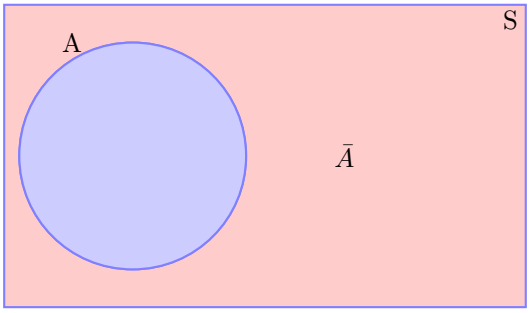
Example. Let S be the sum of two different colored dice. Suppose we are interested in $P(S \leq 4)$. Notice that the pair of dice can fall 36 different ways (6 ways for the first die and six for the second results in 6x6 possible outcomes, and each way has equal probability 1/36. Since the dice cannot simultaneously sum to 2 *and* to 3, we could write

$$\begin{aligned} P(S \leq 4) &= P(S = 2) + P(S = 3) + P(S = 4) \\ &= P(\{1,1\}) + P(\{1,2\} \text{ or } \{2,1\}) + P(\{1,3\} \text{ or } \{2,2\} \text{ or } \{3,1\}) \\ &= \frac{1}{36} + \frac{2}{36} + \frac{3}{36} \\ &= \frac{6}{36} \\ &= \frac{1}{6} \end{aligned}$$

Fact. $P(A) + P(\bar{A}) = 1$.

The above statement is true because the probability of whole space S is one (remember S is all possible outcomes), then either we get an outcome in which A occurs or we get an outcome in which A does not occur.

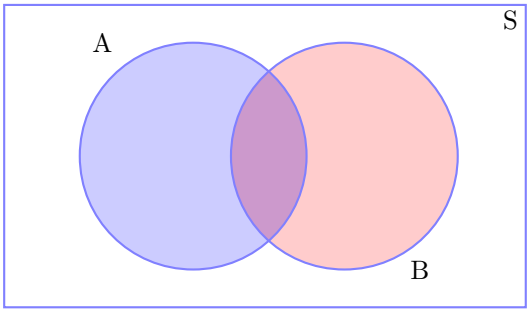
$$P(A) + P(\bar{A}) = 1$$



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

The reason behind this fact is that if there is if A and B are not disjoint, then some area is added *twice* when I calculate $P(A) + P(B)$. To account for this, I simply subtract off the area that was double counted.

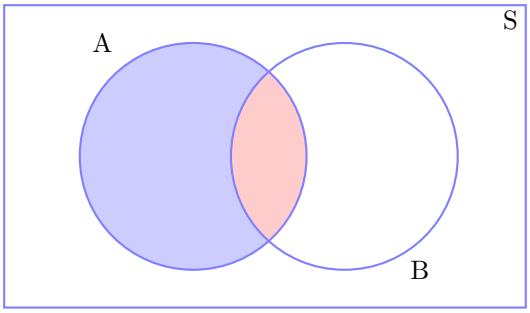
$$P(A \cup B) = P(A) + P(B) - P(A \cap B)$$



Fact 3. $P(A) = P(A \cap B) + P(A \cap \bar{B})$

This identity is just breaking the event A into two disjoint pieces.

$$P(A) = P(A \cap \bar{B}) + P(A \cap B)$$



2.2.2 Conditional Probability

We are given the following data about insurance claims. Notice that the data is given as $P($ *Category* $\cap$ *PolicyType* $)$ which is apparent because the sum of all the elements in the table is 100%:

	Type of Policy (%)		
Category	Fire	Auto	Other
Fraudulent	6%	1%	3%
Non-fraudulent	14%	29%	47%

Summing across the rows and columns, we can find the probabilities of for each category and policy type.

	Type of Policy (%)			
Category	Fire	Auto	Other	Total %
Fraudulent	6%	1%	3%	10%
Non-fraudulent	14%	29%	47%	90%
Total	20%	30%	50%	100%

It is clear that fire claims are more likely fraudulent than auto or other claims. In fact, the proportion of fraudulent claims, given that the claim is against a fire policy is

$$\begin{aligned} P(\text{ Fraud } | \text{ FirePolicy }) &= \frac{\text{proportion of claims that are fire policies and are fraudulent}}{\text{proportion of fire claims}} \\ &= \frac{6\%}{20\%} \\ &= 0.3 \end{aligned}$$

In general we define conditional probability (assuming $P(B) \neq 0$) as

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

which can also be rearranged to show

$$\begin{aligned} P(A \cap B) &= P(A \,|\, B)\, P(B) \\ &= P(B \,|\, A)\, P(A) \end{aligned}$$

since the order doesn't matter and $P\,(A \cap B) = P\,(B \cap A)$.

Using this rule, we might calculate the probability that a claim is an Auto policy given that it is not fraudulent.

$$\begin{aligned} P\,(\,Auto \,|\, NotFraud\,) &= \frac{P\,(\,Auto \,\cap\, NotFraud)}{P\,(\,NotFraud\,)} \\ &= \frac{0.29}{0.9} \\ &= 0.3\bar{2} \end{aligned}$$

Definition 4. Two events A and B are said to be **independent** if

$$P(A|B) = P(A) \;\text{ and }\; P(B|A) = P(B)$$

What independence is saying that knowing the outcome of event A doesn't give you any information about the outcome of event B.

- In simple random sampling, we assume that any two samples are independent.
- In cluster sampling, we assume that samples within a cluster are not independent, but clusters are independent of each other.

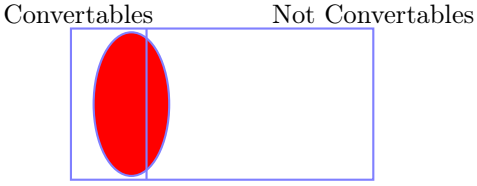
Fact 5. *If A and B are independent events, then*

$$\begin{aligned} P(A \cap B) &= P(A|B)P(B) \\ &= P(A)P(B) \end{aligned}$$

Example 6. Suppose that we are interested in the relationship between the color and the type of car. Specifically I will divide the car world into convertibles and non-convertibles and the colors into red and non-red.

Suppose that convertibles make up just 10% of the domestic automobile market. This is to say $P(\,Convertable\,) = 0.10$. Of the non-convertibles, red is not unheard of but it isn't common either. So suppose $P(\,Red \mid NonConvertable\,) = 0.15$. However red is an extremely popular color for convertibles so let $P(\,Red \mid Convertable\,) = 0.60$.

We can visualize this information via another Venn diagram:



Given the above information, we can create the following table:

	Convertable	non-Convertable	
Red			
Not Red			
	0.10	0.90	

We can fill in some of the table using our the definition of conditional probability. For example:

$$\begin{aligned} P\left(Red \cap Convertable\right) &= P\left(Red \,|\, Convertable\right) P\left(Convertable\right) \\ &= 0.60 * 0.10 \\ &= 0.06 \end{aligned}$$

Lets think about what this conditional probability means. Of the 90% of cars that are not convertibles, 15% those non-convertibles are red and therefore the proportion of cars that are red non-convertibles is $0.90 * 0.15 = 0.135$. Of the 10% of cars that are convertibles, 60% of those are red and therefore proportion of cars that are red convertibles is $0.10 * 0.60 = 0.06$. Thus the total percentage of red cars is actually

$$\begin{aligned} P\left(\, Red\,\right) &= P\left(\, Red \,\cap\, Convertible\,\right) + P\left(\, Red \cap NonConvertible\,\right) \\ &= P\left(\, Red \,|\, Convertable\,\right) P\left(\, Convertible\,\right) + P\left(\, Red \,|\, NonConvertible\,\right) P\left(\, NonConvertible\,\right) \\ &= 0.60 * 0.10 + 0.15 * 0.90 \\ &= 0.06 + 0.135 \\ &= 0.195 \end{aligned}$$

So when I ask for $P($ *red* | *convertable* $)$, I am narrowing my space of cars to consider only convertibles. While there percentage of cars that are red and convertible is just 6% of all cars, when I restrict myself to convertibles, we see that the percentage of this smaller set of cars that are red is 60%.

Notice that because $P\left(Red\right) = 0.195 \neq 0.60 = P\left(Red \,|\, Convertable\right)$ then the events *Red* and *Convertable* are not independent.

2.2.3 Summary of Probability Rules

$$0 \leq P\left(A\right) \leq 1$$

$$P\left(A\right) + P\left(\bar{A}\right) = 1$$

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

$$P\left(A \cap B\right) = \begin{cases} P\left(A \,|\, B\right) P\left(B\right) \\ P\left(B \,|\, A\right) P\left(A\right) \\ P(A)P(B) & \text{if A,B are independent} \end{cases}$$

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

2.3 Discrete Random Variables

The different types of probability distributions (and therefore your analysis method) can be divided into two general classes:

1. Continuous Random Variables - the variable takes on numerical values and could, in principle, take any of an uncountable number of values. In practical terms, if fractions or decimal points in the number make sense, it is usually continuous.

2. Discrete Random Variables - the variable takes on one of small set of values (or only a countable number of outcomes). In practical terms, if fractions or decimals points don't make sense, it is usually discrete.

Examples:

1. Presence or Absence of wolves in a State?

2. Number of Speeding Tickets received?

3. Tree girth (in cm)?

4. Photosynthesis rate?

2.3.1 Introduction to Discrete Random Variables

The following facts hold for discrete random variables:

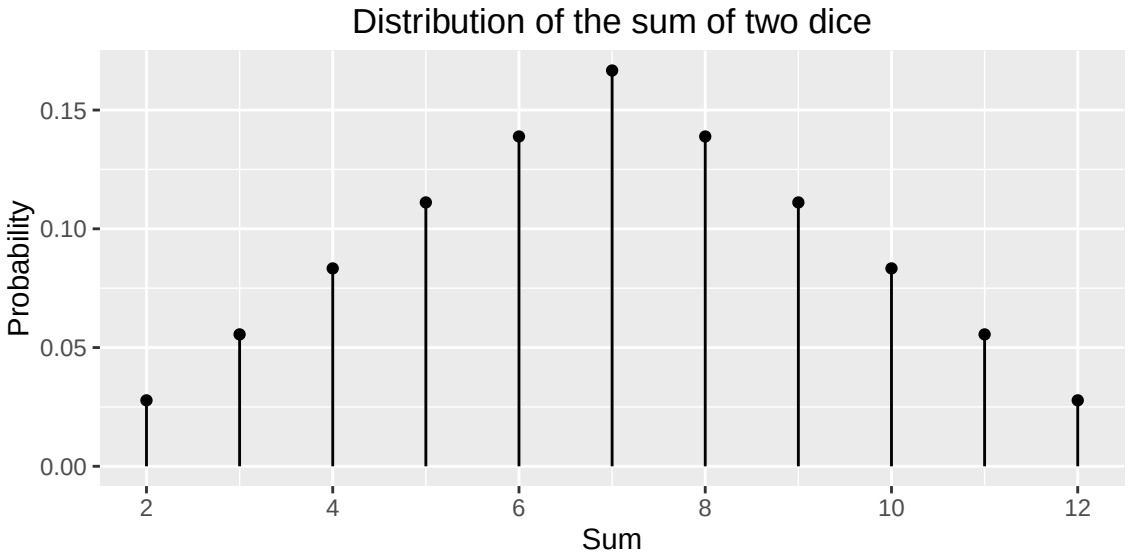
1. The probability associated with every value lies between 0 and 1

2. The sum of all probabilities for all values is equal to 1

3. Probabilities for discrete RVs are additive. i.e., $P(3 \text{ or } 4) = P(3) + P(4)$

Expected Value

Example: Consider the discrete random variable S, the sum of two fair dice.



We often want to ask 'What is expected value of this distribution?' You might think about taking a really, really large number of samples from this distribution and then taking the mean of that *really really* big sample. We define the expected value (often denoted by μ) as *a weighted*

average of the possible values and the weights are the proportions with which those values occur.

$$\begin{aligned}
\mu = E[S] &= \sum_{\text{possible } s} s \cdot P\left(S = s\right) \\
&= \sum_{s=2}^{12} s \cdot P(S = s) \\
&= 2 \cdot P\left(S = 2\right) + 3 \cdot P\left(S = 3\right) + \cdots + 11 \cdot P\left(S = 11\right) + 12 \cdot P\left(S = 12\right) \\
&= 2\left(\frac{1}{36}\right) + 3\left(\frac{2}{36}\right) + \cdots + 11\left(\frac{2}{36}\right) + 12\left(\frac{1}{36}\right) \\
&= 7
\end{aligned}$$

Variance

Similarly we could define the variance of S (which we often denote σ^2) as *a weighted average of the squared-deviations that could occur.*

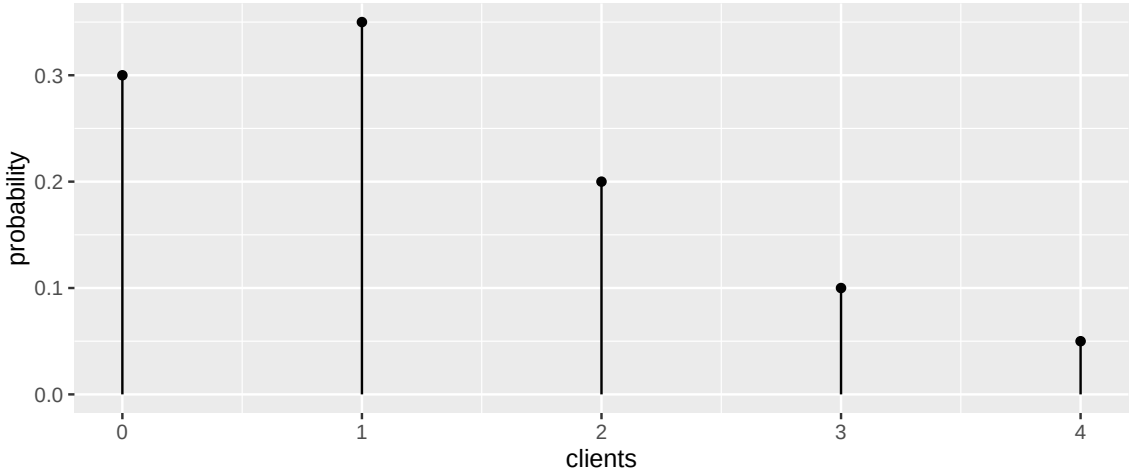
$$\begin{aligned}
\sigma^2 = V[S] &= \sum_{s=2}^{12} \left(s - \mu\right)^2 P(S = s) \\
&= (2-7)^2\left(\frac{1}{36}\right) + (3-7)^2\left(\frac{2}{36}\right) + \cdots + (12-7)^2\left(\frac{1}{36}\right) \\
&= \frac{35}{6} = 5.8\bar{3}
\end{aligned}$$

We could interpret the expectation as the sample mean of an infinitely large sample, and the variance as the sample variance of the same infinitely large sample. These are two very important numbers that describe the distribution.

Example 7. My wife is a massage therapist and over the last year, the number of clients she sees per work day (denoted Y) varied according the following table:

Number of Clients	0	1	2	3	4
Frequency/Probability	0.3	0.35	0.20	0.10	0.05

```
library(ggplot2) # graphing package

distr <- data.frame(    clients = c( 0,   1,    2,    3,    4   ),    # two columns
                     probability = c(0.3, 0.35, 0.20, 0.10, 0.05 ) )   #

ggplot(distr, aes(x=clients)) +                 # graph with clients as the x-axis
  geom_point(aes(y=probability)) +              # where the dots go
  geom_linerange(aes(ymax=probability, ymin=0)) # the vertical lines
```



Because this is the long term relative frequency of the number of clients (over 200 working days!), it is appropriate to interpret these frequencies as probabilities. This table and graph is often called a *probability mass function (pmf)* because it lists how the probability is spread across the possible values of the random variable. We might next ask ourselves what is the average number of clients per day? It looks like it ought to be between 1 and 2 clients per day.

$$\begin{aligned} E(Y) &= \sum_{\text{possible } y} y\,P(Y=y) \\ &= \sum_{y=0}^{4} y\,P(Y=y) \\ &= 0\,P(Y=0)+1\,P(Y=1)+2\,P(Y=2)+3\,P(Y=3)+4\,P(Y=4) \\ &= 0\,(0.3)+1\,(0.35)+2\,(0.20)+3\,(0.10)+4\,(0.05) \\ &= 1.25 \end{aligned}$$

Assuming that successive days are independent (which might be a bad assumption) what is the probability she has two days in a row with no clients?

$$\begin{aligned} P(0 \text{ on day1 } \textit{and } 0 \text{ on day2}) &= P(0 \text{ on day 1})\,P(0 \text{ on day 2}) \\ &= (0.3)\,(0.3) \\ &= 0.09 \end{aligned}$$

What is the variance of this distribution?

$$\begin{aligned} V(S) &= \sum_{\text{possible y}} (y-\mu)^2 \, P(Y=y) \\ &= \sum_{y=0}^{4} (y-\mu)^2 \, P(Y=y) \\ &= (0-1.25)^2(0.3) + (1-1.25)^2(0.35) + (2-1.25)^2(0.20) + (3-1.25)^2(0.10) + (4-1.25)^2(0.05) \\ &= 1.2875 \end{aligned}$$

Note on Notation: There is a difference between the upper and lower case letters we have been using to denote a random variable. In general, we let the upper case denote the random variable and the lower case as a value that the the variable could possibly take on. So in the massage example, the number of clients seen per day Y could take on values $y = 0, 1, 2, 3$, or 4.

2.4 Common Discrete Distributions

2.4.1 Binomial Distribution

Example: Suppose we are trapping small mammals in the desert and we spread out three traps. Assume that the traps are far enough apart that having one being filled doesn't affect the probability of the others being filled and that all three traps have the same probability of being filled in an evening. Denote the event that a trap is filled as F_i and if it is empty E_i (note I could have used $\bar{F}_i$). Denote the probability that a trap is filled by $\pi = 0.8$. (This sort of random variable is often referred to as a Bernoulli RV.)

The possible outcomes are

Outcome
$E_1E_2E_3$
$F_1E_2E_3$
$E_1F_2E_3$
$E_1E_2F_3$
$E_1F_2F_3$
$F_1E_2F_3$
$F_1F_3E_3$
$F_1F_2F_3$

Because these are far apart enough in space that the outcome of Trap1 is independent of Trap2 and Trap3, the

$$\begin{aligned} P(E_1 \cap F_2 \cap E_3) &= P(E_1)P(F_2)P(E_3) \\ &= (1-0.8)0.8(1-0.8) \\ &= 0.032 \end{aligned}$$

Notice how important the assumption of independence is!!! Similarly we could calculate the probabilities for the rest of the table.

Outcome	Probability	S outcome	Probability
$E_1E_2E_3$	0.008	$S = 0$	0.008
$F_1E_2E_3$	0.032	$S = 1$	3(0.032)
$E_1F_2E_3$	0.032		
$E_1E_2F_3$	0.032		
$E_1F_2F_3$	0.128	$S = 2$	3(0.128)
$F_1E_2F_3$	0.128		
$F_1F_3E_3$	0.128		
$F_1F_2F_3$	0.512	$S = 3$	0.512

Next we are interested in the random variable S, the number of traps that were filled:

Outcome	Probability
$S = 0$	$1(0.008) = 0.008$
$S = 1$	$3(0.032) = 0.096$
$S = 2$	$3(0.128) = 0.384$
$S = 3$	$1(0.512) = 0.512$

S is an example of a **Binomial Random Variable.** A binomial experiment is one that:

1. Experiment consists of n identical trials
2. Each trial results in one of two outcomes (Heads/Tails, presence/absence). One will be labeled a success and the other a failure.
3. The probability of success on a single trial is equal to π and remains the same from trial to trial.
4. The trials are independent (this is implied from property 3)
5. The random variable Y is the number of successes observed during n trials

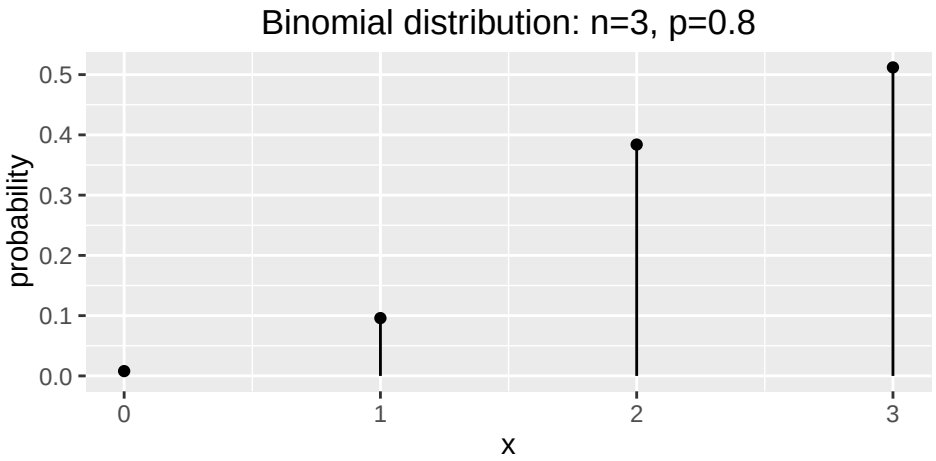
Recall that the probability mass function (pmf) describes how the probability is spread across the possible outcomes, and in this case, I can describe this via a nice formula. The pmf of a a binomial random variable Y taken from n trials each with probability of success π is

$$P(Y = y) = \underbrace{\frac{n!}{y!(n-y)!}}_{orderings} \underbrace{\pi^y}_{y\ successes} \underbrace{(1-\pi)^{n-y}}_{n-y\ failures}$$

where we define $n! = n(n-1)\dots(2)(1)$ and further define $0! = 1$. Often the ordering term is written more compactly as $\binom{n}{y} = \frac{n!}{y!(n-y)!}$.

For our small mammal example we can create a graph that shows the binomial distribution with the following R code:

```
library(ggplot2)
library(dplyr)
dist <- data.frame( x=0:3 ) %>%
  mutate(probability = dbinom(x, size=3, prob=0.8))
ggplot(dist, aes(x=x)) +
  geom_point(aes(y=probability)) +
  geom_linerange(aes(ymax=probability, ymin=0)) +
  ggtitle('Binomial distribution: n=3, p=0.8')
```



To calculate the height of any of these bars, we can evaluate the pmf at the desired point. For example, to calculate the probability the number of full traps is 2, we calculate the following

$$\begin{aligned} P(S=2) &= \binom{3}{2}(0.8)^2(1-0.8)^{3-2} \\ &= \frac{3!}{2!(3-2)!}(0.8)^2(0.2)^{3-2} \\ &= \frac{3\cdot 2\cdot 1}{(2\cdot 1)1}(0.8)^2(0.2) \\ &= 3(0.128) \\ &= 0.384 \end{aligned}$$

You can use R to calculate these probabilities. In general, for any distribution, the "d-function" gives the distribution function (pmf or pdf). So to get R to do the preceding calculation we use:

```
# P( Y = 2 | n=3, pi=0.8 )
dbinom(2, size=3, prob=0.8)

## [1] 0.384
```

The expectation of this distribution can be shown to be

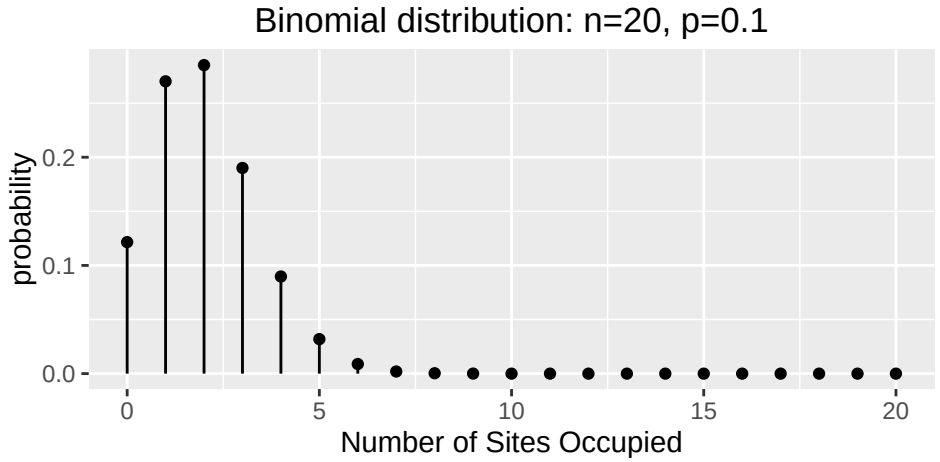
$$\begin{aligned} E[Y] &= \sum_{y=0}^{n} y\, P(Y=y) \\ &= \sum_{y=0}^{n} y\, \frac{n!}{y!\,(n-y)!}\pi^y\,(1-\pi)^{n-y} \\ &= \vdots \\ &= n\pi \end{aligned}$$

and the variance can be similarly calculated

$$\begin{aligned} V[Y] &= \sum_{y=0}^{n} (y - E\,[Y])^2\; P\,(Y=y|n,\pi) \\ &= \sum_{y=0}^{n} (y - E\,[Y])^2\; \frac{n!}{y!\,(n-y)!}\pi^y\,(1-\pi)^{n-y} \\ &= \vdots \\ &= n\pi(1-\pi) \end{aligned}$$

Example 8. Suppose a bird survey only captures the presence or absence of a particular bird (say the mountain chickadee). Assuming the true presence proportion at national forest sites around Flagstaff $\pi = 0.1$, then for $n = 20$ randomly chosen sites, the number of sites in which the bird was observed would have the distribution

```
dist <- data.frame( x=0:20 ) %>%
  mutate(probability = dbinom(x, size=20, prob=0.1))
ggplot(dist, aes(x=x)) +
  geom_point(aes(y=probability)) +
  geom_linerange(aes(ymax=probability, ymin=0)) +
  ggtitle('Binomial distribution: n=20, p=0.1') +
  xlab('Number of Sites Occupied')
```



Often we are interested in questions such as $P(Y \leq 2)$ which is the probability that we see 2 or fewer of the sites being occupied by mountain chickadee. These calculations can be tedious to

calculate by hand but R will calculate these cumulative distribution function values for you using the "p-function". This cumulative distribution function gives the sum of all values up to and including the number given.

```
# P(Y=0) + P(Y=1) + P(Y=2)
sum <- dbinom(0, size=20, prob=0.1) +
       dbinom(1, size=20, prob=0.1) +
       dbinom(2, size=20, prob=0.1)
sum

## [1] 0.6769268

# P(Y <= 2)
pbinom(2, size=20, prob=0.1)

## [1] 0.6769268
```

In general we will be interested in asking four different questions about a distribution.

1. What is the height of the probability mass function (or probability density function). For discrete variable Y this is $P(Y = y)$ for whatever value of y we want. In R, this will be the `d-function`.
2. What is the probability of observing a value less than or equal to y? In other words, to calculate $P(Y \leq y)$. In R, this will be the `p-function`.
3. What is a particular quantile of a distribution? For example, what value separates the lower 25% from the upper 75%? In R, this will be the `q-function`.
4. Generate a random sample of values from a specified distribution. In R, this will be the `r-function`.

2.4.2 Poisson Distribution

A commonly used distribution for count data is the Poisson.

1. Number of customers arriving over a 5 minute interval
2. Number of birds observed during a 10 minute listening period
3. Number of prairie dog towns per 1000 hectares
4. Number of alga clumps per cubic meter of lake water

For a RV is a Poisson RV if the following conditions apply:

1. Two or more events do not occur at precisely the same time or in the same space
2. The occurrence of an event in a given period of time or region of space is independent of the occurrence of the event in a non overlapping period or region.
3. The expected number of events during one period or region, λ, is the same in all periods or regions of the same size.

Assuming that these conditions hold for some count variable Y, the the probability mass function is given by

$$P(Y = y) = \frac{\lambda^y e^{-\lambda}}{y!}$$

where λ is the expected number of events over 1 unit of time or space and e is the constant 2.718281828.

$$\begin{aligned} E[Y] &= \lambda \\ Var[Y] &= \lambda \end{aligned}$$

Example 9. Suppose we are interested in the population size of small mammals in a region. Let Y be the number of small mammals caught in a large trap (multiple traps in the same location?) in a 12 hour period. Finally, suppose that $Y \sim Poi(\lambda = 2.3)$. What is the probability of finding exactly 4 critters in our trap?

$$\begin{aligned} P(Y = 4) &= \frac{2.3^4\, e^{-2.3}}{4!} \\ &= 0.1169 \end{aligned}$$

What about the probability of finding at most 4?

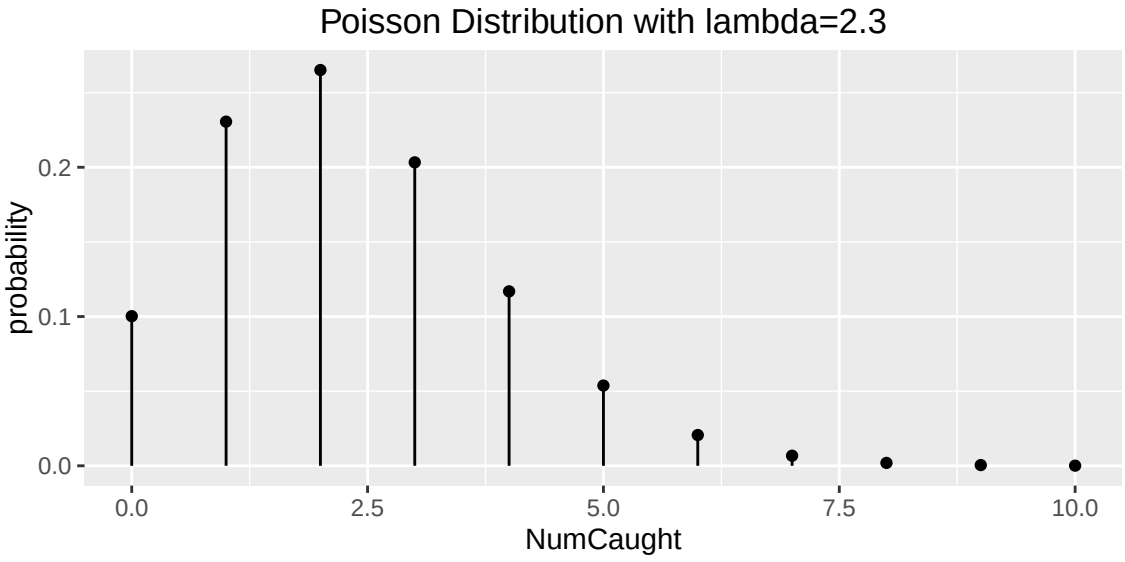
$$\begin{aligned} P(Y \leq 4) &= P(Y = 0) + P(Y = 1) + P(Y = 2) + P(Y = 3) + P(Y = 4) \\ &= 0.1003 + 0.2306 + 0.2652 + 0.2033 + 0.1169 \\ &= 0.9163 \end{aligned}$$

What about the probability of finding 5 or more?

$$\begin{aligned} P(Y \geq 5) &= 1 - P(Y \leq 4) \\ &= 1 - 0.9163 \\ &= 0.0837 \end{aligned}$$

These calculations can be done using the distribution function (`d-function`) for the poisson and the cumulative distribution function (`p-function`).

```
dist <- data.frame( NumCaught = 0:10 ) %>%
  mutate( probability = dpois( NumCaught, lambda=2.3 ) )
ggplot(dist, aes(x=NumCaught)) +
  geom_point( aes(y=probability) ) +
  geom_linerange(aes( ymax=probability, ymin=0)) +
  ggtitle('Poisson Distribution with lambda=2.3')
```



```r
# P( Y = 4)
dpois(4, lambda=2.3)

## [1] 0.1169022

# P( Y <= 4)
ppois(4, lambda=2.3)

## [1] 0.9162493

# 1-P(Y <= 4)  ==  P( Y > 4)  ==  P( Y >= 5)
1-ppois(4, 2.3)

## [1] 0.08375072
```

2.5 Continuous Random Variables

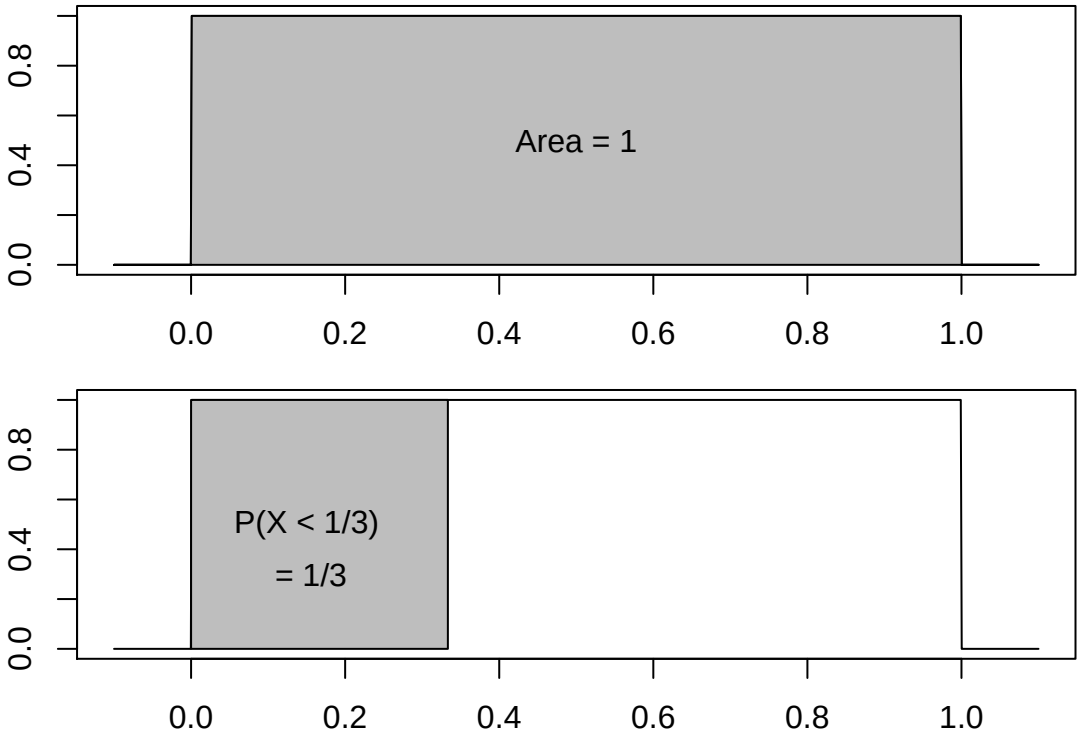
Finding the area under the curve of a particular density function $f(x)$ requires the use of calculus, but since this isn't a calculus course, we will resort to using R or tables of calculated values.

2.5.1 Uniform(0,1) Distribution

Suppose you wish to draw a random number number between 0 and 1 and each number should have an equal chance of being selected. This random variable is said to have a *Uniform(0,1)* distribution.

Because there are an infinite number of rational numbers between 0 and 1, the probability of any particular number being selected is $1/\infty = 0$. But even though each number has 0 probability of being selected, some number must end up being selected. Because of this conundrum, probability theory doesn't look at the probability of a single number, but rather focuses on a *region of numbers*.

To make this distinction, we will define the distribution using a *probability density function* instead of the probability mass function. In the discrete case, we had to constrain the probability mass function to sum to 1. In the continuous case, we have to constrain the probability density function to integrate to 1.



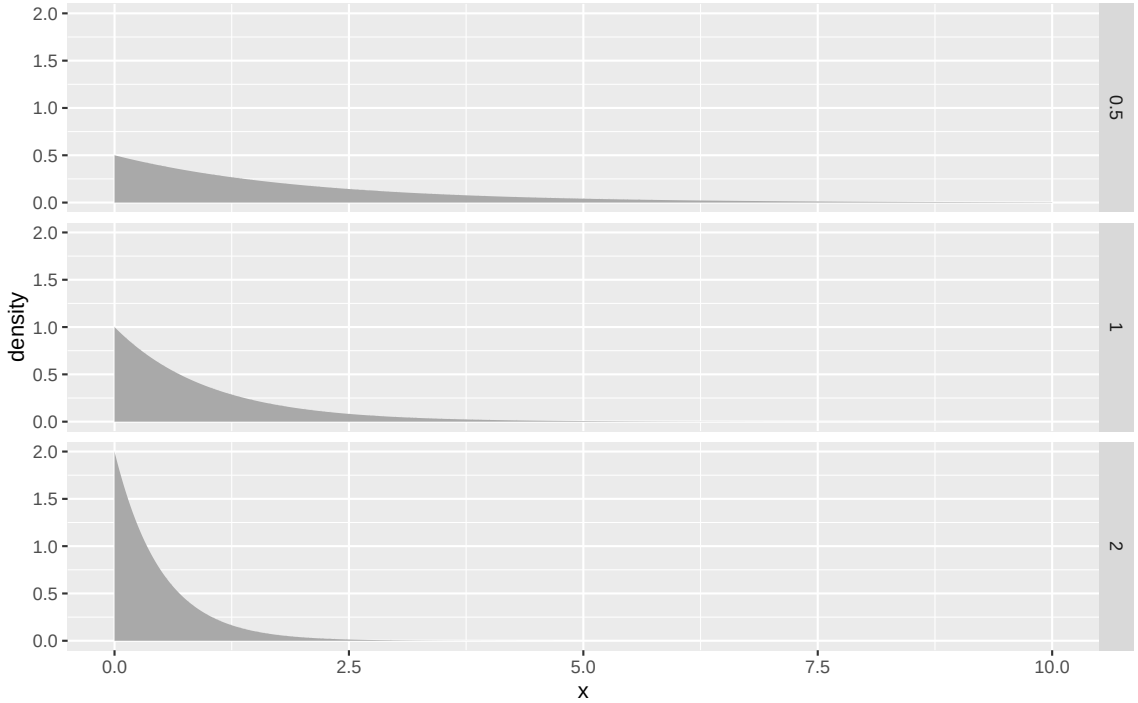
Finding the area under the curve of a particular density function $f(x)$ usually requires the use of calculus, but since this isn't a calculus course, we will resort to using R or tables of calculated values.

2.5.2 Exponential Distribution

The exponential distribution is the continuous analog of the Poisson distribution and is often used to model the time between occurrence of successive events. Perhaps we are modeling time between transmissions on a network, or the time between feeding events or prey capture. If the random variable X has an Exponential distribution, its distribution function is

$$f(x) = \begin{cases} \lambda e^{-\lambda x} & x \geq 0 \text{ and } \lambda > 0 \\ 0 & \text{otherwise} \end{cases}$$

```
##            x lambda   density
## 1 0.00000000    0.5 0.5000000
## 2 0.01001001    0.5 0.4975037
## 3 0.02002002    0.5 0.4950200
## 4 0.03003003    0.5 0.4925486
## 5 0.04004004    0.5 0.4900895
## 6 0.05005005    0.5 0.4876428
```



Analogous to the discrete distributions, we can define the Expectation and Variance of these distributions by replacing the summation with an integral

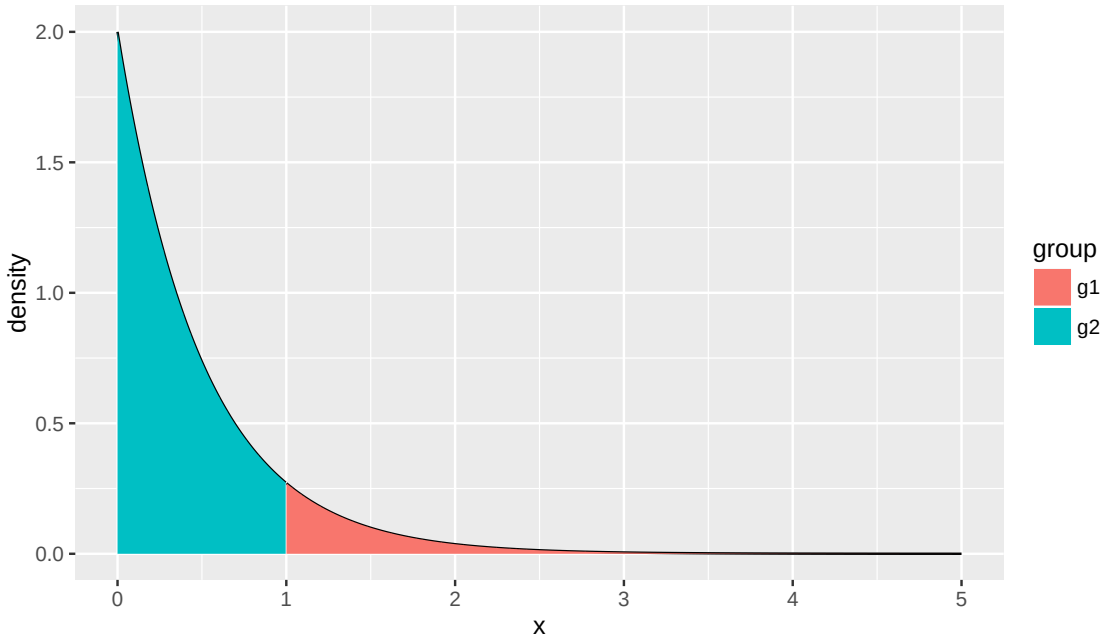
$$\begin{aligned} E[X] &= \int_0^\infty x\, f(x)\, dx \\ &= \vdots \\ &= \frac{1}{\lambda} \\ Var[X] &= \int_0^\infty (x - E[X])^2\, f(x)\, dx \\ &= \vdots \\ &= \frac{1}{\lambda^2} \end{aligned}$$

Since the exponential distribution is defined by the rate of occurrence of an event, increasing that rate *decreases* the time between events. Furthermore since the rate of occurrence cannot be negative, we restrict $\lambda > 0$

Example 10. Suppose the time between insect captures X during a summer evening for a species of bat follows a exponential distribution with capture rate of $\lambda = 2$ insects per minute and therefore the expected waiting time between captures is $1/\lambda = 1/2$ minute. Suppose that we are interested in the probability that it takes a bat more than 1 minute to capture its next insect.

$P(X > 1) =$

```
data <- data.frame( x=seq(0,5,length=1000) ) %>%
    mutate(density = dexp(x, rate=2),
           group   = ifelse( x >= 1, 'g1', 'g2')) # if(x>1) group is 1, otherwise 2
head(data)

##             x  density group
## 1 0.000000000 2.000000    g2
## 2 0.005005005 1.980080    g2
## 3 0.010010010 1.960358    g2
## 4 0.015015015 1.940833    g2
## 5 0.020020020 1.921502    g2
## 6 0.025025025 1.902364    g2

ggplot(data, aes(x=x, y=density, fill=group)) +
  geom_line() +
  geom_area()
```



We now must resort to calculus to find this area. Or use tables of pre-calculated values. Or use R (remembering that `p-functions` give the area under the curve *to the left of the given value.*

```
# P(X > 1)  == 1 - P(X <= 1)
1 - pexp(1, rate=2)

## [1] 0.1353353
```

2.5.3 Normal Distribution

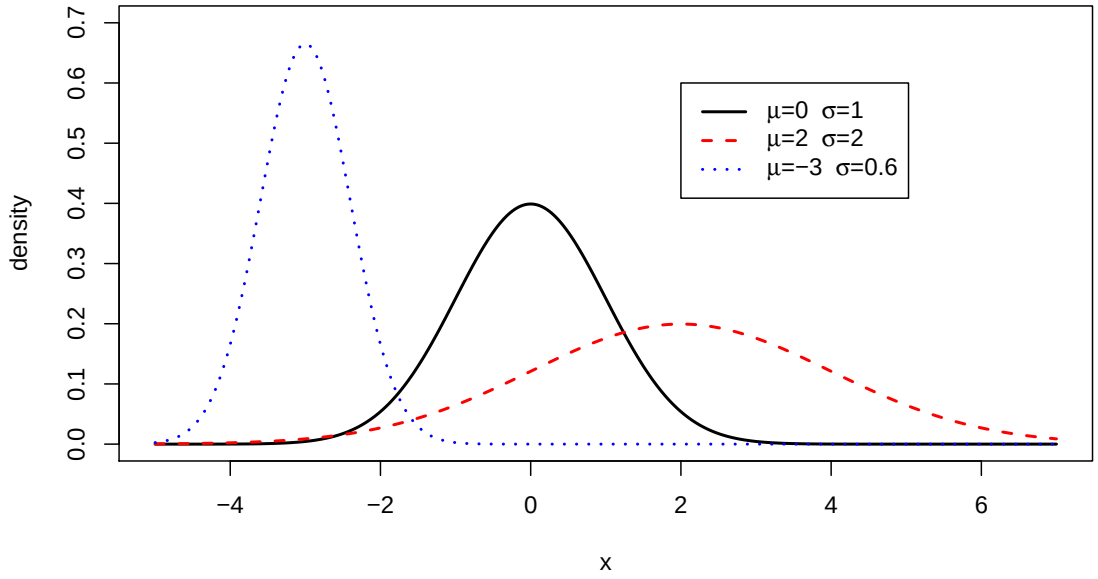
Undoubtably the most important distribution in statistics is the normal distribution. If my RV X is normally distributed with mean μ and standard deviation σ, its probability density function is given by

$$f(x) = \frac{1}{\sqrt{2\pi}\sigma} \exp\left[\frac{-(x-\mu)^2}{2\sigma^2}\right]$$

where $\exp[y]$ is the exponential function e^y. We could slightly rearrange the function to

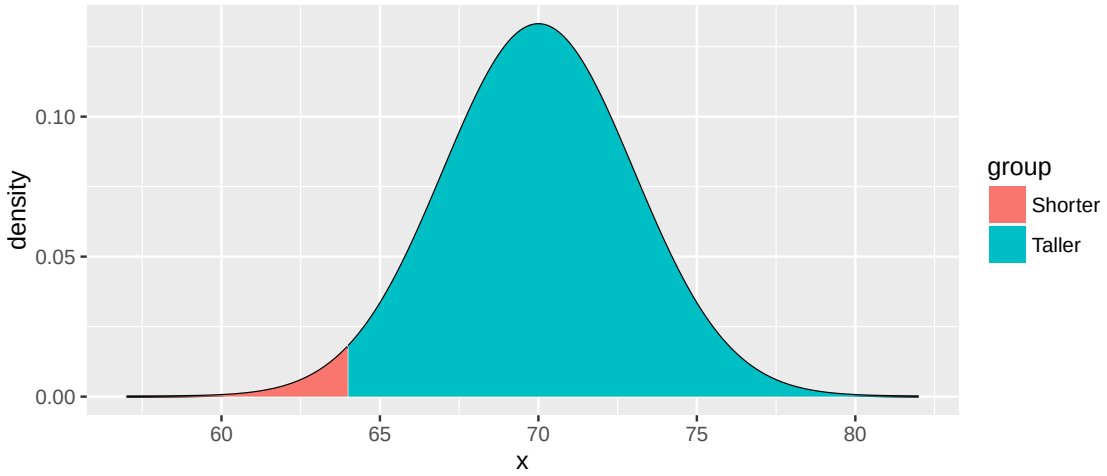
$$f(x) = \frac{1}{\sqrt{2\pi}\sigma} \exp\left[-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2\right]$$

and see this distribution is defined by its expectation $E[X] = \mu$ and its variance $Var[X] = \sigma^2$. Notice I could define it using the standard deviation σ, and different software packages will expect it to be defined by one or the other. R defines the normal distribution using the standard deviation.



Example 11. It is known that the heights of adult males in the US is approximately normal with a mean of 5 feet 10 inches ($\mu = 70$ inches) and a standard deviation of $\sigma = 3$ inches. Your instructor is a mere 5 feet 4 inches (64 inches). What proportion of the population is shorter than your professor?

```
distr <- data.frame(x=seq(57,82,length=1000)) %>%
  mutate( density = dnorm(x, mean=70, sd=3),
          group = ifelse(x<=64, 'Shorter','Taller') )
ggplot(distr, aes(x=x, y=density, fill=group)) +
  geom_line() +
  geom_area()
```



Using R you can easily find this

```
pnorm(64, mean=70, sd=3)

## [1] 0.02275013
```

2.5.3.1 Standardizing

Before we had computers that could calculate these probabilities for any normal distribution, it was important to know how to convert a probability statement from an arbitrary $N\left(\mu, \sigma^2\right)$ distribution to a question about a *Stanard Normal* distribution, which is a normal distribution with mean 0 and standard deviation 1. If we have $X \sim N\left(\mu, \sigma^2\right)$, then

$$Z = \frac{X - \mu}{\sigma} \sim N\left(0, 1\right)$$

You might remember doing something similar in an undergraduate statistics course in order to use a table to look up some probability. From the height example, we calculate

$$\begin{aligned} z &= \frac{64 - 70}{3} \\ &= \frac{-6}{3} \\ &= -2 \end{aligned}$$

note that this calculation shows that he is -2 standard deviations from the mean. Next we look at a table for $z = -2.00$. To do this we go down to the -2.0 row and over to the .00 column and find 0.0228. Only slightly over 2% of the adult male population is shorter!

How tall must a male be to be taller than 80% of the rest of the male population? To answer that we must use the table in reverse and look for the 0.8 value. We find the closest value possible (0.7995) and the z value associated with it is $z = 0.84$. Next we solve the standardizing equation

for x

$$\begin{aligned} z &= \frac{x-\mu}{\sigma} \\ 0.84 &= \frac{x-70}{3} \\ x &= 3(0.84)+70 \\ &= 72.49 \text{ inches} \end{aligned}$$

Alternatively we could use the quantile function for the normal distribution `(q-function)` in R and avoid the imprecision of using a table.

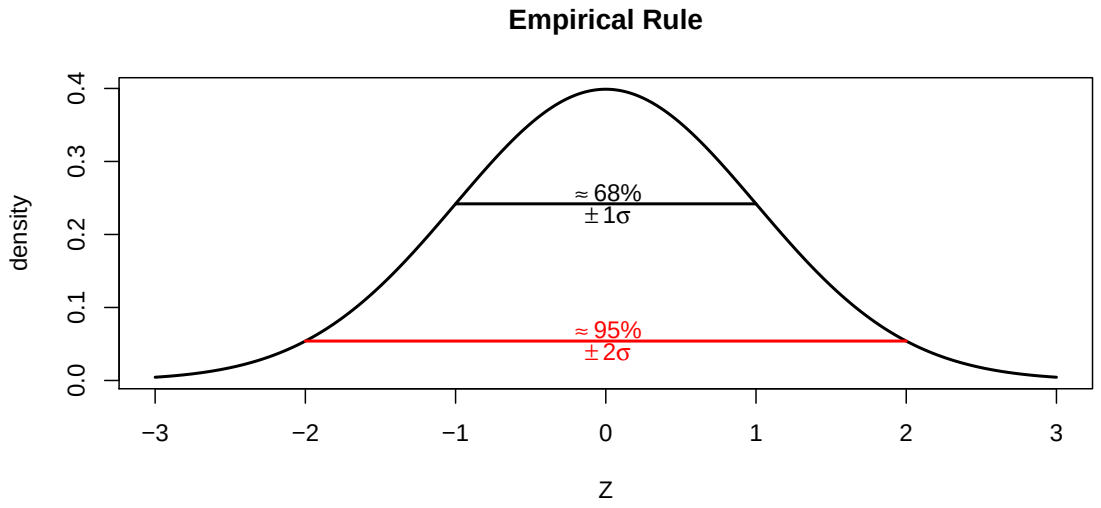
```
qnorm(.8, mean=0, sd=1)
```

```
## [1] 0.8416212
```

$$\begin{aligned} x &= 3(0.8416)+70 \\ &= 72.52 \text{ inches} \end{aligned}$$

Empirical Rule - It is from the normal distribution that the empirical rule from the previous chapter is derived. If $X \sim N(\mu, \sigma^2)$ then

$$\begin{aligned} P(\mu-\sigma \leq X \leq \mu+\sigma) &= P(-1 \leq Z \leq 1) \\ &= P(Z \leq 1) - P(Z \leq -1) \\ &\approx 0.8413 - 0.1587 \\ &= 0.6826 \end{aligned}$$



2.6 R Comments

There will be a variety of distributions we'll be interested in and R refers to them using the following abbreviations

Distribution	R stem	parameters (and defaults)	parameter interpretation
Binomial	`binom`	`size` `prob`	number of trials probability of success
Poisson	`pois`	`lambda`	mean
Exponential	`exp`	`rate` or `lambda`	λ represents the mean, while rate is $\frac{1}{\lambda}$.
Normal	`norm`	`mean=0` `sd=1`	mean standard deviation
Uniform	`unif`	`min=0` `max=1`	lower bound upper bound

All the probability distributions available in R are accessed in exactly the same way, using a `d-function`, `p-function`, `q-function`, and `r-function`.

Function	Result	Example

`d-function(x)`	Discrete: $P(X = x)$
	Continuous: the height of the density function at the given point
		`dbinom(0, size=20, prob=.1)`
		`dnorm(0, mean=0, sd=1)`
		is the height ≈ 0.40

`p-function(x)`	$P(X \leq x)$	`pnorm(-1.96, mean=0, sd=1)` is $P(Z < 1.96) = 0.025$
`q-function(q)`	x such that $P(X \leq x) = q$	`qnorm(0.05, mean=0, sd=1)` is z such that $P(Z \leq z) = 0.05$ which is $z = -1.645$
`r-function(n)`	n random observations from the distribution	`rnorm(n=10, mean=0, sd=1)` generates 10 observations from a N(0,1) distribution

2.7 Exercises

1. The population distribution of blood donors in the United States based on race/ethnicity and blood type as reported by the American Red Cross is given here:

	Blood Type				
Ethnicity	O	A	B	AB	Total
White	36%	32.2%	8.8%	3.2%	
Black	7%	2.9%	2.5%	0.5%	
Asian	1.7%	1.2%	1%	0.3%	
Other	1.5%	0.8%	0.3%	0.1%	
Total					

Notice that the numbers given in the table sum to 100%, so the data presented are the probability of a particular ethnicity and blood type.

   (a) Fill in the column and row totals.

   (b) What is the probability that a randomly selected donor will be Asian and have Type O blood? That is to say, given a donor is randomly selected from the list of all donors, what is the probability that the selected donor will Asian with Type O?

   (c) What is the probability that a randomly selected donor is white? That is to say, given a donor is randomly selected from the list of all donors, what is the probability that the selected donor is white?

   (d) What is the probability that a white donor will have Type A blood? That is to say, given a donor is randomly selected from the list of *all the white donors,* what is the probability that the selected donor has Type A blood? (Notice we already know the donor is white because we restricted ourselves to that subset!)

2. For each of the following, mark if it is Continuous or Discrete.

(a) _____ Milliliters of tea drunk per day.
(b) _____ Different brands of soda drunk over the course of a year.
(c) _____ Number of days per week that you are on-campus for any amount of time.
(d) _____ Number of grizzly bears individuals genetically identified from a grid of hair traps in Glacier National Park.

3. For each scenario, state whether the event should be modeled via a binomial or Poisson distribution.

(a) _____ Number of M&Ms I eat per hour while grading homework
(b) _____ The number of mornings in the coming 7 days that I change my daughter's first diaper of the day.
(c) _____ The number of Manzanita bushes per 100 meters of trail.

4. During a road bike race, there is always a chance a crash will occur. Suppose the probability that at least one crash will occur in any race I'm in is $\pi = 0.2$ and that races are independent.

(a) What is the probability that the next two races I'm in will both have crashes?
(b) What is the probability that neither of my next two races will there be a crash?
(c) What is the probability that at least one of the next two races will have a crash?

5. My cats suffer from gastric distress due to eating house plants and the number of vomits per week that I have to clean up follows a Poisson distribution with rate $\lambda = 1.2$.

(a) What is the probability that I don't have to clean up any vomits this coming week?
(b) What is the probability that I must clean up 1 or more vomits?
(c) If I wanted to measure this process with a rate per day, what rate should I use?

6. Suppose that the number of runners I see on a morning walk on the trails near my house has the following distribution (Notice I've never seen four or more runners on a morning walk):

y	0	1	2	3	4+
$p(y)$	0.45	0.25	0.20		0.0

(a) What is the probability that I see 3 runners on a morning walk?
(b) What is the expected number of runners that I will encounter?
(c) What is the variance of the number of runners that I will encounter?

7. If $Z \sim N\left(\mu = 0, \sigma^2 = 1\right)$, find the following probabilities:

(a) $P(Z < 1.58) =$
(b) $P(Z = 1.58) =$
(c) $P(Z > -.27) =$
(d) $P(-1.97 < Z < 2.46) =$

8. Using the Standard Normal Table or the table functions in `R`, find z that makes the following statements true.

(a) $P(Z < z) = .75$
(b) $P(Z > z) = .4$

9. The amount of dry kibble that I feed my cats each morning can be well approximated by a normal distribution with mean $\mu = 200$ grams and standard deviation $\sigma = 30$ grams.

(a) What is the probability that I fed my cats more than 250 grams of kibble this morning?
(b) From my cats' perspective, more food is better. How much would I have to feed them for this morning to be among the top 10% of feedings?

Chapter 3

Confidence Intervals Using Bootstrapping

3.1 Theory of Bootstrapping

Suppose that we had a population of interest and we wish to estimate the mean of that population (the population mean we'll denote as μ). We can't observe every member of the population (which would be prohibitively expensive) so instead we take a random sample and from that sample calculate a sample mean (which we'll denote $\bar{x}$). We believe that $\bar{x}$ will be a good estimator of μ, but it will vary from sample to sample and won't be exactly equal to μ.

Next suppose we wish to ask if a particular value for μ, say μ_0, is consistent with our observed data? We know that $\bar{x}$ will vary from sample to sample, but we have no idea *how much it will vary* between samples. However, if we could understand how much $\bar{x}$ varied sample to sample, we could answer the question. For example, suppose that $\bar{x} = 5$ and we know that $\bar{x}$ varied about ± 2 from sample to sample. Then I'd say that possible values of μ_0 in the interval 3 to 7 (5 ± 2) are reasonable values for μ and anything outside that interval is not reasonable.

Therefore, if we could take many, many repeated samples from the population and calculate our test statistic $\bar{x}$ for each sample, we could rule out possible values of μ. Unfortunately we don't have the time or money to repeatedly sample from the actual population, but we could sample from our best approximation to what the population is like.

Suppose we were to sample from a population of shapes, and we observed 4/9 of the sample were squares, 3/9 were circles, and a triangle and a diamond. Then our best guess of what the population that we sampled from was a population with 4/9 squares, 3/9 circles, and 1/9 of triangles and diamonds.

Using this approximated population (which is just many many copies of our sample data), we can repeated sample $\bar{x}^*$ values to create the sampling distribution of $\bar{x}$.

Because our approximate population is just an infinite number of copies of our sample data, then sampling from the approximate population is equivalent to sampling *with replacement* from our sample data. If I take n samples from n distinct objects with replacement, then the process can be thought of as mixing the n objects in a bowl and taking an object at random, noting which it is, replace it into the bowl, and then draw the next sample. Practically, this means some objects will be selected more than once and some will not be chosen at all. To sample our observed data with replacement, we'll use the `resample()` function in the `mosaic` package. We see that some rows will be selected multiple times, and some will not be selected at all.

```
## Loading required package:  grid
```

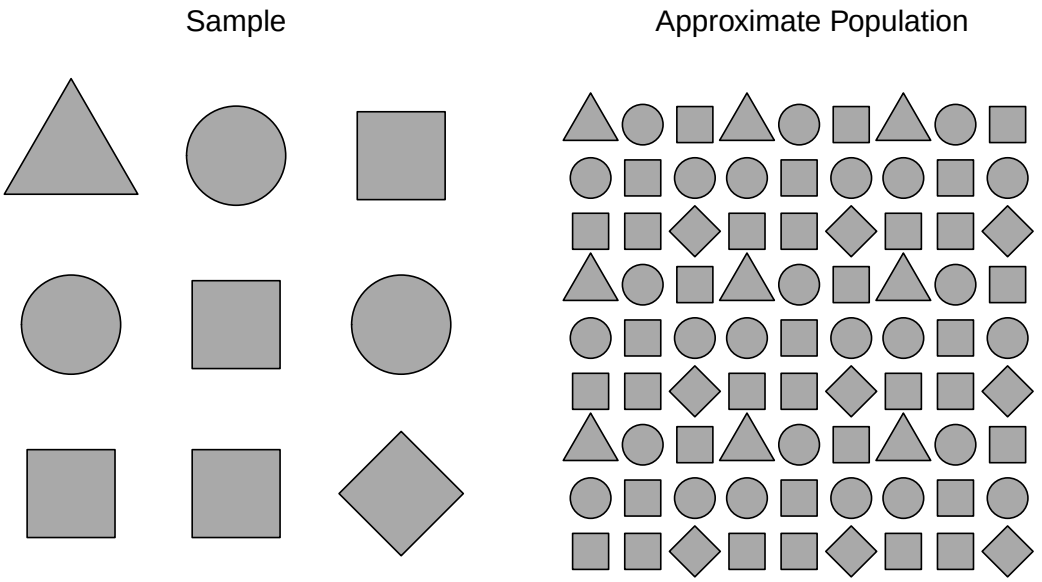


Figure 3.1.1: A possible sample from a population of shapes. Because 4/9 of our sample were squares, our best estimate is that the population is also approximately 4/9 squares. We can think of the approximated population as just many many copies of the observed sample data.

```
Testing.Data <- data.frame(
  name=c('Alison','Brandon','Chelsea','Derek','Elise'))
Testing.Data
```

```
##      name
## 1  Alison
## 2 Brandon
## 3 Chelsea
## 4   Derek
## 5   Elise
```

```
# Sample rows from the Testing Data (with replacement)
resample(Testing.Data)
```

```
##        name orig.id
## 1    Alison       1
## 4     Derek       4
## 3   Chelsea       3
## 1.1  Alison       1
## 5     Elise       5
```

Notice `Alison` has selected twice, while `Brandon` has not been selected at all. We can use the `resample()` function similarly as we did the `shuffle()` function.

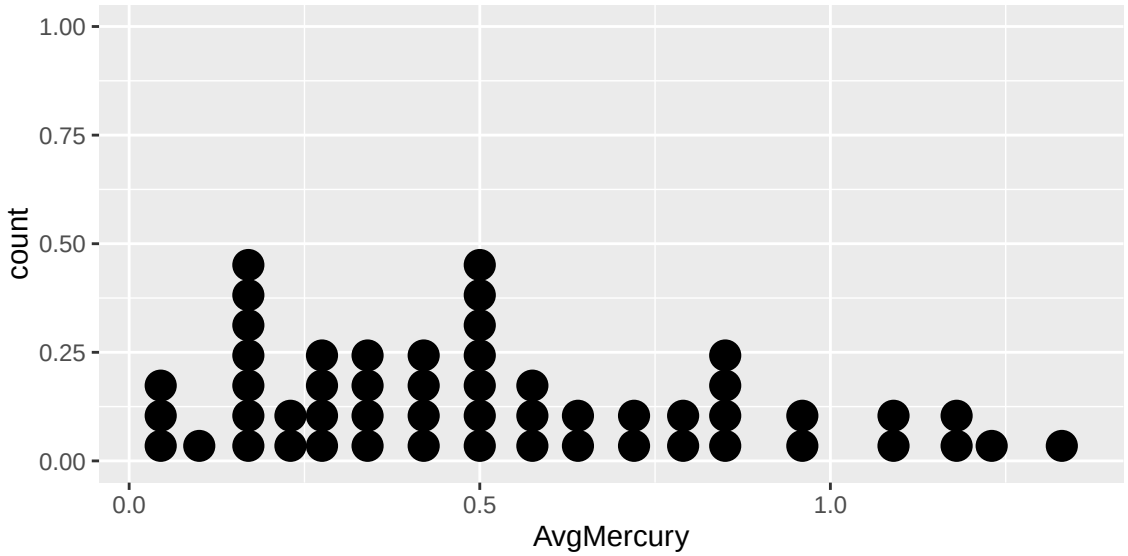
The sampling from the estimated population via sampling from the observed data is called *bootstrapping* because we are making no distributional assumptions about where the data came from, and the idiom "Pulling yourself up by your bootstraps" seemed appropriate.

Example: Mercury Levels in Fish from Florida Lakes

A data set provided by the Lock[5] textbook looks at the mercury levels in fish harvested from lakes in Florida. There are approximately 7,700 lakes in Florida that are larger than 10 acres. As part of a study to assess the average mercury contamination in these lakes, a random sample of $n = 53$ lakes, an unspecified number of fish were harvested and the average mercury level (in ppm) was calculated for fish in each lake. The goal of the study was to assess if the average mercury concentration was greater than the 1969 EPA "legally actionable level" of 0.5 ppm.

```
# as always, our first step is to load the mosaic package
library(mosaic)

# read the Lakes data set
Lakes <- read.csv('http://www.lock5stat.com/datasets/FloridaLakes.csv')
```

```
# make a nice picture... dot plots are very similar to histograms
# but in this case, my y-axis doen't make any sense.
ggplot(Lakes, aes(x=AvgMercury)) +
  geom_dotplot()

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



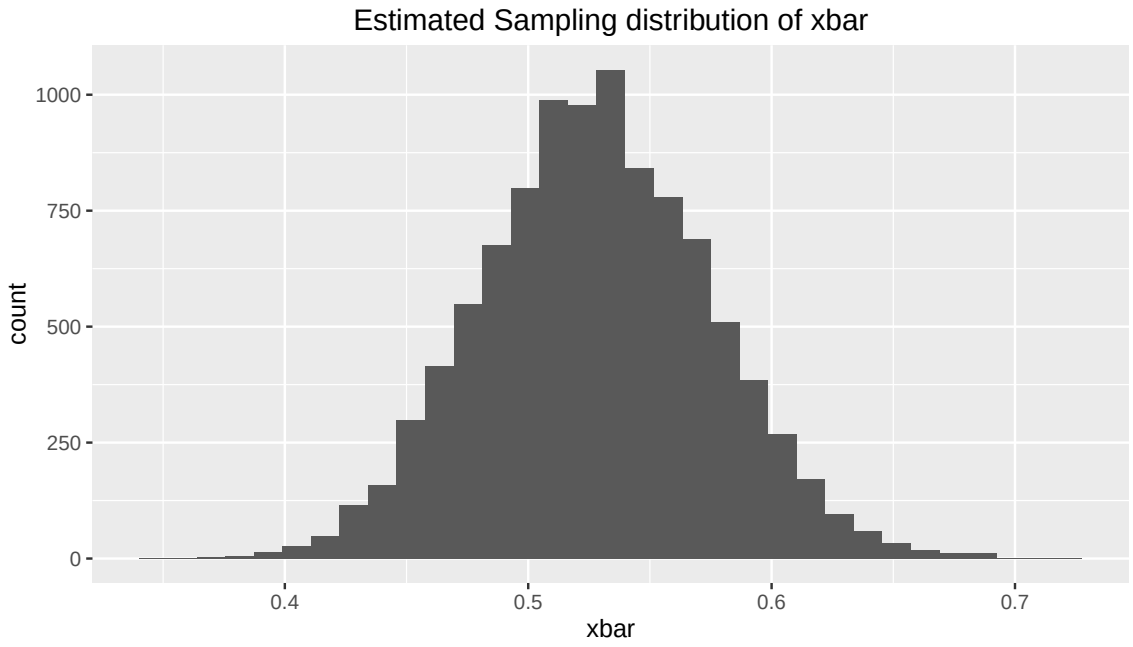
We can calculate mean average mercury level for the $n = 53$ lakes

```
Lakes %>% summarise(xbar = mean( AvgMercury ))

##        xbar
## 1 0.5271698
```

The sample mean is greater than 0.5 but not by too much. Is a true population mean concentration μ_{Hg} that is 0.5 or less incompatible with our observed data? Is our data sufficient evidence to conclude that the average mercury content is greater than 0.5? Perhaps the true average mercury content is less than (or equal to) 0.5 and we just happened to get a random sample that with a mean greater than 0.5?

The first step in answering these questions is to create the sampling distribution of $\bar{x}_{Hg}$. To do this, we will sample from the approximate population of lakes, which is just many many replicated copies of our sample data.

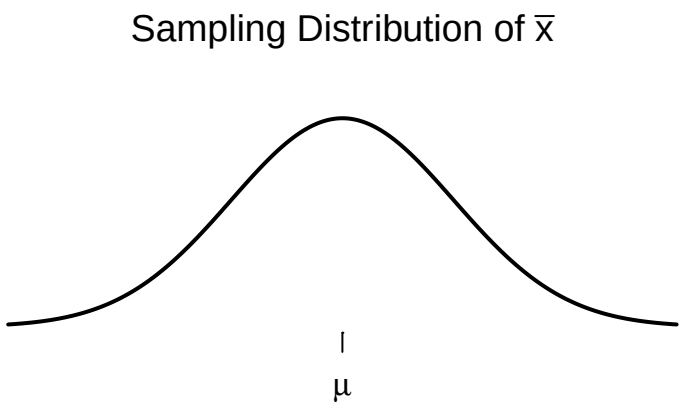
```
# create the sampling distribution of xbar
SamplingDist <- do(10000) * resample(Lakes) %>% summarise(xbar = mean(AvgMercury))

# what columns does the data frame "SamplingDist" have?
head(SamplingDist)

##        xbar
## 1 0.5154717
## 2 0.4864151
## 3 0.5456604
## 4 0.5252830
## 5 0.4920755
## 6 0.6128302

# show a histogram of the sampling distribution of xbar
ggplot(SamplingDist, aes(x=xbar)) +
  geom_histogram() +
  ggtitle('Estimated Sampling distribution of xbar' )

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



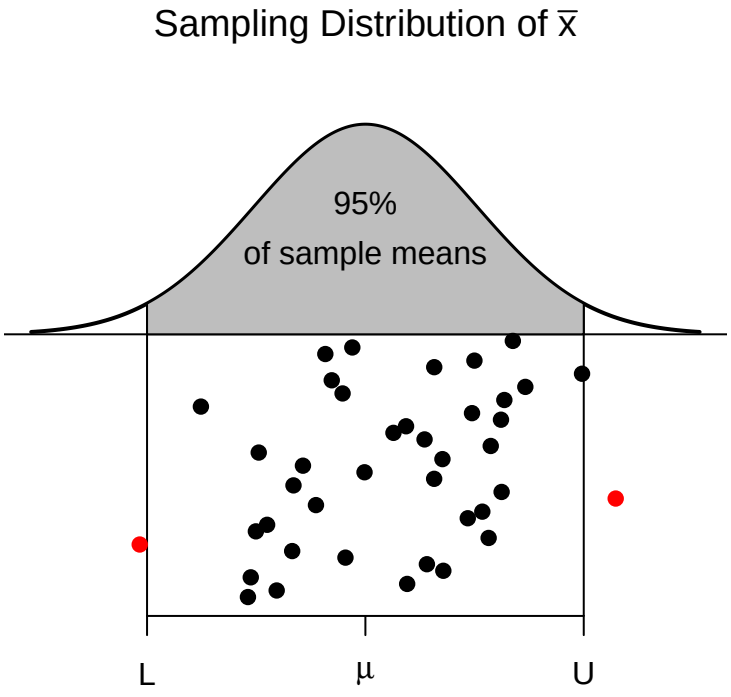
3.2 Using Quantiles of the Estimated Sampling Distributions to create a Confidence Interval

In many cases we have seen, the sampling distribution of a statistic is centered on the parameter we are interested in estimating and is symmetric about that parameter[1]. For example, we expect that the sample mean $\bar{x}$ should be a good estimate of the population mean μ and the sampling distribution of $\bar{x}$ should look something like the following.

[1]There are actually several ways to create a confidence interval from the estimated sampling distribution. The method presented here is called the "percentile" method and works when the sampling distribution is symmetric and the estimator we are using is unbiased.

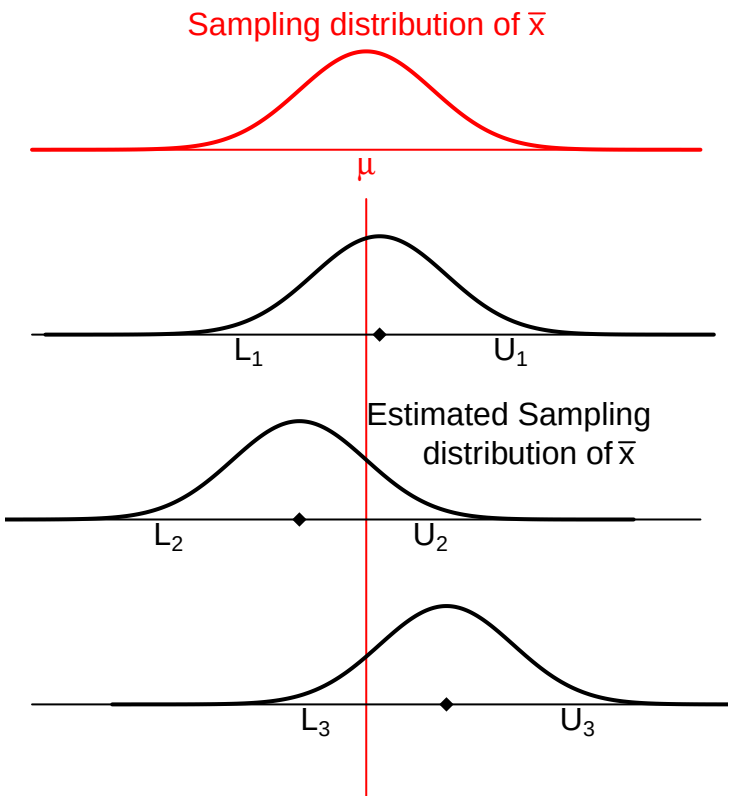


There are two points, (call them L and U) where for our given sample size and population we are sampling from, where we expect that 95% of the sample means to fall within. That is to say, L and U capture the middle 95% of the sampling distribution of $\bar{x}$.

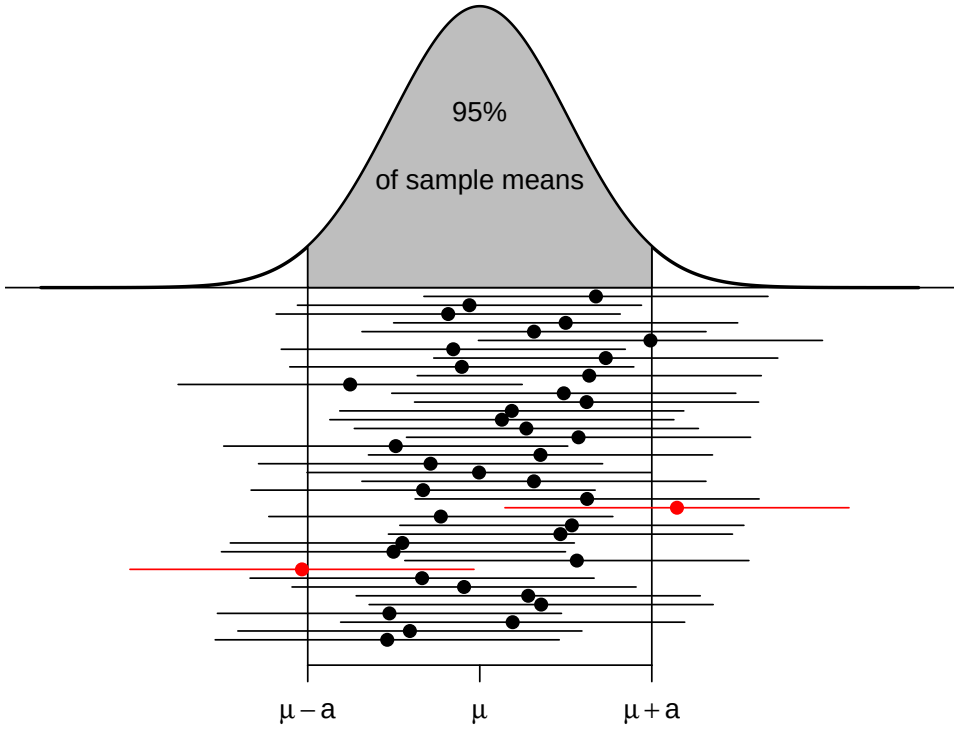


These sample means are randomly distributed about the population mean μ. Given our sample data and sample mean $\bar{x}$, we can examine how our *simulated* values of $\bar{x}^*$ vary about $\bar{x}$. I expect that these simulated sample means $\bar{x}^*$ should vary about $\bar{x}$ in the same way that $\bar{x}$ values vary around μ. Below are three estimated sampling distributions that we might obtain from three different samples

and their associated sample means.



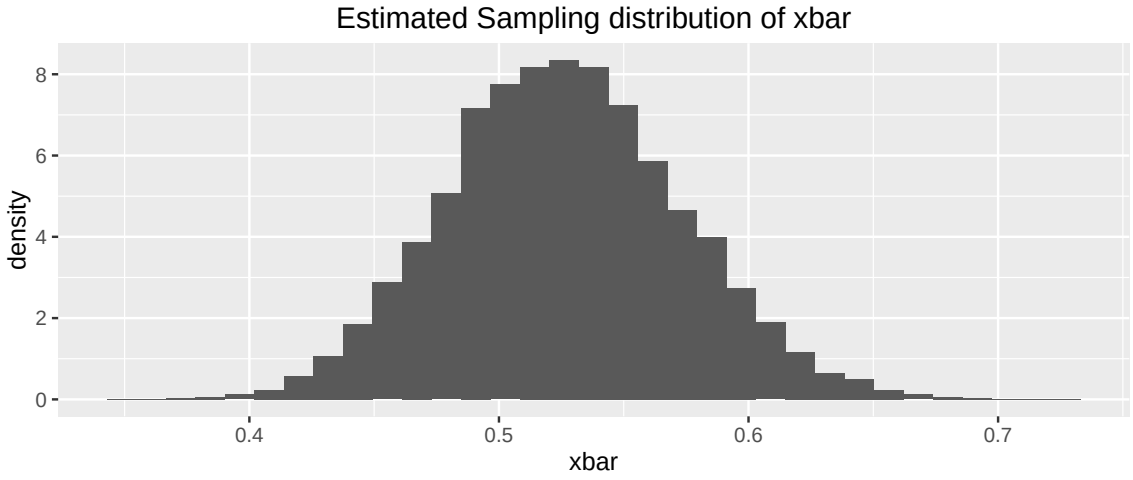
For each possible sample, we could consider creating the estimated sampling distribution of $\bar{X}$ and calculating the L and U values that capture the middle 95% of the estimated sampling distribution. Below are twenty samples, where we've calculated this interval for each sample.



Most of these intervals contain the true parameter μ, that we are trying to estimate. In practice, I will only take one sample and therefore will only calculate one sample mean and one interval, but I want to recognize that the method I used to produce the interval (i.e. take a random sample, calculate the mean and then the interval) will result in intervals where only 95% of those intervals will contain the mean μ. Therefore, I will refer to the interval as a 95% *confidence interval.*

After the sample is taken and the interval is calculated, the numbers lower and upper bounds of the confidence interval are fixed. Because μ is a constant value and the confidence interval is fixed, nothing is changing. To distinguish between a future random event and the fixed (but unknown) outcome of if I ended up with an interval that contains μ and we use the term confidence interval instead of probability interval.

```
# create the sampling distribution of xbar
SamplingDist <- do(10000) * resample(Lakes)%>%summarise(xbar=mean(AvgMercury))

# show a histogram of the sampling distribution of xbar
ggplot(SamplingDist, aes(x=xbar, y=..density..)) +
  geom_histogram() +
  ggtitle('Estimated Sampling distribution of xbar')

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




```
# calculate the 95% confidence interval using middle 95% of xbars
quantile( SamplingDist$xbar, probs=c(.025, .975) )

##      2.5%     97.5%
## 0.4375472 0.6211368
```

There are several ways to interpret this interval.

1. The process used to calculate this interval (take a random sample, calculate a statistic, repeatedly resample, and take the middle 95%) is a process that results in an interval that contains the parameter of interest on 95% of the samples we could have collected, however we don't know if the particular sample we collected and its resulting interval of (0.44, 0.62) is one of the intervals containing μ.

2. We are 95% confident that μ is in the interval (0.44, 0.62). This is delightfully vague and should be interpreted as a shorter version of the previous interpretation.

3. The interval (0.44, 0.62) is the set of values of μ that are consistent with the observed data at the 0.05 threshold of statistical significance for a two-sided hypothesis test[2].

Example: Fuel Economy

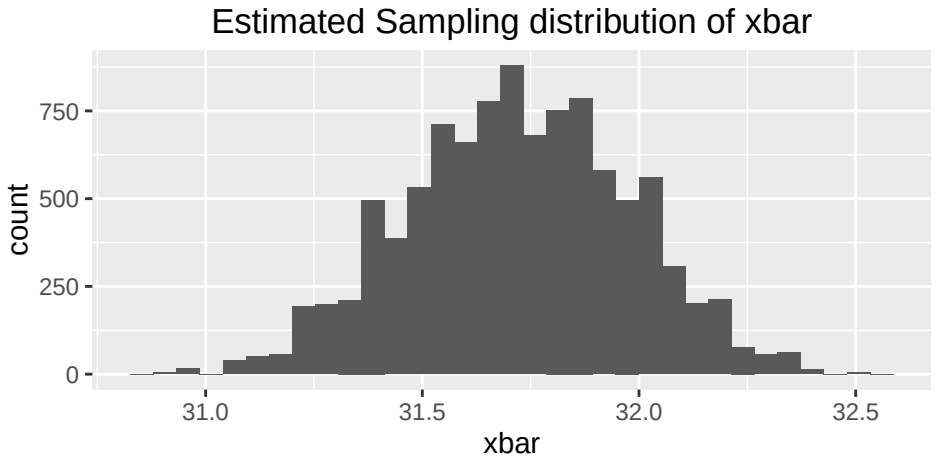
Suppose we have data regarding fuel economy of 5 new vehicles of the same make and model and we wish to test if the observed fuel economy is consistent with the advertised 31 mpg at highway speeds. We the data are

[2]See the chapters on hypothesis testing.

```
CarMPG <- data.frame( ID=1:5, mpg = c(31.8, 32.1, 32.5, 30.9, 31.3) )
CarMPG %>% summarise( xbar=mean(mpg) )

##    xbar
## 1 31.72
```

We will use the sample mean to assess if the sample fuel efficiency is consistent with the advertised number. Because these cars could be considered a random sample of all new cars of this make, we will create the estimated sampling distribution using the bootstrap resampling of the data.

```
SamplingDist <- do(10000) * resample(CarMPG) %>% summarise(xbar=mean(mpg))
# show a histogram of the sampling distribution of xbar
ggplot(SamplingDist, aes(x=xbar)) +
  geom_histogram() +
  ggtitle('Estimated Sampling distribution of xbar')

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




```
# calculate the 95% confidence interval using middle 95% of xbars
quantile( SamplingDist$xbar, probs=c(.025, .975) )

##  2.5% 97.5%
## 31.22 32.20
```

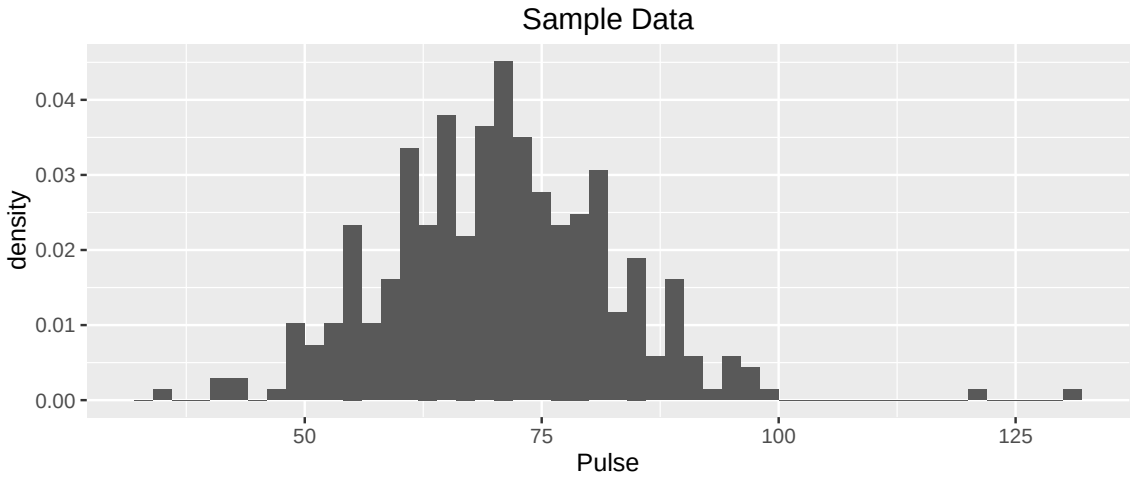
We see that the 95% confidence interval is (31.2, 32.2) and does not actually contain the advertised 31 mpg. However, I don't think we would object to a car manufacturer selling us a car that is *better* than advertised.

Example: Pulse Rate of College Students

In the package `Lock5Data`, the dataset `GPAGender` contains information taken from undergraduate students in an Introductory Statistics course. This is a convenience sample, but could be considered representative of students at that university. One of the covariates measured was the students pulse rate and we will use this to create a confidence interval for average pulse of students at that university.

First we'll look at the raw data.

```
library(Lock5Data)   # load the package
data(GPAGender)      # from the package, load the dataset

# Now a nice histogram
ggplot(GPAGender, aes(x=Pulse, y=..density..)) +
  geom_histogram(binwidth=2) +
  ggtitle('Sample Data')
```

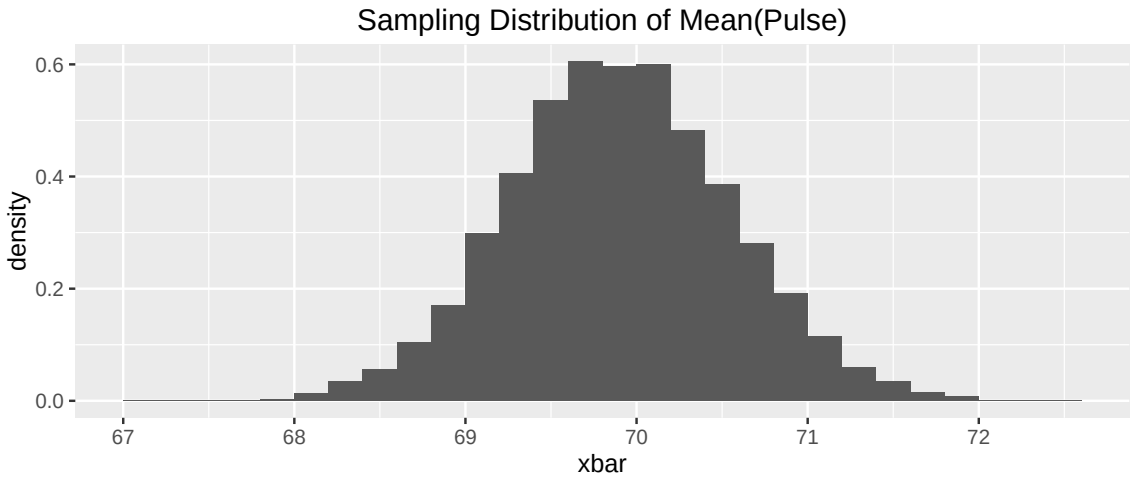


It is worth noting this was supposed to be measuring resting heart rates, but there are two students had extremely high pulse rates and six with extremely low rates. The two high values are approximately what you'd expect from someone currently engaged in moderate exercise and the low values are levels we'd expect from highly trained endurance athletes.

```
# Summary Statistics
GPAGender %>% summarise(xbar = mean(Pulse),
                        StdDev = sd(Pulse))

##       xbar   StdDev
## 1 69.90379 12.08569
```

So the sample mean is $\bar{x} = 69.9$ but how much should we expect our sample mean to vary from sample to sample when our sample size is $n = 343$ people? We'll estimate the sampling distribution of $\bar{X}$ using the bootstrap.

```
# Create the bootstrap replicates
SampDist <- do(10000) * {
  resample(GPAGender) %>% summarise(xbar = mean(Pulse))
}

ggplot(SampDist, aes(x=xbar, y=..density..)) +
  geom_histogram(binwidth=.2) +
  ggtitle('Sampling Distribution of Mean(Pulse)')
```



Just by sampling variability, we expect the sampling mean $\bar{X}$ to vary from approximately 68 to 72. The appropriate quantiles for a 95% bootstrap confidence interval are actually

```
quantile( SampDist$xbar, probs=c(0.025, 0.975) )

##     2.5%    97.5%
## 68.64431 71.18076
```

3.3 Exercises

For several of these exercises, we will use data sets from the R package `Lock5Data`, which greatly contributed to the pedagogical approach of these notes. Install the package from CRAN using either the following R commands or using the RStudio point-and-click interface `Tools -> Install Packages...`.

1. Load the dataset `BodyTemp50` from the `Lock5Data` package. This is a dataset of 50 healthy adults. Unfortunately the documentation doesn't give how the data was collected, but for this problem we'll assume that it is a representative sample of healthy US adults.

   ```
   library(Lock5Data)
   data( BodyTemp50 )
   ?BodyTemp50
   ```

   One of the columns of this dataset is the `Pulse` of the 50 data, which is the number of heartbeats per minute.

   (a) Create a histogram of the observed pulse values.

   (b) Calculate the sample mean $\bar{x}$ and sample standard deviation s of the pulses.

   (c) Create a dataset of 10000 bootstrap replicates of $\bar{x}^*$.

(d) Create a histogram of the bootstrap replicates. Calculate the mean and standard deviation of this distribution.

(e) Using the bootstrap replicates, create a 95% confidence interval for μ, the average adult heart rate.

2. Load the dataset `EmployedACS` from the `Lock5Data` package. This is a dataset drawn from American Community Survey results which is conducted monthly by the US Census Bureau and should be representative of US workers. The column `HoursWk` represents the number of hours worked per week.

(a) Create a histogram of the observed hours worked.

(b) Calculate the sample mean $\bar{x}$ and sample standard deviation s of the worked hours per week.

(c) Create a dataset of 10000 bootstrap replicates of $\bar{x}^*$.

(d) Create a histogram of the bootstrap replicates. Calculate the mean and standard deviation of this distribution.

(e) Using the bootstrap replicates, create a 95% confidence interval for μ, the average worked hours per week.

Chapter 4

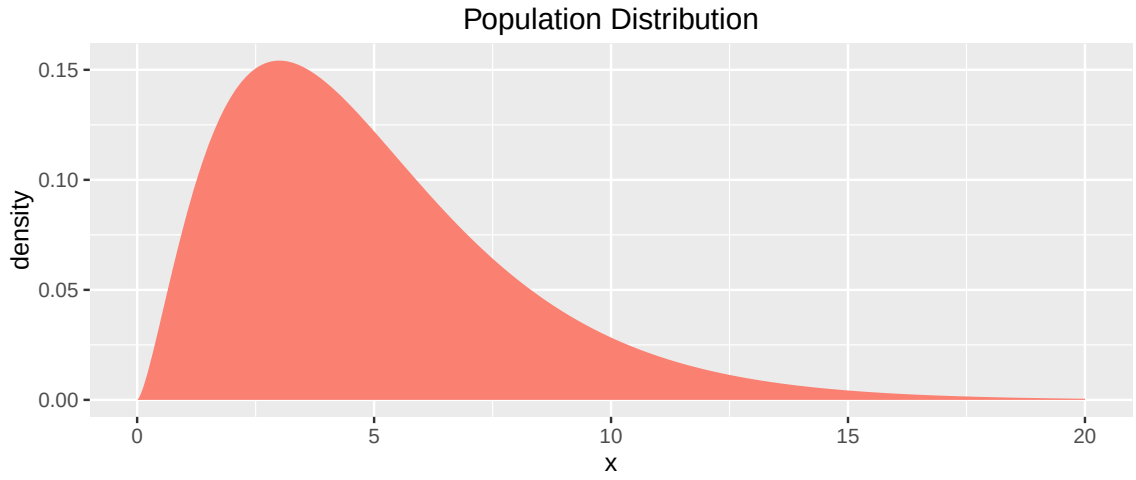
Sampling Distribution of $\bar{X}$

In the previous chapter, we using bootstrapping to estimate the sampling distribution of $\bar{X}$. We then used this bootstrap distribution to calculate a confidence interval for the population mean. Prior to the advent of modern computing, statisticians used a theoretical approximation known as the Central Limit Theorem (CLT). Even today, statistical procedures based on the CLT are widely used and often perform as well or better than the corresponding resampling technique.

4.1 Enlightening Example

Suppose we are sampling from a population that has a mean of $\mu = 5$ and is skewed. For this example, I'll use a Chi-squared distribution with parameter $\nu = 5$.

```
# load the ggplot2 and dplyr librarys... which I use constantly.
library(ggplot2)
library(dplyr)

# Population is a Chi-sq distribution with df=5
PopDist <- data.frame(x = seq(0,20,length=10000)) %>%
  mutate(density=dchisq(x,df=5))

ggplot(PopDist, aes(x=x, y=density)) +
  geom_area(fill='salmon') +
  ggtitle('Population Distribution')
```



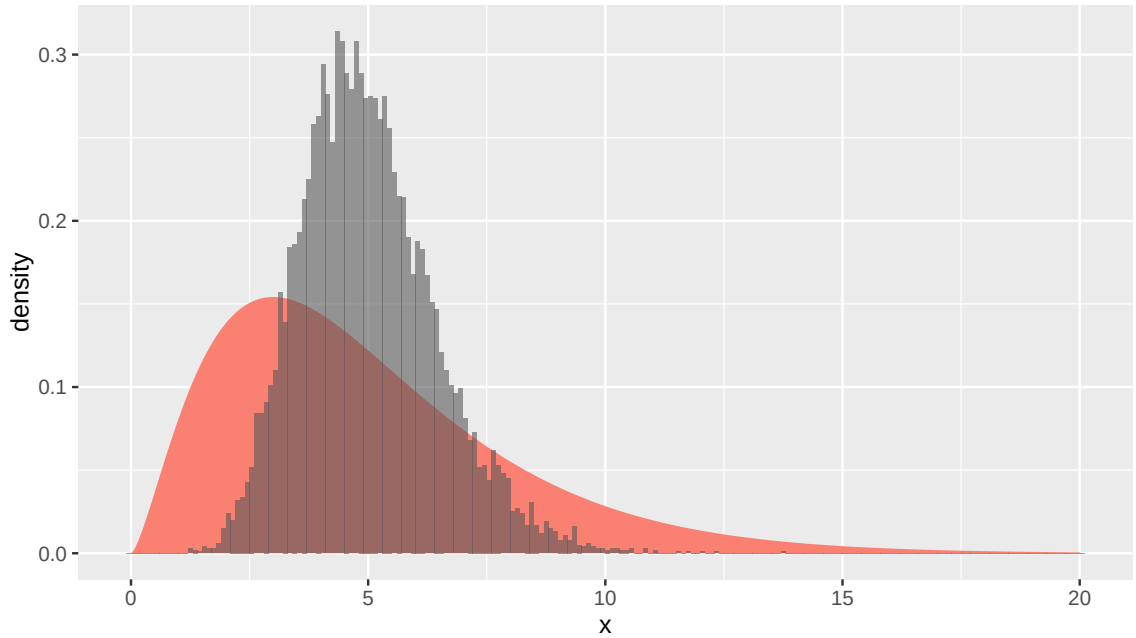
We want to estimate the mean μ and take a random sample of $n = 5$. Lets do this a few times and notice that the sample mean is never *exactly* 5, but is a bit off from that.

```
library(mosaic)  # For the do() loop mechanism
n <- 5  # Our Sample Size!
do(3) * {
  Sample.Data <- data.frame( x = rchisq(n,df=5) )
  Sample.Data %>% summarise( xbar = mean(x) )
}

##       xbar
## 1 6.252452
## 2 4.614849
## 3 3.398105
```

```
n <- 5
SampDist <- do(10000) * {
  Sample.Data <- data.frame( x = rchisq(n,df=5) )
  Sample.Data %>% summarise( xbar = mean(x)     )
}
```

We will compare the population distribution to the sampling distribution graphically.

```
ggplot() +
  geom_area(data=PopDist, aes(x=x, y=density),
            fill='salmon') +
   geom_histogram(data=SampDist, aes(x=xbar, y=..density..),
                  binwidth=.1,
                  alpha=.6)     # alpha is the opacity of the layer
```



From the histogram of the sample means, we notice three things:

- The sampling distribution of $\bar{X}$ is centered at the population mean μ.
- The sampling distribution of $\bar{X}$ has less spread than the population distribution.

- The sampling distribution of $\bar{X}$ is less skewed than the population distribution.

4.2 Mathematical details

4.2.1 Probability Rules for Expectations and Variances

Claim: For random variables X and Y and constant a the following statements hold:

$$\begin{aligned} E(aX) &= aE(X) \\ Var(aX) &= a^2 Var(X) \\ E(X+Y) &= E(X)+E(Y) \\ E(X-Y) &= E(X)-E(Y) \\ Var(X \pm Y) &= Var(X)+Var(Y) \text{ if X,Y are independent} \end{aligned}$$

Proving these results is relatively straight forward and is done in almost all introductory probability text books.

4.2.2 Mean and Variance of the Sample Mean

We have been talking about random variables drawn from a known distribution and being able to derive their expected values and variances. We now turn to the mean of a collection of random variables. Because sample values are random, any function of them is also random. So even though the act of calculating a mean is not a random process, the numbers that are feed into the algorithm *are random.* Thus the sample mean will change from sample to sample and we are interested in how it varies.

Using the rules we have just confirmed, it is easy to calculate the expectation and variance of the sample mean. Given a sample $X_1, X_2, \ldots, X_n$ of observations where all the observations are independent of each other and all the observations have expectation $E[X_i] = \mu$ and variance $Var[X_i] = \sigma^2$ then

$$\begin{aligned} E\left[\bar{X}\right] &= E\left[\frac{1}{n}\sum_{i=1}^{n} X_i\right] \\ &= \frac{1}{n} E\left[\sum_{i=1}^{n} X_i\right] \\ &= \frac{1}{n}\sum_{i=1}^{n} E[X_i] \\ &= \frac{1}{n}\sum_{i=1}^{n} \mu \\ &= \frac{1}{n} n\mu \\ &= \mu \end{aligned}$$

and

$$\begin{aligned} Var\left[\bar{X}\right] &= Var\left[\frac{1}{n}\sum_{i=1}^{n} X_i\right] \\ &= \frac{1}{n^2} Var\left[\sum_{i=1}^{n} X_i\right] \\ &= \frac{1}{n^2}\sum_{i=1}^{n} Var\left[X_i\right] \\ &= \frac{1}{n^2}\sum_{i=1}^{n} \sigma^2 \\ &= \frac{1}{n^2}\, n\sigma^2 \\ &= \frac{\sigma^2}{n} \end{aligned}$$

Notice that the sample mean has the same expectation as the original distribution that the samples were pulled from, *but it has a smaller variance!* So the sample mean is an unbiased estimator of the population mean μ and the average distance of the sample mean to the population mean decreases as the sample size becomes larger.

4.3 Distribution of $\bar{X}$ if the samples were drawn from a normal distribution

If $X_i \overset{iid}{\sim} N\left(\mu, \sigma^2\right)$ then it is well known (and proven in most undergraduate probability classes) that $\bar{X}$ is also normally distributed with a mean and variance that were already established. That is

$$\bar{X} \sim N\left(\mu_{\bar{X}} = \mu,\ \sigma^2_{\bar{X}} = \frac{\sigma^2}{n}\right)$$

Notation: Because the expectations of X and $\bar{X}$ are the same, I could drop the subscript for the expectation of $\bar{X}$ but it is sometimes helpful to be precise. Because the variances are different we will use $\sigma_{\bar{X}}$ to denote the standard deviation of $\bar{X}$ and $\sigma^2_{\bar{X}}$ to denote variance of $\bar{X}$. If there is no subscript, we are referring to the population parameter of the distribution from which we taking the sample from.

Exercise: A researcher measures the wingspan of a captured Mountain Plover three times. Assume that each of these X_i measurements comes from a $N\left(\mu = 6 \text{ inches}, \sigma^2 = 1^2 \text{ inch}\right)$ distribution.

1. What is the probability that the first observation is greater than 7?

$$\begin{aligned} P\left(X \geq 7\right) &= P\left(\frac{X-\mu}{\sigma} \geq \frac{7-6}{1}\right) \\ &= P\left(Z \geq 1\right) \\ &= 0.1587 \end{aligned}$$

2. What is the distribution of the sample mean?

$$\bar{X} \sim N\left(\mu_{\bar{X}} = 6,\ \sigma^2_{\bar{X}} = \frac{1^2}{3}\right)$$

3. What is the probability that the sample mean is greater than 7?

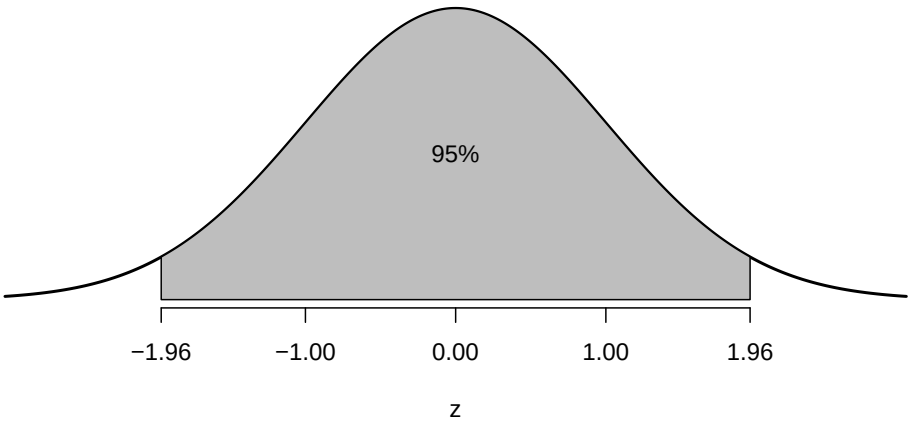
$$\begin{aligned} P\left(\bar{X} \geq 7\right) &= P\left(\frac{\bar{X} - \mu_{\bar{X}}}{\sigma_{\bar{X}}} \geq \frac{7-6}{\sqrt{\frac{1}{3}}}\right) \\ &= P\left(Z \geq \sqrt{3}\right) \\ &= P\left(Z \geq 1.73\right) \\ &= 0.0418 \end{aligned}$$

Example: Suppose that the weight of an adult black bear is normally distributed with standard deviation $\sigma = 50$ pounds. How large a sample do I need to take to be 95% certain that my sample mean is within 10 pounds of the true mean μ?

So we want $\left|\bar{X} - \mu\right| \leq 10$ which we rewrite as

$$\begin{aligned} -10 &\leq \bar{X} - \mu_{\bar{X}} \leq 10 \\ \frac{-10}{\left(\frac{50}{\sqrt{n}}\right)} &\leq \frac{\bar{X} - \mu_{\bar{X}}}{\sigma_{\bar{X}}} \leq \frac{10}{\left(\frac{50}{\sqrt{n}}\right)} \\ \frac{-10}{\left(\frac{50}{\sqrt{n}}\right)} &\leq Z \leq \frac{10}{\left(\frac{50}{\sqrt{n}}\right)} \end{aligned}$$

Next we look in our standard normal table to find a z-value such that $P\left(-z \leq Z \leq z\right) = 0.95$ and that value is $z = 1.96$.



So all we need to do is solve the following equation for n

$$\begin{aligned} 1.96 &= \frac{10}{\frac{50}{\sqrt{n}}} \\ \frac{1.96}{10}\left(50\right) &= \sqrt{n} \\ 96 &\approx n \end{aligned}$$

4.4 Central Limit Theorem

> I know of scarcely anything so apt to impress the imagination as the wonderful form of cosmic order expressed by the "Law of Frequency of Error". The law would have been personified by the Greeks and deified, if they had known of it. It reigns with serenity and in complete self-effacement, amidst the wildest confusion. The huger the mob, and the greater the apparent anarchy, the more perfect is its sway. It is the supreme law of Unreason. Whenever a large sample of chaotic elements are taken in hand and marshaled in the order of their magnitude, an unsuspected and most beautiful form of regularity proves to have been latent all along. - Sir Francis Galton (1822-1911)

It was not surprising that the average of a number of normal random variables is also a normal random variable. Since the average of a number of binomial random variables cannot be binomial since the average could be something besides a 0 or 1 and the average of Poisson random variables does not have to be an integer. The question arises, what can we say the distribution of the sample mean if the data comes from a non-normal distribution? The answer is quite a lot![1]

Central Limit Theorem

Let $X_1, \ldots X_n$ be independent observations collected from a distribution with expectation μ and variance σ^2. Then the distribution of $\bar{X}$ converges to a normal distribution with expectation μ and variance σ^2/n as $n \to \infty$.

In practice this means that if n is large (usually n >30 is sufficient), then

$$\bar{X} \dot{\sim} N\left(\mu_{\bar{X}} = \mu,\ \sigma^2_{\bar{X}} = \frac{\sigma^2}{n}\right)$$

So what does this mean?

1. Variables that are the sum or average of a bunch of other random variables will be close to normal. Example: human height is determined by genetics, pre-natal nutrition, food abundance during adolescence, etc. Similar reasoning explains why the normal distribution shows up surprisingly often in natural science.

2. With sufficient data, the sample mean will have a known distribution and we can proceed as if the sample mean came from a normal distribution.

Example: Suppose the waiting time from order to delivery at a fast-food restaurant is a exponential random variable with rate $\lambda = 1/2$ minutes and so the expected wait time is 2 minutes and the variance is 4 minutes. What is the approximate probability that we observe a sample of size $n = 40$ with a mean time greater than 2.5 minutes?

$$\begin{aligned} P\left(\bar{X} \geq 2.5\right) &= P\left(\frac{\bar{X} - \mu_{\bar{X}}}{\sigma_{\bar{X}}} \geq \frac{2.5 - \mu_{\bar{X}}}{\sigma_{\bar{X}}}\right) \\ &\approx P\left(Z \geq \frac{2.5 - 2}{\frac{2}{\sqrt{40}}}\right) \\ &= P\left(Z \geq 1.58\right) \\ &= 0.0571 \end{aligned}$$

[1] Provided the distribution sample from has a non-infinite variance and we have a sufficient sample size.

```
# Answer obtained via simulation
SampDist <- do(10000) *{                                  # make 10,000
  Sample <- data.frame( x= rexp(n=40, rate=1/2 ) )        # simulated xbar
  Sample %>% summarise( xbar = mean( x )          )       # values
}
SampDist %>%                                              # What proportion of those
  mutate(Greater = ifelse(xbar >= 2.5, 1, 0)) %>%         # xbar values are
  summarise( ProportionGreater = mean(Greater) )          # greater than 2.5?

##   ProportionGreater
## 1            0.0642
```

4.5 Summary

- Often we have sampled n elements $Y_1, Y_2, \ldots, Y_n$ independently and $E(Y_i) = \mu$ and $Var(Y_i) = \sigma^2$ and we want to understand the distribution of the sample mean, that is we want to understand how the sample mean varies from sample to sample.
  - $E\left(\bar{Y}\right) = \mu$. That states that the distribution of the sample mean will centered at μ. We expect to sometimes take samples where the sample mean is higher than μ and sometimes less than μ, but the average underestimate is the same magnitude as the average overestimate.
  - $Var\left(\bar{Y}\right) = \frac{\sigma^2}{n}$. That states that as our sample size increases, we trust the sample mean to be close to μ. The larger the sample size, the greater our expectation that the $\bar{Y}$ will be close to μ.
- If $Y_1, Y_2, \ldots, Y_n$ were sampled from a $N\left(\mu, \sigma^2\right)$ distribution then $\bar{Y}$ is normally distributed.

$$\bar{Y} \sim N\left(\mu_{\bar{Y}} = \mu, \ \sigma^2_{\bar{Y}} = \frac{\sigma^2}{n}\right)$$

- If $Y_1, Y_2, \ldots, Y_n$ were sampled from a distribution that is not normal but has mean μ and variance σ^2, and our sample size is large, then $\bar{Y}$ is *approximately* normally distributed.

$$\bar{Y} \dot{\sim} N\left(\mu_{\bar{Y}} = \mu, \ \sigma^2_{\bar{Y}} = \frac{\sigma^2}{n}\right)$$

4.6 Exercises

1. Suppose that the amount of fluid in a small can of soda can be well approximated by a Normal distribution. Let X be the amount of soda (in milliliters) in a single can and $X \sim N(\mu = 222, \ \sigma = 5)$.
   (a) $P(X > 230) =$
   (b) Suppose we take a random sample of 6 cans such that the six cans are independent. What is the expected value of the mean of those six cans? In other words, what is $E\left(\bar{X}\right)$?
   (c) What is $Var\left(\bar{X}\right)$? (Recall we denote this as $\sigma^2_{\bar{X}}$)
   (d) What is the standard deviation of $\bar{X}$? (Recall we denote this as $\sigma_{\bar{X}}$)
   (e) What is the probability that the sample mean will be greater than 230 ml? That is, find $P\left(\bar{X} > 230\right)$.

2. Suppose that the number of minutes that I spend waiting for my order at Big Foot BBQ can be well approximated by a Normal distribution with mean $\mu = 10$ minutes and standard deviation $\sigma = 1.5$ minutes.

   (a) Tonight I am planning on going to Big Foot BBQ. What is the probability I have to wait less than 9 minutes?

   (b) Over the next month, I'll visit Big Foot BBQ 5 times. What is the probability that the mean waiting time of those 5 visits is less than 9 minutes? (This assumes independence of visits but because I don't hit the same restaurant the same night each week, this assumption is probably ok.)

3. A bottling company uses a machine to fill bottles with a tasty beverage. The bottles are advertised to contain 300 milliliters (ml), but in reality the amount varies according to a normal distribution with mean $\mu = 298$ ml and standard deviation $\sigma = 3$ ml. (For this problem, we'll assume σ is known and carry out the calculations accordingly).

   (a) What is the probability that a randomly chosen bottle contains less than 296 ml?

   (b) Given a simple random sample of size $n = 6$ bottles, what is the probability that the sample mean is less than 296 ml?

   (c) What is the probability that a single bottle is filled within 1 ml of the true mean $\mu = 298$ ml? *Hint: Draw the distribution and shade in what probability you want... then convert that to a question about standard normals. To find the answer using a table or R, you need to look up two values and perform a subtraction.*

   (d) What is the probability that the mean of 10 randomly selected bottles is within 1 ml of the mean? What about a sample of 100?

   (e) If a sample of size $n = 50$ has a sample mean of $\bar{x} = 298$, should this be evidence that the filling machine is out of calibration? i.e., assuming the machine has a mean fill amount of $\mu = 300$ and $\sigma = 3$, what is $P\left(\bar{X} \leq 298\right)$?